



ABSTRACT BOOK

Edited by

Gregory T. Sullivan and Sebahat K. Ozman-Sullivan

http://www.acarology.org/ica/ica2018/



XV INTERNATIONAL CONGRESS OF ACAROLOGY 2-8 SEPTEMBER 2018, ANTALYA - TURKEY

ABSTRACT BOOK

Edited by
Gregory T. Sullivan and Sebahat K. Ozman-Sullivan

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International Standard Book Number: – ISBN (online) 978-605-65607-0-5

Publication date: 28 December 2018

Congress web site: http://www.acarology.org/ica/ica2018/

Logo: Designed by Mujdat Tos

Cover page: Designed by Hakkı Bayındır & Sebahat K. Ozman-Sullivan

Publisher:

Bilkon Turizm Organizasyon Yayıncılık Ltd. Şti.

Cinnah Cad. Gelibolu Sok. No: 3/11 Kavaklıdere, Ankara, Turkey

Tel: +90 312 466 1 466 | Fax: +90 312 466 1 468

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2-8 September 2018, Antalya - TURKEY

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PREFACE

This abstract book is an updated version of the hard copy produced for the XV International Congress of Acarology (XV ICA) in Antalya, Turkey from 2 to 8 September, 2018. The keynote presentations, general sections and symposia are in the areas of taxonomy and systematics, evolution and phylogeny, ecology and behaviour of mites and ticks, invasive species and biosecurity, chemical control and resistance, alternative pesticides, biological control, integrated pest management, biodiversity, dispersal of mites and ticks, population dynamics, agricultural acarology, soil acarology, aquatic acarology, veterinary acarology and medical acarology. The submitted abstracts were reviewed by scientific committee members before acceptance for oral or poster presentation. Where necessary, the selected abstracts were formatted and edited for length and syntax. Only the abstracts presented at the congress are included.

Gregory T. Sullivan, PhD Scientific Secretary XV ICA 2018

WELCOME

Dear colleagues

It seems like only months ago that many of us were together at the XIV ICA in the beautiful city of Kyoto in Japan but in reality that was four years ago. It is therefore my great pleasure, on behalf of the organising committee, to officially welcome you, our honoured official guests, keynote speakers and participants from six continents to the XV International Congress of Acarology 2018 (XV ICA 2018) in Antalya, Turkey.

Firstly, I acknowledge our official guests and six keynote speakers, Emeritus Prof. James W. Amrine Jr. from West Virginia University in the USA; Dr Maria Navajas, a senior scientist at the French Institute of Agricultural Research in France; Prof. Peter Schausberger of the University of Vienna, Austria; Prof. Kosta Mumcuoglu of the Hebrew University-Hadassah Medical School in Israel; Professor Hans Klompen, from the Ohio State University in the USA; and Professor Edward A. Ueckermann of the North West University in South Africa.

These six distinguished speakers are outstanding scholars and leaders in their respective fields of acarology, I am sure you are very much looking forward to hearing their keynote addresses. I also extend my appreciation to you as researchers, students, and government and plant protection industry representatives, who have made the effort, and in some cases extraordinary efforts, to be with us today. I'm sure that you will all be richly rewarded in terms of new friendships and renewed friendships, knowledge gained and cultural experience.

The keynote presentations, symposia, general oral sessions and posters at this congress will showcase a large volume of applied and cutting-edge research across all aspects of acarology, continuing the long tradition of the International Congress of Acarology as a major event on the scientific calendar. The theme of many presentations is the challenge of providing the high quality, sustainably produced food that is vital for healthy communities. Biological control agents and associated environmentally friendly technologies are now at the forefront of improved productivity at much lower environmental costs. Separately, the four symposia explore the massive challenges to human and animal health that ticks and some mites represent, especially in the context of invasive species and climate change.



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Our theme for XV ICA 2018 is, **The Acari: very small but impossible to deny!** The word 'small' could equally refer to the small group of acarologists globally with very small budgets who are being asked to answer bigger and more urgent questions for society. These questions are being asked in an increasingly complex and uncertain international environment and against a backdrop of worsening environmental conditions, including the degradation of natural resources and tragic loss of biodiversity across the planet.

The many presentations at this congress will show you how the collective creativity, energy and persistence of acarologists is finding novel solutions to aspects of these complex problems facing society. You will also see presentations on the absolutely extraordinary diversity of the Acari across our planet and I urge you to make a personal and public commitment to the protection of that diversity.

Separately, I am sure that this congress will help expand the existing network of international scientific cooperation and information sharing. Cooperation on the global level is essential, not just in the field of acarology but in all areas because of the mounting global environmental, social and economic challenges. The exchange of information and ideas over the next 5 days will further our individual and collective understandings of the current situation of acarology and what we need to do to respond to the many pressing challenges.

On a more informal note, please enjoy the extensive hospitality, facilities and entertainment offered here at the Swandor Topkapi Palace Resort and in Antalya. When time allows, take the opportunity to soak up some sun and swim in the turquoise waters of the Mediterranean and experience the delectable tastes of Turkish cuisine. I also encourage you all to join the post-congress tour to experience magical glimpses of some of the historic sites and natural landscapes that make Turkey a tourist's paradise.

In closing, I again offer a heartfelt welcome to all congress participants and delegates to XV ICA 2018. I hope that this congress will be a fruitful and inspiring experience for all of you and I sincerely thank you again for your support. Please enjoy the congress experience and the many attractions of Antalya.

Yours sincerely

Prof. Dr. Sebahat K. Ozman-Sullivan President, XV ICA 2018



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ACKNOWLEDGEMENTS

The Organising Committee of XV ICA expresses its sincere thanks to the following sponsors, Biobest, Koruma Tarim, Leica, Agrobio, Arslanturk Ltd., Dogal Tarim, Koppert, Bayer, Ecaser, Karimex and SG Koleoglu Ltd., and supporting organisations, the Turkish Ministry of Food, Agriculture and Livestock, Acarologia, Acarological Society of America, Acarological Society of Iran, Acarological Society of Japan, Latin American Society of Acarology, Biological Control Society of Turkey, Entomological Society of Turkey, Turkish Phytopathological Society, Turkish Weed Science Society, and The University of Queensland, Erzincan University, Hitit University, Suleyman Demirel University and Uludag University. The Organising Committee also thanks Mujdat Tos for designing the congress logo, the tulip – shaped mite*, Gregory. T. Sullivan for the congress theme, "The Acari: very small but impossible to deny!", and David E. Walter, Ronald Ochoa, Kosta Y. Mumcuoglu, Sevgi Sevsay, Salih Dogan, Sebahat K. Ozman-Sullivan and Mustafa Acici for kindly allowing their images of mites to be displayed on the website.

*The tulip is a cultural symbol of Turkey

CONTACTS

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GENERAL INFORMATION

1. Registration

The registration desk is located in the foyer and will operate from Sunday, 2 September to Friday, 7 September between 08.00 am and 18.00 pm.

2. Presentation guidelines

Oral presentations

Oral presentations will be 15 minutes, including question time.

All speakers at the general sessions and symposia should bring presentation files to the preparation room at least 3 hours before the session / symposium begins. Please bring your file on a USB flash drive. Only PowerPoint files (.ppt or .pptx) can be accepted. Personal computers cannot be used. The congress laptop PCs have the Windows 7 English version in which Microsoft PowerPoint 2013 is installed.

Only PowerPoint files (.ppt or .pptx) in the standard (4:3) format can be accepted.

Poster presentations

The author(s) is/are strongly advised to prepare posters in advance.

Sections include Title, Author(s), E-mail address of corresponding author, Introduction or Literature Review, Materials and Methods, Results and Discussion (including figures, tables, color photographs, charts) and a list of key references.

Posters must be 100 cm long x 70 cm wide. Please prepare your poster so that it is easily readable from a distance. Font size should not be smaller than 14 p Times New Roman or similar and in high quality.

The poster sessions will take place in Yavuz Sultan Selim Hall over two days. Presenters will be required to attend their posters during a specified period.

Poster presentation sessions and sections are as follows:

Tuesday, 4 September

Alternative pesticides, Biological control, Biodiversity, Evolution and phylogeny, Invasive species and biosecurity, Soil acarology, Mites of medical and veterinary importance, Ticks and tick-borne diseases

Thursday, 6 September

Agricultural acarology, Chemical control and resistance, Dispersal of mites, Ecology and behaviour of mites, Population dynamics, Taxonomy and systematics

All posters should be put up at 9:00 am and removed at 19:00 pm of the same day.

3. Student awards

The Organising Committee of XV ICA has created six awards from congress sponsorships for the best oral and poster presentations by students. The Scientific Committee of XV ICA 2018 will select the three best presentations in both categories and the awards will be presented during the closing ceremony of the congress. The three best oral and poster presentations will each receive 500 euros and 250 euros, respectively.



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4. Publication of the congress proceedings

The congress proceedings will be published by **Acarological Studies** which is a peer reviewed, open access, on-line journal with no publication fees. Manuscripts should be prepared according to the instructions of Acarological Studies (http://dergipark.gov.tr/acarolstud) and can be submitted until 30 November, 2018. It is expected that the accepted manuscripts will be published in June 2019.

5. Location of venues

Congress: Swandor Hotels & Resorts Topkapı Palace

Registration: Congress foyer

Oral presentations: Congress Center - Osman Gazi, Fatih Sultan Mehmet, Kanuni Sultan Suleyman Halls

Poster presentations: Yavuz Sultan Selim Hall

Coffee breaks: Congress foyer

Lunch: Congress Hotel - Hünkar Restaurant

Welcome reception: Congress Hotel - Kubbe Bar

Gala Dinner: On a yacht



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SCIENTIFIC PROGRAMME

1st DAY – 3 September 2018 (MONDAY)				
10.00-10.45	OPENING CEREMONY			
	Sebahat K. Ozman-Sullivan – President, XV ICA 2018 Ferit Turanli – President, Entomological Society of Turkey Peter Schausberger-Secretary, Executive Committee, ICA: Remembrance of lost colleagues Zhi-Qiang Zhang – President, Systematic and Applied Acarology Society: James Allen McMurtry Awards			
10.45-11.00	Coffee break			
11.00-11.40	Keynote speaker / Fatih Sultar Maria NAVAJAS - Mites in a			
11.40-11.50	Presentations to sponsors			
11.50-12.30	Keynote speaker / Fatih Sultar Kosta Y. MUMCUOGLU - T	n Mehmet The influence of global warming	on tick vectors	
12.30-14.00	Lunch			
	Section 1. SYMPOSIUM: Parasitic and free living mites of medical and veterinary importance Section 1. 1. Mites of medical importance	Section 1. Ecology and behavior of mites	Section 1. Taxonomy and systematics	
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman	
Chairs	Kosta Y. MUMCUOGLU Aysegul TAYLAN-OZKAN	Norman FASHING Rostislav ZEMEK	Tetsuo GOTOH Qing-Hai FAN	
14.00-14.15	Humidity perception in four astigmatid mite species Elena GAGNARLI, Franca TARCHI, Neri ORSI BATTAGLINI, Donatella GOGGIOLI, Silvia GUIDI, Laura SALVINI, Cristina TINTI, Sauro SIMONI	Different strokes for different folks: Strategies evolved by two related species in adapting to a similar habitat Norman J. FASHING	Mites of the family Parasitidae Oudemans, 1901 (Acari: Mesostigmata) from	
14.15-14.30	Bibliometric analysis of publications on house dust mites Emre DEMIR, Djursun KARASARTOVA, Ayşe SEMRA GÜRESER, Kosta Y. MUMCUOĞLU, Ayşegül TAYLAN-ÖZKAN	Intra- and transgenerational effects in generalist and specialist predatory mites induced by prey limitation Andreas WALZER, Peter SCHAUSBERGER	Spider mites of the Balkan Peninsula: a review, new records and recent outbreaks <u>Ivana MARIĆ</u> , Stanislav TRDAN, Tanja BOHINC, Snježana HRNČIĆ, Sanja RADONJIĆ, Dejan MARČIĆ	
14.30-14.45	Skin prick test reactivity to aeroallergens in pulmonary medicine and dermatology clinics in Çorum Province: a 2-year retrospective study Sertaç ARSLAN, Engin ŞENEL, Aynure ÖZTEKİN, Meral GÜLHAN, Nezahat KOŞAR-ACAR, Ayşegül TAYLAN-ÖZKAN	Diapause termination factors of <i>Tetranychus</i> spider mites (Acari: Tetranychidae) Sergei Y. POPOV	Raphignathoidea (Acari: Trombidiformes) of Turkey: a review of progress on the systematics, with an updated checklist Salih DOĞAN	



1st DAY - 3 S	eptember 2018 (MONDAY)		
	Section 1. SYMPOSIUM: Parasitic and free living mites of medical and veterinary importance Section 1. 1. Mites of medical importance	Section 1. Ecology and behavior of mites	Section 1. Taxonomy and systematics
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
14.45-15.00	A pandemic of pilosebaceous demodecid mites (Acari: Demodecidae) Ting-huan WEN	Costs and benefits of mating with fertilized females in a species with first male sperm precedence Leonor R. RODRIGUES, Alexandre R.T. FIGUEIREDO, Thomas Van LEEUWEN, Isabelle OLIVIERI, Sara MAGALHÃES	Phytoseiidae (Acari: Mesotigmata) of the Indian Ocean: biodiversity and new potential for development of biological control in this area Serge KREITER, Rose-My PAYET, Olivier FONTAINE, Jacques FILLÂTRE, Hamza Abdou AZALI, Fabrice Le BELLEC
15.00-15.15	Demodex infestation and cellular immunity Umut GAZI, Ayse Semra GURESER, Aynure ÖZTEKIN, Djursun KARASARTOVA, Nezahat KOSAR-ACAR, Kursat DERICI, Ferda ARTUZ, Kosta Y. MUMCUOGLU, Aysegül TAYLAN-OZKAN	A parental RNAi-based reverse genetics system for analyzing embryonic development of <i>Tetranychus urticae</i> Shun SHIBAYA, Takeshi SUZUKI	Trombidioid mites (Acari: Prostigmata) and their habitat preferences in Dumanlı Forest in Erzincan Province, Turkey Rukiye YILDIRIM, Sevgi SEVSAY
15.15-15.30	Characteristics of patients with scabies in Corum Province of Turkey: a five-year retrospective analysis Aynure ÖZTEKIN, Ayşe Semra GÜRESER, Coşkun ÖZTEKIN, Djursun KARASARTOVA, Engin ŞENEL, Ayşegül TAYLAN- ÖZKAN	Temperature effects on the developmental time and body size of the invasive mite Aceria tosichella (Eriophyoidea) Kamila KARPICKA- IGNATOWSKA, Alicja LASKA, Lechosław KUCZYŃSKI, Anna RADWAŃSKA, Anna SKORACKA	Phytophagous mites (Acari: Eriophyoidea) of two northern districts of West Bengal, India Sanjay SARKAR
15.30-15.45		Host-parasite associations between arthropods and Trombidioidea (Actinotrichida, Prostigmata), excluding Trombiculidae Magdalena FELSKA, Andreas WOHLTMANN, Joanna MĄKOL	Research progress on the taxonomy of Phytoseiidae (Acari: Mesostigmata) in China Xiao-Duan FANG, Gecheng OUYANG, Wei-Nan WU
15.45-16.00	Coffee break		



1st DAY - 3 S	September 2018 (MONDAY)		
	Section 1.2. Mites of veterinary importance	Section 2. Evolution and phylogeny	Section 2. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Ewan M. CAMPBELL Mustafa ACICI	Enrico de LILLO Xiao-Yue HONG	Serge KREITER Markus KNAPP
16.00-16.15	Why chiggers (Actinotrichida: Parasitengona) share a host? Cases of co-parasitism from temperate climate zone Hanna MONIUSZKO, Magdalena FELSKA, Joanna MĄKOL	First molecular phylogenetic and implications for the taxonomy of the family Phytoseiidae (Acari: Mesostigmata) Marie-Stéphane TIXIER, Victor DOS SANTOS	Laboratory evaluation of entomopathogenic fungi against the bulb mite, Rhizoglyphus robini (Acari: Acaridae) Jana KONOPICKÁ, Rostislav ZEMEK, Andrea BOHATÁ, Jiří NERMUT, Zdeněk MRÁČEK, Eric PALEVSKY, Vladislav ČURN
16.15-16.30	Rapid increase in the incidence of sand-mite fever or chigger-borne rickettsiosis (Acari: Trombiculoidea) Ting-huan WEN	Mites associated with Ambrosia beetles (Curculionidae: Scolytinae) on avocado orchards in Michoacan, Mexico Estefanni Nataly SANDOVAL- CORNEJO, Edith G. ESTRADA-VENEGAS, Armando EQUIHUA- MARTINEZ, Jesús ROMERO- NAPOLES, Dionicio ALVARADO-ROSALES	Screening of potential predators for the control of tomato russet mite, Aculops lycopersici Dominiek VANGANSBEKE, Juliette PIJNAKKER, Lotte SIMILON, Marcus DUARTE, Rob MOERKENS, Patrick DE CLERCQ, Raf DE VIS, Felix WACKERS
16.30-16.45	A survey of chigger mites (Acari: Trombiculidae) from wild rodents and soricomorphs in Turkey Mustafa ACICI, Ali T. GURLER, Cenk S. BOLUKBAS, Sinasi UMUR, Sadik DEMIRTAS	A jump from five to five thousand species: New morphological evidence from the mouthparts strengthens support for the paraphyly of Nematalycidae (Acariformes) with respect to Eriophyoidea (Acariformes) Samuel J. BOLTON, Philipp E. CHETVERIKOV, Gary R. BAUCHAN	Pollen provisioning following flonicamid application has a positive impact on <i>Amblydromalus limonicus</i> Konstantinos SAMARAS, Maria L. PAPPAS, Vassileios MORAITIS, Apostolos SIGOUNAS, Alberto POZZEBON, George D. BROUFAS
16.45-17.00	Varroa mite saliva contains bioactive factors that aid mite feeding and manipulate the honeybee immune response facilitating viral pathogen proliferation Ewan M. CAMPBELL, Alan S. BOWMAN	Genetic divergence predicts reproductive isolation in a social spider mite Yukie SATO, Hironori SAKAMOTO, Tetsuo GOTOH, Yutaka SAITO, Jung-Tai CHAO, Martijn EGAS, Atsushi MOCHIZUKI	Cannibalism and intraguild interactions between an exotic predator, <i>Amblyseius swirskii</i> , and three other phytoseiids occurring in papaya orchards in southern Florida <u>İsmail DÖKER</u> , Cengiz KAZAK, Daniel CARRILLO



1st DAY – 3 S	september 2018 (MONDAY)		
17.00-17.15	Establishment of a novel in vitro feeding system for the honeybee mite, Varroa destructor Craig R. CHRISTIE, Giles E. BUDGE, Ewan M. CAMPBELL, Alan S. BOWMAN		Selection of strains of Amblyseius tamatavensis (Acari: Phytoseiidae) for improved potential to control Bemisia tabaci Marcela MASSARO, Antônio A. D. COELHO, Gilberto J. de MORAES
17.15-17.30	Observation on the life stages of the wool carder bee mite, Sennertionyx manikati (Acari: Acaridae) Qing-Hai FAN, Dongmei LI, Sherly GEORGE		MOTORIES
19.00-20.00	Welcome reception		
2 nd DAY - 4 S	September 2018 (TUESDAY)		
09.00-09.30	Keynote speaker / Fatih Sultan Peter SCHAUSBERGER Behavioral plasticity of plant-i	Mehmet nhabiting predatory mites shape	ed by early life experiences
	Section 1. Agricultural Acarology	Section 1. SYMPOSIUM: Invasive species and biosecurity: understanding and preventing mite invasions Section 1.1. Understanding and preventing mite bioinvasions	Section 1. SYMPOSIUM: Mite-plant interactions: from responses to tolerance/ resistance Section 1.1. Mite-plant interactions
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Peter SCHAUSBERGER Nabi Alper KUMRAL	Maria NAVAJAS Denise NAVIA	Maria PAPPAS, Raul A. SPEROTTO, Merijn KANT
09.45-10.00	Displacement of a phytoseiid predator, Neoseiulus womersleyi, by another phytoseiid predator, N. californicus (Acari: Phytoseiidae) Tetsuo GOTOH, Mohammad Shaef ULLAH, Masumi HANAWA, Shuichi YANO	Phytophagous mite bioinvasions in South America	First steps in the plant responses to spider mite infestation M. Estrella SANTAMARIA,
10.00-10.15	Colomerus vitis (Acari: Trombidiformes: Eriophyoidea): comparison of some morphometric, biomolecular and biological aspects of the deutogyne and protogyne forms Domenico VALENZANO, Maria Teresa TUMMINELLO, Enrico DE LILLO	– What are we learning from that? Denise NAVIA	M. Estrella SANTAMARIA, Ana ARNAIZ, Irene ROSA- DIAZ, Manuel MARTINEZ, Isabel DIAZ



2 nd DAY - 4 S	September 2018 (TUESDAY)		
	Role of <i>Colomerus vitis</i> (Pagenstecher) in the epidemiology of grapevine leaf mottling and deformation in north-eastern Italy		The SHOT family of the spider mite <i>Tetranychus urticae</i> : salivary protein genes showing fast transcriptional plasticity
10.15-10.30	Domenico VALENZANO, Lucio SIMONETTI, Enrico DE LILLO, Pasquale SALDARELLI, Raed Abou KUBAA, Valeria MALAGNINI, Valeria GUALANDRI	Why are <i>Brevipalpus</i> and <i>Raoiella</i> successful invaders?	Wannes DERMAUW, Wim JONCKHEERE, Mousaalreza KHALIGHI, Luc TIRRY, Merijn KANT, Bartel VANHOLME, Thomas VAN LEEUWEN
	Mite diversity and the population dynamics of phytophagous mites and their predators in olive orchards in Aegean Region of Turkey	Jose Carlos VERLE RODRIGUES	Suppression of plant defences by herbivorous mites is not associated with adaptation to host plants
10.30-10.45	Firdevs ERSIN, Ibrahim CAKMAK, Evsel DENIZHAN INANC, Serkan KAPTAN, Halil KOKTURK, Bülent GUMUSAY, Latife ERTEN		<u>Jéssica T. PAULO</u> , Diogo P. GODINHO, Anabela SILVA, Cristina BRANQUINHO, Sara MAGALHÃES
10.45-11.00	Coffee break		
	Section 2. Agricultural Acarology	Section 1.2. Understanding and preventing mite bioinvasions	Section 1.2. Mite-plant interactions
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Alireza SABOORI Sultan COBANOGLU	Maria NAVAJAS Denise NAVIA	Maria PAPPAS, Raul A. SPEROTTO, Merijn KANT
11.00-11.15	Phytoseiulus persimilis: a new member of the acarofauna in Costa Rica? Hugo AGUILAR, Ana María SOLANO	<i>Raoiella indica</i> , arrival and	Versatility of plant-mite interactions
11.15-11.30	Studies on the damage potential of the vegetable spider mite, T. <i>neocaledonicus</i> , on cassava	establishment in Mexico	Vojislava GRBIC, Cristina RIOJA, Vladimir ZHUROV, Kristie BRUINSMA, Nicolas BENSOUSSAN, Miodrag GRBIC
11.13 11.30	Thalakkattil Raghavan SOBHA, Mohamed Abdul HAQ, Othu Pally UMMKULSOOM		



2 nd DAY - 4 S	September 2018 (TUESDAY)		
11.30-11.45	Potential of xylophagous oribatid mites in biodegradation and nutrient	Adventive and/or invasive phytophagous mites in Serbia: an overview and recent data	Local awareness of emergency: spatiotemporal dynamics of spider-mite herbivory on cucumber
	release Mohamed Abdul HAQ	Radmila U. PETANOVIĆ, Dejan MARČIĆ, Biljana VIDOVIĆ, Ivana MARIĆ	Federico MARTINEZ- SEIDEL, Xi ZHANG, Harro J. BOUWMEESTER, Robert D. HALL, <u>Iris F. KAPPERS</u>
11.45-12.00	Feeding impact of Cisaberoptes kenyae Keifer (Acari: Eriophyidae) on the photosynthetic efficiency and biochemical parameters of Mangifera indica L. Ramani NERAVATHU	The spider mite, <i>Tetranychus</i>	Fusarium solani strain K alters tomato responses against spider mites to the benefit of the plant
		truncatus, spreads fast in mainland China Peng-Yu JIN, <u>Xiao-Yue</u> <u>HONG</u>	Maria L. PAPPAS, Maria LIAPOURA, Dimitra PAPANTONIOU, Marianna AVRAMIDOU, Nektarios KAVROULAKIS, Alexander WEINHOLD, George D. BROUFAS, Kalliope K. PAPADOPOULOU
12.00-12.15	Oribatid mites (Acari: Cryptostigmata) from garlic (<i>Allium sativum</i> L.) cultivation areas in Kastamonu, Turkey	Tetranychus okinawanus Ehara (Prostigmata: Tetranychidae) emerging as a potential invasive pest in Kerala, India	Effect of metal-accumulation on the performance of plants and herbivorous mites that cope differently with organic plant defences
	Cihan CILBIRCIOĞLU, <u>Sultan ÇOBANOĞLU</u>	Arunima VADATHALA, <u>Haseena BHASKAR</u> , Abida P. SALIM, Shylaja M. RAMAN	<u>Diogo P. GODINHO</u> , Helena SERRANO, Anabela SILVA, Cristina BRANQUINHO, Sara MAGALHÃES
12.15-12.30	Seasonal distribution and damage potential of <i>Raoiella indica</i> (Hirst) (Acari: Tenuipalpidae) on plantation crops of Kerala	Population dynamics of the coconut mite, <i>Aceria</i> guerreronis Keifer, in Kerala, India	Response of caraway, <i>Carum carvi</i> L., to <i>Aceria carvi</i> Nal. (Acari: Eriophyidae) infestation: is phytoplasma involved?
	Prabheena PRABHAKARAN, Ramani NERAVATHU	Thalakkattil Raghavan SOBHA, <u>Mohamed Abdul</u> <u>HAQ</u>	<u>Rostislav ZEMEK,</u> Jiří PETERKA, Jana FRÁNOVÁ
12.30-14.00	Lunch		
14.00-14.30	Keynote speaker / Fatih Sultan James W. AMRINE, Jr. Project for a world-wide intera		



2 ^{nu} DAY – 4 S	September 2018 (TUESDAY)		
	Section 3. SYMPOSIUM: Tick and tick-borne diseases Section 3.1. Ticks and tick- borne diseases in Turkey	Section 1.3. Understanding and preventing mite bioinvasions	Section 1.3. Mite-plant interactions
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Aysegul TAYLAN-OZKAN Ali Kemal ERENLER	Maria NAVAJAS Denise NAVIA	Maria PAPPAS, Raul A. SPEROTTO, Merijn KANT
	(14.45-15.05) Plenary Lecture		Response of <i>Medicago</i> truncatula plants to drought and spider mite attack
14.45-15.00	Crimean Congo hemorrhagic fever Derya YAPAR	International trade, biosecurity, agriculture and mites: a South African perspective	Chrystalla ANTONIOU, Ioanna FRAGKOUDI, Angeliki MARTINOU, Menelaos C. STAVRINIDES, Vassilis FOTOPOULOS
15.00-15.15	(15.05-15.25) Plenary Lecture	Davina L. SACCAGGI, Isabel J. COLLETT, Nompumelelo P. NGUBANE-NDHLOVU	Induced tomato plant resistance against <i>Tetranychus</i> urticae triggered by the phytophagy of Nesidiocoris tenuis
13.00-13.13	Tick-borne pathogens other than CCHF found in Turkey Ayşe Semra GÜRESER		Meritxell PÉREZ-HEDO, Angela M. ARIAS- SANGUINO, <u>Sarra</u> <u>BOUAGGA</u> , Alberto URBANEJA
15.15-15.30	(15.25-15.45) Plenary Lecture		Reducing tomato leaf hairs promotes herbivory yet also improves biological control such that the plant ultimately is better protected
	Characteristics of patients admitted to the emergency	Of mites and islands: Preventing invasions with minimum resources	Saioa LEGARREA, Joris J. GLAS, Yvonne M. VAN HOUTEN, Merijn R. KANT
	department of Hitit University Hospital in Çorum, Turkey due to tick bite	Menelaos C. STAVRINIDES	Two phytophagous and two predatory mites on tomatoes: changes in behavior?
15.30-15.45	Ali Kemal ERENLER		Sauro SIMONI, Mabrouk BOUNEB, Elena GAGNARLI, Franca TARCHI, Donatella GOGGIOLI, Silvia GUIDI
15.45-16.00	Coffee break		•



2 nd DAY – 4 September 2018 (TUESDAY)			
	Section 3.2. Ticks and tick- borne diseases in Turkey	Section 1.4. Understanding and preventing mite bioinvasions	Section 2. Soil Acarology
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Alparslan YILDIRIM Ayse Semra GURESER	Maria NAVAJAS Denise NAVIA	Frédéric BEAULIEU Shahrooz KAZEMI
16.00-16.15	Phylogenetic characterization of ixodid ticks infesting different hosts from the Kayseri region of Turkey Onder DUZLU, Alparslan YILDIRIM, Zuhal ONDER, Arif CILOGLU, Osman IBIS, Gamze YETISMIS, Coskun	Detection and identification of invasive mites and regulatory measures: a global update	An entomopathogenic nematode as a potential biological control agent for vector mites and vector borne diseases Thalakkattil Raghavan SOBHA, Mohamed Abdul
16.15-16.30	Molecular identification, phylogeny and geographic distribution of <i>Hyalomma</i> (Acari: Ixodidae) species in Turkey Olcay HEKIMOGLU, Nurdan OZER	Ronald OCHOA, <u>Cal</u> <u>WELBOURN</u> , Jurgen OTTO, Denise NAVIA, Maria NAVAJAS, Francisco FERRAGUT, Gary R. BAUCHAN	I can't live without you (of the opposite sex): Parasitus aff. fimetorum (Mesostigmata: Parasitidae), a mite that requires a partner to complete its development Diana RUEDA-RAMIREZ, Diana RIOS-MALAVER, Amanda VARELA-RAMÍREZ, Gilberto J. de MORAES
16.30-16.45	Genetic characterization and expression analyses of the protective antigen subolesin in <i>Hyalomma anatolicum</i> and <i>H. rufipes</i> lineages infesting cattle in the Kayseri region of Turkey Alparslan YILDIRIM, Onder DUZLU, Zuhal ONDER, Arif CILOGLU, Gamze YETISMIS, Abdullah INCI	Rules for importation of natural enemies to Europe and secure identification: the case of Phytoseiidae Marie-Stephane TIXIER,	Taxonomic studies on oribatid mites of the superfamily Galumnoidea (Acari: Oribatida) in Japan Wataru HAGINO, Satoshi SHIMANO
16.45-17.00	Molecular investigation of the natural transovarial transmission of tick-borne pathogens in Turkey Ömer ORKUN	Serge KREITER	Mesostigmatid mites (Acari: Mesostigmata) from soils of rose crops and natural vegetation on the Bogotá high plateau, Colombia <u>Diana RUEDA-RAMIREZ</u> , Amanda VARELA, Gilberto J. de MORAES



2 nd DAY - 4 S	September 2018 (TUESDAY)		
17.0017.15	Prevalence of <i>Hemolivia</i> mauritanica in natural populations of <i>Testudo graeca</i> in Çorum Province, Middle Black Sea Region, Anatolia, Turkey Arzu COMBA, <u>Gönül</u> ARSLAN AKVERAN	General discussion Invasions and biosecurity: lessons gained and perspectives	Soil-inhabiting mites of the family Parasitidae (Mesostigmata: Gamasina) from the central and northwestern regions of Iran, with a new record Ali AHADIYAT, Mohamed W. NEGM, Reyhaneh ABUTALEB KERMANI, Celine ORDOUKHANIAN, Hajar AGHA ALIKHANI, Omid JOHARCHI
17.15-17.30	Diagnosis of Crimean Congo haemorrhagic fever virus by Real-time PCR between 2010 and 2017 in Samsun and neighbouring provinces of Turkey Seda GUDUL-HAVUZ, Ayşegul TAYLAN-OZKAN	Morphological and molecular characterization of <i>Eutetranychus</i> mite populations collected from different hosts and regions of Saudi Arabia Jawwad H. MIRZA, Amgad A. SALEH, Hafiz M. S. MUSHTAQ, Muhammad KAMRAN, Fahad J. ALATAWI	Section 3. Aquatic acarology Chairs: Olga MAKAROVA Ismail DOKER
17.30-17.45	Comparison of real-time PCR and IFA for the detection of Crimean Congo haemorrhagic fever virus Seda GUDUL-HAVUZ, Ayşegul TAYLAN-OZKAN	Poster session	Dermal glands of the freshwater mite <i>Limnochares</i> aquatica (L., 1758) (Acariformes, Limnocharidae) and their functional and evolutionary significance Andrey B. SHATROV
17.45-18.00	A molecular survey of <i>Babesia microti</i> in wild rodents in Turkey <u>Selma USLUCA</u> , Bekir CELEBİ, Djursun KARASARTOVA, Ayse Semra GURESER, Ferhat MATUR, Mehmet Ali OKTEM, Mustafa SOZEN, Ahmet KARATAS, Cahit BABUR, Aysegul TAYLAN OZKAN	Poster session	New records and a checklist of marine mites of Turkey Furkan DURUCAN
18.00-18.15	Molecular evidence for transstadial transmission of Ehrlichia canis by Rhipicephalus sanguineus sensu lato under field conditions Neval Duygu SAYIN IPEK, Sezayi OZUBEK, Munir AKTAS	Poster session	Poster session
18.15-18.30	Poster session		
	September 2018 (WEDNESDA		LTOURS
09.00-12.00 14.00-19.00	Technical tour: Batı Akdeniz A Social tour: Aspendos Antique		
14.00-19.00	Bociai tour. Aspendos Antique		2018 Antolyo TUDKEV



4 th DAY – 6 September 2018 (THURSDAY)			
09.00-09.30	Keynote speaker / Fatih Sultar	Mehmet	
		- South African and African ac	arology
	Section 1. SYMPOSIUM: Ticks and tick-borne diseases Section 1.1. Ticks and tick- borne diseases worldwide	Section 1. Taxonomy and systematics	Section 1. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Kosta Y. MUMCUOGLU	Marie-Stephane TIXIER	Hans KLOMPEN
	Michael LEVIN	Dejan MARCIC	Prakya Sreerama KUMAR
09.45-10.00	Plenary Lecture	New observations on the genus Chyzeria (Acari: Acariformes: Chyzeriidae), with notes on Chyzeriidae Cal WELBOURN, Rossana FUENTES, Maria E. CASANUEVA, Gary R. BAUCHAN, Ronald OCHOA	Eriophyid mites as biocontrol agents of weeds: challenges for future research Massimo CRISTOFARO, Enrico DE LILLO, Francesca MARINI, Philip WEYL, Lincoln SMITH, Brian G. RECTOR, Radmila PETANOVIĆ, Biljana VIDOVIĆ
10.00-10.15	Changing paradigms of tick- borne rickettsioses Michael L. LEVIN	Genetic variability of the tomato russet mite, <i>Aculops lycopersici</i> (Eriophyidae), populations associated with cultivated and wild solanaceous plants Mércia E. DUARTE, Renata S. MENDONÇA, Maria L. S. C. M. ALVES, João F. M. RORIZ, Marselle R. CAPPSSA, Denise NAVIA	Diversity and distribution of beneficial mites from cherry (<i>Prunus avium</i> L.) (Rosaceae) and sour cherry (<i>Prunus cerasus</i> L.) (Rosaceae) in Ankara, Turkey <u>Tuğba ERDOĞAN</u> , Sultan ÇOBANOĞLU
10.15-10.30	Plenary Lecture Seasonal activity of Ixodes inopinatus and Ixodes ricinus and prevalence of pathogens in a sympatric focus in Southeastern Germany Lidia CHITIMIA-DOBLER, Silke WÖLFEL, Ramona RIESS, Sabine SCHAPER, Giulia LEMHÖFER,	A new species of spider mite in the genus <i>Oligonychus</i> (Acari: Tetranychidae) from Japan Tea ARABULI, Tetsuo GOTOH Taxonomic and molecular characters of some Phytoseiidae	
10.30-10.45	MALENA BESTEHORN, Gerhard DOBLER	species from Turkey <u>Sultan COBANOĞLU</u> , Tuğba ERDOĞAN, Marie-Stéphane TIXIER	nematode, <i>Meloidogyne incognita</i> (Kofoid & White, 1919) Chitwood, 1949 <u>Nithinya RAMAKRISHNAN,</u> Ramani NERAVATHU
10.45-11.00	Coffee break		



4th DAY - 6 S	September 2018 (THURSDAY)	
	Section 1.1. Ticks and tick- borne diseases worldwide	Section 2. Biodiversity	Section 2. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Kosta Y. MUMCUOGLU Michael LEVIN	Eddie A. UECKERMANN Maka MURVANIDZE	George BROUFAS Norihide HINOMOTO
11.00-11.15	Vectorial capacity of Rhipicephalus sanguineus and Rhipicephalus turanicus in Israel Kosta Y. MUMCUOGLU	Is a cataclysmic mass extinction of mite species occurring in the shadows of high profile insect and vertebrate extinctions? Gregory T. SULLIVAN, Sebahat K. OZMAN-SULLIVAN	Performance of the generalist predatory mite <i>Amblyseius</i> swirskii Athias-Henriot (Acari: Phytoseiidae) on tomato genotypes with different trichome phenotypes <u>Angeliki PASPATI</u> , Joel GONZÁLEZ-CABRERA, Alberto URBANEJA
11.15-11.30	Blood Meal Analysis and what it tells about the TBE virus natural transmission cycle Malena BESTEHORN, Sabine SCHAPER, Lidia CHITIMIA-DOBLER, Gerhard DOBLER	Spider mites on medicinal and endemic plants of Serbia and the Balkans Dejan MARČIĆ, Ivana MARIĆ, Irena MEĐO, Slobodan JOVANOVIĆ, Radmila PETANOVIĆ, Philippe AUGER	Effect of low relative humidity on the predatory mite <i>Phytoseiulus persimilis</i> Sophie LE HESRAN, Tom GROOT, Markus KNAPP, Marcel DICKE
11.30-11.45	Taxonomic analysis of <i>Hyalomma anatolicum</i> based on morphological and molecular characteristics Ze CHEN, Qianyun REN,	Problems and challenges for the study of gamasoid mite (Acari, Gamasida) diversity in Georgia Maka MURVANIDZE, Levan	Hierarchical analysis of in-and out-breeding in the haplodiploid predatory mite, <i>Phytoseiulus persimilis</i> <u>Demet ÇEKİN</u> , Peter SCHAUSBERGER
	Jin LUO, Kaifei GUO, Andrew LI, Tinghuan WEN, Xiaocui LIU, Shahid KARIM, Guangyuan LIU, Hong YIN	MUMLADZE, Nino TODRIA	SCHAUSBERGER
	Section 1.2. Tick biology and physiology	Section 2. Biodiversity	Section 2. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Olaf KAHL, Kimiko OKABE	Eddie A. UECKERMANN Maka MURVANIDZE	George BROUFAS Norihide HINOMOTO
11.45-12.00	Active water vapor uptake in unfed and engorged Dermacentor marginatus (Acari, Ixodidae)	Case studies with oribatid mites reveal wood ant nest mounds as biodiversity hotspots	Life history of <i>Typhlodromus</i> athiasae as a predator of <i>Tetranychus urticae</i> (Acari: Phytoseiidae, Tetranychidae)
11.73-12.00	<u>Olaf KAHL,</u> Wilhelm KNÜLLE	<u>Riikka ELO,</u> Ritva PENTTINEN, Jouni SORVARI	at different temperatures İsmail KASAP, Serkan PEHLİVAN, Şahin KÖK, <u>Remzi ATLIHAN</u>



4 th DAY – 6 S	4 th DAY – 6 September 2018 (THURSDAY)		
12.00-12.15	The role of three enzymes in embryonic development of the tick, <i>Haemaphysalis longicornis</i> Tiantian ZHANG, Zhaoxi QIU, Yuan LI, Wenying WANG, Mengmeng LI, Zhijun YU, Xiaolong YANG, Jingze LIU	Species richness and biodiversity of Uropodina mites (Acari: Mesostigmata) from Brazil, Belize and Mexico Maria Magdalena VÁZQUEZ GONZÁLEZ, Gilberto DE MORAES, Jandir CRUZ SANTOS, Jorge SANCHEZ, Leticia Henrique AZEVEDO, Geovanny SOARES, David Miguel MEDINA, Kamira Zuelane COOCH, Abigail Liliana AGUIRRE CORTÉS	The effects of <i>Cardinium</i> and <i>Wolbachia</i> on the reproduction and fitness of a predatory mite and its prey <u>Yiying ZHAO</u> , Yanna ZHANG, Qian Zhao, Feng LIU
12.15-12.30	Cloning and characterization of two defensin-like antimicrobial peptides from the tick, <i>Hyalomma asiaticum</i> Xiaolong YANG, Weili LI, Zhihua GAO, Zhijun YU, Peijing ZHENG, Jingze LIU	Biodiversity of spider mites in the Tara National Park in Serbia <u>Ivana MARIĆ</u> , Irena MEĐO, Slobodan JOVANOVIĆ, Radmila PETANOVIĆ, Dejan MARČIĆ, Philippe Auger	Evaluation of seventeen entomopathogenic <i>Beauveria bassiana</i> Bals. (Vuill) isolates against the two-spotted spider mite (<i>Tetranychus urticae</i> Koch, Acari: Tetranychidae) <u>Dürdane YANAR</u> , Yusuf YANAR, Kadriye ATEŞ
12.30-12.45	Life cycle parameters of two common cattle tick species, Amblyomma integrum and Rhipicephalus microplus Kalpani O. BANDARANAYAKA, Rupika S. RAJAKARUNA		
12.45-14.00	Lunch		
14.00-14.30		Mehmet der relationships in the Uropod	ina (Mesostigmata)
	Section 1.3. Tick epidemiology and systematics	Section 3. Evolution and phylogeny	Section 3. Agricultural acarology
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Lidia CHITIMIA-DOBLER Munir AKTAS	Sergey MIRONOV Gregory T. SULLIVAN	Joanna MAKOL Ibrahim CAKMAK
14.30-14.45	Ticks (Acari: Ixodidae) and laelapid mites (Acari: Mesostigmata: Laelapidae) on small rodents in Lithuania Jana RADZIJEVSKAJA, Evelina KAMINSKIENĖ, Algimantas PAULAUSKAS, Linas BALČIAUSKAS		Evaluation of Xenorhabdus and Photorhabdus spp. culture supernatants against Tetranychus urticae (Acari: Tetranychidae) Ibrahim CAKMAK, Selcuk HAZIR, Ceren EROGLU, Mehmet KARAGOZ, Derya ULUĞ, Harun ÇIMEN



4th DAV 65	Contombou 2019 (THIIDSDAY		
14.45-15.00	Human otoacariasis in Sri Lanka: Tick species associated and risk factors Rupika S. RAJAKARUNA, Kalpani BANDARANAYAKA, Sodini ARIYARATNE	Codispersals and host shifts inferred by double dating of host and parasite phylogenies in proctophyllodid feather mites (Astigmata: Proctophyllodidae) associated with passerines (Aves: Passeriformes) Pavel B. KLIMOV, Sergey V. MIRONOV, Barry M.	The expression pattern of ecdysteroid biosynthesis and signaling genes during the molting process in a spider mite Gang LI, Jinzhi NIU, Guy SMAGGHE, Jin-Jun WANG
15.00-15.15	A survey on cattle hard ticks fauna in Maragheh, Iran <u>Sohrab RASOULI</u> , Farshad MAZAHERI CHORS, Navid MOHAMMADI	OCONNOR Genomics of Cardinium Brevipalpus mites endosymbionts suggest metabolic connections with host mite and with other symbionts Thi-Phuong LE, Zaichao ZHANG, Yao-Cheng LIN, Denise NAVIA, Valdenice M. NOVELLI, Juliana FREITAS- ASTUA, Renata Santos de MENDONÇA, Maria Andreia NUNES, Thomas VAN LEEUWEN, Johannes AJ BREEUWER, Yves VAN DE PEER	The diversity and ecology of mites (Acari) in South African vineyards Mia VERMAAK, Pia ADDISON, Ruan VELDTMAN, Eddie A. UECKERMANN
15.15-15.30	Integrative taxonomy of Afrotropical Ornithodoros (Ornithodoros) (Acari: Ixodida: Argasidae) Deon K. BAKKES, Daniel De KLERK, Abdalla A. LATIF, Ben J. MANS	Preliminary phylogenetic hypothesis of the subfamily Tarsoneminae (Heterostigmatina: Tarsonemidae) based on the local species assemblage	A preliminary study of mites in the cork oak forests of Tunisia Amani BELLAHIRECH, Hajer SAHRAOUI, Sabrine ATTIA, Mohamed Lahbib BEN JAMAA, Kaouther LEBDI GRISSA
15.30-15.45 15.45-16.00	Tick predation by the pseudoscorpion, Megachernes ryugadensis (Pseudoscorpiones: Chernetidae), associated with Japanese wood mice Kimiko OKABE, Shun'ichi MAKINO, Takuya SHIMADA, Takuya FURUKAWA, Hayato IIJIMA, Yuya WATARI Coffee break	Revision of the genus Neotropacarus Cunliffe, 1964 (Acaridae) with the description of three new species Marina F.C. BARBOSA	Molecular phylogeny of Phytoptidae s.str. inferred from the partial sequences of three genes Philipp E. CHETVERIKOV, Tatjana CVRKOVIĆ, Biljana VIDOVIĆ, Pavel B. KLIMOV, Samuel BOLTON, James W. Jr. AMRINE and Radmila U. PETANOVIĆ



4th DAY - 6 S	September 2018 (THURSDAY		
	Section 2. Integrated pest management	Section 4. Biodiversity	Section 4. Taxonomy and systematics
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Sergei Y. POPOV Firdevs ERSIN	Cal WELBOURN Edith G. ESTRADA- VENEGAS	James W. AMRINE Enric VILA
16.00-16.15	A good combination of phytoseiid mite with UVB in spider mite management Masahiro OSAKABE, Nariaki SUGIOKA, Kazuhiro NAKAI, Mari KAWAKAMI, Yasumasa MURATA, Nobuhiro HIRAI	the coldest territory in the Old	Sarah ZUKOFF, James W.
16.15-16.30	Adaptation of physical control of <i>Tetranychus urticae</i> featuring UVB	World: diversity, distributions, assemblages Olga MAKAROVA	Phyllocoptes (Acari: Eriophyoidea) from rose: how many species?
10.13-10.30	Masaya TANAKA, Junya YASE, Takeshi KANTO, Masahiro OSAKABE		<u>Tobiasz DRUCIAREK,</u> Mariusz LEWANDOWSKI, Ioannis TZANETAKIS
16.30-16.45	Side effects of zeolite on the predatory mite, <i>Amblyseius</i> swirskii	Invited Speaker Lindquist et al. 1979 revisited: knowledge status and taxonomic gaps on the acarine diversity in Canada	The Megalolaelapidae awakens: systematic revision and biology of Megalolaepidae (Mesostigmata: Dermanyssina) Orlando COMBITA-
	Mehmet KEÇECİ, Ali ÖZTOP	Frédéric BEAULIEU, Wayne KNEE, Victoria NOWELL, Marla SCHWARTZFELD,	HEREDIA, Edwin Javier QUINTERO-GUTIÉRREZ, <u>Hans KLOMPEN</u>
16.45-17.00	Poster session	Zoë LINDO, Monica YOUNG, Heather PROCTOR, Terry GALLOWAY, Lisa LUMLEY, Ian SMITH, Valerie BEHAN-PELLETIER, David WALTER, Evert LINDQUIST	Prostigmata) in amber material Marta KONIKIEWICZ, Jacobson MAKOI
17.00-17.15	Poster session	Invited Speaker	A new, interesting tenuipalpid (Acari: Trombidiformes: Tenuipalpidae) Eddie A. UECKERMANN, Ronald OCHOA, Gary R.
17.15-17.30	Poster session	A review of the feather mite family Gabuciniidae Gaud & Atyeo (Astigmata: Pterolichoidea) from Brazil Fabio Akashi HERNANDES	BAUCHAN One new genus, two new species, three new records and an updated record of mites in Thailand Ploychompoo KONVIPASRUANG, Angsumarn CHANDRAPATYA



Ath DAV	Santambar 2019 (THUDSDAY		
4" DAY - 6 S	September 2018 (THURSDAY)	
17.30-17.45	Poster session	Poster session	A new species of the genus Storchia (Acari: Stigmaeidae) from Pakistan <u>Bilal Saeed KHAN,</u> Muhammad Asif QAYYOUM, Muhammad FAROOQ
17.45-18.00	Poster session	Poster session	Description of a new species (Acari: Mesostigmata: Trematuridae) from Pakistan Muhammad Asif QAYYOUM, Bilal Saeed KHAN
18.00-18.30	Poster session		
20.30	Gala dinner: On a yacht		
5th DAY - 7 S	September 2018 (FRIDAY)		
	Section 1. Alternative pesticides	Section 1. Biodiversity - Dispersal of mites - Taxonomy and systematics	Section 1. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Masahiro OSAKABE Andrey B. SHATROV	Zhi-Qiang ZHANG Fabio Akashi HERNANDES	Andreas WALZER Dürdane YANAR
09.00-09.15	Toxicity and durability of two types of nanoformulation of Achillea spp. (Asteraceae) essential oil against the two spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae) Moosa SABER, Zeinab AHMADI, Gholamreza MAHDAVIN	Feather mites from brood parasitic birds of the world: new data from the shiny cowbird (<i>Molothrus bonariensis</i> , Icteridae) <u>Luiz Gustavo de A.</u> <u>PEDROSO</u> , Fabio Akashi HERNANDES	Phytoseiid mites (Acari: Phytoseiidae) of Turkey: from past to present Ismail DOKER, Cengiz KAZAK, Kamil KARUT
09.15-09.30	Alternative control agents of the dried fruit mite, Carpoglyphus lactis (L.) (Acari: Carpoglyphidae) on dried apricots Vefa TURGU, Nabi Alper KUMRAL	Brevipalpus mites (Tenuipalpidae) of the Azores Islands Jorge Laerson S. ALVES, Renata S. MENDONÇA, Francisco FERRAGUT, Aline D. TASSI, Elliot W. KITAJIMA, Denise NAVIA	The effect of birch pollen on the biological control of the two spotted spider mite, <i>Tetranychus urticae</i> , by the predatory mite, <i>Kampimodromus aberrans</i> İsmail KASAP
09.30-09.45	RNAi in <i>Tetranychus urticae</i> by feeding on dsRNA-coated leaves Hebatallah Galal Mansour ABOUELMAATY, Noureldin Abuelfadl GHAZY, Takeshi SUZUKI	Acarine biodiversity associated with bark beetles in Mexico Martha Patricia CHAIRES-GRIJALVA, Edith G.ESTRADA-VENEGAS, Iván F. QUIROZ-IBÁÑEZ, Armando EQUIHUA-MARTÍNEZ, John C. MOSER	biological parameters of the predatory mite Kampimodromus aberrans on Tetranychus urticae Tuğba ERDOĞAN, Sultan



5 th DAY – 7 September 2018 (FRIDAY)			
	Section 1. Alternative pesticides	Section 1. Biodiversity - Dispersal of mites - Taxonomy and systematics	Section 1. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Masahiro OSAKABE Andrey B. SHATROV	Zhi-Qiang ZHANG Fabio Akashi HERNANDES	Andreas WALZER Dürdane YANAR
09.45-10.00	Control of mite pests with botanical acaricides in Thailand Ammorn INSUNG, Jarongsak PUMNUAN	Biodiversity and impacts of plant feeding mites on the tea plant, <i>Camellia sinensis</i> , in South Africa Pholosi A. MAAKE, <u>Eddie A. UECKERMANN</u>	Use of the predatory mite Phytoseiulus persimilis (Acari: Phytoseiidae) in the control of the two-spotted spider mite (Tetranychus urticae Koch, Acari: Tetranychidae) in greenhouse cucumber production in Tokat Province, Turkey Dürdane YANAR, Naif
			GEBOLOĞLU, Tuğba ÇAKAR, Merve ENGÜR
10.00-10.15	Acaricidal activity of <i>Allium</i> sativum L. extracts against the stored product mite, <i>Suidasia</i> pontifica	Behavioural, morphological and environmental interactions predict passive dispersal in the invasive wheat curl mite (WCM)	Observations of sperm and the sperm transfer process in <i>Phytoseiulus persimilis</i> (Acari: Phytoseiidae)
	Mark Anthony Angeles MANGOBA	Alicja LASKA, Lechosław KUCZYŃSKI, Brian G. RECTOR, Anna SKORACKA	Xiaohuan JIANG, Jiale LV, Endong WANG, <u>Xuenong XU</u>
		Understanding Indian tetranychid diversity – a perusal of molecular evidence	Biology and potential of the predatory mite, <i>Amblyseius swirskii</i> Athias-Henriot (Acari: Phytoseiidae), for controlling thrips in Thailand
10.15-10.30		Srinivasa NAGAPPA, Chinnamadegowda CHANNEGOWDA, Rakesh HADLAHALLI PUTTASWAMYGOWDA	Athitiya KAEWPRADIT, Pichate CHAOWATTANAWONG, Ploychompoo KONVIPASRUANG, Atcharabhorn PRASOETPHON
10.30-10.45		Fauna and diversity of poultry manure-inhabiting mites (Acari: Mesostigmata) from the Punjab Province, Pakistan Muhammad Asif QAYYOUM, Bilal Saeed KHAN, Abid Mahmood ALVI	Are predatory mites efficient vectors for entomopathogenic fungi: a comparative study? Gongyu LIN, Claude GUERTIN, Sean-Anthony PAOLO, Silvia TODOROVA, Jacques BRODEUR
10.45-11.00	Coffee break		



	Section 2. Chemical control and resistance	Section 2. Ecology and behavior of mites - Population dynamics	Section 2. Biological control
Room	Osman Gazi	Fatih Sultan Mehmet	Kanuni Sultan Suleyman
Chairs	Sauro SIMONI Mohamed Abdul HAQ	Jose Carlos VERLE RODRIGUES, Katsura ITO	Hugo AGUILAR Ismail KARACA
11.00-11.15	Tomato russet mite, Aculops lycopersici: status in Belgian tomato greenhouses, screening of pesticides and estimation of population densities Eva REYBROECK, Lotte SIMILON, Ibrahim ISMAEIL, Rob MOERKENS, Thomas VAN LEEUWEN, Lieve WITTEMANS, Raf DE VIS		Improvement of biocontrol with releases of astigmatid mites Enric VILA, M del Mar MORALES, Anabel PARRA, Ana Belén ARÉVALO, Don GRIFFITHS
11.15-11.30	The resistance status to abamectin and pyridaben of <i>Panonychus citri</i> (Acari: Tetranychidae) collected from the eastern Mediterranean region of Turkey <u>Ismail DOKER</u> , Cengiz KAZAK, Recep AY	Do spider mites evolve antagonistic traits against cytoplasmic incompatibility induced by <i>Wolbachia</i> ? Flore ZÉLÉ, Inês SANTOS, Leonor R. RODRIGUES, Paula MARTINEZ JIMINEZ, João ALPEDRINHA, Sara MAGALHÃES	The castor bean plant, <i>Ricinus communis</i> , as an alternative host plant for <i>Tetranychus urticae</i> for the mass rearing of the common phytoseiid predators, <i>Phytoseiulus persimilis</i> and <i>Neoseiulus californicus</i> in Egypt <u>Ahmed Y. M. ELLAITHY,</u> Amira A. ABDELKHALEK
11.30-11.45	Establishment of integrative resistance levels and acaricide resistance level status in Korea for <i>Tetranychus urticae</i> Deok Ho KWON, Taek Jun KANG, Si Hyeock LEE	Spider mites on apparent versus unapparent plants: what changes? <u>Jinzhi NIU</u> , Qun YANG, Qinzhe SUN, Jinjun WANG	Phenotypic plasticity of a predatory mite under high temperatures and its application in Chongqing, China Ya Ying LI, Zi Ying WANG, Huai LIU, Jin Jun WANG
11.45-12.00	Abamectin and milbemectin resistance in European populations of the two-spotted spider mite, <i>Tetranychus urticae</i> Wenxin XUE, Emre INAK, Simon SNOEK, Wannes DERMAUW, Thomas VAN LEEUWEN	New types of attacking behaviors against predators inside and outside nests of Schizotetranychus brevisetosus Ehara (Acari: Tetranychidae) on blue Japanese oak Katsura ITO	Plant feeding by two <i>Euseius</i> species (Acari: Phytoseiidae): there is more to it than meets the eye! Prakya Sreerama KUMAR



5 th DAY – 7 September 2018 (FRIDAY)			
12.00-12.15		How opilioacarids (Parasitiformes: Opilioacarida) live, love and take care of their offspring María Magdalena VÁZQUEZ, Daniel MAY, Elvia ALAMILLA, Hans KLOMPEN	
12.15-12.30	The resistance levels to some acaricides of <i>Tetranychus urticae</i> Koch (Acari: Tetranychidae) collected from vegetable greenhouses in Antalya Province, Turkey <u>Yasin Nazım ALPKENT,</u> Abdullah YILMAZ, Recep AY, Selçuk ULUSOY, Züleyha YAVUZ, Emre İNAK, Başak COŞKUN, A. Emre ATIŞ	Changes in the amplitude of temperature affect the biological parameters of <i>Tetranychus macfarlanei</i> and <i>Oligonychus biharensis</i> Mohammad Shaef ULLAH, Tetsuo GOTOH	Bionomics of the predatory mite, Neoseiulus californicus, as affected by feeding on Tetranychus urticae inhabiting three different rose cultivars, with and without the mycelia of Podosphaera pannosa var. rosae Ahmed Y. M. ELLAITHY, Morad F. HASSAN, Ayman M. HANFY, Fareed ABD ELKAREEM
12.30-14.00	Lunch		
	CLOSING CEREMONY		
	Sebahat K. Ozman-Sullivan – President, XV ICA 2018		
	Sebahat K. Ozman-Sullivan – Presentation of student awards		
	Peter Schausberger – Secretary, Executive Committee, ICA: General assembly, including the announcement of the host country for XVI ICA 2022		
14.00-15.30	President – XVI ICA 2022 – Presentation on the congress		
	Andreas Walzer – Presentation on the IOBC-WPRS Working Group "Integrated control of mite pests", 2019		
	Enrico de Lillo – Presentation	on the European Acarology Co	ongress, 2020
	Maria Pappas – Presentation on the European Entomology Congress, 2022		
	Denise Navia - Presentation of 2018	n the III Latin American Congre	ess of Acarology held in July



6th DAY - 8 S	September 2018 (SATURDAY)
	Post congress tour
	— Payment required
	Tour includes:
	— Pick up from the hotel at approx. 8:00am
	— All entrance fees mentioned in the itinerary
08.00-18.00	— Myra (Castle)
	— St. Nicholas Church
	— Boat to Sunken City, Kekova, Theissuma, Simena Castle + swimming break
	— Lunch included (drinks are extra)
	— Transportation in a fully air-conditioned coach
	— Return transfer to the hotel at approx. 18:00 pm



2-8 September 2018, Antalya - TURKEY

POSTER PRESENTATIONS -Tuesday, 4th September

ALTERNATIVE PESTICIDES

Contact toxicity to spirodiclofen resistant and susceptible *Tetranychus urticae* Koch (Acari: Tetranychidae) populations of some essential oils

Sibel YORULMAZ SALMAN, Cenk KESKİN

Demographic response of the two-spotted spider mite (Acari: Tetranychidae) to egg treatment with biopesticides

Irena MEĐO, Dejan MARČÍĆ

The efficacy of soft soap and garlic bulb extracts in controlling *Polyphagotarsonemus latus* (Prostigmata: Tarsonemidae) on Barbunia bean (*Phaseolus vulgaris* L. cv. '*Barbunia*')

Rana AKYAZI, Mete SOYSAL, Yunus E. ALTUNÇ

Repellent and mortality effects of different essential oils on *Tetranychus urticae* (Acarina: Tetranychidae)

Alime BAYINDIR EROL, İsmail KARACA

Efficacy of Tagetes minuta L. extracts against Tetranychus urticae Koch

Sebahat K. OZMAN-SULLIVAN, <u>Elnaz LATIFIAN</u>, Soner SERT, Onur OZYUREK, Funda S. ARSLANOGLU

Efficacy of some endophytic fungi against Tetranychus urticae Koch

Sebahat K. OZMAN-SULLIVAN, Berna TUNALI, B. Muge MALDAR, Fatma OKSUZ, Seyma CAKIR

BIOLOGICAL CONTROL

Mortality effect of vermiwash extracted from cow manure on Tetranychus urticae

Amir ASADI, Jamasb NOUZARI, Ali AHADIYAT, Sohrab IMANI

The effects of milbemectin resistance on some biological parameters and life table of *Phytoseiulus persimilis* A.-H. (Acari: Phytoseiidae)

Sibel YORULMAZ SALMAN, Cenk KESKİN

Compatibility of *Beauveria bassiana* and *Phytoseiulus persimilis* against *Tetranychus urticae* on potted bean plants

Mohammad Shaef ULLAH, Un Taek LIM

Effect of cold storage on the survival and fecundity of the predatory mite *Neoseiulus californicus* (McGregor) (Acari: Phytoseiidae)

Rana AKYAZI, Mete SOYSAL, Yunus E. ALTUNÇ

A new species of *Cosmolaelaps* (Mesostigmata: Laelapidae) of rose greenhouses in The Netherlands with potential to control the edaphic phases of thrips

Diana RUEDA-RAMIREZ, Karen MUÑOZ-CÁRDENAS, Alexandra SIERRA

POSTER PRESENTATIONS -Tuesday, 4th September

Increasing biological control by providing alternative food for the litter-inhabiting predator, *Cosmolaelaps* n. sp. (Mesostigmata: Laelapidae)

<u>Karen MUÑOZ-CÁRDENAS</u>, Diana RUEDA-RAMIREZ, Firdevs ERSIN, Farid FARAJI, Arne JANSSEN

Laboratory evaluation of predators of the Citrus leprosis virus vector, *Brevipalpus yothersi* (Acari: Tenuipalpidae)

<u>İsmail DÖKER</u>, Daniel J. ANDRADE, Marielle BERTO, Jessica MORENO, Alexandra REVYNTHI, Carina ALLEN, Amy RODA, Daniel CARRILLO

Eriophyoid mites on weeds in three families in wheat fields in the Central Anatolian Region of Turkey

Heval DILER, Sebahat K. OZMAN-SULLIVAN

BIODIVERSITY

South-East Asia, the biodiversity hotspot of the Uropodina mites (Acari: Mesostigmata)

Jenő KONTSCHÁN

The diversity of oribatid mites (Acari: Oribatida) in arid and semi-arid ecosystems of eastern Georgia

Nino TODRIA, Maka MURVANIDZE, Levan MUMLADZE

Biodiversity of mites in caves in south Spain

Jaime G. MAYORAL, Pablo BARRANCO, María Lourdes MORAZA

First insight into quill mite (Prostigmata: Syringophilidae) microbiomes

Eliza GLOWSKA, Zuzanna FILUTOWSKA, Miroslawa DABERT, Michael GERTH

Trombidiid mites (Acari: Trombidiidae) of park and garden areas of Erzincan Province, Turkey

Ebru AKMAN, Sevgi SEVSAY

A new locality record and distribution of *Enemothrombium bifoliosum* (Canestrini, 1884) (Acari: Microtrombidiidae) in Turkey

Evren BUĞA, Mert ELVERİCİ, Sevgi SEVSAY

Mite species on wild mushrooms on the campus of Ondokuz Mayis University in Samsun, Turkey

Esra CALTEPE, Aysun PEKSEN, Wojciech WITALINSKI, Joanna MAKOL, Marie-Stephane TIXIER, Olga MAKAROVA, Sebahat K. OZMAN-SULLIVAN

EVOLUTION AND PHYLOGENY

Searching for the sister-group of Eriophyoidea based on rDNA sequence data

Natalia SZUDAREK-TREPTO, Anna SKORACKA, Mirosława DABERT, Jacek DABERT



2-8 September 2018, Antalya - TURKEY

POSTER PRESENTATIONS -Tuesday, 4th September

INVASIVE SPECIES AND BIOSECURITY

Intraguild aggressiveness between an alien and a native predatory mite

Lucia Adriana ESCUDERO-COLOMAR, Eva CREUS, Alice CHORĄŻY, Andreas WALZER

Alien, non-indigenous spider mites and flat mites (Acari: Tetranychidae and Tenuipalpidae) in Hungary

Jenő KONTSCHÁN, Enikő KİSS, Géza RİPKA

New quarantine mite detections in South Africa

Nompumelelo P. NGUBANE-NDHLOVU, Isabel J. COLLETT, Davina L. SACCAGGI

SOIL ACAROLOGY

A tool of pollution estimation: soil mites and other microarthropod groups

Adina CĂLUGĂR

Mesostigmatic mites (Acari) of the mangrove forests in southern Iran

Shahrooz KAZEMI

Two new records of Mesostigmata (Acari) from Turkey

Shahrooz KAZEMI, Hasan H. ÖZBEK

Mite communities (Acari) of salt marshes in the Russian Arctic: taxonomic structure and spatial organization

Mikhail BIZIN, Olga MAKAROVA

First report on soil-inhabiting mites of the cohort Gamasina (Acari: Mesostigmata) in the Kashan region, Isfahan Province, Iran

Reyhaneh ABUTALEB KERMANI, Ali AHADIYAT, Omid JOHARCHI

MITES OF MEDICAL AND VETERINARY IMPORTANCE

Role of house dust mite and CD14 (C-159T) polymorphism in the development of asthma among the West Bengal population, India

Sanjoy PODDER, Goutam K. SAHA

Contribution to the fauna of chigger mites (Acariformes: Trombiculidae & Leeuwenhoekiidae) parasitizing small mammals in Iran

Mohsen SHAMSI, Alireza SABOORI, Alexandr A. STEKOLNIKOV, Azadeh ZAHEDI GOLPAYEGANI, Masoud HAKIMITABAR

Prevalence and body distribution of the poultry red mite (*Dermanyssus gallinae*) in layer farms in Western Azerbaijan Province of Iran

Sohrab RASOULI, Farshad MAZAHERI

POSTER PRESENTATIONS -Tuesday, 4th September

TICKS AND TICK-BORNE DISEASES

DNA barcoding and phylogenetics of neotropical *Amblyomma* (Acari: Ixodideae) from the ICMT collection, Colombia

Lyda CASTRO, Adriana SANTODOMINGO, Gustavo LOPEZ-VALENCIA

Ticks and tick-borne pathogens in Sudan

Yassir Adam SHUAIB, Mohamed Abdelsalam ABDALLA, Saad El-Tiab MOHAMED-NOOR, Ahmed Mohamed Ahmed WAD-ELHAJ, Yassir Abakar Brima ISMAEL, Giulia LEMHÖFER, Sven POPPERT, Sabine SCHAPER, Gerhard DOBLER, <u>Deon K. BAKKES</u>, Lidia CHITIMIA-DOBLER

Gertrud Theiler Tick Museum - Standing on the shoulders of giants

Deon K. BAKKES

To sequence or not to sequence: Comparison of high-throughput sequencing and quantitative PCR for detection of pathogen prevalence in *Ixodes* ticks

Satu MÄKELÄ, Jani SORMUNEN, Maija LAAKSONEN, Eero VESTERINEN

The exploration of the cold response genes of *Dermacentor silvarum* and functional analysis of its important genes

Zhijun YU, Qingying JIA, Tianhong WANG, Xiaolong YANG, Hui WANG, Jingze LIU

Attachment sites of the tick *Hyalomma aegyptium* on the *Mediterranean spur-thighed* tortoise, *Testudo graeca* in Nevsehir, Cappadocia in central Anatolia, Turkey

Gönül ARSLAN AKVERAN

Molecular detection and characterization of tick-borne encephalitis virus in ixodid ticks in Lithuania (PP100)

Marina SIDORENKO, Jana RADZIEVSKAJA, Algimantas PAULAUSKAS

The genetic diversity of Anaplasma marginale isolates in the Moscow region of Russia

Ekaterina FEDORINA, Svetlana KOVALCHUK, Anna ARKHIPOVA

An investigation of *Dermacentor reticulatus* genetic diversity using the 12S rRNA marker

Matas GALDIKAS, Algimantas PAULAUSKAS, Greta NARADOVSKAJA, Jana RADZIJEVSKAJA, Michal STANKO, Olaf KAHL, Gregorz KARBOWIAK

Genetic diversity of *Ehrlichia canis* in dogs from Turkey inferred by TRP36 sequence analysis and phylogeny

Munir AKTAS, Sezayi OZUBEK

Molecular evidence for a novel species of *Babesia* in unfed *Rhipicephalus sanguineus sensu lato*

Sezayi OZUBEK, Munir AKTAS

A survey of canine haemoprotozoan parasites from Turkey, including molecular evidence of an unnamed *Babesia*

Munir AKTAS, Sezayi OZUBEK



2-8 September 2018, Antalya - TURKEY

POSTER PRESENTATIONS -Thursday, 6th September

AGRICULTURAL ACAROLOGY

Mites living in the galleries of the almond bark beetle, *Scolytus amygdali* Guerin-Meneville (Coleoptera: Curculionidae: Scolytinae), attacking almond trees in southern Taleghan, Qazvin Province, Iran

Saeed BABAEI, Ali AHADIYAT, Omid JOHARCHI

Eriophyid mite species on olive orchards and their distribution in Hatay Province of Turkey

Kamuran KAYA, Evsel DENİZHAN

Metabolomic changes in a model system of gallogenesis induced by eriophyoid mites

<u>Philipp E. CHETVERIKOV</u>, Irina E. DODUEVA, Anatoly A. PAUTOV, Elena G. KRYLOVA, Svetlana S. PAPONOVA, Alexey L. SHAVARDA

Alterations in leaf developmental program and expression of regulatory genes in a model system of gallogenesis induced by eriophyoid mites

<u>Svetlana S. PAPONOVA</u>, Irina E. DODUEVA, Anatoly A. PAUTOV, Elena G. KRYLOVA, Sarah ZUKOFF, Philipp E. CHETVERIKOV

Natural acarofauna in intensive greenhouse horticultural crops in Almeria, Spain

Patricia CASTILLO, Margarita IBÁÑEZ, Sofía Isabel GÓMEZ, Sofía del Carmen PÉREZ, Pablo BARRANCO, M. Dolores ALCÁZAR

Interaction between two-spotted spider mite (*Tetranychus urticae* Koch, Acari: Tetranychidae) density and the leaf chlorophyll content of different strawberry varieties

Tuğba ÇAKAR, <u>Dürdane YANAR</u>, Çetin ÇEKİÇ

Genome and transcriptome sequencing of *Phytoseiulus persimilis* (Acari: Phytoseiidae) and comparative analyses of potential sex-determination genes

Jiale LV, Dianyi SHI, Xiaohuan JIANG, Sijia BI, Endong WANG, Xuenong XU

Population development of the European red mite, *Panonychus ulmi* (Koch) (Acari: Tetranychidae) in apple orchards in Çanakkale Province of Turkey

İsmail KASAP, Şahin KÖK, Serkan PEHLİVAN, Gökhan BAŞTUĞ

Hazelnut big bud mites in Georgia and an innovative method for their PCR analysis

Tea ABRAMISHVILI, Dali GAGANIDZE, Sebahat K. OZMAN-SULLIVAN

Mite species associated with cultivated mushrooms in Samsun Province, Turkey

Vahit TEKBAS, Wojciech WITALINSKI, Aleksandr A. KHAUSTOV, Olga MAKAROVA, Sebahat K. OZMAN-SULLIVAN

Two potential targets for RNAi-based pest mite management

Yiying ZHAO, Qian ZHAO, Kaiyang LIU, Feng LIU

Development of *Tetranychus evansi* Baker and Pritchard (Acari: Tetranychidae) on *Solanum tuberosum* L. in Tunisia

Sabrine ATTIA, <u>Amani BELLAHIRECH</u>, Ali MBARKI, Hajer SAHRAOUI, Kaouthar GRISSA LEBDI

POSTER PRESENTATIONS -Thursday, 6th September

CHEMICAL CONTROL AND RESISTANCE

Spirodiclofen resistance levels in *Tetranychus urticae* Koch (Acari: Tetranychidae) populations on eggplant in Turkey

Sibel YORULMAZ SALMAN, Selin Nur ÖZDEMİR, Selçuk ÇİFTÇİ

Registered acaricides in Turkey

Emre İNAK, Sultan ÇOBANOĞLU

Status of insecticide resistance and associated mutations in two spotted spider mite, *Tetranychus urticae*, from China

Shaoli WANG, Dandan XU

Determination of resistance, inheritance and some detoxification enzymes in a *Panonychus ulmi* Koch (Acari: Tetranychidae) population selected with milbemectin

Mehmet Ali İNANICI, Recep AY

Monitoring of abamectin resistance in *Tetranychus urticae* Koch (Acarina: Tetranychidae) populations collected-from cut flower greenhouses in Antalya, Turkey

Erdem SOLMAZ, Recep AY

Metabolism of xenobiotics in mites

Narin GÖK, Emre İNAK, Sultan ÇOBANOĞLU

Detection of endosymbiont bacteria in *Tetranychus urticae* collected from cut-flower greenhouses

Erdem SOLMAZ, Nadire SAKALLI, Bayram ÇEVİK, Recep AY

DISPERSAL OF MITES

Testing the interplay between specialization and dispersal in the invasive wheat curl mite, *Aceria tosichella* (Acariformes: Eriophyidae)

<u>Kamila KARPICKA-IGNATOWSKA</u>, Alicja LASKA, Lechosław KUCZYŃSKİ, Sara MAGALHÃES, Jacek RADWAN, Mariusz LEWANDOWSKİ, Agnieszka MAJER, Ewa PUCHALSKA, Jarosław RAUBİC, Anna RADWAŃSKA, Anna SKORACKA

Dispersal factors of the shiso rust mite, Shevtchenkella sp. (Acari: Eriophyidae)

Yusuke HASEGAWA, Akio TATARA, Fujio KADONO, Satoshi KAGIWADA

Dispersal strategies in cereal-feeding eriophyoid mites

Agnieszka MAJER, <u>Alicja LASKA</u>, Lechosław KUCZYNSKI, Mariusz LEWANDOWSKI, Heather PROCTOR, Anna SKORACKA

ECOLOGY AND BEHAVIOR OF MITES

Do females evolve to avoid incompatible crosses?

Inês SANTOS, Leonor RODRIGUES, Sara MAGALHÃES Flore ZÉLÉ



2-8 September 2018, Antalya - TURKEY

POSTER PRESENTATIONS -Thursday, 6th September

Does an increased male mating rate evolve in response to *Wolbachia*-induced cytoplasmic incompatibility?

Paula MARTINEZ JIMÉNEZ, Inês SANTOS, Sara MAGALHÃES, Flore ZÉLÉ

Leptus (Trombidiformes: Erythraeidae) larvae parasitizing Odonata – a case study of terrestrial parasitengones associated with dragonflies in Zambia

Joanna MAKOL, Magdalena FELSKA, Rafał BERNARD

POPULATION DYNAMICS

Are r and K genetically correlated?

André MIRA, Leonor R. RODRIGUES, Claus RUEFFLER, Sara MAGALHÃES

Spatio-temporal distribution of *Oligonychus afrasiaticus* on date palm fruits: a step towards early detection and establishment of a sampling program

Fahad J. ALATAWI, Syed ZAIN-UL-ABIDIN, Mohamed W. NEGM, Muhammad KAMRAN

TAXONOMY AND SYSTEMATICS

A newly recorded mite species from Turkey: Eutogenes frater Volgin (Acari: Cheyletidae)

Salih DOĞAN, Sibel DOĞAN, Orhan ERMAN

A species being worthy of its name: Intraspecific variations on the gnathosomal characters in topotypic heteromorphic males of *Cheylostigmaeus variatus* (Acari: Stigmaeidae)

Salih DOĞAN, Sibel DOĞAN, Qing-Hai FAN

First record of *Cheletonella* (Acariformes, Cheyletidae) in Poland, with comments on other members of the genus

Salih DOĞAN, Sibel DOĞAN, Joanna MAKOL

Phytoseiid species (Acari: Mesostigmata) in Bursa Province, Turkey, with their original illustrations

Nabi Alper KUMRAL, Sultan ÇOBANOĞLU, Elif SADE, Gözde KILINÇ

New host and country records for the genus *Imparipes* (Acari: Scutacaridae)

Sibel DOĞAN, Şifanur UĞURLU, Salih DOĞAN

Redescription of six feather mite species of the genus *Proterothrix* Gaud, 1968 (Analgoidea: Proctophyllodidae: Pterodectinae) from the "Edouard Louis Trouessart" Collection

Ioana C. CONSTANTINESCU, Gabriel B. CHIŞAMERA, Costică ADAM

New data on the genus *Dissorhina* Hull, 1916 (Acari, Oribatida, Oppiidae), based on a review of species from the Romanian fauna

Otilia IVAN, Nicolae A. VASILIU

Relationships between columbiform birds (pigeons and doves) and quill mites of the genus *Gunabopicobia* (Acariformes: Syringophilidae: Picobiinae)

Katarzvna KASZEWSKA, Natalia MARCINIAK

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Natalia MARCINIAK, Katarzyna KASZEWSKA

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Jaime G. MAYORAL, Pablo BARRANCO, Vicente M. ORTUÑO

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Yunus Emre ALTUNÇ, Rana AKYAZI

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Sibel DOĞAN, Salih DOĞAN, Meryem BİNGÜL TÜRK, Orhan ERMAN

A review of the erythraeoid mites (Acari: Prostigmata) of Turkey

Sevgi SEVSAY

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Evren BUĞA, Sevgi SEVSAY

The genus *Oligonychus* Berlese (Prostigmata: Tetranychidae) from Saudi Arabia; new records and some morphological and webbing behavioral variations between *Oligonychus ephamnus* and *Oligonychus afrasiaticus*

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İsmail DÖKER

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Spider mites of the genus *Oligonychus* Berlese, 1886 (Trombidiformes: Tetranychidae) on coniferous plants in the territory of the former USSR

Ilya O. KAMAYEV



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Keynote Presentations





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Mites in a changing world

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Invasive species and climate change are two independent major threats to global biodiversity and ecosystem sustainability. The globalization of trade and travel are the main drivers of invasions, and may present a rather more immediate threat than climate change. At the same time, climate change poses a risk for the long-term. However, it is clear that both stressors interact and can act synergistically. Climate change can favor pest range expansions, as illustrated by species originating from subtropical areas establishing in more temperate geographical regions. An example is the tomato red spider mite, Tetranychus evansi, which by the end of the last century had moved from South America to other continents where it is now regarded as an emerging pest of solanaceous crops. By distinguishing among multiple pathways and the timing of introduction, there is evidence of different genotypes of *T. evansi* responding to climate in distinct ways. Likewise, native species can be favored by the higher temperatures and episodes of drought associated with climate change. This is the case for spider mites, for which modelling predicts increasing impacts. By focusing on Tetranychus mites, a group that includes a number of damaging pests, this presentation will explore how not only host plant shifts, but also adaptation to drought and harsh environmental conditions, can explain the growing numbers of outbreaks. It will also be emphasized that pests will not be the only group affected by global change, with their predators and competitors also having to be considered. Therefore, biodiversity changes must be approached at the community level. Moreover, a better understanding of the influence of environmental disturbance on the success of mites will be necessary for the prediction of the associated risks of damage.

Keywords: Bioinvasions, climate change, spider mites, pests, population genetics

The influence of global warming on tick vectors

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Together with mosquitoes, ticks are the vectors of many severe and less severe diseases of humans, domestic and wild animals. They are responsible for nearly 95% of the vector-borne diseases reported annually in the USA. There is increasing evidence that climate change is widening the geographic range of some important ticks. In addition, in some areas of the globe the tick population has increased dramatically, leading to an increase of tick-borne diseases. Ticks spend the largest proportion of their lives in their environment and accordingly their development, survival and population dynamics depend on many factors, including climate (temperature, relative humidity), soil (moisture, permeability), vegetation (density, leaf litter) and host animals. The ecology and epidemiology of vector-borne diseases can be described by using the "disease triangle" of hostpathogen-vector environment, with each of these factors influencing the other two. In the USA, Amblyomma maculatum was originally limited to the south-eastern states bordering the Gulf of Mexico and the south Atlantic states. However, in the past several decades, its range has expanded significantly. In Canada, *Ixodes scapularis*, one of the main vectors of Lyme disease (LD, is becoming established in areas where temperatures are now more favorable, with an increased number of LD cases also being reported. A marked northward spread of *Ixodes ricinus* has been observed over the past two decades in Sweden. It has increased its range by about 100 km, and the higher incidence of tick-borne encephalitis it transmitted between the early 1980s and mid-1990s was closely related to warmer summers and winters in the 1990s compared with the previous three decades. A long-term study carried out in Russia reported an increase in the abundance of I. ricinus in the eastern part of its range. The shift of ticks was noted not only in plains areas but also at higher altitudes. Ecological models for I. ricinus in Europe under a changing climate scenario predicted a potential habitat expansion of 3.8% in all of Europe, indicating habitat expansion in some areas, e.g., Scandinavia, the Baltics, and Belarus, and habitat contraction in other areas, e.g., the Alps, Pyrenees, interior of Italy and north-western Poland. Climate change has also been implicated as an important driving force for the expansion of the range of *Ixodes persulcatus*, the vector of tick-borne encephalitis in the north of European Russia. A cluster of Mediterranean spotted fever cases related to a warmingmediated increase in the aggressiveness of the vector, the brown dog tick, *Rhipicephalus sanguineus*, was correlated to the increase in temperatures in Europe. However, an assessment of the effects of climate on the presence of human cases of Crimean Congo hemorrhagic fever (CCHF) in Turkey concluded that climate was no different at sites with active foci of the disease compared with sites where Hyalomma marginatum is common but human cases are not reported. Accordingly, it is not always possible to predict, based solely on climate grounds, where new cases should appear in the near future. Hyalomma-endemic areas with the mildest autumns and winters in the Mediterranean basin have been free and are currently free of the disease. In conclusion, it is likely that climate warming overall will increase the number of ticks and tick-borne clinical cases in many areas of the globe and we should be prepared accordingly.

Keywords: Ixodoidea, ticks, tick-borne diseases, vector, climate



2-8 September 2018, Antalya - TURKEY

Behavioral plasticity of plant-inhabiting predatory mites shaped by early life experiences

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Behavioral plasticity is variation in behavior of the same genotype induced by environmental stimuli. Behavioral variation may be short-lived and easily reversible or long-lasting and persistent, depending on the life stage, age and state of the organism; the behavioral context; and the nature of the stimuli. Conceptually, behavioral plasticity may be categorized as mutually non-exclusive and often interacting, trans-generational (TBP), developmental (DBP) and activational (contextual) (ABP). TBP refers to usually persistent behavioral variation based on environmental stimuli in previous, including the parental, generation(s); DBP encompasses phenomena where experiences result in changes of the underlying neural substrate, allowing time-lagged persistent behavioral changes based on memory of previous experiences, i.e., learning; and ABP builds on existing neural networks, does not require neural modification, and allows immediate, short-term contextual changes. Here I review how and why (i.e. proximate and ultimate aspects) early life experiences shape the DBP of plant-inhabiting predatory mites in foraging, anti-predator and social contexts. For illustration of the conceptual framework, I also touch on topically pertinent examples of TBP (maternal effects) and ABP, and their interactions with DBP. The prey experiences of generalist predatory mites, such as Neoseiulus californicus and Amblyseius swirskii, in early life enhance foraging by adult predators on matching prey (DBP). In contrast, the prey experiences of adult A. swirskii result in prey-unspecific changes in foraging behavior, qualifying as ABP. In A. swirskii, maternal experience of predation risk influences the microhabitat preference of offspring (TBP), interacting with predation risk induced-DBP. Social enrichment and familiarization early in life profoundly and persistently affect the grouping behavior, cannibalism and anti-predator behavior (DBP) of Phytoseiulus persimilis. The complexity and sophistication of DBP is illustrated by interference in early dual-task learning (at simultaneous presence of multiple stimuli) in N. californicus, and finely-tuned behavioral adjustment based on memorizing multiple contextual features in group-living P. persimilis. Subject to data availability, the fitness implications of behavioral plasticity are highlighted. I conclude by emphasizing the relevance of early life experiences and DBP for the supposed occurrence of mite personalities.

Keywords: Phytoseiidae, predatory mites, behavioral plasticity, developmental plasticity, learning

Project for a world-wide interactive eriophyoid database

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The aim of this project is to enable researchers anywhere with access to the Internet, to enter an online database, to view current "information" on known eriophyoid mites, by author, species, genus, correlated with publications pertaining to specific genera and species of eriophyoids and their hosts, location and other data. The two first authors began a computerized catalog of Eriophyoidea in 1994, combining their personal databases and placing them into four files and layouts in Filemaker Pro® [current entries]: "Allpapers" [8600], "Allspecies" [4700], "Genera" [485], and "Hostindex" [7800+]. "Allpapers" is a relational file, such that entering a unique reference number into fields in the related databases, "Allspecies", "Genera", & "Hostindex", results in a listing of that reference ["References" Layout from Allpapers.]. The Filemaker Pro® "Scriptmaker" enabled us to create scripts to sort and list mites by genus, species name, year, host, relationship to host, host family, location, date, et al. and topics. Over the years, each researcher had to "reinvent the wheel", finding references, and other information for each mite studied. This project will allow researchers to find the authors, titles, journals, abstracts (when known), and other information for particular eriophyoid genera/species. Once known, pdf copies of citations can be sought via library loans, journals, authors or on-line requests. We will enable researchers to enter their new citations, and other information on Eriophyoidea, into this database as they publish their papers. We hope that use of this database will be as automatic as meeting requirements for publication in recognized journals. Additional comments will be made on the Eriophyoidea.

Keywords: Eriophyoidea, database, catalogue, citations, hosts, scripts



2-8 September 2018, Antalya - TURKEY

Higher order relationships in the Uropodina (Mesostigmata)

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The Uropodina forms one of the most diverse and abundant lineages of mesostigmatid mites in soil and litter habitats, especially in tropical areas. Unfortunately, genus and family level classification of this group is poorly resolved and plagued with taxonomic confusion. Werner Hirschmann and colleagues described the majority of known species, especially from the tropics, but their idiosyncratic approach to descriptions and classification is difficult to follow and partially incompatible with more traditional views. On the other hand, traditional approaches are perhaps more easily understood, but are geographically much more limited, with poor coverage of the diversity in tropical regions. So far, there have been no published phylogenetic analyses of genus and family level relationships in the entire group. The goal of this study is to conduct such an analysis. To do so, a matrix of DNA sequence data for 3-4 standard markers is being assembled, in addition to a morphological matrix based on the specimens used for DNA extraction. Data in the literature for most described supra-specific taxa is added to the morphological matrix to allow examination of the match between monophyletic groups and these taxonomic concepts.

Keywords: Uropodina, phylogeny, classification, monophyletic, mesostigmatid

South African and African acarology

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The establishment and development of acarology in South Africa and its influence on the rest of Africa, are discussed. This development is divided into two epochs, namely 1834 to 1994 and 1994 to the present. The role players in establishing and maintaining acarology in South Africa and their connections with the rest of Africa are also discussed. It all started with tick species recorded in 1834 from Cape Town and Port Elizabeth. The Metastigmata (ticks) is the best explored group of Acari in South Africa and the rest of Africa though not so much with reference to diversity. The study of soil mites laid the foundation for research on all the other mite taxa since the 1950's. South African and African mites are discussed under three topics, namely, 1. Parasitic mites, including ticks; 2. Oribatids; and, 3. Soil, plant feeding and predatory mites. For about three decades acarology was mainly a means to obtain a qualification, without continuing mite research. Therefore, the maintenance and furthering of acarology during that period and later has rested on the shoulders of about 16 specialists. Acarology in South Africa and in a sense also in Africa reached its climax after 1994 with four highlights discussed. An overview of the present situation and future of acarology in South Africa is outlined.

Keywords: South Africa, Africa, ticks, mites, acarologists



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Oral Presentations



Monday, 3 September

Osman Gazi Hall

Section 1. SYMPOSIUM: Parasitic and free living mites of medical and veterinary importance

Section 1. 1. Mites of medical importance

Humidity perception in four astigmatid mite species

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Indoor relative humidity (RH) is a key environmental factor greatly affecting the survival and population growth of both house dust and storage mites. In this study, the capacity to perceive and movement behaviour under different indoor RH conditions of three species of dust mites in Pyrogliphidae, *Dermatophagoides pteronyssinus*, *D. farinae* and *Euroglyphus maynei*, and one pest species infesting various stored products, the glycyphagid, *Glycyphagus domesticus*, was evaluated. All specimens tested came from mass reared populations cultured for diagnostic tests and immunotherapy at 25 °C and 75% RH; each test was carried out in a simple apparatus that allowing mites to choose between ≥75% RH and lower indoor humidity. Within two hours, the mite's position/movement was recorded, with the time interval depending on the mite species, with the mites tested alone or in small groups of 10 specimens. In addition, a preliminary screening, based on a molecular approach, of the microbiota associated with the same four mite species was conducted to evaluate interspecific similarities. The analysis of the data generated with the General Linear Model and aggregation indexing facilitated consideration of the particular habits of the mite species. Results regarding their ability to select microhabitat with different RHs and on the composition of their microbiota are discussed.

Keywords: Dermatophagoides pteronyssinus, Dermatophagoides farinae, Euroglyphus maynei, Glycyphagus domesticus, microhabitat selection



2-8 September 2018, Antalya - TURKEY

Bibliometric analysis of publications on house dust mites

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House dust mites, which are microscopic organisms that feed on flakes of skin, shed and excrete potential allergens to their surroundings that can trigger allergies in susceptible, predisposed persons. House dust mites produce some of the most common indoor allergens and they can be present year round, causing illnesses and diseases such as allergic rhinitis and asthma. Bibliometric analysis is the statistical analysis of published articles. In addition, citation analysis is a method of measuring the impact of an author or an article. This study aimed to produce a bibliometric overview of research published between 1980 and 2017 on dust mites by using the Thomson Reuters Web of Science (WoS; Thomson Reuters, New York, NY, USA) database. The keywords, «dust mite», «dust mites" and "Dermatophagoides", were used in the initial search. Statistical analyses were then conducted using VOS viewer (Version 1.6.6) software. A total of 11,743 publications were found; 8,331 (70.9%) of them were articles, 1,597 (13.6%) meeting abstracts, 1,143 (9.7%) reviews, 500 (4.7%) proceedings papers and 4.6% were publications such as letters, book chapters, discussions and corrections. Most of the articles were on subjects related to immunology (4,058; 48.7%) and allergies (3,887; 46.7%). The journal with the most publications in it was the Journal of Allergy and Clinical Immunology (702; 8.4%). Authors from the United States of America contributed most to the literature with 1,850 (22.2%) articles. The most active author was M.D. Chapman (116; 1.4%).

Keywords: Dermatophagoides, house dust mites, bibliometric analysis, publications, indoor allergens

Skin prick test reactivity to aeroallergens in pulmonary medicine and dermatology clinics in Çorum Province: a 2-year retrospective study

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Allergic sensitization to aeroallergens is a major risk factor in allergic diseases. The prevalence of aeroallergen sensitization varies in different regions and countries. The aim of this study was to determine the prevalence of common aeroallergen sensitization and the atopic status in the Corum Province, Turkey. A cross-sectional, retrospective study was conducted. The data were collected from medical records and database of the results of skin prick tests of patients who had allergic symptoms in the Pulmonary Medicine and Dermatology Clinics of Hitit University Hospital in Corum from January 2016 to April 2018. A total of 179 patients (female, 119 [66.4%]) were enrolled. The mean age of participants was 31.4 (standard deviation, ± 17.6) years. Thirtynine percent of the patients were diagnosed with allergic contact dermatitis, and 16.2%, 13.9%, 3.3%, and 3.3% with asthma, allergic rhinitis, atopic dermatitis and chronic urticaria, respectively. Mites were responsible for the most common inhaled allergen sensitizations, with 24.5% related to Dermatophagoides farinae and 18.4% to Dermatophagoides pteronyssinus. The dog (Canis familiaris) was the next most common aeroallergen sensitization agent at 15.6%, followed by cockroach (13.4%), grass pollen (8.9%) and cat (4.4%). In conclusion, mites were the most common cause of aeroallergen sensitization in patients in Corum Province, followed by dog, cockroach, grass pollen and cat allergens.

Keywords: Aeroallergens, allergy, *Dermatophagoides*, Corum, allergic contact dermatitis



2-8 September 2018, Antalya - TURKEY

A pandemic of pilosebaceous demodecid mites (Acari: Demodecidae)

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Demodecid mites are obligatory, permanent dermal parasites of mammals with host-parasite specificity. There are more than 120 named species belonging to 7 genera. Around 100 demodecid species have been reported from more than 80 different mammalian species. Two human specific, parasitic demodecids are *Demodex folliculorum* infesting the hair follicles, and *D. brevis* inhabiting the sebaceous glands. Humans can also be accidentally infested by D. canis from its dog host. The minute worm-like bodies of demodecids are highly adapted to living and breeding in their niches, namely the pilosebaceous unit. The dominant symptom caused by the mites is heterogeneous rosacea with papules and pustules. It has been estimated that 50% of the Chinese population are affected and 10% of them have rosacea symptoms. In addition, 16 million Americans were affected in 2007. The symptoms are characterized by vascular and inflammatory lesions. The mites primarily infest the skin surrounding the nose and mouth, the eyes and meatus of the ears, and other parts of the body with pilosebaceous units. Infestation by the mites may occur as early as the new born period and persist lifelong. Mechanically, the mite disrupts the cutaneous barrier which facilitates secondary infection and triggers a cascade of allergic responses. Around infested pilosebaceous units there is infiltration by inflammatory cells, expressing cytokine IL17, in turn strongly activating TLR2, then causing the expression of CAMP and KLK5, and over-expression of the altered peptide LL37, and finally inflammation, angiogenesis and telangectasia. Mite commensal microbes, temperature fluctuations and exposure to ultraviolet light can exacerbate the symptoms. There are two abbreviated, susceptible human genes, SELL and DDB2, closely statistically related to serious rosacea symptoms in the Chinese Han population. Traditional acaricides, the ivermectin group and natural essential oils are effective topical remedies for pilosebaceous mite infestation.

Keywords: Demodecid mites, pilosebaceous unit, rosacea, susceptible genes, acaricides

Demodex infestation and cellular immunity

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Rosacea is a chronic inflammatory skin disease with unclear etiology. Among the organisms associated with rosacea, *Demodex* are the most common in humans. The aim of this study was to determine the cutaneous immune responses triggered in human subjects with or without Demodex infestation and/or rosacea diagnosis. Literature on the immune response triggered by Demodex is very limited because it cannot be cultured in vitro. Seventeen patients with neither rosacea diagnosis nor *Demodex* infestation (control group), 16 non-rosacea patients with *Demodex* infestation (Demodex group), 7 rosacea patients without Demodex infestation (rosacea group), and 20 rosacea patients with *Demodex* infestation (rosacea/*Demodex* group), were included in the study. Skin-infiltrating T_H1 , T_H2 , T_H9 , T_H17 , T_H22 and T_{reg} cell levels were monitored by using antibodies against the cutaneous lymphocyte-associated antigen, IFN-y, IL-4, IL-9, IL-17, IL-22, Foxp3 and CD25 for flow cytometry analysis of whole blood samples isolated. Control and PP rosacea subjects displayed T_H1-biased cutaneous immune responses while rosacea/Demodex and *Demodex* group members exhibited T₁₁22 and Treg-dominant immune responses, respectively. When compared with controls, subjects with Demodex infestation only, those with rosacea symptoms only, and those with rosacea and *Demodex*, had higher levels of T_H9 and T_{reg} but a lower T_H^2 2 cell level; elevated levels of T_H^2 1 cells; and increased frequencies of T_H^2 1, T_H^2 9, and T_H^2 22 cells, respectively. On the other hand, subjects with rosacea and *Demodex* infestation had lower $T_H 1$ and higher $T_H 22$ levels, and higher $T_H 1$ and $T_H 22$ and lower T_{reg} cell levels, than subjects with rosacea and subjects with *Demodex* only, respectively. The cutaneous immune responses triggered by Demodex infestation and rosacea formation seem to influence each other by altering skininfiltrating frequencies of CD4+ T-cell subsets. More studies would contribute to the development of effective treatment strategies not only for demodicosis and rosacea but also for other associated skin diseases.

Keywords: *Demodex*, rosacea, CLA, T_H1, T_H22



2-8 September 2018, Antalya - TURKEY

Characteristics of patients with scabies in Corum Province of Turkey: a five-year retrospective analysis

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Scabies is a global health problem that affects more than 300 million people throughout the world annually. In this study, it was aimed to evaluate the demographic characteristics of the patients diagnosed with scabies between 2013 and 2018 in Corum Hitit University Erol Olcok Education and Research Hospital and investigate changes in these characteristics according to the number of patients and by year. The information was obtained from the patient's examination data registered in the hospital information management system. A total of 2,317 patients were included in the study, 927 men (40%) and 1,390 women (60 %). The age range of patients was 3 months to 99 years with a mean age of 44.3 years. There were 417 (18%) patients under the age of 18 years. There was a kinship connection in 256 patients (11%). According to the address information of the patients, 425 (18.3%) lived in a village, 504 (21.7%) in the country and 1,313 (56.7%) in the provincial center. Overall, 396 patients (17.1%) were diagnosed with scabies in 2013, 580 (25%) in 2014, 289 (12.4%) in 2015, 290 (12.5%) in 2016, 607 (26.2%) in 2017 and 155 (6.7%) until May 2018. There was a significant increase in the number of patients in 2017. Everyone, regardless of age, sex and socio-economic level, can be affected by scabies. Since it is a very contagious disease, it is very important to diagnose, treat and take measures early. Therefore, we suggest that public epidemiologic data be taken into consideration in the planning and implementation of measures to control scabies, including public education.

Keywords: Scabies, epidemiology, demography, personal hygiene, public health

Section 1.2. Mites of veterinary importance

Why chiggers (Actinotrichida: Parasitengona) share a host? Cases of coparasitism from temperate climate zone

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Trombiculidae (Ewing, 1937), also known as chiggers, contain ca 3,300 nominal species and as larvae, are obligatory parasites of vertebrates, mostly rodents, insectivores and bats. Reports on the simultaneous feeding of distinct trombiculid species on the same host are rarely mentioned in the literature, however, the phenomenon is considered to occur more often in this family than in arthropod-associated parasitengones. Our study aimed to ascertain the frequency of cases of co-feeding but also the specific affiliation of trombiculids infesting *Myodes glareolus*, *Apodemus agrarius* and *A. flavicollis* in the central Palearctic. The first part of the project was carried out from 2012 to 2017 in 18 geographical mesoregions of Poland. Rodents were caught in Sherman traps. The collected mites were preserved in 96% ethyl alcohol whereas the individuals dedicated for laboratory rearing were transferred to glass vials filled with the charcoaled plaster-of-Paris and kept in an environmental test chamber. Larvae and active post-larval forms were identified to species on the basis of morphological criteria, supported by molecular evidence. Recorded cases of co-parasitism accounted for c. 9% of all observed chigger-rodent associations. We discuss the evolutionary background of the phenomenon.

Keywords: Central Palaearctic, co-feeding, COI, host spectrum, Trombiculidae



2-8 September 2018, Antalya - TURKEY

Rapid increase in the incidence of sand-mite fever or chigger-borne rickettsiosis (Acari: Trombiculoidea)

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In 1954, a new English word, "chigger", was proposed by Audy to equate with the Chinese name "sand-mite" given by Ge Hong (314 AD), the vector of the important disease, sand-mite fever or chigger-borne rickettsiosis, in the tropical and subtropical regions. One billion people are at risk of the disease and one million cases occur annually. With 0-30% mortality in untreated patients, the importance of the disease is second only to malaria. In the last 20 years the global incidence of the disease has increased along with the global changes in atmospheric temperature. On the Chinese mainland, the incidence of the fever was 14.8 times higher in 2014 than in 2006. An increase in the incidence also was reported in South Korea from 2001 to 2006 and in most countries of South-East Asia, the islands of the West Pacific Ocean and the Indian subcontinent. Previously, the endemic area of the disease was estimated at 13 million km2 from the Far East to Australia. It has been newly recorded in Dubai in the Middle East, Chiloé Island of South America and on the African continent. In 2010, a second pathogen (Orientia chuto) causing the fever was isolated from a patient infected in Dubai; the first recorded pathogen was O. tsutsugamushi. Several pathogens in different categories have also been newly isolated from trombiculid mites, namely Hantan virus in China, Bartonella tamiae from Leptotrombidium chiangraiense in Thailand, and the Borreliella burgdorferi (the new name of Borrelia burgdorferi since 2014) group, Bl. garinii and Bl. valaisiana, the agents which cause Lyme disease, isolated from Neotrombicula carpathica and N. inopinata infesting wild birds in Europe. Around 50 species belonging to 13 genera of trombiculoids have been recorded as biting pests of humans. Recently, several outbreaks and sporadic cases of trombiculosis or sand-mite biting have been reported in Europe and America. House gardens in the Czech Republic and city parks in China have been reported among breeding places of trombiculids attacking humans. Human nodular trombiculosis caused by Apolonia tigipioensis and avian feather nodular trombiculoids have been reported in Brazil and cases of dog hair follicle nodular trombiculosis, caused by the chigger Straelensia cynotis originating from fox dens, have been reported from France and Portugal.

Keywords: Sand mite, distribution, rickettsiosis, trombiculosis, incidence

A survey of chigger mites (Acari: Trombiculidae) from wild rodents and soricomorphs in Turkey

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Trombiculid larvae or chiggers (Acari: Trombiculidae) are ectoparasites that are distributed worldwide on a wide variety of vertebrates. Chiggers also act as reservoirs and vectors of infectious agents, with wild rodents being the main hosts. These mites are found attached to their ear canals, edge of ears and other body parts. Approximately twenty species are considered to be of medical and veterinary importance. The aim of this study was to determine the distribution of trombiculid mites infesting wild rodents and soricomorphs in six regions of Turkey. All the rodents and insectivores examined for chiggers were captured during a survey that involved the molecular characterisation and epidemiology of Echinococcus multilocularis and the determination of risk areas for alveolar echinooccosis in Turkey from November 2015 to March 2016. A total of 546 small, wild mammals were captured in 20 provinces of Turkey; 325 of them have been checked for the presence of trombiculid larvae. Afterwards, ethanol-preserved larval specimens from four different rodent species were mounted in Faure's fluid on microscope slides and identified by using the characteristics described by Stekolnikov and Daniel (2012). Chigger infestation was recorded on 38 of the 325 examined animals (11.7%). Three trombiculid species were identified. as follows: Neotrombicula vulgaris (Schluger, 1955) was found on Apodemus flavicollis and A. witherbyi from Aydın and Tokat provinces in the Aegean and Black Sea regions, respectively; Schoutedenichia krampitzi (Willmann, 1955) was collected from Microtus guentheri in Ankara Province in the central Anatolia region, and Kepkatrombicula sp. was recorded on M. guentheri in Adana Province in the Mediterranean region of Turkey.

Keywords: Acari, chigger, trombiculosis, wild rodents, Turkey

Acknowledgements: This project was funded by TUBITAK (Project no.1150281). The authors are also most grateful to Dr. Alexandr Stekolnikov (Zoological Institute of the Russian Academy of Sciences, St. Petersburg, Russia) for confirming the chiggers identifications.



2-8 September 2018, Antalya - TURKEY

Varroa mite saliva contains bioactive factors that aid mite feeding and manipulate the honeybee immune response facilitating viral pathogen proliferation

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Varroa destructor is an ectoparasite mite of the honeybee (Apis mellifera) that feeds on the haemolymph of the developing brood and transmits numerous pathogenic viruses, including deformed wing virus (DWV). The adult female mite feeds on developing bee larvae after cell capping and creates a communal wound site from which all of her subsequent offspring feed. It is hypothesised that bioactive factors in adult Varroa saliva supress the developing bee larvae immune response and prevent of the wound. Salivary glands of feeding mites were collected by micro-dissection and discrete saliva droplets were collected from Varroa mouthparts by microinjection of stimulants. Subsequent nano-MS/MS proteomic approaches identified a cohort of putative secreted bioactive factors present in both saliva and salivary gland samples, many of which are homologous to factors found in haematophagous and insectivorous arthropods. In addition, peptides in the saliva mapped to honey bee pathogens, including DWV and bee macula virus. Putative secreted bioactive factors, PLA,, calreticulin and cathepsin, were knocked down in Varroa by RNAi gene silencing. A dramatic impact on feeding physiology and host immune response was observed after PLA, knockdown with host honey bee pupae becoming discoloured and failing to complete eclosion due to immune system disruption. These approaches will help facilitate an in-depth analysis of the transmission of DWV and the role of salivary factors in the pathogen – *Varroa* – honeybee axis.

Keywords: Bioactive factor, host immune response, deformed wing virus, melanisation, proteomics

Establishment of a novel *in vitro* feeding system for the honeybee mite, *Varroa* destructor

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Varroa destructor is an ectoparasitic mite of Apis mellifera, the eastern honeybee. The role of V. destructor as a vector of pathogens, most notably deformed wing virus (DWV), is viewed as a leading cause of declining honeybee health globally. Previous research has enabled the formation of various control agents against Varroa, which has become resistant to many of the chemical treatments. A better understanding of Varroa biology and the process by which it transmits pathogens may permit the development and implementation of new control methods. Here, we present a novel in vitro feeding platform, a tool by which Varroa can be maintained off-host, allowing research into their physiology, the testing of novel treatments, and its role as a vector of honeybee pathogens. Through this platform Varroa survival was extended to >50% after 10 days through the incorporation of honeybee haemolymph at 25% (v / v) into the artificial diet. Additionally, this protocol was employed to evaluate the efficacy of a broad-spectrum pesticide, ivermectin, demonstrating the assay's role as a screening platform for potential varroacides. By substituting honeybee haemolymph in the diet with a virus-free alternative from the desert locust, Schistocerca gregaria, DWV transmission was examined. Following 4 days of in vitro feeding by Varroa, diet packets contained detectable DWV. This platform presents an artificial system in which Varroa can be maintained in vitro for similar periods as on their natural host, providing a useful tool for studies requiring long-term survival. The system also presents a tightly controlled, standardised platform for varroacide testing and vector-pathogen transmission studies.

Keywords: Varroa destructor, in vitro, feeding, haemolymph, honeybee



2-8 September 2018, Antalya - TURKEY

Observation on the life stages of the wool carder bee mite, Sennertionyx manikati (Acari: Acaridae)

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Many species of the family Acaridae are known only from hypopi (heteromorphic deutonymphs). For nearly 120 years, the monotypic genus Sennertionyx (Acari: Acaridae) represented by the wool carder bee mite, Sennertionyx manicati (Giard, 1900), was recognized only on the basis of its hypopi. This species is in close association with bees in the family Megachilidae (Hymenoptera), e.g., Anthidium manicatum, A. florentinum, A. diadema, A. oblongatum and A. cingulatum. It has been recorded from the Palearctic countries, e.g., Armenia, Belgium, France, Georgia, Greece, Italy, Kazakhstan, The Netherlands, Russia, Spain and Turkmenistan. In 2015, all stages of S. manicati were isolated from a nest of the wool carder bee, Anthidium manicatum in Auckland, New Zealand. DNA sequences of the 18S and D2/D3 regions of the 28S genes of the mite shared 100% and 99.5% identity, respectively, with S. manicati. Morphologically, this species is consistent with the other members of Acaridae in having a sejugal furrow, a rectangular prodorsal shield, smooth cuticle, stout condylophores and strong empodial claws, and the typical idiosomal setal arrangement. However, it is unusual in having the anterolateral areas of the prodorsal shield fused with the lateral sclerites in both sexes, solenidia omega 2 and omega 3 situated at the same level on the apical half of tarsus I in adult female, and omega 3 enlarged and at the end of the segment in the adult male. Both homeomorphic and heteromorphic males are observed and the latter can be recognized by having a pair of enlarged leg III. The idiosomal setae h2 are the longest, followed by the internal vertical setae (vi) and internal scapular setae (sci), and the other setae are very small. The morphological and molecular data generated in this study may facilitate the improved diagnostics of the species and assist the phylogenetic analysis of the family.

Keywords: Sarcoptiformes, Anthidium manicatum, Astigmata, phoretic association, Sennertionyx

Monday, 3 September

Fatih Sultan Mehmet Hall Section 1. Ecology and behavior of mites

Different strokes for different folks: Strategies evolved by two related species in adapting to a similar habitat

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Slime flux (a.k.a. sap flux) is the exudate from wounds in the bark or wood on tree trunks caused by an infection of the inner sapwood by pathogenic microbes. Containing sugars and other nutrients, the flux is rapidly colonized by bacteria, filamentous fungi and airborne yeasts. The resultant microbial growth is the habitat for a number of arthropod species, including two mites in the family Algophagidae, subfamily Hericiinae (*Fusohericia lawrencei* and *Hericia janehenleyi*). They have many morphological traits in common, including mouthparts modified for feeding on microbes. However, *H. janehenleyi* is a specialist inhabiting only fermenting flux on oak trees (*Quercus* spp.) and *F. lawrencei* is a generalist inhabiting flux on several different tree species, but none with fermenting flux. Bark containing flux was sampled at variable intervals over a five-year period and the environmental parameters of the flux recorded. Observations on mites in the bark samples were made utilizing a stereomicroscope. The present paper compares the similarities and differences evolved by the two species in adapting to their respective tree flux habitats.

Keywords: Algophagidae, *Fusohericia*, *Hericia*, adaptive strategy, slime flux



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Intra - and transgenerational effects in generalist and specialist predatory mites induced by prey limitation

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Life history theory predicts that females should produce few large eggs under food stress and many small eggs when food is abundant. We tested this prediction in two female-biased, size-dimorphic predatory mites feeding on herbivorous spider mite prey: Phytoseiulus persimilis, a specialized spider mite predator and Amblyseius andersoni, a broad diet generalist. The complexity of the response to the varying availability of spider mite prey correlated with the predators' degree of adaptation to this prey. Most A. andersoni females did not oviposit under severe food stress whereas P. persimilis did oviposit. Irrespective of predator species, the number of female but not male eggs decreased with increasing maternal food stress. This sex-specific effect was probably due to the higher production costs of large female eggs than small male eggs. Under moderate food stress, only *P. persimilis* increased its investment per offspring, at the expense of egg number, and produced few large female eggs. When prey was abundant, P. persimilis decreased the female egg sizes at the expense of increased egg numbers, resulting in a sex-specific egg size/number tradeoff. Maternal effects manifested only in *P. persimilis*. Small egg size correlated with the body size of daughters but not sons. Overall, our study provides a key example of sex-specific maternal effects, i.e., food stress during egg production more strongly affects the sex of the large than the small offspring.

Keywords: Biological control, environmental stress, maternal effects, Phytoseiidae, sex-specific effects

Diapause termination factors of *Tetranychus* spider mites (Acari: Tetranychidae)

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Diapause termination factors of the spider mite *Tetranychus atlanticus* McGregor (sensu Mitrofanov et al. 1987) were investigated under laboratory conditions at 25±0.5 °C and different relative humidities and photoperiods. The first series of experiments were made with females, which entered diapause under laboratory conditions after the mites were exposed to a short-day regime (L:D=14:10 h) at 18-19 °C during post-embryonic development. It was found that those diapausing females did not require any chilling for diapause termination. High humidity accelerated the diapause termination of females. There were no significant differences between diapause durations at different length of natural short-day photoperiod ($L_1 = 8.4 - 10.4 \text{ h vs. } L_2 = 11.3 - 13.2 \text{ h}$). However, the diapause period was significantly shorter at long-day photoperiod (L>15.2 h). No significant difference was found in diapause duration of females that were exposed as immature stages to a long- (14.1-15.0 h) and a short-day (9.0-10.4 h) natural photoperiod at 18-19 °C. The lack of light during the whole period of diapause in the presence of leaf culture as a food did not prevent the termination of diapause. However, it significantly increased the duration of diapause. The second series of experiments were done with spider mite females that entered winter diapause in strawberry plantations before September 1 in the Moscow region. They were sampled on November 18 and 22 and on December 6. The females kept at 25±0.5 °C and photoperiod of L:D=16:8 h required from 3.0 to 7.9 additional days of diapause. Cold treatment of diapausing females by pushing the temperature below 0 °C compared with low, above-freezing temperatures hastened the termination of diapause. The lack of light in comparison to L:D=16:8 h photoperiod did not delay the time of diapause termination of those diapausing females. It was also found that high humidity (55-85% vs. 40-45% RH) hastened diapause termination. The diapause duration of mated and unmated females did not differ significantly. The results obtained may also be relevant to other species of the genus Tetranychus.

Keywords: Tetranychidae, Tetranychus, diapause, termination of diapause, photoperiod



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Costs and benefits of mating with fertilized females in a species with first male sperm precedence

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Different patterns of sperm precedence are expected to result in specific mating costs and benefits for each sex, generating different selection pressures on males and females. However, most studies concern species with mixed paternity or last male sperm precedence, neglecting species with first male sperm precedence, in which only the first mating is effective. Here, we measured the costs and benefits of polyandry for both sexes of the spider mite, *Tetranychus urticae*. Firstly, we assessed the degree of sperm precedence, using a pesticide resistance marker. We found complete first male precedence, independently of the mating interval and number of matings. In addition, females paid a cost of polyandry, as multiply-mated females showed reduced longevity and laid fewer eggs than females that mated once or twice. Males showed reduced survival when in patches with five virgin females but such costs were absent when they were exposed to mated females only. Moreover, by mating multiple times with mated females, males decreased the total number of offspring sired by first males, which suggests that mating with mated females may entail a relative benefit for second males. Overall, our results suggest that polyandry may provide a benefit to second males, despite first male precedence. Whether such benefit is sufficient to maintain selection on polyandry in this system remains an open question.

Keywords: Spider mites, multiple mating, sperm precedence, mating costs, polyandry

A parental RNAi-based reverse genetics system for analyzing embryonic development of *Tetranychus urticae*

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The two-spotted spider mite, Tetranychus urticae, is one of the most important agricultural pest arthropods and the first chelicerate whose complete genome was sequenced and annotated. In this recent model system, efficient protocols for reverse genetics approaches are required to characterize gene function. RNA interference (RNAi)-mediated gene silencing is a powerful tool for the functional analysis. For functional characterization of genes involved in embryonic development, parental RNAi (pRNAi), the systemic RNAi in the embryonic stage of the progeny from mothers injected with double-stranded RNA (dsRNA), has been utilized in insects. However, the small body size of *T. urticae* often involves difficulties in dsRNA injection, even into adults. Here we describe a minimally-invasive method for microinjection of small molecules into *T. urticae*. Using this method, we performed parental RNAi targeting on Eyes absent (Eya), a conserved gene involved in eye development in insects. We found that higher survival and fecundity was observed in adult females injected at 3 days after final molting (DAFM) than those injected at 1 or 2 days DAFM. In addition, a tracer dye was delivered to ~20% of eggs laid by mothers injected at 2 or 3 DAFM whereas no delivery was found when injected at 1 DAFM. The relative level of TuEya expression was reduced in adult females injected with dsRNA-TuEya at 3 DAFM. Absence of eyes was observed in the progeny from the injected mothers. These results indicate that microinjection of dsRNA to mothers at 3 DAFM is promising for pRNAi in T. urticae and that TuEya is involved in eye development.

Keywords: dsRNA, embryogenesis, eye development, microinjection, pRNAi



2-8 September 2018, Antalya - TURKEY

Temperature effects on the developmental time and body size of the invasive mite *Aceria tosichella* (Eriophyoidea)

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Temperature has a great impact on developmental time and consequently on population growth rates, especially in ectothermic organisms. To cope with annual temperature changes some ectotherms develop different strategies such as accelerated or delayed development throughout the year. Investigation of complex interactions between temperature and the development of herbivorous invertebrates is important in order to improve the ability to predict their outbreaks and population dynamics. For instance, the invasive eriophyoid mite species, Aceria tosichella (wheat curl mite, WCM; genotype MT-1), which is one of the most important crop pests, causing huge economic losses worldwide, constantly increases its range. Therefore, the understanding of the ecology and biology of WCM is crucial for the further development of effective plant protection and management strategies. The aim of our study was to investigate the developmental time of WCM MT-1 at different temperatures. Furthermore, we tested whether there was a relationship between the development temperature and asymptotic body size. Eriophyoid mites were reared on plant samples and then placed on plant tissue culture medium. Wheat leaves with a single female of WCM MT-1 on them were placed on plates filled with Murashige and Skoog (MS) medium. Females were incubated at constant temperatures ranging between 17 °C and 33 °C at 2 °C intervals. When the female laid an egg, she was removed, and the entire development period, including egg, larva, nymph and adult stage, were monitored daily, until the individual of the next generation (F1) laid an egg. Afterwards, the F1 females were mounted on slides and their body size was measured. Our results were used to develop a mathematical model that describes the relationship between ambient temperature during ontogenetic development and both development time and asymptotic body size.

Keywords: Eriophyidae, temperature, morphology, phytophagous mites, wheat curl mite

Acknowledgement: This study was funded by the National Science Centre (Grant number: 2016/21/B/NZ8/00786).

Host-parasite associations between arthropods and Trombidioidea (Actinotrichida, Prostigmata), excluding Trombiculidae

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Trombidioidea, like other terrestrial Parasitengona, have a complex life cycle, with alternate occurrence of active and inactive instars. Parasitengona larvae (excl. Trombiculidae), except for few species, are ectoparasites of arthropods (Chilopoda, Diplopoda, Hexapoda and Arachnida). The aim of this study was to review the current knowledge of the host spectrum of Trombidioidea, host specificity, infestation, prevalence and topic preferences of larvae. The previous comprehensive survey of hosts of trombidioid larvae was provided by Welbourn (1983) and contained information on the hosts of 76 Trombidioidea species (excl. Trombiculidae). Our analysis, based on literature data and our own observations, includes around 1,150 parasite-host pair-wised associations involving the representatives of 254 nominal species assigned to 86 genera and 12 families of Trombidioidea. New data about host-parasite associations were obtained during field studies and in the course of laboratory experiments. For the majority of cases observed, the host spectrum revealed a high level of diversity at the intra- and intergeneric level. The number of parasites per host varies, reaching the median value at four, and revealing a tendency to increase with the increase of host size e.g. up to 175 larvae of Eutrombidium locustarum on one Orthoptera specimen. Very little is known about the prevalence; the index varies between a few percent and up to 100%. The disproportion between the number of species in the world fauna, for which at least one host is known, in comparison with data on the total number of nominal species and the possible consequences of incorrect identification, points to the need for further, intensive research and verification of previous data.

Keywords: Trombidioidea, larvae, parasitic associations, arthropods, ectoparasite



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Section 2. Evolution and phylogeny

First molecular phylogenetic and implications for the taxonomy of the family Phytoseiidae (Acari: Mesostigmata)

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The predatory mites of the family Phytoseiidae are well known for their use in biological control. Phytoseiidae systematics has a long and complex history due to the difficulty of establishing the evolutionary meaning of the morphological structures. The classification presently accepted is essentially based on the dorsal chaetotaxy but some authors have proposed that other structures be taken into account. However, none of the classifications proposed are based on phylogenetic relationships. Thus, it is impossible to say if one of these hypotheses is truer than another. Due to methodological advances, molecular markers are available to test deep phylogenetic relationships. This study aimed to test the monophyly of the three sub-families, some tribes and genera, using a combination of six DNA markers, namely 12S rRNA, COI mtDNA, CytB mtDNA, 28S rRNA, ITSS and HSP90. A total of 3,454 bp were analysed. The main results do not match with the present classification. The sub-family concept is questioned. Species of the genus *Phytoseius* (Phytoseiinae) are included in a clade also containing taxa of Typhlodrominae. The majority of the Typhlodrominae taxa considered are included in the same clade; however this study questions the validity of some tribes, for instance the Typhlodromini, and some genera and sub-genera, including Typhlodromus (Typhlodromus) and Typhlodromus (Anthoseius). Some species of Typhlodrominae (Galendromimini and Metaseiulini) are included in the sub-family Amblyseiinae. Finally, this latter sub-family appears to be polyphyletic, as well as several tribes, namely Amblyseiini, Neoseiulini and Typhlodromipsini, and the genus Amblyseius. This study confirms the monophyly of the tribes Euseiini and Phytoseiulini and of some taxa within the Kampimodromini. The molecular characters associated with these evolutionary relationships are discussed. Finally, other taxa need to be considered and additional analyses conducted to confirm the present findings in order to propose a modification of the current classification system.

Keywords: Molecular markers, phylogeny, taxonomy, Phytoseiidae, monophyly

Molecular phylogeny of Phytoptidae s.str. inferred from the partial sequences of three genes

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Earlier, we inferred the basal phylogeny of Eriophyoidea based on two markers (COI and D1-2 rRNA), and found several well-supported molecular clades which can be distinguished by genital anatomy and prodorsal shield setation: Loboquintus (Pentasetacus ((Eriophyidae s.str. + Diptilomiopidae), (Phytoptidae s.str., Nalepellidae)))). In this study, we used a concatenated partitioned alignment of three genes (COI, 28S, and EF1 α , 2191 nt aligned) to reconstruct the eriophyoid phylogeny, focusing on the clade Phytoptidae s.str., comprising phytoptids restricted to angiosperms. Pentasetacids, tydeoids and various groups of early derivative acariform mites, including nematalycids, were chosen as outgroups. Although the resulting ML tree had poor resolution, the following conclusions can be reported: (1) in accordance with our earlier results, Eriophyoidea has basal divergence with monophyletic Pentasetacidae (Loboquintus + Pentasetacus) and three large clades (Phytoptidae s.str., Nalepellidae and Eriophyidae s.l.). However, the position of Nalepellidae was uncertain; (2) There were no well supported clades corresponding to suprageneric groupings of Phytoptidae s.str. from the generic key of Eriophyoidea of Amrine et al. (2003). Additionally, phytoptids from monocots and dicots do not form two distinct clades, suggesting possible host shifts between these two groups of hosts; (3) the genus Oziella is monophyletic, as well as a group of Oziella spp. associated with Poales; (4) The endoparasitic genus Novophytoptus is nested within Phytoptus, suggesting a possible origin of Novophytoptus from dicot-inhabiting Phytoptus-like ancestors, and (5) The set of three gene markers used in this study is suboptimal and does not allow the resolution of the phylogeny of Phytoptidae s. str. The set of six genes, 18S, 28S, EF1-α, SRP54, HSP70 and CO1, which were recently used for inferring the position of Eriophyoidea within Acariformes, offer future prospects for improving phylogenetic support.

Keywords: Eriophyoidea, *Pentasetacus, Loboquintus*, Phytoptidae, phylogeny Acknowledgement: This study was partly supported by the Russian Foundation for Basic Research (RFBR grant 16-04-01292).



2-8 September 2018, Antalya - TURKEY

A jump from five to five thousand species: New morphological evidence from the mouthparts strengthens support for the paraphyly of Nematalycidae (Acariformes) with respect to Eriophyoidea (Acariformes)

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A recently published morphology-based phylogenetic analysis of basal Acariformes shows weak support for the paraphyly of Nematalycidae with respect to Eriophyoidea, and so additional morphological characters were sought to further test support for this relationship. Both Eriophyoidea and Nematalycidae have mouthparts that are too small to show much detail under a conventional light microscope. Therefore, these taxa were examined with a confocal laser scanning microscope, which allowed their mouthparts, including both external and internal features, to be visualized as 3D models. This investigation revealed a suite of characters that strengthens support for the paraphyly of Nematalycidae. These characters show that the mouthparts can be broadly categorized into two main forms: 1) a plesiomorphic form that closely resembles that of other basal acariform mites; and 2) an apomorphic form that has undergone a series of large scale and interdependent modifications, including thickening of the subcapitulum, thinning of the labrum, and the reorientation of the pharynx to a more upright position. In accordance with the most-parsimonious trees from the published phylogenetic analysis, the basal nematalycids, cf. Psammolycus and Osperalycus, have the plesiomorphic form, whereas the late derivative nematalycids, Cunliffea, Gordialycus and Eriophyoidea, have the apomorphic form. Eriophyoidea have undergone the most extreme modifications with respect to the apomorphic form, which is consistent with their highly derived position in all the most parsimonious trees.

Keywords: Eriophyoidea, Nematalycidae, Acariformes, confocal, gnathosoma

Genetic divergence predicts reproductive isolation in a social spider mite

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Reproductive barriers prevent diverging groups from merging back into one gene pool. The evolution of such barriers, therefore, has been paid much attention as a speciation mechanism. The prevalent view is that reproductive barriers evolve gradually as a byproduct of genetic changes accumulated by natural selection and genetic drift in groups that are segregated spatially and/or temporally. Reproductive barriers, however, can also be reinforced by natural selection against maladaptive hybridization. Both views are empirically supported by comparative studies analyzing relationships between intensity of reproductive barrier and genetic distance in sympatric taxa and allopatric taxa, mainly in *Drosophila* and other model organisms. In this study, to test these two views in a social spider mite, Stigmaeopsis miscanthi, we focused on three forms in the mite, which are different in the intensity of male lethal fight for nest ownership and have been diverging recently. We carried out crossing experiments and measured genetic distance among the three forms collected from parapatric and allopatric areas, and found that the three forms were reproductively isolated and that post-mating, prezygotic barriers most contributed to the isolation. As predicted by the former view, genetic distance explains the intensities of reproductive barriers. The latter view predicts that prezygotic barriers evolve faster in their parapatric area than in their allopatric area. However, we did not find such a clear tendency, although the low-aggression form slightly showed such a tendency and it is in line with their ecological and behavioral relationships.

Keywords: Tetranychidae, haplodiploidy, herbivore, cryptic reproductive isolation, *Stigmaeopsis miscanthi*



2-8 September 2018, Antalya - TURKEY

Monday, 3 September

Kanuni Sultan Suleyman Hall Section 1. Taxonomy and systematics

Mites of the family Parasitidae Oudemans, 1901 (Acari: Mesostigmata) from Japan: a new species of *Vulgarogamasus* Tichomirov, 1969, and a key to species

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Faunistic studies about parasitid mites in Japan are still limited. *Vulgarogamasus* sp. nov. (Acari: Parasitidae), extracted from leaf litter and soil in Ami, Ibaraki Prefecture, is described, based on females, deutonymphs and males. Morphological differences between the new species and its closely related species, *Vulgarogamasus fujisanus* (Ishikawa, 1972), were recorded on the basis of the examination of type materials. Information about parasitid mites reported in the Japanese literature was also collated, and a key to the species is provided.

Keywords: Parasitiformes, Vulgarogamasus, morphology, Japan, new species

Spider mites of the Balkan Peninsula: a review, new records and recent outbreaks

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Knowledge of the diversity of spider mites (Acari: Tetranychidae) is incomplete in some regions of Europe, including the Balkan Peninsula. This study reviews the species diversity of spider mites found on crop plants and native vegetation in the Balkan countries. The review is based on data available from the Spider Mites Web (SMW) database and other sources, including scientific literature, media and personal communications. According to SMW, 56 species have been recorded in Greece, the southern-most Balkan country, while the number of records in other countries is much smaller, specifically, Serbia (15), Bulgaria (12), Romania (8), Slovenia (4), Croatia (3) and Albania (1). In Serbia, very recent data from a five-year survey across the country have increased the number of tetranychid species to 37. There are also reports from the scientific literature of six common Palearctic species new to Slovenia, as well as two invasive, non-European species in Croatia. However, there is no published data from Albania, Bosnia and Herzegovina, FYR Macedonia and Montenegro. However, from personal communications and from field experiments, there is data on the cosmopolitan and Palearctic spider mite species present in these countries. In addition to the review of species diversity, this study gives recent reports of the spread and outbreaks of several tetranychid pest species in Balkan countries. Considering the geographical and biological diversity of the Balkan Peninsula, the aims and objectives of further research are also discussed, with emphasis on the need for highly qualified taxonomists.

Keywords: Tetranychidae, spider mites, species diversity, taxonomy, Balkans



2-8 September 2018, Antalya - TURKEY

Raphignathoidea (Acari: Trombidiformes) of Turkey: a review of progress on the systematics, with an updated checklist

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This paper provides a historical review of research on the superfamily Raphignathoidea in Turkey, with an updated list of the species known from Turkey. The taxonomic study of Raphignathoidea in Turkey is relatively deficient. Most species reported from the country have been published in a wide range of journals, mainly by Turkish researchers and a few by their colleagues from other countries. To date, about 250 papers on the taxonomy, fauna, morphology, biology and related fields have been published by more than 75 authors. Presently, this group is represented in Turkey by 206 species in 26 genera of 8 families. The recorded species richness of the Turkish Raphignathoidea is about 20% of the known world Raphignathoidea fauna.

Keywords: Checklist, faunistic, mite, Raphignathoidea, taxonomy

Phytoseiidae (Acari: Mesotigmata) of the Indian Ocean: biodiversity and new potential for development of biological control in this area

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The Indian Ocean contains many islands and archipelagos. Surveys of the phytoseiid faunas of some of these poorly-known territories only started recently, especially in Mauritius (3 species), Rodrigues (0) and for the four main islands of Comoros (only 1 species) but also in La Réunion (33 species, among which 8 are new to science). All data concerning earlier surveys in these archipelagos were published in seven papers. Surveys done more recently (2015-2018) have added: La Réunion: 22 new species (19 newly recorded and 3 new to science), with a total of 55 species presently known, among which 5 are well-known as biological agents (BCA); Mauritius: 4 newly recorded species, 7 species presently known and 2 well-known BCAs; Comoros Archipelago: 6 newly recorded species, 7 species presently known and 3 well-known BCAs. A better knowledge of the biodiversity and of its local role in the control of pests will allow a better response to the difficulties of introducing new BCAs to a territory. Since the French Government Decree of 2012 concerning the authorization of introduction into the environment of a BCA useful for biological control on cultivated plants, it is mandatory to deposit a permit for each introduction, and for research, experiments and commercial issues. France has various territories considered different under the law: France Metropolitan Main Territories (FMMT), Corsica, Caribbean Islands and La Réunion. A species present in FMMT cannot be introduced into La Réunion without permit and viceversa. Permits are expensive to lodge and quite difficult to obtain, if there are any risks associated with the introduction. Demonstration of the natural occurrence of already known, efficient BCAs in these foreign territories is consequently of very great agricultural and commercial interest, in addition to the importance of the knowledge of the biodiversity.

Keywords: Predatory mites, biological control agents, La Réunion, Mauritius, Comoros Archipelago



2-8 September 2018, Antalya - TURKEY

Trombidioid mites (Acari: Prostigmata) and their habitat preferences in Dumanlı Forest in Erzincan Province, Turkey

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Branches, leaves, bark and other organic debris deposited on the forest floor form a very favorable living environment for small animals. Mites are one of the richest invertebrate groups in terms of both species and the number of individuals in forest and soil ecosystems. There are numerous small arthropods in the litter of the forest floor, and most of them are mites. Turkey is one of the richest countries in terms of flora and fauna. The Dumanlı Forest, which is 2,000 m above sea level, is rich in biodiversity, since it has many variations in elevation and aspect and hence many different habitats. The forest has a special flora influenced by the Black Sea climate, featuring large numbers of specimens of the Scots pine. Velvet mites prefer habitats where shelter is abundant. Their distribution varies according to humidity and temperature. Some prefer stream edges or mossy areas adjacent to water, while others prefer dry areas. In this study, velvet mite groups were studied systematically for the first time in the different habitats of Dumanlı Forest. Soil samples were collected from a total of 255 different sites between April and November, 2017. The ecological characteristics of the habitats where the samples were collected were separately recorded. In this study, a total of 18 species belonging to five families were found. The examined specimens were deposited in the collection of the Acarology Laboratory of Erzincan University, Turkey.

Keywords: Acari, distribution, fauna, Parasitengona, Turkey

Acknowledgement: This study was supported by the Scientific Research Fund of Erzincan University (EÜBAP) (Project number: FYL-2017-469).

Phytophagous mites (Acari: Eriophyoidea) of two northern districts of West Bengal, India

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Among the Acari, eriophyoid mites are the second largest group with regard to their economic importance as phytophagous pests throughout the world. The great diversity of these tiny plant feeders is related to their extreme host specificity and intimate host relationships. Several of them are directly responsible for causing various disease symptoms in plants. The present work deals with the systematic study of eriophyoid mites done from 2006 to 2016 in two northern districts, Malda and Dakshindinajpur, of West Bengal, India. The objective of this work was to provide a taxonomic account of these mites and to record the nature of damage inflicted on their host plants. The study revealed 51 eriophyoid species in 28 genera, eight tribes, six subfamilies and two families. Of these species, 27 are in the subfamily Phyllocoptinae, 8 in Diptilomiopinae, 6 in Eriophyinae, 2 in Rhyncaphytoptinae, and 4 each in Nothopodinae and Cecidophyinae. The highest number of species (8) are in the genus Diptilomiopus Nalepa. Of the total number of species, 19 are considered new to science. To the present, 8 new species and two new genera have been described. In addition, 31 species are reported for the first time from this area. The host plants include 26 economically important species, including herbs, shrubs and trees. The other 17 host plants are wild. The systematic account of these species, their periods of infestation, the nature of damage and host associations are discussed in this paper.

Keywords: Diversity, eriophyoids, taxonomy, host association, West Bengal



2-8 September 2018, Antalya - TURKEY

Research progress on the taxonomy of Phytoseiidae (Acari: Mesostigmata) in China

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Phytoseiid mites are some of the most common natural enemies of pest mites and some other small arthropods. They are diverse and widespread on plants and on the soil, playing an important role in the ecological balance. To date, more than 2,700 species in about 100 genera and 3 subfamilies have been recorded worldwide. The taxonomy and field investigation of phytoseiids in China began in 1958, mainly in Taiwan and Hong Kong. Forty nine species were reported. A survey on the mainland from 1978 to 2002 recorded nearly 300 species. In 1997, some new genera were proposed, based on the collection in China and compared to species in nearby countries. In 2009, 307 species belonging to 15 genera and 3 subfamilies were reported in 'Fauna Sinica', among which 204 species are endemic to China. Some species were widespread in the 33 districts or provinces. The southern provinces had more species, with Guangdong, Fujian, Hainan and Jiangxi having 80, 72, 65 and 56 species, respectively. The Phytoseiidae of China overlap with those of its neighboring nations, Japan and South Korea. The species shared with Japan and South Korea are 38 and 18, respectively. Due to its huge land mass, geographical position and diverse environments, there is a rich diversity of phytoseiid mites in China and it is expected that substantially more phytoseid mite species will be described in the near future.

Keywords: Phytoseiidae, taxonomy, China, distribution, natural enemies

Section 2. Biological control

Laboratory evaluation of entomopathogenic fungi against the bulb mite, Rhizoglyphus robini (Acari: Acaridae)

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The bulb mite, *Rhizoglyphus robini*, is a serious pest of garlic and onion. The mite is also an important vector of plant pathogens such as *Fusarium* spp. Control of this pest is difficult because it has high reproductive potential, broad food niche, unique adaptations for dispersal and the ability to develop resistance to acaricides. Several studies revealed some compounds in *R. robini* which have been shown to possess antifungal activity and attempts to control this pest using the acaropathogenic fungus *Hirsutella thompsonii* failed. The aim of this study was to conduct a survey to determine the occurrence of entomopathogenic fungi (EPF) in onion and garlic fields in Israel and the Czech Republic and further assess the efficacy of selected strains against adult females of *R. robini*. Strains of *Beauveria* sp., *Isaria* sp., *Lecanicilium* sp., *Metarhizium* sp. and *Purpureocillium* sp. were isolated from soil samples in both countries. The concentration of EPF was significantly higher in soil samples collected in the Czech Republic than in Israel. The results further showed high differences among tested fungal strains in virulence against *R. robini*. While the reference strain CCM 8367 *Isaria fumosorosea* showed no efficacy, a strain of the genus *Metarhizium* sp. isolated from Israel caused almost 100% mortality of bulb mites. Perspectives on the use of EPF in the biological control of *R. robini* will be discussed.

Keywords: Biological control, entomopathogenic fungi, *Rhizoglyphus robini*, soil samples, virulence



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Morphological and molecular characterization of *Eutetranychus* mite populations collected from different hosts and regions of Saudi Arabia

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Spider mites of the genus Eutetranychus (Acari: Trombidiformes: Tetranychidae) are primarily phytophagous, mostly feeding on shrub and tree leaves, and making little webs on the leaves. Among Eutetranychus species, the oriental red spider mite, E. orientalis, is considered a major pest of citrus in many tropical and subtropical countries. Within the populations of E. orientalis, variations in the length and shape of dorsal body setae, pattern of striations between setae d1 and el, and chaetotaxy on the femora and tibiae, have been reported. Such morphological variations in the E. orientalis species complex have resulted in misidentification of its populations. For this reason, molecular methods can help taxonomists precisely identify and/or confirm different mite species. The present study aimed to confirm the identity of Eutetranychus mites collected from different plant hosts in different regions of Saudi Arabia. The second internal transcribed spacer (ITS2) region was amplified and sequenced from the morphologically-characterized mite samples. The cleaned and edited DNA sequences were compared with the NCBI-GenBank database for possible matches. DNA sequence analysis confirmed the identity of morphologically-characterized mites belonging to E. orientalis. Moreover, three different ITS-2 genotypes of E. orientalis were identified, suggesting that the Saudi E. orientalis populations may be genetically very diverse. In addition, a new Eutetranychus species was morphologically and molecularly identified. On-going studies will be conducted to elucidate the phylogenetic relationships among the Saudi mites and their counterparts worldwide. It is anticipated that the outcomes of the present study will help in resolving some problems associated with cryptic mite species. In addition, the proper identification of pest species can contribute to the development of effective management strategies.

Keywords: ITS2, *orientalis*, genotypes, genetic diversity, phenotypic variations

Pollen provisioning following flonicamid application has a positive impact on Amblydromalus limonicus

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Flonicamid (Teppeki 50WG) is an insecticide with moderate toxicity against phytoseiid mites. In the present study we evaluated the effect of pollen as a supplementary food source following the spray application of flonicamid on the survival, reproduction and prey (*Frankliniella occidentalis* larvae) consumption of the predatory mite, *Amblydromalus limonicus*. For the experiments, two application frequencies of fresh *Typha angustifolia* pollen were used: a) pollen was provided only once, within half an hour following the application of flonicamid and b) the same amount of pollen was gradually provided to the mites in smaller amounts every 48 hours. Pollen provisioning resulted in increased prey consumption by *A. limonicus*, irrespective of its application frequency. Frequent provisioning of fresh pollen had a positive effect on juvenile survival of the predatory mite; however, a mixed diet (thrips and pollen) provided in flonicamid-treated arenas did not affect its oviposition and adult survival. The results of this study highlighted the role of pollen provisioning in mitigating the negative side effects of pesticide residues on phytoseiid predatory mites.

Keywords: Amblydromalus limonicus, flonicamid, pollen, performance, prey consumption



2-8 September 2018, Antalya - TURKEY

Cannibalism and intraguild interactions between an exotic predator, Amblyseius swirskii, and three other phytoseiids occurring in papaya orchards in southern Florida

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The two-spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae) is one of the most important pests of papaya (Carica papaya L.) plantations in southern Florida. In recent decades, an Asian mite, Neoseiulus longispinosus (Evans), has become the most frequent predator associated with T. urticae. Neoseiulus chilenensis (Dosse) and Amblyseius largoenesis (Muma), one of the most common predatory mite species on various host plants in the area, are rarely observed on papaya. Papaya growers trying to control T. urticae have released Amblyseius swirskii, an exotic predator. In this study, we aimed to clarify whether competition among these four predators can influence the biological control of *T. urticae* on papaya. We tested the aggressiveness of adult female predators towards conspecific and heterospecific larvae in absence and presence of extraguild prey (T. urticae) for all four species of phytoseiids and their combinations. Neoseiulus longispinosus was the most cannibalistic species, followed by A. largoensis, A. swirskii and N. chilenensis. Both Neoseiulus species were able to recognize extra-guild prey, while in some cases, both Amblyseius species were not. In a second experiment, we tested single or combined releases of A. swirskii and N. longispinosus against T. urticae on potted papaya plants under greenhouse conditions. The mean numbers of T. urticae decreased dramatically in the N. longispinosus single release treatment, whereas prey populations gradually increased in all other treatments. Similar population levels of *T. urticae* were observed in the single and combined release of *A. swirskii* treatments throughout the experiment. In addition, our results showed that the biological control potential of N. longispinosus was negatively affected by the presence of A. swirskii.

Keywords: Phytoseiidae, biological control, intraguild predation, cannibalism, papaya

Selection of strains of *Amblyseius tamatavensis* (Acari: Phytoseiidae) for improved potential to control *Bemisia tabaci*

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Intraspecific biological differences have been observed in numerous organisms, including mites. These findings led to the inference that the performance of predatory mites in pest control could be improved through artificial selection. Amblyseius tamatavensis Blommers is a predatory mite found throughout the tropics. Promising results were obtained in laboratory evaluations of this predator as a control agent of Bemisia tabaci (Gennadius) (Aleyrodidae), an insect that causes great damage to various crops around the world. The study reported here refers to an attempt to obtain a more efficient population of A. tamatavensis for the control of B. tabaci by selecting for higher oviposition and predation rates. Sixteen populations of A. tamatavensis were collected from various parts of Brazil. From each population, 40 females were randomly taken and isolated in experimental units. They remained there for 11 days for the initial determination of those variables, when fed daily with 15 eggs of B. tabaci. Highest rates of predation and oviposition were determined for a population from the state of Alagoas. The process was conducted for several cycles, always selecting from successive progenies from that population. At the end of the selection cycles, the daily predation rate had increased from 7.7 to 8.8 eggs/female but no significant increase in oviposition rate was observed. A field study will now be conducted to compare the performance of the selected population with other populations used as controls.

Keywords: Biological control, *Bemisia tabaci*, selection of predatory mite, *Amblyseius tamatavensis*, intraspecific variation



2-8 September 2018, Antalya - TURKEY

Tuesday, 4 September
Osman Gazi Hall
Section 1. Agricultural Acarology

Displacement of a phytoseiid predator, *Neoseiulus womersleyi*, by another phytoseiid predator, *N. californicus* (Acari: Phytoseiidae)

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Neoseiulus womersleyi (NW) and N. californicus (NC) are two important predators that are frequently used to control spider mites in fruit tree orchards. Neoseiulus womerslevi used to be the dominant predatory species in Japan but since the 1990s in central and southwestern Japan, N. californicus populations have been increasing and have displaced populations of N. womersleyi. We confirmed this phenomenon under laboratory conditions, demonstrating that N. californicus could exclude N. womersleyi if they initially coexisted in a ratio of 1:1. It was concluded that neither reproductive interference nor differential female fecundity but asymmetric intraguild predation seemed to explain the competitive exclusion of N. womerslevi by N. californicus. However, the ratio in fruit tree orchards could be different from 1:1. Therefore, we hypothesized that differential susceptibilities to pesticides might accelerate species displacement of N. womersleyi by N. californicus, even if the ratio between these two species was extremely skewed in favor of N. womersleyi and no species displacement occurred otherwise. Among 21 pesticides examined, two neonicotinoids (acetamiprid and imidacloprid) had more negative effects on N. womersleyi than on N. californicus and thus could possibly account for its displacement. If the two species were released on leaf arenas at an NC:NW ratio of 1:9 in the absence of insecticide, no displacement was observed. However, just after acetamiprid or imidacloprid application, the proportion of N. californicus increased, causing displacement of N. womersleyi. Our results indicate that displacement in predator complexes in fruit tree orchards could be due to different degrees of pesticide susceptibility.

Keywords: Species displacement, asymmetric intraguild predation, neonicotinoids, dominant predator, pesticide susceptibility

Colomerus vitis (Acari: Trombidiformes: Eriophyoidea): comparison of some morphometric, biomolecular and biological aspects of the deutogyne and protogyne forms

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Eriophyoid mites overwinter in a winter form (deutogyne) morphologically distinct from the springsummer form (protogyne). The grapevine erineum mite (GEM), Colomerus vitis (Pagenstecher), which is widespread in the main viticultural areas of the world, was recently demonstrated to be the vector of the grapevine pinot gris virus (GPGV). The females overwinter mainly under the outer scales of buds and a deutogyne has been described. Colomerus oculivitis (Attiah) and other strains of C. vitis (bud and a leaf-roll strains) are known so GEM requires better characterization. In this study, a morphometric, biomolecular and biological approach was applied in order to better characterize the deutogyne and protogyne forms. Buds and leaves of the vineyard cultivar Luisa infested by C. vitis were sampled 6 times from December 2015 to January 2017. Females were studied for about 70 traits commonly used for taxonomic identification. The Kruskal-Wallis test was applied to the measured populations. ITS1 was investigated in individuals collected from buds in winter and erinea in spring. Groups of protogynes and deutogynes were separately submerged in water or vaseline oil at $5/25\pm1$ °C, and mite survival was assessed every week/day, respectively. Data were analyzed with regression analysis. Length of the tibial setae l' on the forelegs and of the tarsal setae ft' on the hindlegs, as well as the numbers of smooth dorsal semiannuli, differed significantly between protogynes and deutogynes. ITS1 analysis confirmed the homogeneity of the populations composed of these two forms. The year-long study demonstrated the presence of both protogynes and deutogynes in July and September, 2016. As expected, only protogynes were collected in April and May 2016, whereas only deutogynes were collected in December 2015 and January 2017. The deutogynes showed a higher survival percentage than the protogynes under all experimental conditions.

Keywords: Grape erineum mite, morphometry, biology, ITS1, ecology



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Role of *Colomerus vitis* (Pagenstecher) in the epidemiology of grapevine leaf mottling and deformation in north-eastern Italy

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The grapevine pinot gris virus (GPGV), a new virus discovered at Trentino-Alto-Adige in Italy, is currently spreading worldwide. It is associated with symptoms of chlorotic mottling and leaf deformation in the grapevine, Vitis vinifera. The virus was demonstrated to be transmitted by Colomerus vitis (Pagenstecher) (Eriophyoidea, Eriophyidae). The epidemiology and the acquisition/ transmission times of GPGV were studied. The acquisition and transmission trials were carried out under controlled conditions of 22±2 °C, 70% RH±10 and 16:8 L:D. Eriophyid mites collected from overwintering buds of GPGV-free grapevines were transferred to infected grapevine leaves. Some mites were resampled for GPGV detection after a predefined period. Others were transferred to GPGV-free leaves and removed after 24 hours. Those leaves and those mites were analyzed for the presence of GPGV. The assessment of GPGV infection in the field was done in 2016 and 2017 by means of potted grapevine plants that were GPGV-free, i.e., bait plants, which were placed close to symptomatic vines in two infected vineyards. Groups of ten bait plants were exposed in the field and replaced monthly with a new group until September. The exposed bait plants were stored in a screen house to avoid unwanted infections; concurrently, bait plants were inspected for the presence of leaf erinea and eriophyid mites were sampled for virus screening purposes. In winter, plants were analyzed for GPGV infection. All screenings for GPGV detection purposes were conducted by total-RNA extraction from eriophyid mites or plant tissues and amplification by RT-PCR and RT-qPCR. Acquisition trials showed that C. vitis can be infected by GPGV in four hours. Transmission trials involved some inoculations of healthy grapevine leaves with the virus. GPGV was subsequently detected in bait plants placed in the infected vineyards. Eriophyid mites collected from the leaf erinea and buds of these vines were positive for GPGV. These results increase the knowledge of the intimate involvement of C. vitis in GPGV transmission.

Keywords: GPGV, transmission, acquisition, eriophyid, grapevine

Mite diversity and the population dynamics of phytophagous mites and their predators in olive orchards in the Aegean Region of Turkey

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This study was carried out between 2015 and 2017 in order to determine the phytophagous mites and their predators in olive orchards in Balıkesir, İzmir and Manisa Provinces of Turkey. In addition, the population dynamics of the phytophagous mites were monitored in five olive orchards in Bornova and Kemalpaşa (Izmir), and Saruhanlı and Akhisar (Manisa). Weekly sampling was done between March and November. The phytophagous mites, Aceria oleae and Tegolophus hassani (Eriophyidae), Cenopalpus lineola and Brevipalpus sp. (Tenuipalpidae); the predatory mites, Amblyseius andersoni, Euseius stipulatus, Neoseiulus barkeri, Paraseiulus talbii, Typhlodromus (Anthoseius) athenas, Typhlodromus (Typhlodromus) psyllakisi, Typlodromus rarus, Typhlodromus (Anthoseius) recki, Typhlodromus (Typhlodromus) athiasae (Phytoseiidae), Raphignathus gracilis (Raphignathidae), Agistemus duzgunesae (Stigmaeidae); and the neutral mite, Tydeus californicus (Tydeidae), were collected. The eriophyid mites, A. oleae and T. hassani, were widely distributed in the spring (April-May) and autumn (September-October) in all the orchards. The predator, T. athenas, which was commonly observed throughout the year in all the orchards, is a first record for the Turkish fauna. It was also observed that the predatory mite, A. duzgunesae, fed on eriophyid mites. Further studies are needed to investigate the prey ranges of T. athenas and A. duzgunesae and their potential for the biological control of eriophyid mites.

Keywords: Olive, Eriophyidae, predatory mites, damage, Turkey

Acknowledgement: This study was supported by the Ministry of Food, Agriculture and Livestock of the Republic of Turkey (Tagem-BS-14/08-06/01-12).



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Section 2. Agricultural Acarology

Phytoseiulus persimilis: a new member of the acarofauna in Costa Rica?

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Phytoseiulus persimilis (Acari: Phytoseiidae) is an exotic species in Costa Rica that has apparently been introduced several times during the last few years to control Tetranychus urticae (Acari: Tetranychidae) on various field and greenhouse crops without, in most cases, government supervision. On collecting trips unrelated with this research, populations of *P. persimilis* were found associated with different crops, e.g., tomatoes, peppers, common beans and strawberries. Thus, an investigation was proposed to determine whether this predactions mite has become established in the Central Valley of Costa Rica. Surveys were undertaken in the four main provinces that compose the Central Valley, namely San José, Alajuela, Cartago, and Heredia, from January, 2016 to August, 2017. Ninety four sampling sites were chosen for the surveys, representing the following crops: tomato (Solanum lycopersicum), pepper (Capsicum annuum), bean (Phaseolus vulgaris), chayote squash (Sechium edule), and strawberry (Fragaria sp.), as well as some associated weeds, e.g., Rytidostylis gracilis, Ipomoea purpurea and Solanum americanum. Phytoseiulus persimilis was found at 27 of the 94 sampling sites. Traditional and molecular taxonomy were used to identify and/ or verify the phytoseiid mites present. They were P. persimilis and Phytoseiulus macropilis, which was collected from only one site, as well as other species. The highest densities of *P. persimilis* were found in El Yas and La Flor, Paraíso, in the province of Cartago, Santa Ana, in San José, and Poasito, and El Rosario de Naranjo, in Alajuela. Climatic conditions were taken into account to infer whether or not *P. persimilis* has adapted to the conditions in the Central Valley of Costa Rica. Some hypotheses are proposed as to why *P. persimilis* has become naturalised in some areas of the country.

Keywords: Phytoseiidae, *Phytoseiulus persimilis*, *Tetranychus urticae*, introduced species, Costa Rica

Studies on the damage potential of the vegetable spider mite, *T. neocaledonicus*, on cassava

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Cassava (Manihot esculenta Crantz) is infested by a number of pests, especially mites and insects. A survey of acarine fauna associated with this tuber crop revealed the presence of six species of mites. Among the phytophagous spider mites, the vegetable spider mite, Tetranychus neocaledonicus André, is one of the major agricultural pests, not only because of the damage it causes but also because it has a wide host range on various economically important crops. The present study was carried out in experimental plot with different sets of cultivated plants, both uninfested and infested, at Farook College campus in Kerala, India from April 2016 to March 2017. Qualitative assessment of damage was made by collecting both uninfested and infested leaves from the field and experimental plots to determine visual symptoms as well as by the leaf sectioning method to reveal various types of cellular damage caused by the mite, *T. neocaledonicus*. A quantitative assessment of leaf damage caused by its feeding activity was also made through the estimation of biochemical parameters such as photosynthetic pigments (chlorophyll a and b), carotenoids, carbohydrates, phenol and proline on mite infested and uninfested *M. esculenta* leaves. The feeding of *T. neocaledonicus* was found to induce a significant decrease in chlorophyll level and an increase in the total phenol and proline contents in infested cassava leaves. The reduction in the chlorophyll a and b, total chlorophyll and carotenoid contents were 60.23%, 71.86%, 65.57% and 25.06%, respectively. The increases in proline and phenol content were 0.89 µg/g and 38µg/g of tissue, respectively, compared to the control. The percentage of carbohydrate was low in infested leaves. A preliminary study that involved the protein profiling of M. esculenta leaves following infestation and damage by *T. neocaledonicus* revealed a decrease in protein concentration.

Keywords: *Manihot esculenta*, *Tetranychus neocaledonicus*, damage potential, leaf sectioning method, biochemical parameters



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Potential of xylophagous oribatid mites in biodegradation and nutrient release

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Degradation of litter is an essential process of soil ecosystem leading to nutrient cycling and it is mediated by a heterogeneous group of soil organisms. Oribatid mites represent one of the predominant agents of litter biodegradation in the soil. The ubiquitous presence and extensive diversity of this group of mites make them integral to the process of mineralization of litter in almost all types of soil ecosystems. However, an overall assessment of the mineralization potential of different groups of oribatid mites depicts the relative advantage of lower groups of oribatids viz. the lohmannoid and phthiracaroid members in the degradation of leafy and woody elements of litter. Degradation of such complex materials primarily necessitates additional qualities such as strong and well developed oral and holding appendages and the presence of the necessary enteric microflora and associated enzymes for continuation of the degradation process. In-depth field and laboratory studies of two representative species of the above two groups, namely Heptacarus hirsutus and Hoplophorella (Hoplophorella) chaliyamensis, through half a dozen methods, clearly indicated that these species provide a remarkable contribution to the process of nutrient cycling. The combined feeding activity of these two species on the woody elements of litter of two species of plants, namely Anacardium occidentale L. and Artocarpus integrifolia L., enhanced the release of nitrogen, phosphorous and potassium as evidenced by the increased concentration of these minerals in their fecal pellets. However, a decrease in the levels of calcium and magnesium was observed in the case of A. occidentale while for A. integrifolia there was a decrease in the level of calcium and an increase in the magnesium level owing to the feeding activity of the mites. The decrease in the calcium level may be attributable to its immediate requirement in the maintenance of bodily functioning.

Keywords: Oribatid mites, biodegradation, nutrient cycling, fertility, plant productivity

Feeding impact of *Cisaberoptes kenyae* Keifer (Acari: Eriophyidae) on the photosynthetic efficiency and biochemical parameters of *Mangifera indica* L.

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Cisaberoptes kenyae Keifer, the mango leaf coating mite, is a widely distributed eriophyid species in the tropics, infesting all varieties of mango tree. The mite produces a white coloured leaf coating on the adaxial surface of mango leaves, which extends over the entire leaf lamina in severely infested leaves. The present paper discusses the feeding impact of the mite on the photosynthetic pigments and other biochemical parameters of mango leaves. Biochemical studies revealed a significant decrease in the level of chlorophyll and carotenoid pigments in mite infested mango leaves when compared to uninfested leaves. The percentage loss of chlorophyll 'a', 'b', total chlorophyll and carotenoids were 65.80-84.64%, 76.57-95.29%, 68.69-87.13% and 39.31-56.75%, respectively. The photosynthetic efficiency determined through chlorophyll fluorescence measurement (fv/ fm) using the Handy PEA (Hansatech Instruments, UK) revealed a 25.15% to 28.43% reduction. Mite infestation also induced a significant reduction in total carbohydrates of 57.86% to 80.58% when estimated through the Anthrone method. In contrast to the above, a significant increase was observed in the proline and total phenol concentrations in mite infested leaves. The proline concentration increased from 2.9578±0.36 µ mol/g to 5.2611± 0.61 µ mol/g in the infested leaf tissue. Total phenol content increased from 55.14± 1.72 mg/g to 81.16± 0.85 mg/g in mite infested leaves. The results were statistically significant (P<0.05), confirming that infestation by C. kenyae induced severe stress which caused increased production of defense compounds like proline and total phenol and adversely affected photosynthetic efficiency and primary metabolite production of the host.

Keywords: Cisaberoptes kenyae, Mangifera indica, chlorophyll, carotenoids, proline



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Oribatid mites (Acari: Cryptostigmata) from garlic (*Allium sativum* L.) cultivation areas in Kastamonu, Turkey

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Garlic (*Allium sativum* L.) (Asparagales: Amaryllidaceae) is one of the most commonly produced and widely used vegetable crops in the world. It is used as a spice mash, canned product, dried powder, garlic oil and as garlic pellets. Oribatid mites (Acari) are saprophagous microarthropods inhabiting almost all types of soil ecosystems. In huge abundance, they feed mainly on dead organic matter, fungi, algae and lichens, and have considerable potential as bioindicators. Oribatid mites mainly live below ground and reach their highest densities in acidic forest soils, e.g., up to 200,000 individuals per m² in a boreal forest. They are important for litter decomposition, soil formation, nutrient cycling and the regulation of fungal and nematode populations. Cryptostigamatid mites have an important role in the decomposition of organic matter. In this study, cryptostigamatid species were determined from garlic cultivation areas in Kastamonu, Turkey. For this purpose, weekly samplings were made from March to July in garlic cultivaton areas in 2015-2016. After collection, the mites were preserved in 70% ethyl alcohol before clearing in lactic acid and mounting in Hoyer's medium for identification. A total of nine mite species belonging to the Oppiidae, Punctoribatidae, Protoribatidae, Tectocepheidae, Euphthiracaridae, Liebstadiidae, Epilohmanniidae and Galumnidae of Cryptostigmata were recorded.

Keywords: Oribatida, Acari, Cryptostigmata, garlic, Kastamonu

Acknowledgement: This study was supported by The Scientific and Research Council of Turkey (TÜBİTAK-114 O 416).

Seasonal distribution and damage potential of *Raoiella indica* (Hirst) (Acari: Tenuipalpidae) on plantation crops of Kerala

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Tenuipalpid mites represent an important group of phytophagous Acari characterized by polyphagous habit on a wide variety of crops. Among the injurious species of tenuipalpids, Raoiella indica (Hirst), the red palm mite (RPM), is a serious pest on a variety of plants. In the present study, infestation of the species on an important plantation crop of Kerala, viz. Areca catechu L., was studied. Field sampling of mite-infested leaves was carried out in areca plantations in two districts of North Kerala from 2011 to 2013. Both uninfested and infested leaf samples were observed under a Stereo Zoom Microscope (MVNSZ - 450) in the laboratory to determine the population density of the mite. Feeding impact of the RPM on the areca palm was assessed through quantitative estimation of total nitrogen, phenol, total chlorophyll and proline levels in the leaves. Results of population studies revealed that peak population of RPM occurs during April and May. A positive correlation was recorded between mite population and temperature and a negative correlation between mite population and relative humidity. The percentage losses of total nitrogen and total chlorophyll content were estimated at 51-53% and 59-60%, respectively in RPM-infested leaves. The percentage increase recorded for proline and phenol contents of miteinfested leaf samples were 182 - 198% and 90-92%, respectively, thereby revealing the stress induced by RPM in A catechu palms.

Keywords: Raoiella indica, Areca catechu, total nitrogen, total phenol, total chlorophyll



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Section 3. SYMPOSIUM: Tick and tick-borne diseases Section 3.1. Ticks and tick-borne diseases in Turkey Plenary lecture

Crimean Congo hemorrhagic fever

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Crimean Congo hemorrhagic fever is the most common viral hemorrhagic fever worldwide. CCHF virus is a Nairovirus in the Bunyaviridae family. Ticks of the *Hyalomma* genus, especially *H*. marginatum marginatum, are both reservoirs and vectors of CCHF virus. The prevalence of CCHF is closely related to the amount of wildlife, climate and socioeconomic status. Healthcare providers are the second most commonly affected group. Human-to-human transmission occurs to healthcare providers or other contacts via blood and body fluids, although the pathogenesis hasn't been fully elucidated. The primary pathology is bleeding which results in micro-vascular injury, increased vascular permeability and impaired hemostasis. CCHF, which causes infection only in humans, has 4 phases, namely incubation, pre-hemorrhagic, hemorrhagic and convalescent. The duration of incubation phase is 1-9 days; followed by the pre-hemorrhagic phase which is characterized by non-specific symptoms such as flu-like presentation, fatigue, diffuse myalgia, fever, nausea, vomiting, diarrhea, epigastric and abdominal pain. In addition, hemorrhages such as hematemesis, melena, hematochezia, metroragia, epistaxis, gingival hemorrhage, hemoptysis and hematuria can be seen. Multi-organ failure, DIC, shock and death can occur with hemorrhages. Death occurs after 7 to 10 days Laboratory findings include thrombocytopenia, leucopenia, elevated AST, ALT, LDH, CPK and INR, and prolonged PT and aPTT. IgM and IgG antibodies can be detected on day 7 after the onset of disease by using ELISA or IFA. Reverse-transcriptase PCR is highly specific and sensitive for the rapid diagnosis of CCHF. There are no specific agents for use in the treatment of CCHF. Supportive therapy is the mainstay of the management of CCHF. Although its mechanism of action is unknown, ribavirin is the only antiviral agent recommended by the World Health Organization. However, the subject of its effectiveness is controversial. Personal protective measures that minimize the risk of infection are therefore essential.

Keywords: Crimean Congo hemorrhagic fever, epidemiology, *Hyalomma marginatum*, ticks, vector borne infections

Plenary lecture

Tick-borne pathogens other than CCHF found in Turkey

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Ticks are known vectors of many pathogenic microorganisms like bacteria, viruses and protozoa harmful to humans and domestic animals. All ticks require blood for development and reproduction. In recent years, shifts in climatic conditions and changes in land use have increased the infestation probability with ticks and infection with tick-borne diseases (TBDs) worldwide. Turkey has suitable habitats for ticks due to its diverse climate, vegetation and large variety of wild and domestic animals. Today, 48 tick species are known in Turkey, 31 of which have been found infesting humans. Nineteen TBDs have been detected either in animals or humans in Turkey, one of the most important being Crimean Congo haemorrhagic fever (CCHF). The virus is mainly transmitted by Hyalomma marginatum ticks. Moreover, CCHF might also be transmitted by contact with the blood or tissues of viremic humans during the acute phase of the disease. Overall, 9,787 CCHF cases were reported between 2002 and 2015, with 469 of them resulting in death. Tularemia is another common disease that is transmitted by tick bites; 4,824 human tularemia cases were reported to the Ministry of Health between 2005 and 2011. Lyme borreliosis is also known in Turkey. The seroprevalence of Borrelia burgdorferi in humans has been reported at 4%. In addition, the anaplasmosis seroprevalence was 10.6% in humans, and the bartonelloses seroprevalence was 6% in human blood donors, and 22.2% in veterinarians. In addition, numerous pathogens such as Rickettsia spp., Ehrlichia spp., Coxiella burnetii, Bartonella spp., Leishmania spp., Toxoplasma gondii, Babesia spp., Theileria spp., Hepatozoon spp. and Hemolivia mauritanica has been reported from ticks collected in Turkey. Tick control is often based on the use of chemicals in animals and the environment, while biological control agents such as entomopathogenic fungi have also been tested. Protective clothing and the application of tickrepellent chemicals on clothing and skin are recommended, especially in areas where the contact risk is high.

Keywords: Seroprevalence, tick borne diseases, tick borne pathogens, tularemia, Turkey



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Plenary lecture

Characteristics of patients admitted to the emergency department of Hitit University Hospital in Corum, Turkey due to tick bite

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Crimean Congo haemorrhagic fever (CCHF) is a tick borne disease which has been endemic in Turkey since 2002 and Çorum is one of the leading five cities in Turkey for its occurrence. The disease is an acute illness affecting multiple organ systems that is characterized by thrombocytopenia, and/or leukopenia, elevated levels of alanine aminotransferase (ALT), aspartate aminotransferase (AST), lactate dehydrogenase (LDH) and creatine kinase (CK) and it has a case-fatality proportion of 8% to 80%. In the current study, the medical data of the patients admitted to the emergency department (ED) due to tick bite was retrospectively analyzed. These patients were divided into two groups according to their transcriptase-polymerase chain reaction (RT-PCR) test results. The findings of PCR (+) (Group 1) and PCR (-) (Group 2) patients were compared. Epistaxis was a statistically significant clinical finding in Group 1. In addition, while aspartate transaminase (AST) levels and potassium (K) level were significantly higher, platelet count and white blood count (WBC) were significantly lower in Group 1 than in Group 2. Predictors of CCHF in the ED are epistaxis, leukopenia, thrombocytopenia and elevated K and AST levels. In this study, the fatality rate for CCHF in Çorum was 6.8% to 21.6%. The examination of 970 blood samples showed that 560 of them were PCR (+), including 38 fatalities.

Keywords: Tick borne disease, Crimean Congo haemorrhagic fever, thrombocytopenia, enzyme level, fatality rate

Section 3.2. Ticks and tick-borne diseases in Turkey

Phylogenetic characterization of ixodid ticks infesting different hosts from the Kayseri region of Turkey

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Knowledge of the inter-population and intra-population genetic structure and variability amongst tick populations is important for exploring the dispersal and transmission dynamics of the tickborne pathogens. To compare the phylogenetic relationships of some ixodid tick isolates collected from several animal species in the Kayseri region of Turkey with the published sequences in GenBank, this study examined sequence variations in the mitochondrial gene, cytochrome c oxidase subunit I (COI). Genomic DNA was extracted from individual, adult male and female tick specimens that had been identified according to the morphological keys. A 523 bp of the COI gene was successfully amplified by using C1-J-1718M and C1-N-2191M primers in PCR. Sequence analysis was performed on 472 bp of COI after trimming the PCR primers. The COI data set comprised a total of 61 sequences from ixodid ticks of which 40 sequences from 13 species, namely Rhipicephalus annulatus, R. turanicus, R. sanguineus, R. bursa, Haemaphysalis parva, Hae. sulcata, Hyalomma marginatum, H. anatolicum, H. excavatum, H. detritum, H. dromedarii, Dermacentor marginatus and Ixodes ricinus, were characterized in this study. The highest and lowest intra-specific genetic distances were determined as 10.6±1.8% and 0.1±0.1% for R. turanicus and Hae. parva, respectively. All the haplotypes, except the ones belonging to H. dromedarii and H. rufipes, formed monophyletic clusters based on species. The highest interspecific genetic distance (31.6±3.1%) was determined between Hae. sulcata and H. excavatum and the lowest distance (0.3±0.2%) was between H. dromedarii and H. rufipes. Consequently, this study reports the first genetic characterization of ixodid tick species from several animal species in the Kayseri region of Turkey.

Keywords: Ixodid ticks, COI, phylogenetic characterization, Kayseri, GenBank

Acknowledgement: This study was supported by the Erciyes University Research Fund (Research project TSA-2018-8060).



2-8 September 2018, Antalya - TURKEY

Molecular identification, phylogeny and geographic distribution of *Hyalomma* (Acari: Ixodidae) species in Turkey

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The genus *Hyalomma* Koch, 1844 is one of the most important genera in the Ixodidae family because it transmits many pathogens to humans and animals. To elucidate the current distribution of the species of *Hyalomma*, field studies were carried out in 65 localities in Turkey and five localities in Cyprus between 2011 and 2015. Additionally, the sequence variation of mitochondrial 16S and 12S rDNA of the *Hyalomma* species collected from Turkey and Cyprus was compared with the sequences on Genbank. Morphological examination and molecular analyses showed the presence of four species, namely *Hyalomma marginatum*, *Hyalomma excavatum*, *Hyalomma aegyptium* and *Hyalomma asiaticum*. The molecular data verified the morphological identifications. Phylogenetic trees demonstrated five different clades, placing *H. asiaticum*, *Hyalomma scupense*, *Hyalomma dromedarii* and *H. aegyptium* in different clades with high bootstrap values. Specimens of the *Hyalomma anatolicum* group and *H. marginatum* complex are sister groups. Pairwise distance analyses of these groups showed 2.8% and 3% differences for 12S rDNA and 16S rDNA, respectively. The results of this study provide a tool to further investigate the distribution of *Hyalomma* species and intraspecies and interspecies variation in order to understand the dynamics of Crimean Congo hemorrhagic fever (CCHF) in the regions where it is endemic.

Keywords: *Hyalomma marginatum*, mitochondrial rDNA, distribution, phylogeny, Turkey

Genetic characterization and expression analyses of the protective antigen subolesin in *Hyalomma anatolicum* and *H. rufipes* lineages infesting cattle in the Kayseri region of Turkey

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Subolesin has been characterized as an evolutionarily conserved, intracellular, protective antigen in several tick species which functions in regulating gene expression as a transcription factor. Immunization and RNAi trials have demonstrated that subolesin affects a number of cellular processes such as the innate immune response, digestion, reproduction and development which result in reduced vectorial capacity, fertility and vitality. Thus, subolesin is considered one of the important protective antigens for developing universal vaccines for the management of tick infestations. In the current study, the open reading frame (ORF) of the subolesin gene was amplified from the cDNA library of some Hyalomma anatolicum and Hyalomma rufipes lineages infesting cattle in the Kayseri region of Turkey. cDNA from both H. anatolicum and H. rufipes lineages contained 492 bp open reading frame with a predicted molecular mass of approximately 40.4 kilodaltons and an isoelectric point of 5.16. There were no intraspecific nucleotide differences within the sequences of H. anatolicum while a mean distance of 0.2% was found among the H. rufipes lineages. The subolesin ORF nucleotide and amino acid sequences of H. anatolicum showed 97.4 to 100% and 98.2 to 100% identities, respectively, with all full length ORF sequences of H. anatolicum from several countries in GenBank. The nucleotide and amino acid sequences of *H. rufipes* exhibited a mean of 99.8 to 100% and 100% identities, respectively, to the only available, partial ORF sequence of *H. rufipes* from Spain (GenBank accession: JX193849). A mean of 0.8% interspecific genetic distance was determined between H. anatolicum and H. rufipes lineages within the subolesin ORF region. In conclusion, this study provides the first data on the protective antigen subolesin of *Hyalomma* species in Turkey.

Keywords: *Hyalomma*, protective antigen, subolesin, Kayseri Province, Turkey

Acknowledgement: This study was supported by the Erciyes University Research Fund (Research project TSG-2016-7052).



2-8 September 2018, Antalya - TURKEY

Molecular investigation of the natural transovarial transmission of tick-borne pathogens in Turkey

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Transovarial transmission is an advantageous adaptation of tick-borne pathogens (TBP). Investigations determining the presence of natural transovarial transmission in ticks contribute to the knowledge of ecology and biology of TBP. This study aimed to investigate the presence of TBP in unfed larvae obtained from engorged female ticks from domestic animals in Turkey. A total of 131 engorged female ticks from cattle, sheep, goats and a dog were incubated under conditions suitable for egg laying. Unfed larvae were successfully harvested from 75 females. In total, 75 larval pools (n = 2,250) obtained from individual females were produced, and DNA/ RNA were simultaneously extracted. All pools were screened for the presence of *Anaplasma* spp., Babesia spp., Borrelia spp., Crimean-Congo hemorrhagic fever virus (CCHFV) and Rickettsia spp. with PCR. In the sequence and phylogenetic analyses, *Babesia occultans* was detected in three Hyalomma marginatum larval pools and one Hyalomma excavatum larval pool, and Babesia ovis was detected in one Rhipicephalus bursa larval pool. Additionally, Rickettsia aeschlimannii was detected in five H. marginatum larval pools, and Rickettsia raoultii in one Dermacentor marginatus larval pool. From these, B. occultans and R. aeschlimannii were detected as a mixed infection in one *H. marginatum* larval pool. Thus, this study identified natural transovarial transmission of *B*. occultans, B. ovis, R. aeschlimannii and R. raoultii in Turkish ticks. This is first demonstration of transovarial transmission of B. occultans in naturally infected H. excavatum. These data suggest that *H. excavatum* may act as a vector in the natural cycle of *B. occultans*, and also confirm that *R.* aeschlimannii and R. raoultii can pass to the larvae of infected H. marginatum and D. marginatus females transovarially. In conclusion, R. aeschlimannii and R. raoultii, which are pathogenic rickettsiae for humans, and B. occultans and B. ovis, which are pathogenic for livestock, can be transmitted transovarially in Turkish ticks, posing a substantial health threat to humans and livestock in Turkey.

Keywords: Transovarial transmission, natural ecology, tick-borne pathogens, *Babesia occultans*, *Hyalomma excavatum*

Prevalence of *Hemolivia mauritanica* in natural populations of *Testudo graeca* in Corum Province, Middle Black Sea Region, Anatolia, Turkey

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In this study, the blood samples of 25 (11 $\lozenge\lozenge\lozenge$, 14 $\lozenge\lozenge\lozenge$) individuals of the tortoise, *Testudo graeca* (Testudinidae), in Corum Province in the central Black Sea Region of Anatolia, Turkey were examined for *Hemolivia mauritanica*, a hemogregarine protozoan, between April and September, the activity period of T. graeca, in 2017. It has been suggested that co-evolution has occurred within the Testudo-Hyalomma (tick genus)-Hemolivia host-parasite complex. In the first stage of this study, T. graeca individuals were examined for the presence of ticks and then blood samples were collected from the dorsal coccygeal vein. Three blood smears were prepared per individual. The smears were air-dried, fixed in absolute methanol for 5 min, stained with Giemsa (diluted 1:10 in buffered water, pH 7) for 20 min and washed in buffered water for 2 min. The stained smears were examined with a light microscope at 100x magnification; parasitaemia was determined for each tortoise as the occurrence of infected erythrocytes in 10⁴ cells. The infestation prevalence for Hyalomma aegyptium was 92%. Among the examined blood smears from infested tortoises, 83% of them were H. mauritanica-positive. The mean intensity of perasitaemia was 4.7% in H. mauritanica-positive individuals. In this study, we detected the occurrence of H. mauritanica in T. graeca infested by H. aegyptium in a new area of Turkey. Turkey has both a suitable environment for the transmission of tick borne pathogens and also a diversity of tick species that are abundant. It is important to determine the biological and epidemiological role of H. aegyptium infesting tortoises in Corum Province because it is an endemic area for the important tick-borne disease, CCHF.

Keywords: Hemolivia, Hyalomma aegyptium, Testudo graeca, parasitaemia, blood smear

Acknowledgement: This study was supported by the Scientific Research Unit of Hitit University in Çorum, Turkey (Project number: ALACA19003.16.001).



2-8 September 2018, Antalya - TURKEY

Diagnosis of Crimean Congo haemorrhagic fever virus by Real-time PCR between 2010 and 2017 in Samsun and neighbouring provinces of Turkey

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Crimean Congo hemorrhagic fever virus (CCHFV), which belongs to the Bunyaviridae family and Nairovirus genus, is transmitted to humans by tick bites; in addition, human to human transmission may occur by direct contact with blood or other infected tissues. The disease became endemic and has been a public health problem in Turkey since 2002. The real-time PCR method has a very high sensitivity and specificity for CCHFV. Presence of the viral RNA in acute infection is a "definitive diagnosis" which is used in the diagnosis of acute infections in Turkey. The purpose of this study was to determine retrospectively the CCHFV positive percentage of patients suspected of being infected with CCHF in Samsun Province and neighbouring provinces between 2010 and 2017. Serum samples submitted to Samsun Public Health Laboratory with a suspicion of CCHF were analysed with the real-time PCR method (RealStar CCHFV qRT-PCR Kit1.0, Altona Diagnostics Hamburg, Germany). Overall, 40.86% of 460 samples in 2010, 47.12% of 783 in 2011, 40.53% of 634 in 2012, 47.40% of 616 in 2013, 39.90% of 807 in 2014, 37.67% of 645 in 2015, 30.03% of 323 in 2016 and 26.97% of 278 samples in 2017, were positive for CCHFV. The primary reason for the gradual decrease in the positive percentage over the years could be related to the proactive approach taken by the Ministries of Health and Agriculture. The increased awareness of physicians may also have helped them make better selective diagnoses based on clinical findings. The decrease may also be related to the natural decline of the epidemic due to increased immunity in the population.

Keywords: Crimean Congo hemorrhagic fever virus, PCR, immunity, epidemiology, Samsun

Comparison of real-time PCR and IFA for the detection of Crimean Congo haemorrhagic fever virus

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Crimean-Congo hemorrhagic fever virus (CCHFV), a member of the genus Nairovirus of the family Bunyaviridae, causes a severe disease in humans with high mortality rates. It is a fatal zoonotic viral hemorrhagic infection reported from Africa, Asia, Eastern Europe and the Middle East. In this study, the presence of CCHF viral load and CCHF IgM antibodies were investigated in serum samples submitted to the Samsun Regional Laboratory of the Ministry of Health with a suspicion of CCHF between 2010 and 2017 by using real time PCR and IFA methods. RealStar CCHFV qRT-PCR Kit1.0, Altona Diagnostics (Hamburg, Germany) was used for PCR and the CCHFV mosaic 2 IgM (Euroimmun, Luebeck, Germany) kit was used for IFA. Of the 3,426 samples received at the laboratory during the 7 years, 1,096 (32%) were both viral RNA and IgM antibody positive, and 359 (10%) of them were positive for one of the two methods. While 216 (6%) samples were IgM positive, they were viral RNAs negative, meaning that there was a recent CCHFV infection. On the other hand, 143 (4%) samples were viral RNA positive but were negative for IgM, indicating a past infection. Both tests have some advantages for the diagnosis of CCHF. For instance, the level of detection of the CCHF virus with PCR was higher in the samples taken 1-3 days after the appearance of the symptoms, while CCHF IgM seropositivity was greater at 4 or 5 days. Neither of the tests alone was sufficient to be definitive for CCHFV. In conclusion, since early diagnosis and treatment are important for CCHF management, the use of molecular and serologic methods in combination is recommended.

Keywords: Crimean Congo hemorrhagic fever virus, RT-PCR, immunofluorescence assay seropositivity, IgM antibody, Nairovirus



2-8 September 2018, Antalya - TURKEY

A molecular survey of *Babesia microti* in wild rodents in Turkey

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Rodents serve as reservoirs for numerous infectious disease agents, especially tick-borne pathogens. Babesia microti is an important tick-borne zoonotic parasite that uses rodents as reservoir hosts. In this study, rodents were collected from four different regions in Turkey in order to investigate the proportion of positivity to B. microti infection. Between 2010 and 2012, 536 rodents were captured in Burdur, Bartin, Giresun and Yozgat Provinces in Turkey for the collection of blood and tissue samples. DNA was extracted from the samples and screened for Babesia spp. by using conventional PCR which targeted the 18S rRNA gene. The sequences of PCR amplicons were analysed for B. microti, Hepatozoon spp. and Sarcocystis spp. In total, 5.8% of the rodents were positive for B. microti but no other Babesia species were detected. The overall proportion of positivity of Myodes glareolus to B. microti was 41%; in Bartin and Giresun it was 48.7% and 15.4%, respectively. In other rodent species, the extent of positivity to B. microti was lower, specifically, 7.7% in Chionomys roberti, 3.8% in Microtus sp., 2% in Apodemus sp., and 0% in both Mus macedonicus and Pitymys subterraneus. The overall positivity of the rodents for B. microti collected from Bartin, Giresun and Yozgat Provinces was 14.9%, 4.5%, and 1.1%, respectively. None of the rodents collected from Burdur Province were positive for *Babesia* spp. but six were positive for *Hepatozoon* spp. and one was positive for Sarcocystis spp. The sequence analysis of B. microti isolates revealed that all of the isolates belonged to the zoonotic genotype. Isolates obtained from Bartin Province were genotypically closer to the European isolate (Accession number: EF413181 Jane /Germany), whereas the ones obtained from Giresun Province were closer to Russian (Accession number: KU955528) and Mongolian (Accession number; LC005771) isolates.

Keywords: Rodent, *Babesia microti*, PCR, hepatozoon, sarcocystis

Molecular evidence for transstadial transmission of *Ehrlichia canis* by *Rhipicephalus sanguineus sensu lato* under field conditions

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This study investigated possible transstadial transmission of *Ehrlichia canis* by *Rhipicephalus sanguineus sensu lato* collected from dogs in shelters and from the shelter grounds in Diyarbakır Province of south-eastern Turkey. A total of 225 engorged nymphs collected from 8 dogs infected with *E. canis* were incubated at 28 °C to promote moulting. Unfed ticks from the shelter grounds, comprising 1,800 larvae, 3,100 nymphs and 85 adults, were sorted according to sampling origin, life stage and sex into 116 pools and screened with 16S rRNA PCR. Nine out of 26 pools of unfed adult ticks were positive for *E. canis*, with an overall infection rate maximum likelihood estimation (MLE) of 4.83 (CI 2.39-8.87). *Ehrlichia canis* was detected in three of 12 male pools (MLE 3.22, CI 0.86-8.83) and six of 14 female pools (MLE 6.16, CI 2.59-12.90). No adult pools collected from the shelter grounds were positive. Among 62 unfed nymph pools collected from the shelters, six were infected with *E. canis* (MLE 0.20, CI 0.08-0.42). No *E. canis* DNA was detected in any of the larval pools. Our results revealed molecular evidence for transstadial transmission of *E. canis* by *R. sanguineus s.l.*, both from larva to nymph and from nymph to adult but we found no evidence of transovarial transmission.

Keywords: *Ehrlichia canis*, *Rhipicephalus sanguineus sensu lato*, dog, transstadial transmission, transovarial transmission



2-8 September 2018, Antalya - TURKEY

Tuesday, 4 September

Fatih Sultan Mehmet Hall

Section 1. SYMPOSIUM: Invasive species and biosecurity: understanding and preventing mite invasions

Section 1.1. Understanding and preventing mite bioinvasions Plenary lecture

Phytophagous mite bioinvasions in South America – What are we learning from that?

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Invasive, phytophagous mites can greatly impact agroecosystems and natural terrestrial ecosystems. These minute arachnids are not only extremely harmful to their host plants but they also: (i) act as vectors of major plant diseases; (ii) quickly develop resistance to pesticides; (iii) survive adverse environmental conditions; (iv) reproduce parthenogenetically, establishing new colonies from one or a few colonizer females; and (v) adapt to new host plants in invaded areas. In addition, phytophagous mites are extremely small, around 0.5mm or even less. Therefore, they can easily go unnoticed during a naked-eye inspection and be accidentally introduced into new areas. In recent decades, South America has experienced the accidental introduction of phytophagous mites, including the red palm mite, Raoiella indica; the wheat curl mite, Aceria tosichella; the rice mite, Steneotarsonemus spinki; the citrus hindustanicus mite, Schizotetranychus hindustanicus; the lychee erinose mite, Aceria litchi; and the blue oat mite, Penthaleus major. Pathways, dissemination progress, current distribution, host plant range, and impact of these mites in South American countries are discussed related to their bioecological features, genetic variability, invasive history on other continents and quarantine measures. Understanding invasion processes, especially favourable and unfavorable factors, pathways and applied mitigation measures, can be helpful as support for pest risk analysis and the prevention of new invasions.

Keywords: Invasive mites, invasion biology, pathways, pest risk analysis, plant protection

Plenary lecture

Why are Brevipalpus and Raoiella successful invaders?

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Members of the mite genera, Brevipalpus and Raoiella, both share some key features that make them exceptionally successful invasive pests. Both species show high reproductive and behavioral plasticity. Brevipalpus species, mainly the groups 'obovatus', 'yothersi' (=phoenicis) and 'californicus', has telytokous parthenogenesis, while *Raoiella indica*, which has arrhenotoky, is the main pest in its genus. Brevipalpus mites have been reported more frequently as problem pests because of their ability to transmit several new emergent viruses to extensively cultivated tropical and subtropical plants. Raoiella indica invaded the New World as a single "clonal" population and has colonized several palm species, including coconut palms, impacting several plantations. Because palms are a key species in several environments and are widely used as ornamental plants, Raoiella has found an abundance of host plants to reproduce on and can efficiently disperse with the frequent help of human activity. In a similar way, but with different attributes, Brevipalpus mites are also very effective in colonizing many hundreds of species of ornamental plants, which inconspicuously host the mites and their viruses, and are dispersed on cuttings by unaware people. Their plasticity and polyphagous behavior may be associated with their capacity to detoxify a large variety of plant compounds with the help of their endogenous microbial communities. Currently, the largest economic impact of *Brevipalus* is on perennial crops such as sweet orange in both South and Central America and in tea plantations in Asia. In other crops, the damage can also be significant, e.g., passion fruit, but the crop area and costs of control are lower. In addition, Brevipalpus has developed resistance to many acaricides. However, several studies have reported many natural enemies of both Raoiella and Brevipalpus but they are often unable to suppress outbreaks. Both genera are extremely effective in synchronizing their reproductive strategies with their hosts' phenology and weather patterns, and adjusting quickly to the extreme and rapid climatic variations that have become more common.

Keywords: Tenuipalpidae, virus-vectors, plasticity, biological invasion, dispersal



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Section 1.2. Understanding and preventing mite bioinvasions

Raoiella indica, arrival and establishment in Mexico

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Raoiella indica, an exotic tenuipalpid, was found for the first time in the Americas on the island of Martinique in 2004. From there it moved to different Caribbean Islands, and then to the mainland of the continent, and Mexico. In 2009, it was officially declared present on a small island in the south-east of the country called "Isla Mujeres" in the state of Quintana Roo. The species was detected by plant health staff working at that time on the evaluation and control of another invasive species, the cactus moth, Cactoblastis cactorum. With the removal of the infested cacti, this species was finally eradicated from the island in 2009. Unfortunately, due to its small size, the dispersal of R. indica, went unnoticed. A survey on coconut palms on the island found that by October 2009 it had already spread to different points on the island and to a few points on the mainland. The movement of the species is believed to have occurred via vegetable waste, people, boats and wind. A phytosanitary fence was established but the progress of the species was relentless, despite these efforts. The island receives tourists from the U.S.A. and small boats carrying Cuban immigrants; R. indica was present in both countries before 2009. Isla Mujeres represents a potential point of entry but no monitoring work is carried out. The present study indicates that this island represents an area at particular risk of introduction of exotic species through tourism. The presence of the mite species, R. indica, is currently confirmed in 190 municipalities in 15 states across the Mexico.

Keywords: Isla Mujeres, coconut palm, exotic species, quarantine, phytosanitary measures

Adventive and/or invasive phytophagous mites in Serbia: an overview and recent data

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The term adventive species refers to allochthonous, alien or exotic species introduced to, or migrated to, an area outside of their native range. Many of these species are termed invasive because they cause ecological or socio-economic problems around the world. The number of adventive and/or invasive species among the plant feeding mite families is increasing within Tetranychidae, Eriophyidae, Tarsonemidae, Tenuipalipidae and Phytoptidae. The 2010 inventory of the adventive, phytophagous Acari of Europe included 82 species, namely 47 species of Eriophyoidea, 27 of Tetranychidae, seven of Tenuiplapidae and one of Tarsonemidae. In Serbia, 30 species of Eriophyoidea, three of Tenuiplapidae, one of Tetranychidae and one of Tarsonemidae, were recorded. Of these 35 adventive species of phytophaous mites, eight were pests of crops, six were on weeds and 21 were on ornamental plants. In the past eight years, 16 new adventive species of phytophagous mites have been recorded in Serbia: 14 eriophyoids and two species of spider mite. Of them, two eriophyoid species, Aceria kuko and Calepitrimerus bailei, and two species of spider mite, Panonychus citri and Tetranychus evansi, are pests of different crops, while eight eriophyoid species were associated with ornamental plants and trees and four were on weeds. Three adventive eriophyid species are considered promising biological control agents. Two of these species are associated with adventive and invasive weeds (Ambrosia artemisifolia and Ailanthus altissima) in Europe and one with *Taeniaterum caput- medusa*, an invasive weed in the USA. Most of these species are inconspicuous and there is a lack of data regarding adventive and/or invasive species and their distribution. In order to get a better understanding of the ecological and economic effects of introduced plant feeding mites, it is necessary to develop long-term research.

Keywords: Phytophagous mites, adventive species, invasive species, plant pests, biological control agents



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The spider mite, Tetranychus truncatus, spreads fast in mainland China

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Understanding the species assemblages of economically important spider mites is essential for their effective control. From 2002 to 2017 (two periods: 2002-2004 and 2009-2017), we surveyed 177 locations and collected 376 population samples from the field in mainland China. During 2002-2004, *T. urticae* was the predominant *Tetranychus* species with a 56% infestation frequency. Tetranychus truncatus was the second most dominant species with 15% infestation frequency. However, the dominant species has shifted from T. urticae to T. truncatus in recent years. Nine species of Tetranychus were found during the period 2009-2017. Tetranychus truncatus was the most serious pest *Tetranychus* species in almost every agricultural region in China with a 49% infestation frequency. Several mechanisms may dictate the fast spread and outbreak of *T. truncatus* in mainland China. Firstly, we found that species' niche breadth was significantly and positively associated with mite abundance. Tetranychus truncatus has the widest climate breadth and host breadth in China which may be one fundamental reason for their success in the field. Secondly, T. truncatus maintained higher genetic diversity than other Tetranychus species and this may help its adaptation to an unstable agricultural environment, e.g., host transfer and climate change. Thirdly, we speculate that southern populations originated from northern regions based on the genetic data and species distribution modeling. The increase in movement of both people and commodities such as vegetables, fruits and, flowers may have facilitated fast spread and recent outbreaks of T. truncatus in southern regions. Some other factors, such as pesticide spray programs, are also potential reasons for the shift in dominant species. The determination of the exact underlying mechanisms require long-term monitoring as a component of multi-disciplinary research effort at multiple scales.

Keywords: Tetranychus truncatus, outbreak, genetic diversity, niche breadth, China

Tetranychus okinawanus Ehara (Prostigmata: Tetranychidae) emerging as a potential invasive pest in Kerala, India

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Spider mites are serious pests of many economically important agricultural and horticultural crops of Kerala, India. Tetranychus truncatus is the predominant mite species infesting vegetable crops in the Thrissur district of Kerala. Tetranychus okinawanus, an alien species, was reported on cucumber recently in this region. Purposive sampling surveys were undertaken in different localities of central Kerala to collect and study the species composition of spider mites associated with major crops during the period 2016-2017. Morphological characterization of features viz., chaetotaxy of hysterosoma and leg (female), empodium (female) and aedeagus (male) of the slide mounted specimens collected during the survey revealed the presence of three species, namely T. truncatus, T. okinawanus and T. udaipurensis. The data generated by the study suggests that T. okinawanus may be emerging as a major pest on crops in Kerala; five new hosts, namely ash gourd, papaya, eggplant, cowpea and banana, were recorded in three districts of central Kerala. To reinforce the morphological identification of *T. okinawanus*, the *ITS2* region of rDNA was amplified and the amplicons were sequenced. The sequences obtained were subjected to a homology search with BLASTN and all the accessions showed identity as high as 99-100 % with T. okinawanus. The sequences were submitted to GenBank and accession numbers were generated. The new hosts and geographical area in which T. okinawanus was recorded in this study suggests that this alien species has the potential to become an important pest.

Keywords: Tetranychus okinawanus, aedeagus, ITS2, BLASTN, GenBank



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Population dynamics of the coconut mite, *Aceria guerreronis* Keifer, in Kerala, India

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The history of the invasion of Kerala, India by the coconut mite, *Aceria guerreronis* Keifer, dates back to the early 1990s. Within a short period, the pest took a toll on coconut farming and dependent industries of this state. The coconut trees, as well as the economy of Kerala, suffered a serious setback over the years. The current study evaluated the population dynamics of the mite on the Chowghat green dwarf variety of coconut which is highly susceptible to coconut mite infestation. The survey on coconut mite population was carried out on the Calicut University Campus and in surrounding areas from 2015 to 2017. The population density of the mite was estimated by counting the number of mites in the meristematic zone of infested nuts at biweekly intervals. A seasonal fluctuation in population density was observed as a normal trend annually with higher density during January to May and lower density during the period of June to August. Further, an overall decline in the population density was recorded during the rainy season during this study period. This phenomenon would revive coconut production and improve the economy of coconut farming and other coconut based industries in Kerala. The role of predatory mites in regulating the proliferation of the coconut mite population was also studied and will be discussed.

Keywords: Chowghat green dwarf coconut, *Aceria guerreronis*, coconut mite, population dynamics, predatory mites

Section 1.3. Understanding and preventing mite bioinvasions

International trade, biosecurity, agriculture and mites: a South African perspective

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Vast amounts of agricultural produce are traded across South Africa's borders and those of other nations, allowing contaminating organisms to be transported to new regions where they may establish and become invasive. Mites are very easily transported in this way, as detection and exclusion are difficult due to their small size and ability to survive adverse conditions. In South Africa, goods and travelers can legally enter the country via 72 official points of entry, including land borders, airports and seaports. Phytosanitation inspectors are stationed at all major entry points to prevent illegal imports and to inspect legal ones. However, in most cases the volume of incoming goods and/or travelers far exceeds the point's capacity to adequately enact existing biosecurity legislation. Mites are particularly problematic in this regard, as they require a microscopic inspection which takes additional time and trained personnel. An analysis of budwood imported to South Africa (dormant propagation material) revealed that 24% of imports were infested with arthropods, with mites accounting for 84.5% of all detections and 98% of quarantine interceptions. Of the plantfeeding mites detected, Eriophyidae were the most common (80%), followed by Diptilomiopidae (14%), Tetranychidae (3.5%), Tenuipalpidae (2%) and Tuckerellidae (0.5%). In contrast to this, proportionately few mites are recognized as quarantine pests or invasive species. Approximately 30 mite species are listed on South Africa's phytosanitary legislation, as compared to around 100 insect species. A review of quarantine lists, inspection strategies and mitigation measures, as well as increased collaboration regarding phytosanitary issues, is critically needed to improve biosecurity with respect to mites.

Keywords: Biosecurity, phytosanitary, budwood, interceptions, Acari



2-8 September 2018, Antalya - TURKEY

Of mites and islands: Preventing invasions with minimum resources

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Invasive mites represent a significant threat to agricultural crops and native flora. The Mediterranean island of Cyprus is a biodiversity hotspot with more than 140 species of endemic plants. While agriculture contributes less than 2% to the GDP of the island, farmers grow more than 100 different species of vegetables and tree crops. Cyprus lies at the crossroads of Asia, Europe and Africa, and the high volume of agricultural and ornamental plant and commodity trade increases the risk of pest invasions. Important plant feeding mites on the island include around 40 species in the families Eriophyidae, Tetranychidae and Tenuipalpidae. Global species, such as Panonychus ulmi, have never been reported from Cyprus, but only one mite survey has been conducted in the country, and that was more than 60 years ago. In the last 10 years, several new species of arthropods have established in Cyprus, most of which are highly invasive, with the report of just one mite, Panonychus citri. The current and expected future climate of the island make it prone to invasion by a number of destructive mite pests that require specialized personnel for interception at entry points. However, the high volume of plant and commodity trade facilitated by the relatively short distance from three continents, and minimum resources available for inspections, make the country highly vulnerable to new invasions. In most cases new invasions go undetected until the pest is established, meaning that measures must focus on highly expensive long term control, instead of eradication. A well-organized inspection plan for the worst invasive mites at entry points would pay dividends in the future.

Keywords: Invasions, pests, plants, islands, mites

Section 1.4. Understanding and preventing mite bioinvasions

Detection and identification of invasive mites and regulatory measures: a global update

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Mites (Acariformes, Parasitiformes) are considered one of the largest groups in Arthropoda, with estimated numbers from 3 to over 10 million species. The majority of mites are small, with most of them being from ~100 um to 1,000 um, with color tones that help to camouflage them with the environment, making them difficult to detect at ports of entry worldwide. The increased international trade in all kind of commodities, from agricultural to computer products, has resulted in increased interceptions of potentially invasive mite species. On the agricultural commodities, the most commonly intercepted, economically important intercepted mites are the plant feeders. The families Eriophyidae and Tetranychidae are often collected but collections of species in the Tenuipalpidae, Tarsonemidae, Tuckerellidae, Penthaleidae and stored-products Acaridae, e.g. bulb mites, mold mites and cheese mites, have been increasing. In addition, the species of other mite families, e.g., Tydeidae, Iolinidae, Phytoseiidae, Laelapidae, Winterschmidtiidae, Oribatidae, Galumnidae, associated with plants, wood, soil, construction materials and electronic goods and components, are being intercepted in increasing numbers. Many of these mite families include important economic pests or potential pests of crops, fruit trees, stored products, forests, ornamentals, cattle and humans. Trade from regions where there is little or no information on the local mite fauna makes it difficult to identify or prevent the accidental introduction of potentially invasive species. The most common equipment used to identify regulatory mite pests is the light microscope but preparation techniques and quality of the microscopes used may lead to misidentifications. Furthermore, the digital images obtained with such equipment can also compromise identifications. However, the use of high quality phase contrast and DIC lenses can help avoid or minimize some of these problems. In addition, user friendly, table top scanning electron microscopes (SEM) at ports of entry could help in the process of identification of a particular species and understanding its potential to be an invasive or adventive species. In addition, we will be presenting an update on the data available on the interceptions of mite species and the technologies that can be use at ports of entry to detect exotic species and therefore prevent their entry.

Keywords: Crop pests, SEM, interceptions, trade in commodities, port of entry



2-8 September 2018, Antalya - TURKEY

Rules for importation of natural enemies to Europe and secure identification: the case of Phytoseiidae

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Augmentative and classical biological control strategies are based on the introduction of natural enemies to crops, especially protected crops. These natural enemies can be exotic (originating from other continents, countries) or indigenous to Europe. Rules for the introduction/collection of these organisms exist in Europe, even for natural enemies originating in Europe as each country and sometimes each territory (for example, each island) is considered a separate entity, potentially with its own specific fauna and/or its own specific risks. The first part of the presentation will address the rules concerning the importation of natural enemies, import permits required and risk assessment systems. In order to apply these rules, correct diagnosis is clearly the key step and the one legally required by institutions. Several identification methods exist and it is usually their combinations that provides reliable information and informs the decision. The second part of the presentation will present these methods for the case of predatory mites of the family Phytoseiidae. A special focus will be done on the methodological and analytical aspects of molecular techniques. The reliability of molecular methods in diagnostics for making decisions and the associated risks will be discussed, both at species and population levels, for biological control.

Keywords: Exotic organism, biological control, morphological identification, molecular identification, European rules

Tuesday, 4 September

Kanuni Sultan Suleyman Hall

Section 1. SYMPOSIUM: Mite-plant interactions: from responses to

tolerance/resistance

Section 1.1. Mite-plant interactions

First steps in the plant responses to spider mite infestation

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Plants rely on a battery of mechanisms to detect pests and mount appropriate defences. The induction of plant defences is initiated when specific receptors detect either the presence of herbivory through the recognition of herbivore-associated molecular patterns (HAMPs), the damage incurred as the consequence of herbivore feeding, or even the presence of volatiles emitted as plant-plant cues. Among pests, the two spotted spider mite, *Tetranychus urticae*, is the most harmful phytophagous acarine since it feeds on more than 1,100 host plants and causes more than \$1 billion worth of damage annually. We focus our research on Arabidopsis responses to spider mite infestation to identify and characterize molecules involved in defence as potential alternatives to chemical control. Currently, we are interested in the cascade of short-term responses to spider mites. We have assayed transcriptional responses after the first hours of infestation. A large set of data was obtained with a robust list of differentially expressed genes. Candidate genes were selected and validated by RT-qPCR. Molecular and functional characterization of these genes is now in progress. Arabidopsis plants overexpressing or silencing these genes are being generated or accessed from publicly available collections to determine their functionality in the defence process. Leaf damage and biochemical and molecular parameters of the transgenic plants are being measured after mite feeding. In parallel, progression of the infestation, mite behaviour, mortality and the oviposition process are also being assessed. As a result, new genes involved in the perception of herbivory and in the first reactions have been identified and are being characterized. More crop species will be used for the "proof of concept" of defence pipelines.

Keywords: Plant defence genes, plant short-term-responses, *Tetranychus urticae, Arabidopsis*, herbivore-associated molecular patterns



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The SHOT family of the spider mite *Tetranychus urticae*: salivary protein genes showing fast transcriptional plasticity

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The two-spotted spider mite, Tetranychus urticae, is an extremely polyphagous herbivore, with hosts belonging to more than a hundred different plant families. Next to an elaborate detoxification system, the salivary protein repertoire of *Tetranychus urticae* is also assumed to be important for its success as a generalist herbivore. Recently, the salivary protein repertoire of *T. urticae* was elucidated and it was shown that *T. urticae* is able to manipulate plant defenses via effector proteins secreted via their saliva. Here we report on a spider mite-specific protein family that is expanded in *T. urticae*. Peptides of these proteins were identified in the *T. urticae* salivome and expression of their encoding genes was restricted to the anterior podocephalic glands, supporting the salivary origin of these proteins. As these proteins were secreted in a host-dependent manner, we designated this family as the SHOT (Secreted HOst–responsive protein of Tetranychidae) family. Intriguingly, genes belonging to subfamilies SHOT 1 & 2 are highly expressed when T. urticae is feeding on a subset of legume hosts (Fabaceae), while expression is virtually absent on the other tested hosts. Furthermore, SHOT 1 & 2 gene expression can be induced within 24 hours after host transfer, pointing towards transcriptional plasticity rather than adaptation or genetic drift. We suggest that T. urticae adjusts its salivary protein repertoire such that it can optimally cope with its host and that this plasticity is likely driven by host-derived cues. Furthermore, we investigated the occurrence of SHOT genes in related Tetranychidae and could show these to be linked to the diversity and identity of their host plants.

Keywords: Effectors, saliva, plant-mite interactions, host plant range, spider mite

Suppression of plant defences by herbivorous mites is not associated with adaptation to host plants

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Some herbivores suppress plant defences, which may be viewed as a result of the coevolutionary 'arms race' between plants and herbivores. However, this ability is usually studied in a one-herbivore-one-plant system, which hampers comparative studies that could support this hypothesis. Here, we extend this paradigm and ask whether the herbivorous spider mite *Tetranychus evansi*, which suppresses the jasmonic acid pathway in tomato plants, is also able to suppress defences in other host plants. We tested this possibility by using plants from the Order Solanales, namely tomato, Jimsonweed, tobacco and morning glory (three Solanaceae and one Convolvulaceae), and bean plants (Fabales). Firstly, we compared the performance of *T. evansi* to that of the other two most commonly found species of the same genus, *T. urticae* and *T. ludeni*, on several plants. We found that the performance of *T. evansi* is higher than that of the other species only on tomato plants. We then showed, by measuring the activity of trypsin inhibitors, and the life history traits of conspecific mites on either clean or pre-infested plants, that *T. evansi* can suppress the defences of all plants, except tobacco. This study suggests that the suppression of plant defences may occur on host plants other than those to which herbivores are adapted.

Keywords: Plant-herbivore interactions, Solanales, Tetranychidae, host-plant adaptation, jasmonic acid pathway



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Section 1.2. Mite-plant interactions

Versatility of plant-mite interactions

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Plant-herbivore interactions have evolved over long periods of time, resulting in an elaborate 'arms race' between interacting species. While specialist herbivores evolved specific strategies to cope with the defences of a limited number of hosts, our understanding of how generalist herbivores deal with the defences of a plethora of diverse host plants is largely unknown. Understanding the interaction between a plant host and a generalist herbivore requires an understanding of the plant's mechanisms aimed at defending itself and the herbivore's mechanisms intended to counteract diverse defences. Using the two-spotted spider mite (TSSM), *Tetranychus urticae* Koch as an example of a generalist herbivore, we will discuss the ability of TSSM to adapt to marginal hosts, the identification of direct plant defences against spider mite herbivory, and spider mite adaptations to them. Knowledge of plant defence mechanisms that affect mite fitness are of practical importance as it could lead to the development of new control strategies against this important agricultural pest. In parallel, understanding the mechanisms of mite counter adaptations to these defences is required to maintain the efficacy of these control strategies in agricultural practices.

Keywords: *Tetranychus urticae*, evolution of host range, mechanisms of pest xenobiotic resistance, plant-herbivore interactions, generalist herbivore

Local awareness of emergency: spatiotemporal dynamics of spider-mite herbivory on cucumber

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Upon the onset of herbivory, a cascade of events is activated leading to changes in the transcriptome, proteome and eventually the metabolome of the plant that will hinder and sometimes even kill the herbivore. These events start with the recognition of the attacker by the plant through herbivoreassociated molecular patterns (HAMPs) and via elevation of cytosolic calcium, mitogen-activated protein kinases, protein phosphorylation, production of stress-related hormones such as ethylene and jasmonates and expression of defense-response genes which finally results in adaptation of the primary and secondary metabolome, including emission of volatile organic compounds. The response cascade starts locally at the feeding site and spreads systemically throughout the plant. As the intensity of the signaling cues increases, fluxes of metabolism in the surrounding tissue will alter progressively. Although multiple genes involved in the biosynthesis of defense metabolites and regulatory factors have been identified, the spatial and temporal scale of changes in plants at the onset of herbivore attack is still poorly understood. Here we present our work on the spatial and temporal dissection of the triggered molecular responses in cucumber triggered by two-spotted spider mite herbivory by using two strategies that complement each other. Targeted and untargeted analysis of primary and secondary metabolites using different mass spectrometry platforms, key metabolites induced upon infestation and their spatial distribution and temporal changes around the site of infection were identified. Furthermore, transgenic plants expressing promotors of herbivore-induced genes that encode for the production of key metabolites and fused to light emitting reporter genes were used to follow the spatial and temporal dynamics of genes associated with herbivore infestation and/or defence metabolite formation upon mite-infestation. Our results give more insights into how plants dynamically spread the message of herbivory within 'not-yet' infested areas of a local leaf.

Keywords: *Tetranychus urticae, Cucumis stativus*, metabolome, signaling cue, volatile and non-volatile metabolites



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Fusarium solani strain K alters tomato responses against spider mites to the benefit of the plant

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Soil-borne beneficial microbes are known to be capable of protecting plants against pathogens and herbivores via the elicitation of plant responses. In this study, we evaluated the role of *Fusarium solani* K (FsK), a beneficial endophytic fungal strain isolated from the roots of tomato plants grown on suppressive compost, in altering responses to the two-spotted spider mite *Tetranychus urticae* in tomato. Defense-related genes were differentially expressed in FsK-inoculated plants after spider mite infestation compared to FsK-inoculated or spider mite-infested control plants. Spider mite performance was negatively affected on FsK-inoculated plants, with feeding damage lower than on control plants. In addition, FsK-inoculated plants attracted more predators than non-inoculated plants. Headspace volatile analysis revealed significant differences between the volatile blends emitted by FsK-inoculated plants and the control plants which were in agreement with our behavioral assays. Our results highlight the role of endophytic fungi in shaping plantmite interactions and may offer the opportunity for the development of a novel tool for spider mite control.

Keywords: Endophyte, spider mites, tomato, *Fusarium solani* strain K, *Macrolophus pygmaeus*

Effect of metal-accumulation on the performance of plants and herbivorous mites that cope differently with organic plant defences

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Some plants accumulate metals toxic to most organisms. This metal accumulation may have evolved as a defence against herbivores. However, it is yet unclear how metal-based defences interact with organic defences. To fill this gap, we studied the interactions between tomato (Solanum lycopersicum), a plant that accumulates cadmium, and two spider-mites, Tetranychus urticae and T. evansi, that differ in their effects on tomato plant defences. While T. urticae induces organic plant defences, *T. evansi* down-regulates them. We assessed how cadmium affects plant and herbivore performance by exposing tomato plants to different cadmium concentrations and then measuring plant physiological traits and the life-history traits of the spider-mites infesting those plants. The oviposition rate of both spider mites increased with low cadmium concentrations until a threshold, 0.5 mM, was reached, then it progressively decreased, reaching levels below those in cadmium-free plants. There were no effects of cadmium on the biomass, water content and carbon/ nitrogen ratio of the plant, indicating no costs of metal accumulation for the concentrations used. Additionally, we tested how organic defences interacted with the effect of the metal on herbivores by exposing plants to both metal and herbivores. Spider mites had lower oviposition rates on plants previously infested with *T. urticae* and higher oviposition rates on plants pre-infested with T. evansi, as compared to clean plants. These differences, together with the effects of the pattern of production of proteinase inhibitors on herbivory, confirm that *T. urticae* upregulates and *T. evansi* supresses plant defences. The pattern was the same, irrespective of the cadmium concentration the plant was exposed to. Our results indicate that herbivores with contrasting responses to organic defences respond similarly to metal accumulation. Additionally, their effect on organic plant defences is unaffected by cadmium accumulation, suggesting that there is no interaction between these types of defences, at least within the range of the concentrations used.

Keywords: Plant defences, metal accumulation, *Tetranychus evansi, Tetranychus urticae, Solanum lycopersicum*



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Response of caraway, *Carum carvi* L., to *Aceria carvi* Nal. (Acari: Eriophyidae) infestation: is phytoplasma involved?

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Caraway, Carum carvi L., is a traditional minor crop in several European countries. Its seeds are used in cuisine and essential oils extracted from the seeds are used in the pharmaceutical industry. The crop is attacked by Aceria carvi Nal., a gall-inducing eriophyid mite. However, very little is known about the A. carvi-C. carvi interaction. The first objective of our work was to investigate symptoms of A. carvi infestation and its effects on caraway growth and the yield of seeds. The second objective was to search for phytoplasmas in plant samples infested by A. carvi. The study was carried out in commercial caraway fields in the Czech Republic and a small experimental plot at the Faculty of Agriculture in České Budějovice, also in the Czech Republic. Molecular techniques, namely the amplification of 16S rDNA by polymerase chain reaction (PCR) with phytoplasma specific primers R16F2n/R2, followed by restriction fragments length polymorphism analyses (RFLP), and also transmission electron microscopy (TEM), were used for the detection and identification of phytoplasma Several symptoms of A. carvi infestation, specifically phyllody and virescence, and less often the proliferation of witches broom, were observed on flower organs: Infested plants were smaller, had a lower yield of seeds but had more umbels than healthy plants. Artificial infestation of young plants at the vegetative stage (first year of growth) was achieved by deliberate transfer on caraway umbels heavily infested by A. carvi. The infestation resulted in leaf malformations in most plants one month later. However, the molecular analysis of the symptomatic plants did not reveal the presence of phytoplasma. In contrast, the presence of 'Candidatus Phytoplasma asteris' (ribosomal subgroup16SrI-B) was confirmed by both PCR/ RFLP analysis and TEM in wild caraway with similar symptoms but no mites.

Keywords: Gall-inducing mite, symptoms, damage, phyllody, virescence

Section 1.3. Mite-plant interactions

Response of Medicago truncatula plants to drought and spider mite attack

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Biotic and abiotic stresses force plants to optimize their defense mechanisms with the production of reactive oxygen and nitrogen species (RONS) that represent a major defensive response of plants. In the current work, we studied the simultaneous impact of two key stresses, drought and spider mite attack (*Tetranychus urticae*) on *Medicago truncatula* plants. We analyzed the biosynthesis of key RONS representatives and measured the H_2O_2 content of leaves infested by spider mites and neighboring leaves to investigate the local and systemic effects of the two stresses on the nitro-oxidative response. Spider mite feeding on the leaves of the plant did not cause significant cellular damage whereas lipid peroxidation (MDA content) was higher in plants under drought stress and plants under combined drought stress and spider mite feeding than in control plants. Production of hydrogen peroxide (H_2O_2) was significantly induced in plants under drought and spider mite attack, with the highest levels detected on the feeding leaf (local response). Real-time RT-PCR analysis of the expression of genes implicated in the metabolism of RONS (NR, PAO, DAO, AOX) pointed to different patterns of regulation between abiotic and biotic stress, and their combination. Exposure of plants to both drought stress and attack by spider mites affected mainly the local nitro-oxidative response of *Medicago truncatula*.

Keywords: Biotic stress, abiotic stress, spider mites, RONS, climate change



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Induced tomato plant resistance against *Tetranychus urticae* triggered by the phytophagy of *Nesidiocoris tenuis*

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The zoophytophagous predator *Nesidiocoris tenuis* (Reuter) (Hemiptera: Miridae) is capable of inducing plant defences in tomato due to its phytophagy. These induced defenses, which include the release of herbivore-induced plant volatiles (HIPVs), has been proven to affect the oviposition behavior and to reduce the subsequent performance of some tomato pests. However, the effect of these plant defences mediated by *N. tenuis* on the plant selection, development and reproduction of the two spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae) remains unknown. A greenhouse experiment was conducted to determine whether the defence induction mediated by *N. tenuis* had a xenobiotic effect on *T. urticae*. In this field experiment, the infestation of *T. urticae* was significantly reduced by 35% on those plants previously activated by the feeding punctures of *N. tenuis* when compared to the control. The jasmonic acid signaling pathway was significantly upregulated and the concentrations of two plant protein inhibitor markers were higher on activated plants than in the control which could explain the decreased life history traits of *T. urticae* on these activated plants. These results can serve as a basis for the development of new management strategies for *T. urticae*, based on the resistance mechanisms induced by the phytophagy of *N. tenuis*.

Keywords: *Tetranychus urticae*, *Nesidiocoris tenuis*, phytophagy, plant defence, xenobiotic

Reducing tomato leaf hairs promotes herbivory yet also improves biological control such that the plant ultimately is better protected

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Plant hairs or trichomes play an important role as a direct defence against herbivores by entrapping them or by releasing noxious chemical compounds. However, they can also be detrimental to natural enemies used in biological control, in particular the smaller ones such as predatory mites. The predatory mite, Phytoseiulus persimilis, is a well-known biocontrol agent of the two-spotted spider mite, Tetranychus urticae. However, in tomato (Solanum lycopersicum) crops control by P. persimilis is rather limited due to the presence of tomato trichomes. Here, we tested a range of tomato genotypes with abnormal trichomes for their compatibility with herbivorous and predatory mites. Under laboratory conditions, the alteration of the trichome phenotype promoted the reproductive performance of the spider mite. However, the predatory mite could move faster on these plants and did not get entrapped on the distorted trichomes on the stems, as they did on normal tomatoes. Subsequently, we evaluated the population dynamics of prey and predator on a subset of tomato trichome mutants in a greenhouse for a period of 6 weeks. Our results showed that the predatory mites were able to suppress spider mite populations very efficiently on tomato plants with a distorted trichome phenotype and that they reached higher population densities. Overall, we showed that reducing the level of a direct plant defence, i.e., glandular trichomes, may promote herbivory. However, this effect is more than compensated by enhanced biological control that results in a much better protected crop.

Keywords: Spider mites, phytoseiids, predatory mites, plant defences, population dynamics



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Two phytophagous and two predatory mites on tomatoes: changes in behavior?

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Most studies that have evaluated the consequences of herbivory by mites have considered a single species, while a few studies have used a number of species feeding simultaneously. Tomato plants may suffer from attacks by different species of herbivores which feed on different structures and/ or tissues of the plant. In this study, we evaluated some consequences of the interactions between two phytophagous mites and how these affected the responses of two predatory mites. Specifically, we used as phytophages the tetranychid Tetranychus urticae, a spider mite, and the eriophyoid mite Aculops lycopersici (russet mite), and as predators, two phytoseiids, namely the specialist, Phytoseiulus persimilis, and the generalist, Neoseiulus californicus. The objectives of the study were to examine: a) the induced direct defence response of tomato plants to attack by the russet mite alone, the spider mite alone and by the two mites together; and b) the consequence of these interactions on the third trophic level, which was the attraction of predatory mites to volatile organic compounds emitted from tomato plants, under different scenarios. The olfactory choice of each predatory mite to tomato plants infested by the spider mite alone, russet mite alone, or by both herbivores, was assessed at low population density (10 adult spider mites and 100 russet mites/ leaflet) and at high population density (20 adult spider mites and 300 russet mites/leaflet). Both Phytoseiulus persimilis and N. californicus mainly moved towards plants attacked by T. urticae alone. We also report on the headspace volatiles emitted from attacked tomato plants.

Keywords: Tetranychus urticae, Aculops lycopersici, Phytoseiulus persimilis, Neoseiulus californicus, olfactory response

Section 2. Soil acarology

An entomopathogenic nematode as a potential biological control agent for vector mites and vector borne diseases

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The role of oribatid mites as excellent transmitters of cestode diseases in domesticated animals is well established. Farm workers may therefore be exposed to the health hazards associated with cestode infection. Therefore control strategies against cestode diseases in farm animals are necessary. In depth laboratory and field studies helped to disclose the role of entomopathogenic nematodes, viz. *Steinernema* and *Heterorhabditis*, as potential control agents against the oribatid mite vectors. The study was initiated by introducing the above two species of entomopathogenic nematodes from cultures into rearing chambers of the vector mite maintained on fungal colonies. Subsequent to introduction into the culture cells, the nematodes attempted to establish contact with the mites by climbing over the notogaster, though the mites resisted several times. Finally the nematodes successfully pierced the body of the mites through their lateral integument and reached their body cavity. Simultaneous with multiplication of the nematode within the body cavity of the mite, the latter became lethargic and died in due course. The mechanism of penetration into the internal organs of the mite, duration of its development, multiplication, death of the mite and emergence of the nematode are discussed.

Keywords: Vector borne disease, *Galumna flabellifera orientalis*, entomopathogenic nematode, cestode parasites, Kerala



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I can't live without you (of the opposite sex): *Parasitus* aff. *fimetorum* (Mesostigmata: Parasitidae), a mite that requires a partner to complete its development

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Parasitus aff. fimetorum is frequently found in rose crops and associated vegetation in the Bogotá Plateau (Cundinamarca, Colombia). Preliminary observations indicated that it is commonly found aggregated in laboratory rearing units, feeding voraciously on Frankliniella occidentalis (Thripidae), a common rose crop pest, laying a relatively large number of eggs. Apparently, individuals do not reach the adult stage when kept in isolation. The objective of this study was to confirm if this species needs company to complete its development, and the influence of diet on its biology. The variables considered in this study included three types of aggregation: 1) mites always maintained in isolation; 2) each deutonymph maintained together with another deutonymph and adult female maintained with a male for 24 h; and 3) mites paired continuously. Because preliminary trials showed that P. aff. fimetorum did not feed on F. occidentalis during its immature stages, immatures were always fed only with nematodes. Adults of all aggregation types were fed either: pre-pupae and pupae of F. occidentalis (T), free-living rhabditid nematodes (N), or a combination of those (NT). About 87% of the mites of aggregation type 1 died as immatures, about 50% of which were deutonymphs, which lasted up to 56 days. Immature mortality was 24% and 19% for the aggregation types 2 and 3, respectively. The duration of the deutonymphal stage of mites of aggregation type 3 was significantly lower than that of aggregation type 2. Mites of aggregation type 3 had higher biotic potential when the diet included nematodes. However, when fed solely with F. occidentalis, the biotic potential was statistically the same as for mites of aggregation type 2 whose diets included nematodes. These results showed the need for femalemale interaction to allow complete immature development, and repeated insemination and/or the need for nematode availability in the diet.

Keywords: Parasitidae, Colombia, biological control, aggregation, mite diet

Taxonomic studies on oribatid mites of the superfamily Galumnoidea (Acari: Oribatida) in Japan

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Since the first description of four new species by Aoki (1961), 10 genera and 48 species of oribatid mites in the superfamily Galumnoidea have been reported from Japan. In this study, we focus on three genera in Galumnoidea, *Neoribates* Berlese, 1915, *Trichogalumna* Balogh, 1960, and *Cosmogalumna* Aoki, 1988. Species of the first two genera are widely distributed around the world and are found in many places all across Japan. Due to this widespread distribution, members of these two genera have been reported in ecological papers, in which, however, they tend to be left unidentified to species. On the other hand, the other genus, *Cosmogalumna*, has so far been reported only from the south-western islands of the country. In total, we obtained more than 1,200 individuals of oribatids from 14 sampling sites round Japan. We describe and illustrate in detail seven species (five new and two previously known), from mature individuals.

Keywords: Galumnid mites, morphology, oribatid, SEM, taxonomy



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Mesostigmatid mites (Acari: Mesostigmata) from soils of rose crops and natural vegetation on the Bogotá high plateau, Colombia

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Mesostigmatid mites are common predators in the soil, and some of these have been used as biological control agents of pest arthropods. Their use for that purpose in rose crops in Colombia is highly desirable, to complement the adopted pest management strategies. The first step for the establishment of a program for their use is to know their identity. The objective of this study was to determine the species of non-Uropodina Mesostigmata present in rose crops and in the surrounding secondary vegetation of representative fields on the Bogotá Plateau (Cundinamarca). The study was conducted between August 2015 and December 2016 in four greenhouse rose plantations at Nemocon, Tocancipa Cogua and Guasca, and in patches of secondary vegetation next to the latter two localities. Twenty soil samples were taken every two months from each area. Mites were extracted from the samples by using Berlese funnels and mounted with Hoyer's medium. At all sites, mites were most numerous in months with higher rainfall. Deutonymphs were found in higher proportions than any other stages in rose plantations, while adult females were almost invariably found in higher proportions in areas of secondary vegetation. In both rose cultivation and natural vegetation, Parasitidae and Laelapidae were the dominant families throughout the study, but high proportions of Veigaiidae and Blattisociidae were also observed in secondary vegetation. Species of Parasitus and Gaeolaelaps were the most dominant in all areas and at all sampling times. In rose plantations, the second dominant genus was Cycetogamasus (Parasitidae), while in secondary vegetation were Lasioseius (Blattisociidae), Paragamasus, Pergamasus (Parasitidae) and Veigaia (Veigaiidae). The faunistic composition determined in this study is rather different from that of the surrounding neotropical regions, given the high elevation of the study sites (2,460-2,777 m) and the characteristic rose cultivation selection pressure that involves the frequent use of pesticides.

Keywords: Parasitidae, Laelapidae, Veigaiidae, mite species, Andean region

Soil-inhabiting mites of the family Parasitidae (Mesostigmata: Gamasina) from the central and northwestern regions of Iran, with a new record

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During sampling conducted from 2014 to 2016 in different locations of three provinces of Iran, including the Arasbaran Forests in the East Azerbaijan Province, Kashan and adjacent areas in Isfahan Province, and Qom and adjacent areas in Qom Province, mites of the family Parasitidae were collected from soil, leaf-litter and dung by using the Berlese-Tullgren funnel method. The specimens were cleared in lactophenol or Nesbitt's solution and mounted in Hover's medium on microscope slides. A total of six species in four genera of the two subfamilies, Parasitinae and Pergamasinae, were identified as follows, with Neogamasus unicornutus recorded for the first time from Iran (items given for each species are in the respective order of developmental stage, locality, specific site and altitude [m a.s.l.], seperated by a semicolon): 1) Parasitinae Oudemans, 1901: Arasbaran: Parasitus consanguineus Oudemans and Voigts, 1904 (deutonymphs; Asheqloe-Aynalou; oak leaf-litter; 763); *Parasitus hyalinus* (Willmann, 1949) (\bigcirc and deutonymphs; Jananlou; oak forest soil; 395–741); <u>Kashan:</u> Eugamasus sp. (♀; Niyasar; decomposing lumber; 1584); *Neogamasus unicornutus* (Ewing, 1909) (♀; Niyasar; leaf-litter; 1735); *Parasitus consanguineus* (deutonymphs; Hanjan, Jowshagan, Niyasar, Oamsar; farm, orchard and roadside soil, plant-litter; 1400–1625); Parasitus fimetorum (Berlese, 1904) (deutonymphs; Abyaneh, Jowshagan, Mashhad Ardehal, Niyasar; farm, orchard and roadside soil, dung, plant-litter; 1390–1700); Parasitus hvalinus (\textsq and deutonymphs: Hanian, Oamsar; farm, orchard and riverbank soil: 1550–1625); Oom: Parasitus consanguineus (deutonymphs; Alghadir Park of Oom, Salafchegan; soil; 882-996), Parasitus fimetorum (deutonymphs; Alavi Park of Qom, Kahak; alfalfa farm soil, dung; 921–972), *Parasitus hyalinus* (and deutonymphs; Alavi, Alghadir and Pardisan parks of Qom; soil; 966–1000); 2) Pergamasinae Juvara-Bals, 1972: Arasbaran: *Paragamasus* sp. (♀; Aynalou; oak forest soil; 1353-2098).

Keywords: Acari, edaphic mites, fauna, distribution, altitude



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Section 3. Aquatic acarology

Dermal glands of the fresh-water mite *Limnochares aquatica* (L., 1758) (Acariformes, Limnocharidae) and their functional and evolutionary significance

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The presence of dermal glands is thought to be a synapomorphic character of fresh-water mites evolved independently and *de novo* after the invasion of fresh-water basins by their ancestors. Exact functions of dermal glands remain unknown but it is supposed that generally they function in defending against predators. If in the vast majority of water mites dermal glands have undergone oligomerization, in L. aquatica, by contrast, they originally multiplied and are scattered freely at the mite body surface. The dermal glands of L. aquatica were studied using SEM and TEM methods at different stages of activity at the Collective Resource Center in ZIN RAS (http://www. ckp-rf.ru/ckp/3038/?sphrase id=8879024). The opening of the glands is saddle-like, composed of several tightly packed cuticular folds and oriented freely to the axis of the mite body. A small cuticular spine or, rarely, neotrichial seta, occupies one pole of the orifice. From inside, the intraalveolar cavity of the glands has a complex, cuticular armature. The glands are composed of cells situated around the intra-alveolar cavity and that are shaped like a fig-fruit with the base facing the body lumen. Three stages of the gland conditions may be recognized, depending on their secretory activity: (i) glands without secretion, with highly folded cells walls and numerous microtubules within the cytoplasm, (ii) glands with an electron-dense granular secretion in the expanded vacuole, and (iii) glands having extruded secretions and possessing giant, empty vacuoles bordered with slim, cytoplasmic strips on the outside. Summer mites mostly show the first gland types whereas winter mites, conversely, more often demonstrate the second and the third types. Regeneration of the glands after secretion looks problematic because they lack cambial cells.

Keywords: Water mites, Limnocharidae, dermal glands ultrastructure, secretion

Acknowledgement: This study was supported by the RFBR (Grant number: 18-04-00075-a)

New records and a checklist of marine mites of Turkey

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There are two mite families, Halacaridae Murray, 1877 and Pontarachnidae Koenike, 1910, that inhabit the marine environment. They are exclusively small and meiobenthic, with the adult body length less than 2 mm and covered by chitinous cuticle. The family Halacaridae is represented by 64 genera and more than 1,100 known species, while the Pontarachnidae family is represented by only 2 genera and 52 known species worldwide. The investigation of the marine mites of Turkey only started at the beginning of the twenty first century. According to the published records, 34 halacarid and 7 pontarachnid species have been reported from the Turkish coast. In the present paper, a checklist of marine mite species is provided. This paper also includes 11 new halacarid records in the genus *Copidognathus* Trouessart, 1888, and 4 new pontarachnid records in the genera *Litarachna* Walter, 1925 and *Pontarachna* Philippi, 1840, from the Levantine Sea coast at Antalya, Turkey.

Keywords: Acari, Halacaridae, Pontarachnidae, Turkey, new records



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Thursday, 6 September

Osman Gazi Hall Section 1. SYMPOSIUM: Ticks and tick-borne diseases Section 1.1. Ticks and tick-borne diseases worldwide Plenary lecture

Changing paradigms of tick-borne rickettsioses

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Our understanding of vector-pathogen relationships and processes governing natural cycles of tick-borne pathogens to a large degree is based on general paradigms suggested decades ago. Originally advanced as working hypotheses, some of these ideas were accepted by the scientific community as generalizable facts and after numerous reiterations in scientific papers, reviews and textbooks became well-known and rarely challenged axioms. The invention of modern molecular and serological methods allows us to reexamine the generality of some of those commonly accepted paradigms related to tick-borne rickettsial pathogens. In this presentation, I will summarize the existing evidence supporting or contradicting several such axioms including the detrimental effects of pathogenic *Rickettsia* spp. on their vectors, transovarial interference (known as the "East Side Hypothesis") between pathogenic and endosymbiotic rickettsiae, and the requirement for prolonged rickettsial reactivation in the tick-vector before it becomes infectious to the vertebrate host. Although several laboratory attempts at the introduction of certain strains of Rickettsia rickettsii or R. conorii into tick colonies resulted in profound deleterious effects, the naturally infected ticks maintain these and other species of pathogenic *Rickettsia* quite successfully without noticeable increase in mortality. Our recent experiments showed no significant difference in the frequency of vertical transmission of R. rickettsii between A. americanum infected with and free of R. amblyommatis, thus contradicting the hypothesis of transovarial interference. Results of yet another study indicate that Rickettsia present in unfed ticks does not necessarily require a long reactivation period and infected ticks are capable of transmitting the infectious pathogen virtually as soon as they attach to the host. Together, these data demonstrate that processes and mechanisms governing the natural cycles of tick-borne rickettsiae are neither the same across various Rickettsia and vector species nor unidirectional.

Keywords: Ixodidae, vectors, tick-borne, *Rickettsia*, transmission

Plenary lecture

Seasonal activity of *Ixodes inopinatus* and *Ixodes ricinus* and prevalence of pathogens in a sympatric focus in south-eastern Germany

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Ixodes ricinus, an important tick vector of Borrelia burgdorferi s. l. and tick-borne encephalitis (TBE) virus, was considered to occur in Europe and in northern Africa. Ixodes inopinatus, a recently described species, could have been historically confused with and erroneously reported as I. ricinus in parts of Spain, Portugal and northern Africa. In 2016, I. inopinatus was first detected also in south-eastern Germany. To the present, no data is available on the seasonal activity and prevalence of pathogens in this species. In 2017, we collected ticks monthly by flagging in Immenstetten in south-eastern Germany. A total of 1,124 ticks were collected and morphologically identified as I. inopinatus (415/1,124) and I. ricinus (579/1,124). One hundred and thirty of 1,124 (11.5%) could not be identified as they showed morphological features of both species. Ixodes inopinatus was active from March to October, with a peak for males and nymphs in April and a peak for females in July. These first data on the seasonal activities of the two species imply that the activity period of *I. inopinatus* and *I. ricinus* differs in particular developmental stages. All 994 specimens of *I. inopinatus* and *I. ricinus* were tested individually for *Rickettsia* spp. and TBE virus. A total of 83/994 (8.3%) ticks (34/415, 8% I. inopinatus; 49/579, 8.4% I. ricinus) tested positive in screening panRick PCR. Fifty of 83 (30 *I. ricinus* and 20 *I. inopinatus*) were positive in R. helvetica specific qPCR. Thirty three of 83 were negative either due to low DNA amount or due to different Rickettsia species, probably R. monacensis. Two I. inopinatus (2/415; 0.5%) and two *I. ricinus* (3/579; 0.5%) specimens tested positive for TBE virus. This is the first report about *I. inopinatus* activity in comparison to *I. ricinus* activity from a location where the species are sympatric. Furthermore, our data showed that *I. inopinatus* can carry the TBE virus and Rickettsia spp., namely Rickettsia helvetica and Rickettsia monacensis, and therefore provide the first evidence for a potential medical and veterinary role of this tick species.

Keywords: *Ixodes inopinatus*, *Ixodes ricinus*, seasonal activity, tick-borne encephalitis, *Rickettsia* spp.



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Vectorial capacity of *Rhipicephalus sanguineus* and *Rhipicephalus turanicus* in Israel

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Rhipicephalus sanguineus and R. turanicus are the most prevalent tick species in Israel and they can be found in all geo-climatic areas of the country, sometimes on the same host. Both species are either known or suspected vectors of a variety of bacterial (Rickettsia, Ehrlichia and Anaplasma) and protozoal diseases (Babesia and Hepatozoon) of medical and veterinary importance. For years, Rickettsia conorii was considered the primary pathogen of spotted fever group rickettsioses (SFGR) transmitted by R. sanguineus, the causative agent of the Mediterranean spotted fever in humans. Rickettsia conorii is also being found in R. turanicus so it can be assumed that this species is also acting as a vector. Rickettsia massiliae is suspected of causing clinical spotted fever in humans and it serologically cross-reacts with R. conorii antigen. Physicians should be aware of the possible exposure of local communities and travelers to this Rickettsia sp. since a large percentage of R. sanguineus and R. turanicus ticks screened carry this rickettsial DNA. Clinicians should be aware that diseases caused by R. massiliae, Candidatus Rickettsia barbariae, as well as Anaplasma phagocytophilum and Anaplasma platys, that were previously thought to be present only outside of Israel, may occur in residents who have not necessarily traveled overseas.

Keywords: Ixodidae, *Rhipicephalus*, vector, *Rickettsia*, *Ehrlichia*

Blood meal analysis and what it tells about the TBE virus natural transmission cycle

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Tick-borne encephalitis is the most important disease of the human central nervous system in Europe with the number of infections increasing. The causative agent, TBEV, is a flavivirus transmitted by ticks. The associated vector of the European subtype is *Ixodes ricinus*. TBEV-Eu is mainly endemic in Central Europe, as well as the Baltic States and Scandinavia. Recently more and more cases have been reported from regions which had been considered free of TBE. Phylogenetic analyses of the E gene showed a diverse pattern of clusters containing virus isolates with high sequence identities that were sampled in distant regions. It is unclear how TBEV is transmitted over long distances; it cannot be explained by phylogenetic analysis and the so far described natural transmission cycle alone. Migrating birds have been incriminated as possible transfer vehicles for ticks and TBEV but there is not enough supporting evidence to date. For a better understanding of the TBEV transmission cycles it is crucial to identify the interactions of ticks and hosts. Therefore, the source of TBEV detected in single ticks will help to better understand the transmission cycle and its interactions in natural foci. It is possible to find the DNA of a tick's last blood meal, even after the tick has developed to the next stage. Therefore, we used PCR to identify the last blood meal host of ticks. The highly sensitive real time PCR based on the 12S mtDNA of vertebrates uses three different TaqMan probes to distinguish between mammals, birds and rodents. For deeper analysis of the exact species, a second conventional PCR based on the same fragment was used. The first data showed the correct identification of the blood meal sources of ticks that had been collected manually from birds and mammals.

Keywords: TBEV, ticks, blood meal, TBEV transmission cycle, vector-host interactions



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Taxonomic analysis of *Hyalomma anatolicum* based on morphological and molecular characteristics

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Recently, the taxonomic statuses of *Hyalomma anatolicum anatolicum* and *Hy. anatolicum excavatum* were elevated to species level morphologically. However, there still many unresolved issues. In 2016 and 2017, many ticks of Pakistan and China were analyzed morphologically and molecularly. The results suggested that ticks from Pakistan were typical *Hy. anatolicum*, while many from China were intermediate between *Hy. anatolicum* and *Hy. excavatum* morphologically. Molecular analysis indicated that three gene sequences of ticks from Pakistan and China were 99-100% identitical. Further molecular analysis showed that the identity of accurate *Hy. excavatum* ticks from Israel and Tunisia was 97.3-98.2% (16S rDNA), 95.9-97.6% (COI) and 100% (ITS2) to *Hy. anatolicum*, which is higher than that between other separate tick species. Therefore, there are indications of small differences between *Hy. anatolicum* and *Hy. excavatum* morphologically and molecularly. Additional studies, especially the molecular analysis of more *Hy. excavatum* ticks and hybridization experiments should be undertaken to confirm whether they are separate species or subspecies.

Keywords: *Hyalomma anatolicum*, *Hyalomma excavatum*, taxonomic status, morphology, molecular analysis

Section 1.2. Tick biology and physiology

Active water vapor uptake in unfed and engorged *Dermacentor marginatus* (Acari, Ixodidae)

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Active water vapor uptake from unsaturated air is the principal source of water for unfed ticks in a mostly dehydrating atmosphere, i.e., at ≤99% RH. Engorged larvae and nymphs of at least some species in the genera *Ixodes*, *Haemaphysalis* and *Argas* are capable of gaining atmospheric water in this way. The critical lower threshold for this oral process is usually 80-85% RH. It is unknown, however, whether engorged *Dermacentor* ticks are able to do so. This was investigated by exposing unfed and engorged immatures and engorged males of the Eurasian, 3-host tick D. marginatus sequentially to low and high RHs and weighing them intermittently on a microbalance or continuously on a recording ultramicrobalance. Usually, active water vapour uptake results in a measurable body mass gain in ticks and some other terrestrial arthropods. Partially dehydrated, unfed D. marginatus larvae and nymphs compensated for water losses by active water vapour uptake at 95% RH. However, engorged larvae did not. There was also no evidence of active water vapour uptake in engorged nymphs when they were weighed intermittently. However, when their body mass was recorded continuously there were relatively short phases with distinct gains, which suggests that active water vapour uptake occurs in the engorged nymph but is masked for most of the time, particularly by a high rate of spiracular water loss. Engorged D. marginatus males were also found to be capable of active water vapour uptake. These results will be briefly discussed in an ecological context.

Keywords: Engorged, immature, spiracle, ticks, water vapour uptake



2-8 September 2018, Antalya - TURKEY

The role of three enzymes in embryonic development of the tick, Haemaphysalis longicornis

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In the current study, the mRNA expression profiles and the enzymatic activity of cathepsin B, cathepsin D and acid phosphatase were investigated by quantitative relative real-time PCR and enzymatic assays during the embryonic development of the tick, *Haemaphysalis longicornis*. The results revealed that all three enzymes were expressed through the whole embryonic development period. Both cathepsin B and acid phosphatase transcripts were accumulated during the first four days, with cathepsin B reaching its highest level of expression on day 5, whereas the peak expressions of acid phosphatase and cathepsin D occurred on day 11. The highest activity of cathepsin B was observed at the first day of egg development, whereas cathepsin D reached its highest activity on day 13. Acid phosphatase activity increased gradually during the first five days, and then remained stable until the end of egg development. To assess the enzymes function in tick embryogenesis, we injected double-stranded RNA (dsRNA) into engorged females to obtain gene-specific silencing in eggs. The hatchability of the eggs produced by engorged females injected with cathepsin B was not significantly different from the controls which were injected with GFP dsRNA), but the group injected with acid phosphatase dsRNA was significantly lower (P < 0.05) than the controls, suggesting that acid phosphatase may play an indispensable role in embryonic development. The above results indicate the importance of the three enzymes, cathepsin B, cathepsin D and acid phosphatase, during the embryonic development of H. longicornis, and imply that they play multiple roles in embryogenesis.

Keywords: *Haemaphysalis longicornis*, embryonic development, cathepsin B, cathepsin D, acid phosphatase

Acknowledgements: This work was supported by the National Natural Science Foundation of China (Grant No. 31672365) and Graduate Student Innovation Foundation of Hebei Province (Grant number: sj2016011).

Cloning and characterization of two defensin-like antimicrobial peptides from the tick, *Hyalomma asiaticum*

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The tick, Hyalomma asiaticum, which is widely distributed in north-west China, mainly inhabits the desert and semi-desert areas with *Populus euphratica* and weed shrub. They can parasitize cattle, sheep, horses, wild boar and Bactrian camels, and occasionally attach to humans. The tick can spread a variety of natural foci diseases, including Xinjiang hemorrhagic fever, O fever and tropical theileriosis. Defensin is a class of antimicrobial peptides that play an important role in innate, biological immunity. In this study, two novel genes were cloned from a constructed cDNA library of H. asiaticum, with their full-length cDNA being 219 bp and 222 bp. The alignment of their amino acid sequences with other tick defensins showed a similarity of 53%~82%, and hence they were named Ha-defensin-1 and Ha-defensin-2. The numbers of amino acids in the mature peptides were 37 and 38, respectively, and their theoretical pI values were 9.08 and 9.54, respectively. In addition, the prokaryotic expression and functional analyses of Ha-defensin-1 and Ha-defensin-2 were carried out. The results showed that the recombinant proteins had antibacterial activity against Gram-positive bacteria, Gram-negative bacteria and fungi. The antioxidant experiments with their recombinant proteins showed scavenging ability for ABTS++ and DPPH • free radicals. The hemolytic activity test showed the hemolysis rates of the recombinant proteins to be 5.58% and 6.39%, respectively. The above results lay a foundation for revealing the innate immune mechanisms of ticks and developing new biological control agents.

Keywords: *Hyalomma asiaticum*, defensin, prokaryotic expression, antimicrobial assay, innate immunity

Acknowledgements: This work was supported by the National Natural Science Foundation of China (No. 31472050, No. 31071979), the Natural Science Foundation of Hebei Province (No. C2018205054) and the Hebei Introduction Foundation for Returned Overseas Scholars (CL201716).



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Life cycle parameters of two common cattle tick species, *Amblyomma integrum* and *Rhipicephalus microplus*

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Amblyomma integrum and Rhipicephalus microplus are hard ticks infesting mainly cattle and buffalo. Biological data on the life cycle of the two species were collected by experimental infestation on New Zealand white rabbits under controlled laboratory conditions (RH = 70%-80%, $T = 27 \pm 1$ °C). Wild caught females were collected, allowed to oviposit under laboratory conditions and the life cycle parameters, namely latent period, oviposition, feeding and moulting periods, were recorded. The Mean Reproductive Efficiency Index (REI) and Reproductive Aptitude Index (RAI) were calculated. Oviposition started after a 10-25 day and 5-8 day latent period for A. integrum and R. microplus, respectively. The number of eggs laid varied; A. integrum laid a higher number of eggs (55-7,389) within a longer period (2-35 days) while R. microplus laid fewer eggs (19-1,535) within a shorter period (1-11 days). The larvae of A. integrum hatched after 31–105 days, fed for 4-11 days, dropped off and moulted into nymphs within 10-16 days. Nymphs fed for 4-8 days, dropped off and moulted into adults after 11-25 days. The three-host life cycle of A. integrum was completed within 74-245 days; however, the laboratory hatched females did not feed on the rabbits. The parasitic phase of R. microplus, a one host tick, however, was confined to larval engorgement to nymphal moulting (8-14 days) and the non-parasitic phase (29-57 days) including the incubation period (22-31 days). Only the larvae of R. microplus fed and moulted on the host. Neither the nymphs nor adults fed on the rabbits, therefore the life cycle of R. microplus was not completed under controlled conditions. The REI/RAI for A. integrum and R. microplus were 3.6/1.1 and 8.3/5.1, respectively. Rabbits are hosts for immature stages of the two species but not for the mature stages.

Keywords: Ticks, Sri Lanka, life cycle, *Amblyomma integrum*, *Rhipicephalus microplus*

Acknowledgement: The authors are grateful for the financial assistance received from the National Research Council of Sri Lanka (Grant Number: 11-44)

Section 1.3. Tick epidemiology and systematics

Human otoacariasis in Sri Lanka: Tick species associated and risk factors

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The presence of ticks or mites in the external auditory canal is known as otoacariasis and it is a common parasitic otopathy reported in some parts of the world. Studies on intra-aural tick infestations in Sri Lanka are sparse. We investigated the tick species associated with otoacariasis, and their distribution in different agro-climatic zones of the country. Later, risk factors of otoacariasis were determined using a case control study in two selected districts with high tick infestations. Villagers were visited at home and interviewed using a pre-tested questionnaire. Tick collections were done in five districts: Anuradhapura (low country dry zone), Kandy (up country intermediate zone), Kurunegala (low country intermediate zone), Nuwara Eliva (up country wet zone) and Ratnapura (low country wet zone). Of the five districts, the highest number of patients with otoacariasis was reported from Kandy (33.8%), followed by Ratnapura (22.5%). The lowest number was recorded from Nuwara Eliya (8.2%). Five species of ticks, Dermacentor auratus, Rhipicephalus sanguineus, Hyalomma isaaci (formerly Hy. marginatum isaaci), Haemaphysalis bispinosa and Otobius megnini, were recorded lodging in the human ear. Almost all of them (99.1%) were nymphs; only four specimens (0.9%) were adults (three males of D. auratus and one male of R. sanguineus). The most common intra-aural tick species was D. auratus which constituted 90.6% of the collection and was recorded in all five districts. The rest of the collection was represented by the other four species at very low percentages. A case control study carried out in Kandy and Anuradhapura districts showed that involvement in outdoor activities is a risk factor for otoacariasis in both districts while the presence of wild animals around the house and the presence of household animals posed a risk for those in Kandy and Anuradhapura district, respectively.

Keywords: Otoacariasis, ticks, risk factors, Sri Lanka, otopathy

Acknowledgement: The authors thank the National Research Council of Sri Lanka for providing financial assistance (Grant No. 11-44)



2-8 September 2018, Antalya - TURKEY

A survey on cattle hard ticks fauna in Maragheh, Iran

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Ticks, which are the most important ectoparasites, cause heavy economic losses to the livestock industry, including by the transmission of viral, rickettsial, bacterial and protozoal diseases. The Ixodidae family is one of the most important tick families infesting domestic animals, with 13 genera and 650 species in five subfamilies having been reported. The goal of this research, which was conducted on cattle in Maragheh, Iran, was to document the diversity of species and quantify their numbers. A survey was done from the start of autumn in 2015 to the end of summer in 2016. A total of 328 ticks was collected and identified. *Hyalomma* spp. with 224 individuals (68.3%) were the most common, followed by *Rhipicephalus* spp. with 98 (29.9%). There were also three *Dermacentor* spp. (0.9%) and three *Boophilus* spp. (0.9%). In the current survey, 168, 89, 45 and 26 ticks were collected in spring, summer, autumn and winter, respectively, from cattle, with maximum and minimum prevalence in summer and winter, respectively. The highest and lowest numbers of ticks were recorded in the groin region and on the surface of the testicles, respectively.

Keywords: Hard tick, Ixodidae, *Hyalomma*, *Rhipicephalus*, Maragheh

Integrative taxonomy of Afrotropical *Ornithodoros* (*Ornithodoros*) (Acari: Ixodida: Argasidae)

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Afrotropical *Ornithodoros* (*Ornithodoros*) ticks are revised, based on the qualitative morphology of females and nymphs, as well as the tarsus I shape outlines of females measured in a geometric morphometric framework. These lines of evidence corroborate lineages based on 16S rRNA nucleotide sequence data. Four previously unrecognized species are described, along with a revived *nomen nudum* that was previously considered a synonym. Afrotropical *Ornithodoros* (*Ornithodoros*) now comprises ten species. Support is provided for speciation driven by riverine barriers, Pliocene uplift and differential aridity tolerance. Exaggerated tarsus I shape in the *O. savignyi* group suggests adaptation to fossorial habits and soil type. Conversely, reduced tarsus I shape in the *O. moubata* group is suggested as an evolutionary consequence of the life history change from soil to warthog burrows. This study represents an integrative, iterative approach to delimiting Afrotropical *Ornithodoros* (*Ornithodoros*) species, and provides the first application of tarsus I shape outlines in a geometric morphometric framework for testing species boundaries.

Keywords: Argasidae, *Ornithodoros*, African swine fever, human relapsing fever, tarsus



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Tick predation by the pseudoscorpion, *Megachernes ryugadensis* (Pseudoscorpiones: Chernetidae), associated with Japanese wood mice

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Ticks are obligate blood feeders that parasitize a variety of vertebrates and can be serious pests of these animals. Due to public concerns about the spread of tick-borne diseases, information on tick life history traits such as natural enemies is essential. We observed predation of *Haemaphysalis* ticks by the pseudoscorpion, Megachernes ryugadensis, in a laboratory for the first time. Adult and tritonymphal M. ryugadensis were collected in the field during phoresis on Japanese wood mice. These pseudoscorpions preyed on larval Haemaphysalis ticks and nymphal and adult Haemaphysalis megaspinosa. Most pseudoscorpions fed on two to three larval ticks on the first day following tick transfer. There were no significant differences between male and female pseudoscorpions in the numbers of larval ticks consumed or the numbers of days required to consume all ticks. Although there was no significant difference between the numbers of days to consume nymphal and adult male ticks, male pseudoscorpions consumed adult female ticks significantly faster than did female pseudoscorpions. The tritonymphal pseudoscorpion showed similar trends in the predation of larval and nymphal ticks. There seemed to be no counter attack measures by the tick. Further study is required to obtain detailed information on the tick and pseudoscorpion interactions and the impacts of the tick on small rodents to determine the role of M. ryugadensis as a natural enemy of ticks.

Keywords: Biological control, natural enemy, nidicolous species, rodent, symbiosis

Section 2. Integrated pest management

A good combination of phytoseiid mite with UVB in spider mite management

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Earlier studies revealed simultaneous control effects on economically important powdery mildew and spider mites by UVB irradiation in a strawberry greenhouse. UV damage is repaired by photoreactivation which indicates that the damage caused by spider mites is mainly the accumulation of DNA lesions such as cyclobutane pyrimidine dimers caused by the direct effects of UVB irradiation. Thus, efficient direct irradiation and the suppression of photoreactivation by irradiating at midnight were the keys for spider mite control using UVB. Although a light reflection sheet could successfully guide UVB to spider mites on the lower leaf surfaces, it could gradually no longer pass as the leaves grew thickly in May. Therefore, a good combination between the UV method and biological control using phytoseiid mites may be desirable in a practical use of UVB. Unfortunately, previous laboratory experiments in which mites were once irradiated and then checked for mortality after several days showed higher vulnerability of phytoseiid mites to UVB than spider mites. However, we found higher survival rates of *Neoseiulus californicus* than Tetranychus urticae under the irradiation conditions in the strawberry greenhouse when reproduced in the incubator. Moreover, we also found that pollen diets, especially the antioxidant components such as catechin, increased the robustness of phytoseiid mites against the effects of UVB. Our findings indicate the usefulness of phytoseiid mites combined with the physical control of spider mites with UVB.

Keywords: IPM, ultraviolet-B, biological control, integrated mite management, strawberry



2-8 September 2018, Antalya - TURKEY

Adaptation of physical control of Tetranychus urticae featuring UVB

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Based on the recent studies on lethal effects of ultraviolet-B (UVB) on spider mites, we tested the physical control of Tetranychus urticae on greenhouse strawberries by the combined use of overhead UVB lamps and light reflection sheets. To standardize the method for practical use, we compared the control effects among different cumulative UVB irradiances (0, 0.58, 1.15, 1.73 kJ/m²/d) in a strawberry greenhouse in two growing seasons in 2015-16 and 2016-17. Mite densities after artificial introduction (25 November 2015 and 14 November 2016) were reduced by increasing UVB dose. The densities at 0, 0.58, 1.15, 1.73 kJ/m²/d were 96.4, 72.9, 63.4, 1.6 \mathcal{P} /plant, respectively, on 13 May 2016, and 273.4, 116.3, 41.9, 2.4 \mathcal{P} /plant, respectively, on 8 May 2017. In an earlier study, we found that mite density was correlated with UVB irradiance on the lower leaf surfaces, so we assessed the seasonal changes of UVB intensity on the lower leaf surfaces. We also considered that air temperature, the determinant of the growth rate of mites, was important for this UV method, and that the dominant control effect of the UV method was the inhibition of egg hatching ($LD_{50} = 0.58 \text{ kJ/m}^2$). We calculated the egg stage duration in each month based on air temperatures. UVB irradiation on lower leaf surfaces was likely to decline due to flourishing plants, while egg stage duration became shorter with an increase in temperature after March. These results match up with the fluctuations of mite densities.

Keywords: Ultraviolet-B, *Tetranychus urticae*, physical control, strawberry, mite density

Side effects of zeolite on the predatory mite, Amblyseius swirskii

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Zeolites, which are 'green crops' products, are soil ameliorants that are reported to have a wide range of beneficial effects in agriculture, including reduced water consumption, increased plant tolerance to abiotic stress, and increased crop yields. In recent years, studies have been conducted on the potential use of zeolite against diseases in apple orchards and vineyards. This study aimed to determine the side effects of zeolite alone and zeolite + azadirachtin on the predatory mite, *Amblyseius swirskii*. A modified version of the method that uses *Typhlodromus pyri* Scheuten (Acari: Phytoseiidae) for regulatory testing of plant protection products was used in a laboratory residual contact test. The test unit was glass plates (12 cm diameter) with 20 protonymphs used in each replicate and each treatment replicated six times. The mortality rate of *A. swirskii* was not significantly different between Zeolite 850 WP, Zeolite 800 M SC, Zeolite Azadirachtin 450 WP and the untreated control on the first day after application. This situation changed little in seven days, with the mortality rate still below 30%. The standard pesticide, dimethoate, had extremely negative effects, causing 100% mortality. In contrast, the three zeolite products were classified as only slightly harmful to the predatory mite, *A. swirskii*.

Keywords: Zeolite, Amblyseius swirskii, side effects, biological control, predatory mite

Acknowledgement: This work was funded as a European Union Project (Grant Agreement No: 282865)



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Thursday, 6 September
Fatih Sultan Mehmet Hall
Section 1. Taxonomy and systematics

New observations on the genus *Chyzeria* (Acari: Acariformes: Chyzeriidae), with notes on Chyzeriidae

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The genus *Chyzeria* Canestrini, 1897 was proposed for an unusual adult mite, *C. ornata* Canestini, from New Guinea, with dorsal opisthosomal setose projections. Since then, 19 species have been described from the Southern Hemisphere (Australia, New Zealand, South Africa, New Guinea, Chile and Argentina). Most species are only known from one active postlarval instar but the morphology of postlarval instars has not been carefully examined for any species. In January 2017, adult *Chyzeria* sp. were collected in the Andes mountain range in Ñuble Province of the Biobio Region in Chile. Specimens were examined under light microscopy and low temperature scanning electron microscopy (LTSEM). Examination of the dorsal surface revealed five pairs of finger-like projections and an unpaired anteromedial projection on the opisthosoma. Each projection had two types of setae; the most numerous were spine-like setae of variable lengths and with numerous longitudinal slits at the distal end of each seta. The second type of seta was long, thin and scattered along the finger-like projections. *Chyzeria* will be compared with other genera in the family.

Keywords: Chyzeriidae, LTSEM, morphology, Southern Hemisphere, systematics

Genetic variability of the tomato russet mite, *Aculops lycopersici* (Eriophyidae), populations associated with cultivated and wild solanaceous plants

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The tomato russet mite (TRM), Aculops lycopersici, one of the most common pests of tomatoes worldwide, also infests pepper, eggplant and some other cultivated and wild Solanaceae. Among eriophyid mites, TRM is one of the few species infesting host plants of different genera, raising the suspicion that it may consist of a complex of species. To investigate the potential occurrence of cryptic species among TRM populations from different hosts, the molecular variability among 11 populations of A. lycopersici collected from Solanum lycopersicum (tomato and grape tomato) from Brazil and France (6), and from five other solanaceous host plants, Solanum muricatum (1), Solanum aethiopicum (1), Solanum americanum (1), Solanum sessiliflorum (1) and Physalis sp. (1) from Brazil, was assessed. Nucleotide sequences of the D2 region of the 28S rDNA gene, ITS2 and ITS region (spanning the ITS1, 5.8S and ITS2) were produced. Twenty-six new sequences of 552 bp were obtained within the D2 region. The ITS2 and ITS datasets consisted of 69 new sequences of 493 bp and 1090 bp, respectively. Phylogenetic analyses were performed, including sequences of Aculops cajanusis and A. strobilaceae retrieved from GenBank in the D2 dataset and A. lycopersici in the ITS2 dataset. Aceria tosichella was selected as the outgroup. Three D2 genotypes were identified among the analyzed TRM populations, as well as eight for ITS2 and 15 for ITS. The genotypic diversity was 0.1402, 0.2624 and 0.4544 for D2, ITS2 and ITS, respectively. Considering the three markers, the phylogenetic trees showed only one clade clustering the A. lycopersici genotypes. The distance values within the TRM sequences corresponded to intraspecific divergence of D2=0.00%, ITS2=0.065% and ITS=0.094%, indicating the existence of one genetic lineage among the TRM populations studied. Results further showed that the TRM populations collected from six different host plant species consist of a single taxon and confirm that this eriophyid mite is an oligophagous species.

Keywords: Molecular markers, phylogeny, molecular systematics, *Aculops*, Solanaceae

Acknowledgement: This research was supported by CNPq, FAPDF and FUB.



2-8 September 2018, Antalya - TURKEY

A new species of spider mite in the genus *Oligonychus* (Acari: Tetranychidae) from Japan

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Oligonychus is one of the largest genera of tetranychid mites, containing 207 known species. Of them, 18 species have been recorded in Japan. After genetic and morphological investigations, a new species was described as follows. Individuals were collected from Castanea crenata Sieb. et Zucc. (Fagaceae) in Saitama and Tochigi, Japan. The holotype (male) and paratypes (23 males and 27 females) were deposited as NSMT-Ac 14218. A new species, Oligonychus sp. nov., is described and illustrated. The new species closely resembles Oligonychus castaneae Ehara & Gotoh, 2007 but mainly differs in that the aedeagus has a longer distal portion which forms a small sigmoid, acuminate tip, instead of having a shorter distal portion ending in a truncated tip. Several differences were also observed between the two species in the leg setal counts of tarsus II in the male and female; the number of tactile setae and solenidia (in parentheses) was 11(1) for both the female and male in the new species but in O. castaneae these counts were 12(1) for the female and 12(2) for the male. A maximum likelihood tree based on the cytochrome c oxidase subunit I (COI) gene of its mitochondrial DNA (mtDNA) showed that O. sp. nov. is clearly separated from O. castaneae and other related species.

Keywords: Japan, Oligonychus, Castanea crenata, Quercus acutissima, Quercus serrata

Taxonomic and molecular characters of some Phytoseiidae species from Turkey

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Phytoseiid mites are very common biological control agents on plant parasitic mites: the fast and correct identification of these species is critical for biological control success. Furthermore, limited data are available for molecular characterization of phytoseiid species in Turkey. The aim of this study was to investigate the morphological and genetic variability of some predatory mites based on morphometric and molecular analysis methods. Taxonomic and molecular studies were carried out on phytoseiid mites collected from some stone and soft fruit orchards (apple, pear, quince, cherry, sour cherry, apricot) in Ankara, Turkey. The samples were collected from Ayaş, Beypazarı, Kahramankazan during 2014. Temporary preparations of the collected mites were made with lactic acid. Molecular studies were carried out on these samples to determine whether the DNA was degraded or not in the gel display. In this study, phytoseiid species were evaluated by comparing morphometric differences based on their morphological characters such as length of the macrosetae, dorsal idiosomal setae and shape of the spermatheca. The DNA was extracted from the samples with a Qiagen Kit. Molecular analyses were conducted on the mitochondrial 12S ribosomal RNA. The genetic distance between the species was substantially different, depending on the specimens. These results confirm that the target DNA fragment is an important diagnostic tool. The mites were identified to the species level individually and then permanently prepared. An important aspect of this study was obtaining DNA from single specimens and demonstrating their phylogeny for the first time in Turkey.

Keywords: Mitochondria, molecular, Phytoseiidae, predatory mites, Turkey

Acknowledgement: This study was supported by the University of Ankara's Unit for the Coordination of Scientific Research Projects (BAP-12B4347011).



2-8 September 2018, Antalya - TURKEY

Section 2. Biodiversity

Is a cataclysmic mass extinction of mite species occurring in the shadows of high profile insect and vertebrate extinctions?

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An estimated three to ten million species of mites occupy almost every conceivable habitat on the planet. All mite species, which are parasitic, phytophagous, predatory, mycophagous or saprophagous, have complex, dynamic interactions with their abiotic and biotic environments. Mite habitats include an enormous range of microhabitats on plants and animals, with even single animals and plants capable of hosting complex, multispecies communities. The main factors driving the extinction of species are the continually rising human population, non-sustainable use of natural resources, global warming and climate change, habitat destruction, environmental degradation and invasive species. Many of the habitats and microhabitats of mites or their hosts have been destroyed or irreversibly damaged by human activity, with the same processes continuing unabated. Highly specialised mites with restricted distributions, including those that are host specific, such as most of the eriophyoid mites associated with plants and some parasitic mites of birds and mammals, are at great risk of extinction. As an example, six feather mite species have been described from the extinct North American parrot, Conuropsis carolinensis (L.). It is likely that we have lost tens to hundreds of thousands of species to extinction in the last 50 years, especially in tropical and subtropical environments, with an extremely high proportion being undescribed species, with extinctions continuing at a high rate. Moreover, it is arguable that the key driver in this extinction process is anthropocentrism, a cornerstone of many philosophies and religions. Anthropocentrism regards humans as both separate from and superior to nature which is therefore exploitable and disposable for the sole benefit of humans. Unless society fundamentally rejects this philosophy and adopts one that has environment, biodiversity and sustainability at its core, much more of the planet's remaining genetic, evolutionary and ecological heritage, including mites, inevitably will be lost.

Keywords: Economic rationalism, extinction cascade, phoresy, social reality, symbiont

Spider mites on medicinal and endemic plants of Serbia and the Balkans

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This study gives an overview of spider mites (Tetranychidae) found on medicinal and endemic plants of Serbia and the Balkan Peninsula. The overview is based on a five year survey from 2013 to 2017 throughtout Serbia, as well as published data on spider mite species records on medicinal plants in other Balkan countries. In the survey, a total of 23 spider mites species were recorded on 56 important medicinal plant species from 20 plant families. There were 25 new hosts for Tetranychidae and 18 new hosts for 15 spider mite species. Several very well-known medicinal plants e.g. Adonis vernalis, Althaea officinalis, Bellis perrenis, Chamomilla recutita, Hypericum perforatum, Satureja montana, Thymus serpyllum, were recorded as new hosts for spider mites. Two cosmopolitan species, *Tetranychus turkestani* and *T. urticae*, had the highest number of hosts, 26 and 18, respectively, including eight and 13 host species, respectively, new for Tetranychidae. Among 12 host species of Asteraceae, six species were new hosts for tetranychid mites and four species were new hosts for seven spider mites species. Among eight host species from Lamiaceae, three species were new hosts for Tetranychidae and four species were new hosts for five spider mite species. New hosts for tetranychid mites were also found in eight other plant families. Three species recently discovered as new to the Serbian acarofauna, Bryobia praetiosa, Eotetranychus aceri and E. pruni, were found on 11 plant species, including four new hosts for spider mites. Three endemic Balkan plant species, Acer heldreichii, A. intermedium and Ramonda nathaliae, were also recorded as new hosts for spider mites. In addition to the survey data, a review of the literature dealing with this topic in Serbia and other Balkan countries is provided.

Keywords: Tetranychidae, species diversity, medicinal plants, Serbia, Balkans



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Problems and challenges for the study of gamasoid mite (Acari, Gamasida) diversity in Georgia

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The soil inhabiting mesostigmatid mites of Georgia are poorly understood. Investigations of their diversity in Georgia started with the works of Wainstein in the late 1950s and continued to the late 1980s, resulting in a total of 124 recorded species. The main contributors to the investigation of gamasoid faunal diversity were Wainstein (Phytoseiidae), Gomelauri (Phytoseiidae) and Bregetova (Laelapidae). Most sampling locations for the older species records are concentrated around Tbilisi, the capital of Georgia (43 species); the Black Sea coastal side (25 species); and the Borjombakuriani region (24 species). Twenty nine species new for science were described from Georgia (10 of them are found only in the Caucasus region), contributing 7% of the total acarine fauna. There are many problems associated with old Soviet era publications because of substantial inaccuracies in sampling locations. After the 1980s, there was a gap in the investigations of Mesostigmatid mite diversity and new samplings only started after 2010. In recent investigations, 28 new, exactly geo-referenced sampling locations were investigated. These investigations enriched the total fauna by nineteen species, bringing the number of gamasoid species for the country to 143. Uropodine species were also sampled but they are yet to be identified. We expect many more species of mesostgmatid mites to be discovered in Georgia, bearing in mind that more than 500 oribatid mite species are known from the same areas.

Keywords: Mesostigmata, Gamasida, species diversity, Georgia, Caucasus

Case studies with oribatid mites reveal wood ant nest mounds as biodiversity hotspots

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Despite most ant species being predators, their nest mounds are also inhabited by a large variety of other invertebrates known as ant associates. The most numerous associated group, the soil-dwelling oribatid mites, have remained rather unstudied. A few studies conducted in Finland recently have highlighted oribatid diversity in ant mounds. Firstly, our study, based on 10,600 specimens and 74 identified species, showed that the nest mounds of the wood ant, Formica polyctena, were inhabited by an oribatid fauna as abundant and diverse as that in the surrounding soil. Moreover, the results also revealed that predominantly, different species inhabited these two habitats. Secondly, a more extensive study that yielded 18,600 specimens and 94 identified species showed that the oribatids occurred predominantly (78%) on the surface layer of mounds and that their distribution was positively related to mounds' surface moisture content. Forest management practices, such as clear felling, affect the physical properties of mounds which may be harmful not only for ants but also for their rich associated fauna. Indeed, our next study revealed that the surface layer of F. aguilonia mounds was significantly drier in clear fells than in forest. The impacts of forest clear felling and the carry-over effects of the drying of mounds on the oribatid fauna were then investigated. That study, in which 16,500 specimens of 67 species were collected, revealed that while the clear felling had no impact on abundance or community composition of oribatids, their species richness was significantly lower in clear fells and was positively related to the mound's surface moisture content. These results indicate that the oribatid fauna of this distinctive habitat may be considered a useful bioindicator group in studies of environmental changes. As red wood ants build large, dense and long-lasting nest mounds in boreal forest, these nests are important to the maintenance of oribatid biodiversity.

Keywords: Ant associates, biodiversity, Finland, forest management, Oribatida



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Species richness and biodiversity of Uropodina mites (Acari: Mesostigmata) from Brazil, Belize and Mexico

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The Suborder Uropodina comprises mites mainly living on litter in tropical forests but also can be very abundant under moss, stones and in the nests of mammals, and in dung. At a number of sites in the south of Mexico, Belize and Brazil, a study was carried out on the species richness and biodiversity of uropodid mites. Samples of litter, moss, dung and decaying tree trunks were processed through Berlese funnels. A total of 21 families, 23 genera and close to 80 morphospecies were identified. Some genera are more abundant in each country; the family Trigonuropodidae and the genus Trigonuropoda were not collected in Brazil, while in Belize and Mexico the genus is very common and abundant. From Amazonian tropical forest, the genus Chelonuropoda, described by Konstchan from Africa, was collected. In addition, there were very interesting specimen of the genus *Dinychus* from Belize and Brazil. A high species richness and biodiversity of uropodid mites is present in Mexico, Belize and Brazil. Several new species are expected from these countries.

Keywords: Uropodina, mites, biodiversity, Central America, South America

Biodiversity of spider mites in the Tara National Park in Serbia

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Tara Mountain is part of the Dinaric Alps and one of the richest and most biologically valuable forest areas in Europe. It is a medium-high mountain located in western Serbia, in an area declared a National Park in 1981, with a total area of around 25,000 ha. The Tara National Park has been identified as an Important Plant Area (IPA), as well as an area important in the framework of Emerald Ecological Network. This study presents results of a survey carried out for five years (2013-2017) in which spider mites were collected at 41 sampling locations in Tara National Park. In the survey, a total of 21 spider mites species were recorded, including five species new to the Serbian acarofauna, namely Bryobia praetiosa, Eotetranychus aceri, Eotetranychus fagi, Eotetranychus pruni and Panonychus citri; the records of E. aceri and E. fagi were the first for the Balkan Peninsula as well. Spider mites were found on 45 host plant species belonging to 18 plant families. There were new world records among host plants: 13 species were recorded as new hosts for Tetranychidae and 12 species were recorded as new hosts for nine spider mites species. Two species, Tetranychus turkestani and Tetranychus urticae, were clearly distinguished with 13 and 10 recorded hosts that included two and four host species, respectively, that are new for Tetranychidae. Among newly recorded spider mites, B. praetiosa was found on six host plants, five of which were new for Tetranychidae.

Keywords: Tetranychidae, species diversity, host plants, national parks, Serbia



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Section 3. Evolution and phylogeny

Codispersals and host shifts inferred by double dating of host and parasite phylogenies in proctophyllodid feather mites (Astigmata: Proctophyllodidae) associated with passerines (Aves: Passeriformes)

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The Proctophyllodidae (Astigmata), the most species-rich family of feather mites with over 400 species in 50 genera distributed worldwide, is predominately associated with passerine birds (Passeriformes). Inferring co-phylogeographic events requires the matching of the timing of these events for both host and symbiont or parasite phylogenies because divergences of hosts and their symbionts may not temporally coincide, and host switches may occur. We inferred a timecalibrated tree of proctophyllodid feather mites (117 mite species from 116 bird species; six genes, 11,468 nt aligned), using fossils as outgroups. We then compared important time-calibrated mite divergences and dispersal with corresponding events in time-calibrated bird phyloheny. Of 10 putative cophylogeographic events, four well agree in timing for both symbiont and host events being synchronous co-origins or codispersals; three were based on host shifts but agree in timing being very close to the origin of corresponding modern hosts; two disagree; and one large basal mite split was seemingly independent from host phylogeography. Among these events was an ancient (21.0–25.3 Mya), synchronous codispersal from the Old World that led to the origin and diversifications of New World emberizoid passerids and their mites, the thraupis + quadratus species groups of the genus *Proctophyllodes*. Based on temporally concordant cophylogeographic events and host shifts inferred from our double dating analyses, a historical scenario illustrating main phylogenetic diversification and long-distance (transoceanic) dispersal events of the mite subfamily Proctophyllodinae and their avian hosts was reconstructed.

Keywords: Coevolution, molecular clock, double-dating, Proctophyllodidae, Passeriformes

Genomics of *Cardinium Brevipalpus* mites endosymbionts suggest metabolic connections with host mite and with other symbionts

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Intracellular bacteria are drivers of the ecology and evolution of arthropods due to their effects on the host phenotype. Among them are the Cardinium endosymbionts that infect an estimated 7% of arthropod species, including mites, and are primarily known for their ability to manipulate host development in ways that enhance their transmission to the next generation of hosts. Flat mites in the genus Brevipalpus are known to reproduce by thelytoky due to infection by Cardinium bacteria in a way that haploid (unfertilized) eggs develop into females instead of males. Genomic studies of these intracellular bacteria can reveal evolutionary aspects of their relationship with hosts and the environment, based on the degree of reduction and the types of genes that are lost or retained. Genomes of 'feminizing' Cardinium bacteria from three Brevipalpus mite species, B. vothersi, B. papavensis and B. californicus, were sequenced and compared with those of Encarsia wasps and Bemisia whiteflies, as well as with those of Wolbachia endosymbionts. Assembly of Cardinium sequences resulted in ~1Mb, which are close to the genome size of two published Cardinium genomes, whitefly (1,033 Mb) and Encarsia pergandiella (887 kb), which can be considered a highly reduced genome in size and function, even for a facultative endosymbiont bacteria. Annotation of the Brevipalpus-associated Cardinium genome revealed that biosynthetic capabilities of these endosymbionts are very limited: they are not able to synthesize most cofactors or any amino acids, not even biotin; do not have a secretion system for transporting effector proteins, virulence factors and the tricarboxylic acid cycle; and lack a functional respiratory chain. These observations suggest that Brevipalpus-associated Cardinium has to take up essential nutrients from its host cells. Its extremely reduced metabolic capabilities suggest that Cardinium is not a mutualistic symbiont but a parasite. The inability to synthesize some metabolites may be compensated by other facultative endosymbionts of the host, e.g., Wolbachia.

Keywords: Bacteriodetes, flat mites, gene annotation, host relationship, *Wolbachia*



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Preliminary phylogenetic hypothesis of the subfamily Tarsoneminae (Heterostigmatina: Tarsonemidae) based on the local species assemblage

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Phylogenetic relationships within a set of 38 species collected in East Azerbaijan Province of Iran were examined through a cladistic analysis of 97 morphological characters derived from adult females. The species included in the analysis belonged to the genera *Dendroptus* Kramer, 1877 (1), *Steneotarsonemus* Beer, 1954 (7), *Neotarsonemoides* Kaliszewski, 1984 (7), *Xenotarsonemus* Beer, 1954 (1) and *Tarsonemus* Can. & Fanz., 1876 (22), with *Heterotarsonemus lindquisti* Smiley, 1969 as an outgroup. Maximum parsimony analysis was executed using PAUP 4.0 (Swofford 1998). Heuristic searches were carried out with 10,000 random additions followed by branch swapping using tree-bisection-reconnection algorithm. This analysis yielded seven most-parsimonious trees (length 485, RI= 0.613, CI= 0.329). Based upon the strict consensus tree, the two genera, *Steneotarsonemus* and *Neotarsonemoides s. str.*, were found to be monophyletic; and the genus *Xenotarsonemus* was recovered as a sister group of *Neotarsonemoides s. str.*, as suggested by Lindquist (1986). Relationships among *Tarsonemus* species remained mostly unresolved, with the genus appearing as a polyphyletic taxon. Monophyly of the tribes Tarsonemini and Steneotarsonemini (both *sensu* Lindquist) was not supported.

Keywords: Systematics, mites, phylogeny, classification, Iran

Revision of the genus *Neotropacarus* Cunliffe, 1964 (Acaridae) with the description of three new species

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The genus *Neotropacaus* (Cunliffe) is commonly found on plant leaves where they feed on fungi, without causing any damage to the plants. Neotropacarus is characterized by having, at least, setae ex (sce), cp, e2, h1, h2 e h3 very long, extending to the posterior edge of idiosoma; seta ft' (ba) absent on tarsus II; genus I bearing only one solenidium and paranal suckers absent on males. Species belonging to this genus can be differentiated by the presence/absence of seta le; length of seta el that may or may not extend beyond the posterior edge of the body; number of paraproctal seta (one or three pairs); presence/absence of c" on tibiae I-II and the presence/ absence of a" and ft' on tarsi I-II. The two species known in this genus are poorly described. Due to the lack of appropriate morphological characterization of Neotropacarus, the goal of this work was to characterize it, redescribe the two known species, Noetropacarus mumai (Cunliffe) and Neotropacarus bakeri (Collyer), and to describe three new species. The holotype and paratypes of N. mumai and N. bakeri were obtained from the National Museum of Natural History-Washington, DC, USA and the University of Michigan, Ann Arbor, MI, USA, respectively. The collection data of the three new species are as follows: Neotropacarus n. sp.1 on Lophostemon confertus (Myrtaceae), Queensland, Australia; Neotropacarus n. sp.2 on Cupania sp. (Sapindacaceae) from Teotônio Vilela, Brazil; Neotropacarus sp. 3 in nests of Rhipidura sp. (Rhipiduridae).

Keywords: Astigmatina, acarofauna, taxonomy, diversity, plant mites



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Section 4. Biodiversity Invited speaker

Free-living mites (Acari) of the Franz Josef Land Archipelago, the coldest territory in the Old World: diversity, distributions, assemblages

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Processing the first professional sampling of microarthropods from the Franz Josef Land Archipelago has more than four times "increased" its known mite diversity. To the present, 47 mite species from 28 genera and 26 families have been recorded. The fauna and its taxonomical composition resemble those of other polar desert regions (Sverdrup Islands, Severnaya Zemlya Archipelago). The main feature is the prevalence of the suborder Prostigmata (18 species) while the proportions of the suborders Gamasida (12) and Oribatida (9) are lower. Another feature in common is the set of the most diverse families: Ascidae (8 species) and Eupodidae (7), and of the most diverse genera: the gamasid Arctoseius (8 species), the oribatid Liochthonius (3), the endostigmatan Alicorhagia (3), and the prostigmatan Eupodes (3) and Cocceupodes (3). As in the other polar deserts, the mite fauna is rather fragmentary, i.e. most of the genera (almost 80%) are represented only by a single species and nearly all families (92%) include only one genus. Among 34 exactly identified species, 5 are cosmopolitan and 27 species show Holarctic distributions, including 7 polyzonal, 3 arcto-boreal, 6 arcto-montane and 11 Arctic species. The total abundance usually varies from 400 to 1,900 spm./dm² but locally it reaches 4,800 spm./dm² on well-drained meadows with Alopecurus alpinus. As in the polar deserts of the Canadian Arctic Archipelago, Severnaya Zemlya Archipelago, and the Antarctic mainland, small, thin-integumented members of Eupodidae, Tydeidae and Nanorchestidae predominate everywhere. The rather large, wellsclerotized oribatids, Ceratozetes spitsbergensis and Diapterobates notatus (Ceratozetidae), are numerous only in the warmest habitats. The insect fauna of the Franz Josef Land contains only 16 species. A greater diversity of the class Arachnida in the polar desert zone compared to the Insecta, the largest animal class on Earth, is unique for terrestrial biomes.

Keywords: Mesostigmata, Oribatida, circumpolar species, Arctic species, Arctic

Invited speaker

Lindquist et al. 1979 revisited: knowledge status and taxonomic gaps on the acarine diversity in Canada

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In 1979, Lindquist et al. (Mem. Ent. Soc. Can. 108: 252-290) published a detailed synopsis of the Canadian acarofauna, including numbers of known species for each family of Acari, as well as estimates of what is yet unrecorded. This publication was a key resource for Canadian acarologists. Here we present an updated synopsis, providing revised estimates for the known and unknown diversity, as well as directions for future research to address major taxonomic gaps.

Keywords: Acari, Canada, biodiversity, systematics, knowledge gaps



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Invited speaker

A review of the feather mite family Gabuciniidae Gaud & Atyeo (Astigmata: Pterolichoidea) from Brazil

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The feather mite family Gabuciniidae currently includes 16 genera and approximately 60 described species associated with various bird hosts worldwide, namely passerines, eagles, falcons, toucans, cuckoos, vultures, bustards, jacamars, tauracos, bee-eaters, nightjars and New World barbets. In the Neotropical region, about 11 gabuciniid species are known from Argentina, Brazil, Colombia, Cuba, USA (Florida), and Peru, with most of the taxa reported from Colombia and Brazil. This study aimed to investigate the gabuciniid fauna associated with birds in Brazil. The mites were collected from various sources: 1) birds found road-killed; 2) birds which died in captivity; 3) from wild birds captured with mist nets; and a literature survey was conducted. Our survey revealed only 5 named species of 5 distinct genera in Brazil: Piciformobia guirae from Cuculidae; Tocolichus allepimerus from Ramphastidae, Paragabucinia brasiliensis from Caprimulgidae; Cathartacarus coragyps from Cathartidae; and Hieracolichus hirundo from Accipitridae. In addition, at least 11 new species belonging to nine genera were found: two new species of Aetacarus, Coraciacarus, Hieracolichus and Proaposolenidia, and one new species of Capitolichus, Gabucinia, Piciformobia, Paragabucinia and Tocolichus. The hosts represented various orders: Accipitriformes (eagles), Piciformes (woodpeckers, toucans), Cuculiformes (cuckoos), Falconiformes (falcons), and Passeriformes (crows). These findings indicate that Brazil is home to a large diversity of undescribed gabuciniids, which is not surprising considering the vast bird fauna of that country, and especially since most species have yet to be investigated for their feather mites.

Keywords: Ectoparasites, feather mites, symbionts, Psoroptidia, Astigmata

Thursday, 6 September

Kanuni Sultan Süleyman Hall Section 1. Biological control

Eriophyid mites as biocontrol agents of weeds: challenges for future research

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The biological control of weeds is largely based on the selection and evaluation of co-evolved, host specific phytophagous arthropods and pathogens to introduce as agents that reduce the fitness and impact of a given invasive weed species. Eriophyid mites are among the smallest plant feeders and are characterized by having an intimate relationship with their host, with about 80% of currently known species associated with a single host. Eriophyid mites can substantially damage vegetative and reproductive plant parts, have high reproductive rates and have different dispersal strategies which, in addition to high host specificity, indicate their potential as effective biological control agents. In addition, some eriophyid mite species can be so specialized for specific plant ecotypes that they are not able to attack all genotypes of the weed being targeted. The eriophyid mites, Aculops mosoniensis, Aculodes altamurgensis and Aceria chondrillae, are potential or released biological control agents against Ailanthus altissima, Taeniatherum caput-medusae and Chondrilla juncea, respectively. These three eriophyid species are presented as three case studies with a high potential to be effective in classical biological control programs. They are mentioned, together with other eriophyid mite species, as examples for future research studies. In particular, more knowledge of eriophyid mite biology, life history, host range, foraging behaviour, overwintering requirements and dispersal behavior are crucial to the better understanding of mite-host interactions and mitehost coevolution, as well as how to use them as effective biological control agents.

Keywords: Eriophyidae, biological control, weed, invasive plant, host specificity



2-8 September 2018, Antalya - TURKEY

Diversity and distribution of beneficial mites from cherry (*Prunus avium* L.) (Rosaceae) and sour cherry (*Prunus cerasus* L.) (Rosaceae) in Ankara, Turkey

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The cherry tree (*Prunus avium* L.) (Rosaceae) and sour cherry tree (*Prunus cerasus* L.) (Rosaceae) can be important hosts for beneficial mite species. Ankara, which is in the central part of Anatolian Turkey, potentially has a very suitable environment for these species. The current study identified beneficial mite species from both cherry and sour cherry plants in Ankara. Samples were collected monthly from Ankara (Ayaş, Beypazarı, Çubuk, Gölbaşı, Haymana, Kahramankazan and Kızılcahamam) from April to December from 2012 to 2014. From cherry trees, five beneficial, predatory mite species were identified, namely *Typhlodromus (Anthoseius) psyllakisi* (Swirski & Ragusa), *Typhlodromus (Anthoseius) bagdasarjani* (Wainstein & Arutunjan) (Acari: Phytoseiidae), *Kampimodromus aberrans* (Oudemans) (Acari: Phytoseiidae), *Euseius finlandicus* (Oudemans) (Acari: Phytoseiidae) and *Euseius stipulatus* (Athias-Henriot) (Acari: Phytoseiidae). From sour cherry trees, six predatory mite species were identified, namely *T. psyllakisi*, *T. bagdasarjani*, *K. aberrans*, *E. finlandicus*, *E. stipulatus* and *Blattisocius tarsalis* (Berlese) (Acari: Ascidae). On both plant species, *E. finlandicus* (Oudemans) was the most common predatory mite species. In addition, the distributions of beneficial mites from cherry and sour cherry in Ankara, Turkey were determined.

Keywords: Acari, mites, Phytoseiidae, Rosaceae, Turkey

Acknowledgement: This study was supported by the University of Ankara, the Coordination of Scientific Research Projects (BAP-12B4347011).

Banker-Sheet[™]: A new device for allowing predatory mites to long breed, protecting their population against environmental stresses and increasing predator release to crops

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Although predatory mites are widely used for controlling small pests in crops, environmental stresses can adversely affect their performance. The main barriers to the survival and breeding of predatory mites after application are: 1) lack of pollen and pests over a long period after the release of mites; 2) adverse climatic and environmental effects; and 3) population decline due to pesticide application. To minimize these problems, we developed a plant-attached shelter, Banker-Sheet[™], that hold sachets of Neoseiulus californicus (McGregor) or Amblyseius swirskii (Athias-Henriot). The shelter was prepared with water-resistant paper that protects against the adverse effects of chemical application, and rainfall, temperature and humidity fluctuations. The basic features, including shelter function, were published earlier. We conducted laboratory experiments to estimate the number of predatory mites released from the Banker-sheet[™] under different conditions. More mites (N. californicus and A. swirskii) were released from Banker-sheet[™] than from unsheltered sachets at 23 °C and 20 °C. Neoseiulus californicus continued to disperse from Banker-sheet[™] for more than three months at temperatures of 17 °C and 15 °C. The total release of *N. californicus* was 95 at 12 °C, while it increased to 1,061 at an average of 12 °C (max 17 °C, min 8 °C) and continued releasing for more than 3 months. These results indicate that the Banker-sheet[™] is potentially useful for protecting predatory mites and enhancing their release to crops. Banker-sheet[™], with either N. californicus or A. swirskii (called Miyako-Banker[™] and Suwaru-Banker[™], respectively) have become commercially available in Japan. This new technology is being/will be used in various crops such as vegetables, fruit trees, and flowers.

Keywords: Biological control, environmental stress, predatory mite, *Neoseiulus californicus*, *Amblyseius swirskii*

Acknowledgement: This research was financially supported by the Science and Technology Research Promotion Program of the Agriculture, Forestry, Fisheries and Food Industry (26070C and 28022C).



2-8 September 2018, Antalya - TURKEY

Oribatid mites as potential predators of the root knot nematode, *Meloidogyne incognita* (Kofoid & White, 1919) Chitwood, 1949

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Oribatid mites represent the most dominant group among the soil mites and have amazing diversity in feeding habits. Nematodes quite often serve as the most favoured prey choice to oribatids which could be better exploited in biocontrol strategies. Hence the present study was carried out with the intention to explore the predatory habits of selected species of oribatid mites on a notorious nematode pest, namely the root knot nematode, Meloidogyne incognitia, under laboratory conditions. The study was commenced by collecting soil samples from various localities in Kannur and Malappuram districts of Kerala, India, in the period March, 2014 to February, 2015. Among the various species of oribatid mites extracted, three species, Scheloribates viz. S. praeincisus (Berlese, 1910), Scheloribates fimbriatus africanus Wallwork, 1964 and Scheloribates. (Scheloribates)latoincisus Hammer (1973), were selected for studies on their predatory potential on the J2 juveniles of M. incognita. Feeding experiments were conducted by offering adults of each selected mite species twenty J2 juveniles. Observations were made on the feeding behavior of the species, including rate of consumption, to do a comparative evaluation. The percentage consumption per day of J2 juveniles by S. praeincisus, S. f. africanus and S. (S.) latoincisus ranged from 57.00+5.9675 to 60.00+6.37. Statistical analysis following one way ANOVA revealed no significant difference was in the consumption rates among the species (P =0.452; \geq 0.05). It is concluded that all three species of Scheloribates have equal potential to suppress the root knot nematode population.

Keywords: Oribatid mites, predation, *Meloidogyne*, *Scheloribates*, biocontrol

Section 2. Biological control

Performance of the generalist predatory mite *Amblyseius swirskii* Athias-Henriot (Acari: Phytoseiidae) on tomato genotypes with different trichome phenotypes

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Tomato plants are covered in diverse glandular hairy structures (trichomes) that upon touch release toxic or sticky exudates, causing the entrapment and mortality of many species of arthropods. Currently, cultivars used for tomato production are often selected for high density of trichomes since they show increased tolerance to herbivore attacks. However, tomato trichomes are harmful to predatory mites too. These mites usually exhibit greater mobility than their prey, thus increasing the likelihood of getting entrapped. Type VI glandular trichomes, which are responsible for excretion of the sticky acylsugars, are present at low densities on tomato leaves. However, the density of this kind of trichome on stems is higher. Therefore, predatory mites might die during the dispersion from leaf-to-leaf via the stems when trapped in the high concentration of acylsugars present on the stems. In this study, we estimated the dispersal ability of the generalist predatory mite, Amblyseius swirskii, on the tomato cultivar "Raf" and on 3 monogenic mutants with different trichome phenotypes: hairs absent (non-glandular trichomes absent), hairless (trichomes distorted), and hairy (excess of non-glandular trichomes). Moreover, we investigated the success of a biocontrol program based on the augmentative release of A. swirskii against tomato key pests on the three tomato phenotypes mentioned above. We discuss how plant characters that render resistance against arthropods have fitness tradeoffs because they provide enemy-free space to herbivores that are adapted to these defenses. These findings further indicate that the effect of the plant physiology on natural enemies is important and should be taken into account by plantbreeding programs.

Keywords: Biological control, *Solanum lycopersicum*, trichomes, dispersal, trade-offs



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Effect of low relative humidity on the predatory mite, *Phytoseiulus persimilis*

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Predatory mites of the family Phytoseiidae are tiny organisms from 0.2 mm to 0.5 mm long. Despite their small size, they contribute greatly to the success of augmentative biological control, as natural enemies of phytophagous mites and small insects. The predatory mite, *Phytoseiulus persimilis*, is probably the best known example of a phytoseiid mite used for augmentative biocontrol. It was the first mass-reared predatory mite species and it is still successfully applied worldwide to control the spider mites e.g. Tetranychus urticae. As are most phytoseiid mites, P. persimilis is susceptible to low relative humidity, and its performance as a natural enemy can be lowered by dry conditions. Spider mites, on the contrary, perform well in dry conditions. Consequently, the biological control of spider mites on crops grown in arid environments remains a serious problem. With the objective of selectively breeding a drought-resistant strain of *P. persimilis*, we first focused on the effect of low humidity on the egg stage, which is supposed to be the most drought-sensitive. We assessed the effect of constant and variable relative humidity on the egg survival of five populations of this species. In a second experiment, we tried to select for more drought-resistant eggs, using two methods, artificial selection and experimental evolution. In both methods, we assessed the egg survival of the selected populations under low humidity every month. Our results showed that the egg stage is highly sensitive to a constant low relative humidity of 60% but that only a few hours spent at a higher humidity (75%) was enough for the eggs to survive. The results of the selection experiment suggest that we should focus on a different life stage, rather than the egg, to select for a drought-resistant *P. persimilis*.

Keywords: Augmentative biological control, abiotic stress, relative humidity, egg hatching rate, artificial selection

Hierarchical analysis of in-and out-breeding in the haplodiploid predatory mite, *Phytoseiulus persimilis*

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Detrimental effects of close inbreeding are known from numerous animals, with inbreeding commonly reducing fitness. At the genetic level, inbreeding depression results from increased homozygosity of recessive deleterious alleles. Although haplodiploids should suffer less from inbreeding than diplodiploids, excessive inbreeding may also cause significant negative effects in haplodiploids. At the other extreme, mating between genetically distant partners may also be disadvantageous for a variety of reasons, mainly because of genetic incompatibility. Thus, optimal outbreeding theory suggests that intermediate levels of mate relatedness should provide for the highest fitness gains. In the first part of our experiment, we investigated the mating behavior of pseudo-arrhenotokous predatory mites, *Phytoseiulus persimilis*, at different mate relatedness levels and the resulting fecundity of females, and sex ratio of their offspring, using iso-female lines of two populations (Sicily and Greece) that mated with either a sibling, a male from the same population or a male from the other population. Additionally, we recorded mating latency and duration. Females mating with a male from the same population produced more eggs, with a lower female bias, over a longer time than females mating with a sibling or with a male from the other population. Mating duration was disproportionally long in sibling couples, likely indicating female reluctance to mate and sub-optimal spermatophore transfer. In the second part, we monitored founder in- and out-breeding effects on the dynamics of chronically inbreeding lineages over four generations. Cross-generationally, lineages founded by distantly outbred females performed the best, i.e., produced the most descendants. However, this was solely due to superior performance from the F₂ generation onwards. In the F₁ generation, lineages founded by females mated to males from their own population (intermediate relatedness) performed better than lineages founded by closely inbreeding and distantly outbreeding females, as predicted from short-term inbreeding depression effects. At the genetic level, this result was most likely due to distantly outbred founders introducing higher allelic variability and lower homozygosity levels, counterbalancing inbreeding depression from the F₂ generation onwards.

Keywords: Biological control, founder effect, haplodiploid, inbreeding, outbreeding



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Life history of *Typhlodromus athiasae* as a predator of *Tetranychus urticae* (Acari: Phytoseiidae, Tetranychidae) at different temperatures

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The biology of the predatory mite *Typhlodromus athiasae* Porath and Swirski (Acari: Phytoseiidae), a predator of the two spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae), was studied under laboratory conditions. All experiments were conducted on bean leaf discs in an incubator at 20, 25 and 30 ± 1 °C, with 16:8 h L:D, at an average daily relative humidity of $70\pm10\%$. Observations were made twice a day for both the immature stages and the adults to determine the developmental time, survival and fecundity. At 20, 25 and 30 ± 1 °C, the total developmental time of *T. athiasae* females was 9.08, 8.27 and 7.10 days, respectively, and for males it was 8.65, 7.49 and 6.32 days, respectively. The highest total egg production was 17.27 eggs at 25 °C. The longevity of *T. athiasae* females was 27.26, 30.76 and 28.65 days at 20, 25 and 30 ± 1 °C, respectively. *Typhlodromus athiasae* had the highest intrinsic rate of increase (r_m) at 0.1299 $\propeq \$

Keywords: Biological control, Phytoseiidae, *Tetranychus urticae*, *Typhlodromus athiasae*, life table

The effects of *Cardinium* and *Wolbachia* on the reproduction and fitness of a predatory mite and its prey

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Endosymbionts play an important role in arthropod development and reproduction. Different cross combinations were made to explore the effects of endosymbionts on the reproductive manipulation and fitness changes of *Neoseiulus californicus* and its prey *Tetranychus turkestani*, by both single infection and double infection of Cardinium and Wolbachia. The main results were as follows: cytoplasmic incompatibility (CI) was induced by both single infection and double infection of Cardinium and Wolbachia in N. californicus: Single infection with Cardinium and Wolbachia induced strong CI in N. californicus. When Cardinium-infected males were crossed with uninfected females, the fecundity of female adults, hatching rate, survival rate, number of F females and percentage of F₁ females all decreased. Crosses between the Wolbachia-infected males and uninfected females led to a decline in the hatching rate, survival rate, number of F₁ females and percentage of F, females but did not affect female fecundity. Double infection also induced CI, and both endosymbionts affected the inducing and rescue ability of the other. Meanwhile, both Cardinium and Wolbachia could affect the fitness of N. californicus. CI was induced by both single infection and double infection of Cardinium and Wolbachia in T. turkestani; the former showed a decline in fecundity, number of F₁ females and percentage of F₁ females while the latter showed a decline in hatching rate, survival rate, number of F_1 females and percentage of F_1 females. Cardinium and Wolbachia also influenced the fitness of T. turkestani by shortening its lifespan and developmental durations. Furthermore, when infected with Cardinium and Wolbachia, CI was even stronger. Cardinium and Wolbachia had no influence on CI strength or rescue of the other. In summary, the endosymbionts Cardinium and Wolbachia were able to regulate reproduction of T. turkestani and N. californicus by inducing CI, and impact population fitness of the two different mites simultaneously, thus affecting their population dynamics.

Keywords: Cardinium, Wolbachia, Tetranychus turkestani, Neoseiulus californicus, reproductive regulation



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Evaluation of seventeen entomopathogenic *Beauveria bassiana* Bals. (Vuill) isolates against the two-spotted spider mite (*Tetranychus urticae* Koch, Acari: Tetranychidae)

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This study was carried out to determine the biological control potential of 17 entomopathogenic Beauveria bassiana isolates against adult females of the two-spotted spider mite (Tetranychus urticae Koch) under laboratory conditions. A spore suspension was prepared from a 15 day old culture of the isolates on PDA medium. In the pathogenicity tests, 1x10⁷ spore/ml was used. Inoculation was performed by spraying the spore suspension on the adult female mites. Inoculated mites were transferred to bean leaf disks (20 mm in diameter) in sterile Petri dishes and incubated at 25 °C for 5 days. Untreated mites, i.e., mites treated with sterile distilled water containing 0.02% Tween 80, were used as controls. The experiment was established in a completely randomized block design with five replications. Thereafter, the treated adult mites were checked for mortality after the first, third and fifth days of incubation and dead mites were kept separately in humid sterile Petri dishes for another 10 days to determine the mycosis rate. Mortality was observed from the first day and increased with the incubation period. The highest mortality rate of 82% was obtained with isolate GOPT-321 after a three day incubation period. The mortality rates after the 5 day incubation period were 96%, 96%, 94%, 92%, 89%, 89% and 89% for the GOPT-120, GOPT-123, GOPT-247, GOPT-375, GOPT-105, GOPT-283 and GOPT-321 isolates, respectively. Further studies will be conducted, especially with these isolates, to investigate their *in vivo* performance.

Keywords: Beauveria, entomopathogen, Tetranychus, biological control, mortality

Section 3. Agricultural acarology

Evaluation of *Xenorhabdus* and *Photorhabdus* spp. culture supernatants against *Tetranychus urticae* (Acari: Tetranychidae)

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The effectiveness of cell-free supernatants produced by the symbiotic bacteria, Xenorhabdus szentirmaii, X. nematophila, X. bovienii, X. cabanillasi, Photorhabdus luminescens and P. temperata associated with insect parasitic nematodes was investigated against different developmental stages of Tetranychus urticae (Acari: Tetranychidae) in Petri dishes. In addition, the most virulent bacterial supernatants were tested on T. urticae in pot experiments. All studies were conducted at 25±1°C temperature, 70±5% relative humidity and a light cycle of 16h in a climate room. The mortality rates caused by the bacterial supernatants to *T. urticae* eggs, larvae, protonymphs, deutonymphs, adult males and adult females in the Petri dish experiments ranged between 2.5-4.5%, 46-98%, 31-96%, 42-92%, 92-100% and 46-93%, respectively, at 7 days post-treatment. All of the tested bacterial supernatants had a very low effect on the egg stage and no statistical difference was found among the treatments. Xenorhabdus szentirmaii and X. nematophila caused more than 90% mortality on the mobile stages of *T. urticae* and they showed the highest efficacy when compared to the other bacterial supernatants. The application of the supernatants of X. szentirmaii, X. nematophila, and X. szentirmaii + X. nematophila combined, significantly reduced the T. urticae population in pot experiments. Overall, the data showed that X. szentirmaii and X. nematophila supernatants could be potential control agents against *T. urticae*.

Keywords: Spider mites, *Tetranychus urticae*, *Xenorhabdus*, *Photorhabdus*, entomopathogenic nematodes

Acknowledgement: This study was supported by the Scientific and Technological Research Council of Turkey (TUBITAK TOVAG 1170172)



2-8 September 2018, Antalya - TURKEY

The expression pattern of ecdysteroid biosynthesis and signaling genes during the molting process in a spider mite

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Arthropods need to shed their cuticle, i.e, molt, to grow. Ecdysteroids play a crucial role in the regulation of molting and metamorphosis in insects; however, the details of this are still unclear in key pest, including spider mites. In this study, we investigated 14 canonical genes for ecdysteroid biosynthesis and signaling, and also their expression patterns around molting events, in a key spider mite, *Panonychus citri*. The expression of the most analyzed genes followed a "zigzag-like" expression pattern around the molting event, suggesting their involvement in the developmental processes of mites, especially because the expression patterns of *PcRXR1* and *PcRXR2* are relatively opposed to each other and are described as negative zigzag and positive zigzag, respectively. Furthermore, the rescue experiment upon the silencing of *Spook* showed that Ponasterone A but not 20E could rescue the molting. Through the silencing of *PcRXR1* and *PcRXR2* by RNAi, the molting process of mites was significantly inhibited but showed different phenotypes than those resulting from the silencing of *PcSpo*. Furthermore, the expression levels of *PcRXR1* and *PcRXR2*, upon silencing one or the other pointed, to a complex, co-regulated environment together with *PcEcR* during the molting. To better understand the role of *PcRXR1* and *PcRXR2* during molting, a proposed model on how *PcEcR* interacts with *PcRXR1* and *PcRXR2* will be further discussed.

Keywords: Panonychus citri, ecdysteroid, Halloween genes, ecdysone receptor, molting process

The diversity and ecology of mites (Acari) in South African vineyards

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The common grapevine (Vitis vinifera) is the main species used for wine making, with South Africa being one of the top wine exporting countries. Grapevine is vulnerable to a range of threats, one of which is mites. Plant-parasitic mites are extremely damaging pests with a rapid generation time, high fecundity and a tendency to over-exploit their hosts. The diversity of mites on grapevines in South Africa is virtually unstudied. Makeshift surveys have been done, with predatory mites and phytophagous mites being recorded, but no recent studies focussing on their ecology, pest status and seasonal cycles, have been conducted. The aim of this study was to investigate mite diversity, the pest status of phytophagous mites above and below ground, and predatory mites, in vineyards in South Africa. Sampling took place over a two year period on four farms in Wellington and one organic farm in Stellenbosch. Each farm contained a motherblock, nursery and commercial vineyard. The organic farm only consisted of a commercial vineyard. At each site vine, branches, weed samples and soil samples were collected. Vine mites were collected by running the leaf material through a mite brushing machine. Soil samples were placed in Tullgren funnels. In addition, mites were collected directly from weeds. The collected mites were mounted and identified with the help of taxonomic and descriptive keys. A surprisingly low diversity of oribatids was found in the soil. The predatory mite diversity was found to be much higher than expected. Brevipalpus was the dominant phytophagous mite. Tetranychidae was less abundant. It appears that the invasive genus Brevipalpus is out-competing the previously dominant plant pest group, Tetranychidae. Predatory mites have been established as an effective biocontrol measure. The high diversity of the predatory mites could be used for the sustainable control of pests like *Brevipalpus*.

Keywords: Tetranychidae, Tenuipalpidae, vineyards, predatory, phytophagous



2-8 September 2018, Antalya - TURKEY

A preliminary study of mites in the cork oak forests of Tunisia

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Cork oak (Quercus suber) forests cover a total area of about two million hectares across the western Mediterranean basin. The largest continuous cork oak stands are located in the southwest of Portugal and Spain on the Iberian Peninsula. This iconic species is also found in south-western France and southern Italy, and in the northern African countries of Morocco, Algeria and Tunisia. These cork oak forests are of considerable ecological, cultural and economic importance. However, in Europe and especially in North Africa, they have been considerably reduced in total area by conversion to agricultural land and their overall health has suffered from overexploitation of the wood and cork resource, overgrazing and lack of natural regeneration. In Tunisia, outbreaks of pests and diseases have also been major inducers of cork oak forest decline. Despite the importance of these forests to Tunisia there have been no studies of mites and their possible contribution to forest decline. Therefore, the objective of this study was to undertake a preliminary investigation of forest mite diversity in the Tunisian cork oak ecosystem. Three sites in the main cork oak region, which is located in the north-west of Tunisia, were chosen in 2017 and surveyed during the growing season. Phytophagous and predatory mites belonging to four families, Phytoseiidae, Tenuipalpidae, Tetranychidae and Tydeidae, were collected. Further investigations on a larger scale are scheduled and bio-ecological studies may be pursued. The cork oak forests of Tunisia are an extremely important natural asset that is now under even greater threat due to global climate change and the introduction of invasive species. Protection and rehabilitation of the remaining Tunisian forests are essential, as well as research into their ecological processes, including the role of the diverse mite fauna.

Keywords: Mites, investigation, Quercus suber, Tunisia, forests

The castor bean plant, *Ricinus communis*, as an alternative host plant for *Tetranychus urticae* for the mass rearing of the common phytoseiid predators, *Phytoseiulus persimilis* and *Neoseiulus californicus*, in Egypt

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The aim of this investigation was to develop a simpler and cheaper alternative method for the rearing of the predatory phytoseiid mites, *Phytoseiulus persimilis* (Athias-Henriot) and *Neoseiulus californicus* (McGregor), as biological control agents of *Tetranychus urticae* Koch under plastic tunnel conditions in the arid zones of Egypt, to meet the demands of the private sector. The castor bean (*Ricinus communis* L.) shrub was the species tested because it appears to be a cheaper to grow and more tolerant alternative host plant to the common bean, *Phaseolus vulgaris* L., which is suggested by its growing incidentally as a weed in such locations. The biology of the predators and the prey was studied under laboratory condition at a mean temperature of 26 ± 2 °C. The estimated life table parameters for *P. persimilis* and *N. californicus* when fed on *T. urticae* on the green or red leaves of the two castor bean land races showed reproduction rates for both species that were only slightly below the reproductive rate when *T. urticae* was fed on beans. Therefore, the use of both red and green castor bean leaves can be recommended as a cheaper alternative than the common bean for the mass rearing of both of the phytoseiids predators, *P. persimilis* and *N. californicus*, on *T. urticae*.

Keywords: Ricinus communis, land races, pytoseiid mites, life table, Tetranychus urticae



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Section 4. Taxonomy and systematics

On-line database of Eriophyoidea: a project to create an important tool for taxonomists

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Eriophyoidea is among the most studied groups of phytophagous acariform mites in the twenty first century. In the last ten years, more new species of this superfamily have been described than in any other mite superfamily. For the same period, the bibliographical data on eriophyoid species, especially those described before the computer era, are scattered in obscure journals and publications, making literature searches difficult and discouraging researchers from studying this taxon. Twenty years ago an important computerized database was developed by Prof. J. Amrine and Prof. E. de Lillo. At that time, the database included ~3,200 records, each assigned to a single named species and composed of a number of fields, including species name, authors, date, host plant, symptoms and references. Up to now, the database has been constantly updated by Prof. J. Amrine and some eriophyoidologists who have sent their data to be included in the database. Currently, the database includes over 4,500 records; however, many taxa have not been included, mainly because of the huge flow of the new data provided by taxonomists. The database is often cited in literature and confidentially used by some researchers; however, it remains poorly known as it is unavailable to the broader audience. Therefore, we aim to rearrange this proprietary database into a standardized ANSI compliant SQL database which will be available through the Internet and hosted by a well-known scientific or educational organization. The internet based interface will simplify the process of uploading new records along with the corresponding taxonomic publications, conducting searches, inserting comments and adding images and will provide an open source database that we hope will greatly contribute to our understanding of the huge diversity of Eriophyoidea.

Keywords: Taxonomy, Eriophyoidea, plant pest, on-line database, SQL

Phyllocoptes (Acari: Eriophyoidea) from rose: how many species?

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There are few examples of a plant disease epidemic as devastating as rose rosette, the single most significant threat to the rose industry in North America. The disease causes significant losses for home growers, rosarians, municipal gardens and the nursery industry alike. The causal agent is the emaravirus, rose rosette virus (RRV), which is transmitted by the eriophyoid mite, *Phyllocoptes fructiphilus* Keifer. With the identification of the causal agent of rosette, the disease epidemiology is better understood. However, there are still knowledge gaps concerning vector characterization and virus-vector interactions. The situation is further complicated because of the uncertain taxonomic status of rose eriophyoid species, especially those belonging to the genus *Phyllocoptes*. In our crossing experiments *Phyllocoptes adalius* Keifer and *Phyllocoptes resovius* Druciarek & Lewandowski hybridized, with the lack of both pre- and post-zygotic barriers in the F1 generation. An integrative taxonomic approach utilizing both bioassays and molecular tools was used to characterize the vector, and to reveal the taxonomic status of other *Phyllocoptes* species collected from roses. Results also indicate that *P. fructiphilus* is possibly a species complex, with diversity probably playing a role in transmission efficiency.

Keywords: *Phyllocoptes*, rose rosette virus, hybrids, reproductive isolation, virus-vector interactions



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The Megalolaelapidae awakens: systematic revision and biology of Megalolaepidae (Mesostigmata: Dermanyssina)

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Mites of the monotypic family Megalolaelapidae include some of the largest species of Mesostigmata, with females up to 4 mm in body length. However, despite their large size, Megalolaelaps Berlese, is poorly documented, with 10 recognized species. In addition, limited information in descriptions and similarity with Pachylaelapidae and *Neopodocinum* (Macrochelidae), have created difficulties such as: poor diagnoses, exclusion from taxonomic keys and unclear relationships with other families. Here a diagnosis, nomenclatural status clarification and the valid species are presented. Diagnosis: Large mites, idiosomal length 2000-4000 microns. Dorsal shield entire, almost completely covering idiosoma, dorsal setation hypertrichous. Epigynal shield separated from anal shield by a wide area of soft integument, ventral shield absent, exopodal platelets absent, lateral and ventral opisthogastric setation hypertrichous. Palp pretarsal claw 2-tined, palp trochanter with a large ventral horn-like projection. Anal shield free. Male with spermatodactyl long, tightly coiled, and inserted medially in the anti-axial surface of the movable digit. Taxonomy: Family Megalolaelapidae Fonseca, 1946: 179. Type genus Megalolaelaps Berlese, 1892: 72, by monotypy. Type species Megalolaelaps haeros Berlese, 1888, by subsequent designation (Vitzthum 1931; 26). Megalolaelaps includes six valid, recognizable species. Other species previously placed in Megalolaelaps should be transferred to different groups, e.g., all oriental species are transferred to Neopodocinum. Hence, Megalolaelaps is restricted to the "New World". Valid species: M. haeros Berlese, 1888, from Brazil; M. hirtus Berlese, 1904 from Brazil on Passalus interruptus, reported in Ecuador; M. mexicanus Stoll, 1893, from Mexico; M. enceladus Berlese, 1910a from North America on Dichotomius carolinus; M. immanis Berlese 1910b from Venezuela and Brazil; M. colossus Combita-Heredia & Quintero-Gutiérrez 2018 on Oxysternon conspicillatum in Colombia and Brazil; plus two new species that are associated with dung beetles in Colombia and currently under description.

Keywords: Diagnosis, dung beetle, Megalolaelapidae, New World, symbiosis

Inclusions of terrestrial Parasitengona (Actinotrichida, Prostigmata) in amber material

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Terrestrial Parasitengona constitute an ecologically distinct group within the prostigmatid mites (Arachnida, Actinotrichida) and encompass over 5,000 nominal species. Representatives of this world-wide group are highly diversified, both with respect to biology and morphology, and live in a wide range of habitats. They are characterised by a complex life cycle involving alternation of active (larvae, deutonymphs and adults) and inactive (prelarvae, protonymphs and tritonymphs) instars. The representatives of active instars, while looking for prey (deutonymphs and adults) or host (larvae), penetrate litter, lower vegetation layer or tree trunks, which makes them prone to occur in the amber material. The literature published until 2014 contains 23 records of fossil parasitengones; three of them refer to specimens identified to family or superfamily level and 18 (reported by Menge, Koch and Berendt at the middle of the 19th century) refer to species of unclear taxonomic status, due to the lack of type material or inadequacy of morphological descriptions. That means there are only two species, Proterythraeus southcotti, Vercammen-Grandjean 1973 and Atanaupodus bakeri, Judson & Makol 2009, with unquestioned taxonomic position, described from amber inclusions to date. The present analysis of over 2,100 amber lumps from private and museum collections has been carried out on material from different deposits, including Baltic, Bitterfeld, Burma, Dominican, Liodes, Rovno and Siberian amber. We have reported around 2,300 zooinclusions containing representatives of terrestrial Parasitengona mites (ca. 2,100 larvae and ca. 200 postlarval stages). The lumps with the best preserved acaroinclusions have been morphologically analysed. As a result, ten new species of terrestrial Parasitengona mites (Calyptostomatidae, Erythraeidae, Smarididae, Trombidiidae, Trombellidae, Microtrombidiidae) have been described and a further two species assigned to trombidioid families are under description. The overall similarity of the recent findings to the extant fauna and the lack of forms that markedly depart from extant fauna may support the hypothesis that all major evolutionary deviations occurred prior to the Cretaceous Period.

Keywords: Trombidioidea, Erythraeoidea, Calyptostomatoidea, succinite, retinite



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A new, interesting tenuipalpid (Acari: Trombidiformes: Tenuipalpidae)

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A tenuipalpid mite was collected from *Acacia caffra* (Thunb.) Willd. (Fabaceae) in 2009 in Pretoria, South Africa. Although all *Acacia* spp. contain cyanogenic glycosides that are potentially dangerous, it is obviously not particularly harmful to these mites. These mites, which are small and bright red, were found settled in small, wax, clamp shell-shaped structures under the bark of the tree or in blisters. This species is closely related to *Aegyptobia* Sayed and *Phtoptipalpus* Trägårdh in having a 5-segmented palp, 13 pairs of setae on the opisthosoma (*c1*, *c2*, *c3*, *d1*, *d2*, *d3*, *e1*, *e2*, *e3*, *f2*, *f3*, *h1* and *h2*), and tarsal claws uncinate (some species of *Aegyptobia*). However, it is more closely linked to *Phytoptipalpus* in having two pairs of anal setae (*ps1*-2). It differs from both genera in that ventral shields are absent, as well as setae *4a*. Some species of *Phytoptipalpus* have only three pairs of legs but in this species, leg IV is reduced, wrinkled and bearing four setae and one coxal seta. Males have four pairs of legs. Based on these differences, we consider it potentially to be a new genus.

Keywords: Mites, Tenuipalpidae, *Acacia caffra*, new taxa, glycoside

One new genus, two new species, three new records and an updated record of mites in Thailand

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Thailand has a great diversity of mites, such as eriophyoid mites and spider mites, associated with various plants and stored products. Herein we report one new genus, two new species, three new records and one updated record of mites from Thailand. *Rotsukhona* n. gen., n. sp. and *Vareeboona* n. sp. (Eriophyidae) are free living on both leaf surfaces of *Tetracera loureiri* (Finet & Gagnep.) and the lower leaf surface of *Bouae burmanica* Griff., respectively. In addition, we report three new records, namely *Tetranychus parakanzawai* Ehara on *Cucumis melo* L., *Tyrophagus pacificus* Fan & Zhang on *Cordyceps militaris* (L.) Link, and *Tyrophagus tropicus* Robertson on *Ziziphus mauritiana* Lam. In addition, *Vimola artocarpae* (Mohanasundaram), an eriophyoid mite feeding on *Artocarpus heterophyllus* Lam., is an updated record.

Keywords: Eriophyidae, Tetranychidae, spider mite, taxonomy, Thailand



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A new species of the genus Storchia (Acari: Stigmaeidae) from Pakistan

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Mites of the family Stigmaeidae are well known predators of phytophagous mites, lepidopteran eggs and small soft bodied insects. A random survey was conducted to explore the predatory mite fauna of the Punjab, Pakistan. The holotype female (male unknown) of a new species of *Storchia* was collected from the city of Sheikhupura on the millet plant (*Pennisetum americanum*) and is described here. Fourteen (14) paratypes with the same collection data as the holotype were also collected, and seven more from *Oryza sativa*. The description, figures, measurements and a discussion are provided. All specimens were deposited in the Acarology Research Laboratory-I, Department of Entomology, University of Agriculture, Faisalabad, Pakistan.

Keywords: Stigmaeidae, *Storchia*, Acari, new species, predatory mite

Description of a new species (Acari: Mesostigmata: Trematuridae) from Pakistan

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Uropodids have been poorly investigated in Pakistan. During 2014-15, a faunistic survey of poultry manure-inhabiting mites was carried out in eight districts (Faisalabad, Dera Ghazi Khan, Jhang, Bakhar, Rajanpur, Layyah, Muzaffargarh and Rahim Yar Khan) of Punjab Province, Pakistan. Poultry manure samples were collected from three different poultry containing structures (control sheds, semi-control sheds and household poultry cages) in each district. Samples were also collected from a fenced, free range poultry farm in Dera Ghazi Khan. Mite extraction, sample storage and permanent slide preparation were done by using Berlese Funnel, 75% ethyl-alcohol and Hoyer's medium, respectively. The specimens were examined under a stereomicroscope and phase-contrast microscope (MT4210H, Meiji Techno®, Japan) for the separation of mites and detailed taxonomic studies, respectively. Illustrations were done by using Adobe Illustrator® (Adobe Systems Incorporated, USA). All measurements are given in micrometers. Trichouropoda sp. n. is described from the holotype and 10 paratypes from the Dera Ghazi Khan district, and is clearly differentiated on the basis of dorsal chaetotaxy, ornamentation, sternal shield and pedofossal reticulations. All the specimens were deposited in Acarological Laboratory II, Department of Entomology, University of Agriculture, Faisalabad. The manuscript includes the description and illustrations, along with the taxonomic key for uropodid mites from Pakistan.

Keywords: Mesostigmata, uropodids, *Trichouropoda*, poultry manure, Pakistan



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Friday, 7 September
Osman Gazi Hall
Section 1. Alternative pesticides

Toxicity and durability of two types of nanoformulation of *Achillea* spp. (Asteraceae) essential oil against the two spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae)

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Using plant essential oils has been an important pest control option in pest management strategies in recent years. The use of modern technology is necessary to improve the efficacy of essential oils by increasing their volatility and reducing their rapid oxidation properties. Controlled release in nano-encapsulated formulations allows the essential oils to be used more effectively over a given time interval and the minimization of environmental side effects. Preparing formulations of essential oils that may increase their quality and effectiveness in pest control is one of the critical areas in insect pest control. The choice of formulation depends on the physical, chemical and biological properties of essential oils and also their effects, usage and applications. The encapsulation of essential oils in nanocapsules promotes longer biological effect, through the maintenance and controlled release of active ingredients for a longer period. In this study, two types of nanoformulation that included CS/AEO/TPP (chitosan/sodium three polyphosphate) and CS/AEO/k-CAR (chitosan/carrageenan) were prepared with equal amounts of Achillea plant essential oil and evaluated against the two spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae) for 24 hours. The experiments were carried out at 26±1°C, 65±5% RH and a photoperiod of 16:8 h (L:D). The LC₅₀ and LC₉₀ values of first and the second nano-formulation were 8 μl/l and 34μl/l air, and 14 and 58.75 μl/l air, respectively. The experiments therefore showed that the first type of nano-formulation was more toxic than the second. In addition, the second nano-formulation retained its lethal effect 120 hours longer than the first nano-formulation.

Keywords: Nano-formulation, *Achillea*, essential oil, *Tetranychus urticae*, bioassay

Alternative control agents of the dried fruit mite, *Carpoglyphus lactis* (L.) (Acari: Carpoglyphidae) on dried apricots

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Turkey is the biggest dried apricot producer in the world. Carpoglyphus lactis (L.) (Astigmata: Carpoglyphidae) is the most common species on dried apricots. When C. lactis feeds on the fruit sugar of the dried apricot, it accelerates the development of mould fungi and causes unwanted flavours and odours due to the digestive products, secretions and dead bodies of the mite. These contaminants can cause skin diseases and some disorders of the digestive system. Fumigants such as methyl bromide and phosphine are used for the control of this harmful mite. However, these chemicals damage the health of humans, and sometimes cause death, and damage the environment. Biological studies have shown that both reducing the amount of oxygen and/or humidity negatively affect the development of C. lactis. Based on this evidence, the effects of different physical agents, namely ferric oxide and ozone gas (oxygen depleters), and calcium chloride and silica gel (humidity reducers), on packaged dried apricots were studied. The lethal dose concentrations (LC₅₀ and LC₉₀) and lethal times (LT₅₀ and LT₉₀) of each product were determined by probit analysis. In this study, all of the physical agents provided successful control with 100% death rates of females of C. lactis. A death rate of females of 99% was most rapidly obtained with ozone gas treatment, following by ferric oxide treatment. Ozone gas was particularly toxic, causing a significantly high level of mortality after application at 44.4 mg/L (LT_{00} = 34 hrs). When ferric oxide was applied at 5 gr/100 m³ and higher rates, it killed all the female mites within 48 hours. In addition, more than 2 g of calcium chloride/100 m³ killed all C. lactis females within 72 hours. Lastly, silica gel affected mites at a higher dosage of 20 gr/100 m³) and over a longer period, i.e., more than a week.

Keywords: Carpoglyphus lactis, dried apricot, humidity, oxygen, control



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RNAi in Tetranychus urticae by feeding on dsRNA-coated leaves

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RNA interference (RNAi)-mediated gene silencing has proven to be a powerful tool in reverse genetics and an intriguing prospect for application in pest management. The two-spotted spider mite (TSSM) *Tetranychus urticae* is a serious arthropod pest, attacking over 1,100 plant species, and virtually has developed resistance to 95 active ingredients of chemical pesticides, the largest number among arthropod pest species. The availability of the complete genome sequence has led researchers to focus on the application of double stranded RNAs (dsRNAs) triggering RNAi for the control of TSSM. Here we assessed RNAi-mediated pesticidal effects on TSSMs fed on kidney bean leaves on which dsRNA targeting an ATP-binding cassette (ABC) transporter (*TuABC*), a conserved gene among eukaryotes and archaea, was distributed on the upper surface; no surfactants were used because they often induce negative effects on their physiology. The relative level of *TuABC* expression was reduced by dsRNA-*TuABC*. Dose-dependence on dsRNA-*TuABC* was found for mortality, fecundity and body color of TSSM. *TuABC* is a potential target for foliar application of dsRNA as a next-generation pesticide for controlling the TSSM.

Keywords: ABC transporter, coating method, dsRNA delivery, oral RNAi, pest control

Control of mite pests with botanical acaricides in Thailand

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The use of extracts and essential oils from plants as botanical acaricides to control mite pests is an attractive alternative method with high potential because of their generally low toxicity to warm-blood mammals and low impact on the environment. Botanical acaricides also present an opportunity to expand and improve IPM programs as chemical pesticides tend to be of limited use because of the rapid development of resistance. Nowadays, mostly organic farmers in Thailand use water extracts of different medicinal and spicy plants in order to control insect and mite pests. In our study, more than 100 tropical plant species were selected for the possibility of high acaricidal properties against various mite pests. However, only six plant species, especially their essential oils, were found to be extremely toxic to mite pests and could be commercialized. To date, three plant essential oil formulas have been developed and made available in the markets or among farmer communities. The first commercial product is made from a combination of the essential oil of clove, Syzygium aromaticum (L.) Merr. & L.M. Perry, and cinnamon, Cinnamomum bejolghota (Buch.-Ham.) Sweet. It is applied as a spray and is used against the house dust mite, Dermatophagoides pteronyssinus (Trouessart). The second product is also made from those plant essential oils but it is used for the control of the stored product mites, Suidasia pontifica Oudemans and *Tyrophagus* sp. The third product is formulated with the essential oil of the black pepper, Piper nigrum Linn., as a major component and it is used in the control of the mushroom mites, Dolichocybe indica Mahunka, Luciaphorus perniciosus Rack and Formicomotes heteromorphus Magowski. Nanoparticle formulations of some other plant essential oils are showing good effectiveness against spider mites and are under development. Further investigations of other plant species that may contain active compounds with potential acaricidal properties, namely toxicity, repellence and growth inhibition, as well as modified applications, are required.

Keywords: Plant extract, essential oil, acaricidal property, mite pest, nanoparticle



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Acaricidal activity of *Allium sativum* L. extracts against the stored product mite, *Suidasia pontifica*

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Natural products are in demand for pest control because they generally cause less harm to the environment than synthetic pesticides and are less expensive yet at the same time they are effective against a wide range of insect and mite pest. This study aimed to evaluate the efficacy of *Allium sativum* extracts against *Suidasia pontifica* which causes allergenic response and poses a great challenge in post-harvest agricultural products, especially in areas of human activities. In our study, a hexane extract of *A. sativum* at 0.70 g/L was able to kill *S. pontifica*. Chemical compositions were analyzed with the GC-MS method. Our findings support the potential use of *A. sativum* extract as an alternative to synthetic acaricides.

Keywords: Allium sativum, garlic, natural product, stored product mite, synthetic acaricide

Section 2. Chemical control and resistance

Tomato russet mite, *Aculops lycopersici*: status in Belgian tomato greenhouses, screening of pesticides and estimation of population densities

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The tomato russet mite (TRM), *Aculops lycopersici* (Tryon, 1917), Eriophyidae, has recently spread in the main tomato production areas in Belgium and causes important economic damage. A survey of 50 Belgian tomato growers in 2017 indicated the presence of TRM at 94% of the growing facilities compared to 57% in 2016. An infestation of TRM resulted in an average production loss of 2% and led to an extra average labor cost of 5.2 hrs/ha/wk. More than half of the growers indicated that TRM was insufficiently to moderately manageable. At that time, relevant information on the effectiveness of chemical control agents was lacking. Therefore, a semi-field trial was conducted to compare the efficacy of 7 different pesticides against *A. lycopersici* on tomato. Paraffin oil and sulphur showed good results, "Oberon" (Spiromesifen) together with the wetting agent "Trend 90" (isodecyl alcohol ethoxylate) and "Danitron" (fenpyroximate) caused a slight reduction of TRM, and "Vertimec" (abamectin) and "Oberon" (Spiromesifen) showed no effect at all. However, no resistance of the TRM strain to "Vertimec" and "Oberon" was detected. The reason for the low efficacy of some pesticides in this trial, and also in practice, remains unclear. In order to gain a better insight, populations of TRM need to be monitored. Therefore, a binomial sampling plan for estimating TRM densities was developed.

Keywords: Tomato russet mite, chemical control, resistance, monitoring, Aculops lycopersici



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The resistance status to abamectin and pyridaben of *Panonychus citri* (Acari: Tetranychidae) collected from the eastern Mediterranean region of Turkey

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The citrus red mite (CRM), *Panonychus citri*, is one of the most important pests of citrus production in Turkey. Chemical control is the only method applied by growers to keep CRM populations below economic thresholds in Adana, Turkey. Recent population outbreaks of CRM were observed, possibly due to the mite developing resistance to several acaricides commonly used. The aim of this study was to determine the comparative acaricide resistance status of nine populations of CRM collected from commercial orchards with a susceptible strain collected from a pesticide free area. According to management failures experienced by the growers, abamectin and pyridaben were included in the study. Our experimental system consisted of laboratory bioassays and biochemical enzyme analyses. A leaf-disc method was used to determine the LC₅₀ and LC₉₀ values of different CRM populations. The test units were constructed by placing pesticide-free sour orange leafdiscs on water saturated cotton wool pads in Petri dishes. Adult females were transferred to the leaf-discs and the test units were then sprayed with different acaricide concentrations to obtain a range of mortalities in different CRM populations. A total of five to seven population-specific concentrations were estimated and the 5-10% to 90-95% mortalities were determined for each population. Our results showed that all orchard populations had developed resistance to abamectin and pyridaben when compared to a susceptible population. The resistance ratios based on the LC₅₀ values varied between 2.81 and 34.82 for abamectin, and between 2.24 and 75.06 for pyridaben. Biochemical enzyme assays indicated that esterases and glutathion S-transferase may be involved in the methobolic pathway of abamectin and pyridaben in CRM.

Keywords: Citrus red mite, resistance, bioassay, enzyme assay, abamectin

Establishment of integrative resistance levels and acaricide resistance level status for *Tetranychus urticae* in Korea

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Tetranychus urticae is a major pest of rose cultivation area in Korea. Both phenotypic and genotypic resistance detection systems were established earlier, based on residual contact vial (RCV) bioassay and quantitative sequencing (QS), respectively, for the rapid monitoring of acaricide resistance status. In this study, we tried to integrate all available infomation associated with phenotypic and genotypic resistance traits to provide practical management actions. Phenotypic and genotypic resistance levels were determined by applying RCV and QS to 46 field populations collected from roses, strawberries and apple trees. Most populations exhibited multipe resistance to various types of acaricides. Especially, the resistance levels in mites from rose cultivation area were higher than those from stawberry and apple cultivation areas, suggesting that frequent application of acaricides is a major driving force in the development of multiple resistance in the field. The integrated phenotypic and genotific resistance traits were determined by assigning a weight to each resistance value after categorization and then by combining them. The practical management action was empircally suggested by considering the resistance potential based on the integrated resistance allele frequencies and the control efficacy of various acacides. Taken together, about 80% of the rose cultivation areas in Korea exhibited high resistance levels to almost all the acaricides used, suggesting the utmost necessity of alternative control methods, e.g., biological control, whereas alternative acaricides could be used on the other.mite populations.

Keywords: Tetranychus urticae, acaricide, resistance, diagnostics, integrated pest management



2-8 September 2018, Antalya - TURKEY

Abamectin and milbemectin resistance in European populations of the twospotted spider mite, *Tetranychus urticae*

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The macrocyclic lactones, abamectin and milbemectin, are frequently used to control phytophagous mites; consequently, field resistance has been reported. In particular, *Tetranychus urticae* Koch is notorious for its strong ability to rapidly develop resistance. Here, we report on field monitoring where bioassays were used to determine susceptibility in more than 20 field populations of *T. urticae* sampled from different host plants and areas in Europe. Compared with the abamectin and milbemectin susceptible reference strain, adult females from a number of populations exhibited abamectin resistance ranging from 30-fold to 300-fold. In contrast, the decrease in milbemectin susceptibility was much lower, and resistance only reached 30-fold in a single population. Known resistance mechanisms, such as the presence of substitutions in the glutamate-gated chloride channel (GluCl) and the expression levels of the P450 capable of metabolizing abamectin, were assessed. In addition, in a hypothesis free approach, we determined genome-wide expression differences in a number of susceptible and resistance strains, revealing novel genes and pathways associated with abamectin resistance.

Keywords: *Tetranychus urticae*, acaricide resistance, abamectin, milbemectin, glutamate-gated chloride channels

Toxicity of phosphine fumigation to Suidasia pontifica

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Fumigation with phosphine is one of the most effective ways of managing pest infestation in stored agricultural products. In a recent survey of storage warehouses in the Philippines, *Suidasia pontifica* was reported as the most dominant mite species. Their presence remains undetected until the population builds up to a level at which off-odors come from the commodity. The effect of phosphine fumigation on this mite species is not yet known. Therefore, this study was carried out to investigate the biological response of adult *S. pontifica* to phosphine fumigation. A full assay comprising eight concentrations and using a standard testing method of the Food and Agriculture Organization (FAO) for 20 h was conducted. All assays were conducted at 25 °C at 70% RH. Fumigation with phosphine at 0.40 mg/L caused complete mortality of adult *S. pontifica*.

Keywords: Suidasia pontifica, phosphine, fumigation, storage, mortality



2-8 September 2018, Antalya - TURKEY

The resistance levels to some acaricides of *Tetranychus urticae* Koch (Acari: Tetranychidae) collected from vegetable greenhouses in Antalya Province, Turkey

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The two-spotted spider mite (*Tetranychus urticae*), is an important, highly polyphagous pest that can reproduce in a very short period under appropriate conditions. Acaricides used to control this pest can develop resistance in a short time. In this study, the resistance levels to bifenthrin, hexythiazox and cyflumetofen of five different *T. urticae* populations collected from vegetable greenhouses in Antalya Province, Turkey between 2016 and 2018 were investigated. Resistance levels and resistance mechanisms were investigated by bioassay and biochemical methods. Bioassay studies were performed with the aid of a spray tower using the dried residue and leaf disc methods. Resistance levels to bifenthrin ranged from 144.6 to 493.6 times whereas resistance to hexythiazox ranged from 5.05 to 13.9 times. The lowest resistance levels (2.10- 2.18) were detected for cyflumetofen in all populations. In the case of biochemical studies, the levels of esterase and cytochrome P450 mono-oxygenase enzymes among the populations were determined using the substrates, 1-naphthyl acetate and p-nitroanisole, respectively. The results of this study indicate that P450 and esterase enzymes may play a role in resistance of *T. urticae* to the acaricides used in this study.

Keywords: Acaricide, cyflumetophene, resistance, two-spotted spider mite, cytochrome p450

Friday, 7 September

Fatih Sultan Mehmet Hall Section 1. Biodiversity - Dispersal of mites - Taxonomy and systematics

Feather mites from brood parasitic birds of the world: new data from the shiny cowbird (*Molothrus bonariensis*, Icteridae)

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It is widely accepted that the main transmission of feather mites of birds occurs during parental care of the nestlings, resulting in high bird-mite specificity. Brood parasitic birds, however, lay their eggs in the nests of other bird species, leaving the parental care to foster parents. This interspecific relationship raises the question: how do these brood parasitic birds acquire their feather mites? Is it from their foster parents or via intraspecific interactions? Our literature survey revealed 107 brood parasitic bird species from 4 orders and 5 families. While most of these are from the Old World, namely 58 cuckoos (Cuculidae), 20 indigobirds (Viduidae) and 17 honeyguides (Indicatoridae), the New World brood parasites are only 5 species of cowbirds (Icteridae), 3 cuckoos and 1 duck (Anatidae). Only 33 brood parasites have had their feather mites investigated, with most of them (25) being cuckoos and indigobirds, while knowledge of the New World cowbirds is still scarce. Some results suggest the occurrence of horizontal or interspecific transfer of feather mites, while other birds seem to acquire their mites by intraspecific interaction. In 49 analyzed specimens of shiny cowbird (Molothrus bonariensis) from the south of Brazil, most as museum specimens, we found 10 species of feather mites from 6 genera and 4 families, specifically, *Proctophyllodes* spp. 1–4; Amerodectes molothrus (Proctophyllodidae); Analges spp. 1, 2; Strelkoviacarus sp. (Analgidae); Mesalgoides sp. (Psoroptoididae), and Xolalgoides sp. Given that this bird successfully parasitizes more than 60 passerine species, our data suggest that it may acquire at least some of its mites from the foster parents, while other mite taxa seem to be truly associated with M. bonariensis. Samples from other regions of Brazil and from freshly collected birds are currently being analyzed in order to better understand the composition of the feather mite fauna associated with the brood parasitic bird, M. bonariensis.

Keywords: Horizontal transfer, host shift, host specificity, brood parasites, Astigmata



2-8 September 2018, Antalya - TURKEY

Brevipalpus mites (Tenuipalpidae) of the Azores Islands

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The Azorean archipelago, which is composed of volcanic islands located in the Atlantic Ocean, has a high level of endemism. Flat mites of the genus *Brevipalpus* Donnadieu (Tenuipalpidae) are of great economic importance since they can cause direct damage to their hosts or transmit phytoviruses. The objective of this work was to identify *Brevipalpus* mites that occur on endemic and cultivated plants in the Azores islands, based on morphological and molecular traits. A survey was conducted on the islands of Pico, Faial and Flores. Samples from ten hosts and seven families were collected. Morphological study was conducted under optical DIC and scanning electron microscopy. Molecular diagnosis was based on sequences of COI mtDNA and two nuclear regions, ITS2 and 28S (D1-D3). Four species were tentatively identified based on morphological traits: B. obovatus on Melissa officinalis, Ipomoeae indica and Vitis vinifera; B. papayensis on I. indica, Tecomaria capensis, Eleagnus umbellata and V. vinifera; B. azores on Citrus sinensis and Rhododendron indicum; and a new species, B. sp. nov. on Hedera maderensis. However, for the three molecular phylogenies, specimens identified as B. papayensis and B. azores were grouped into a single clade. The genetic distances between B. azores and B. papayensis for COI (1.0%,), ITS2 (4.8%) and 28S (0.9%) were lower than that observed for closely related species, namely 3.0% (B. chilensis x B. obovatus) for COI, 6.7% (B. chilensis x B. ferraguti) for ITS2, and 2.1% (B. obovatus x B. ferraguti) for 28S, fitting as intraspecific distances. Results showed that B. azores and B. papayensis are genetically very close, whic suggests they could be synonyms. Complementary studies must be performed in order to define the taxonomic status of these species. Brevipalpus sp. nov. was morphologically identified as belonging to the cuneatus group; however, molecular phylogeny placed it in a distinct group. These preliminary results raised intringuing questions about *Brevipalpus* systematics.

Keywords: Flat mites, molecular phylogeny, integrative taxonomy, Macaronesia, Tenuipalpidae

Acarine biodiversity associated with bark beetles in Mexico

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The inner bark of dying trees provides suitable habitat for a large number of bark beetles and their associated mites. These mites depend on these scolitids for dispersal, and also directly or indirectly for their nutrition. In Mexico, there have been very few studies of these mite/scolitid associations. A study of Mexican bark beetles and their associated mites is in progress and the data include the records for several states in the country. A total of 55 species of four orders have been reported. The most diverse Order is Mesostigmata with 65% of the total number of confirmed species, followed by Prostigmata with 25%, Astigmatina with 9% and Oribatida with 1%. Trichouropoda polytricha, Proctolaelaps subcorticalis, Proctolaelaps dendroctoni, Schizosthetus lyriformis and Dendrolaelaps neodisetus are the most representative species associated with bark beetles and have been reported in all of the studies from Mexico. Dendroctonus frontalis is the bark beetle with the highest number of associated mites in Mexico and worldwide. There is great mite diversity associated with bark beetles; this situation is mainly due to the great variety of food resources provided by the scolitids, as well as the great adaptability they have to the different environments in which they occur. Among the species mentioned in this study, some have a wide range of eating habits, live in different habitats, and have different associations that make this group interesting to study.

Keywords: *Dendroctonus*, Mesostigmata, phoretic, scolitids, symbiosis



2-8 September 2018, Antalya - TURKEY

Biodiversity and impacts of plant feeding mites on the tea plant, *Camellia sinensis*, in South Africa

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Mites are the most serious pests of tea in almost all tea producing countries. The vast expanse of the tea plantation ecosystem provides a stable, favourable microclimate, uninterrupted food supply and suitable sites for the reproduction and survival of pests. Annual surveys of mites in South Africa were carried out between 1959 and 1990 for the National Collection of Arachnida (NCA), but most of the focus was on natural ecosystems. Mites in tea plantations were neglected and the diversity is unknown. The purpose of this study was to document the diversity, and study the symptoms and impacts of economically important mite groups in tea plantations. Three functional sites were surveyed between 2015 and 2017, with mites collected using various methods to maximise capture. Over 250 slide mounted specimens have been prepared and lodged in the NCA. These represent mites belonging to 10 families, 16 genera and at least 20 species. The ongoing morphological study of the material indicates that at least six new species belonging to three families and five genera, Tetranychidae (Schizotetranychus and Myxonichus), Tenuipalpidae (Brevipalpus and Obuloides) and Tuckerellidae (Tuckerella) have been discovered. In most sections of the tea estates, the mite population was fairly high, with an estimated 30 to 100 mites per leaf causing considerable defoliation. The farm managers reported that there was a clear relationship between infestation level and yield quality, eventually affecting pruning times. Wherephytophagous mites were in high numbers, the leaves appeared red at the sites of attack. As the population increased, the infested leaves became darker, took on a scorched appearance, and a general reduction in size of the new leaves was common. Eventually this resulted in low tea production and even the death of the plant in some cases.

Keywords: Tea, plant feeding mites, phytophagous, predatory mites, Tuckerellidae

Behavioural, morphological and environmental interactions predict passive dispersal in the invasive wheat curl mite (WCM)

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Dispersal is strongly integrated into life history. Therefore, when studying dispersal, correlation between traits associated with dispersal should be examined. In this study, we investigated the relationships between dispersal, morphology, behaviour and wind speed by using the MT-1 genotype of Aceria tosichella Keifer, the eriophyoid wheat curl mite (WCM), as a study system. We tested whether: (i) dispersing and resident mites differ in morphology, (ii) so-called "pre-dispersal behaviours" (standing upright and forming chains) are associated with dispersal. Dispersal was measured as the proportion of mites blown from their host plants. A wind tunnel was used to generate wind speeds between 0.2 - 5.7m/s, with test speeds increased at approximately 0.2m/s intervals. We recorded and analyzed mite behaviour and morphology during five-minute intervals for each treatment. Measurements were made using the GIMP 2 program from video stills of individual mites on the leaf surface. The results showed that the frequency of dispersers in the population was only 1.1%. However, despite few dispersing individuals they colonized new plants efficiently and quickly attained high population density on new plants. Mites formed chains and stood up at each tested wind speed; however, the proportions behaving in these ways were low (10% and 8% of specimens, respectively), with the highest proportion expressed at wind speed ca. 3.5-4m/s. Individuals were blown away by a wind speed of 2m/s whereas chains were blown by a wind speed of 3m/s. We found that the upright position was not related to the likelihood of being blown away. Individual dispersers were not morphologically different from the residents whereas mites in chains that were blown away were more elongated. The results indicate that WCM MT-1 dispersal is influenced by the interaction of behavior, morphology and environment. Our study represents a substantial step toward explaining WCM MT-1 dispersal and colonization potential.

Keywords: Dispersal, Eriophyoidea, phytophagous mites, wheat curl mite, wheat parasites

Acknowledgement: This study was funded by the National Science Centre (Grant number: 2016/21/B/NZ8/00786).



2-8 September 2018, Antalya - TURKEY

Understanding Indian tetranychid diversity – a perusal of molecular evidence

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A revision of Indian Tetranychidae by Gupta and Gupta published in 1994 reported 101 species and opined the occurrence of fourteen species as ambiguous or doubtful. Molecular studies initiated under the aegis of the All India Network Project on Agricultural Acarology since 2012 have generated mitochondrial COI and nuclear rDNA (ITS2) data for many reported spider mite species in the country. DNA isolation by the CTAB method, PCR amplification using COI and ITS2 markers, Sanger sequencing and BLAST analysis enabled the deposition and accession of partial genomic data (COI and ITS2 sequences) of more than 40 tetranychid species by January 2018 in the NCBI - GenBank data base. Slide mounts of mite specimens used for morphological taxonomic identification and wet preservation in 96% ethanol of specimens from isofemale lines used in DNA analysis have been accessioned as voucher specimens in our repository at UAS-B (University of Agricultural Sciences, Bangalore, India). The perusal of morphological data and DNA sequence data resolved the uncertain occurrence of four cosmopolitan species, namely Tetranychus truncatus (GenBank Acc.No.JX497785; BOLD ACI1028), T. turkestani (KF160881; BOLDAAB9985), Oligonychus tylus (KU323485) and O. thelytokus (KX681448), with two new records, T. okinawanus (KX171199) and T. udaipurensis (KU310624), for India. With this molecular evidence the number of tetranychid species in the country had increased to at least 128 by January 2018. This list also includes a relatively new species, T. hirsutus (KU738615), reported on a wild/cultivated medicinal herb, Gymnema sylvestre, but does not include at least 4 to 6 probably new species in the genus *Oligonychus*, whose identity could not be determined precisely. Nuclear gene data (ITS2) is also now available for many polyphagous cosmopolitan species such as T. urticae (31 hosts), T. neocaledonicus (19 hosts), T. ludeni (13 hosts), T. truncatus (14 hosts), T. macfarlanei (26 hosts), T. okinawanus (2 hosts), T. udaipurensis (3 hosts) and T. turkestani (1-2 hosts) across their host/geographical ranges. Phylogenetic analysis of the molecular data obtained in this study will almost certainly reveal intraspecific variation or genetic variability within species which will be helpful in various basic and applied studies, including molecular diagnostics and species delimitation, DNA barcoding, the development of species specific markers, species coexistence and competitive species displacement.

Keywords: Indian tetranychids, diversity, molecular data, species delimitation, DNA barcode

Fauna and diversity of poultry manure-inhabiting mites (Acari: Mesostigmata) from the Punjab Province, Pakistan

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During 2014-15, a survey of poultry manure-inhabiting mites was carried out in nine districts (Faisalabad, Dera Ghazi Khan, Jhang, Bakhar, Rajanpur, Layyah, Muzafargarh and Rahim Yar Khan) of Punjab Province, Pakistan. In this research, a total 1,572 specimens were examined and 23 species (7 new records) from 7 families and 11 genera were identified. Diversity was calculated in three different poultry structures habitats (controlled sheds, semi-controlled sheds and household poultry cages) in each district. The semi controlled shed (Faisalabad) had the maximum mite diversity, with 18 species, while the controlled shed (Muzaffargarh) had lowest mite diversity, with 5 species. The *Macrocheles glaber* group (*Macrocheles perglaber* and *Macrocheles glaber*) were the dominant species with 17.05% and 16.29%, respectively, while *Glyptholaspis americana* and *Trichouropoda* sp. were least common (0.38%). *Macrocheles merdarius* and *M. glaber* were the most widespread species. The results will be presented with list of mesostigmatid mites species (Macrochelidae, Laelapidae, Dermanyssidae, Parasitidae, Trematuridae and Nenteriidae) from Pakistan.

Keywords: Mesostigmata, new records, diversity, poultry manure-inhabiting mites, Pakistan



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Section 2. Ecology and behavior of mites - Population dynamics

Effects of bacterial endophytes on the density and preferences of spider mites (Acari: Tetranychidae)

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Endophytes, which are bacterial or fungal symbionts of plants, often affect the behavior of arthropod pests. It has been reported that some ACC deaminase-producing *Pseudomonas* bacteria isolated from the inner parts of the fruits and vegetables grown on organic farms could reduce the levels of (*E*)-2-hexenal and the other green leaf volatiles (GLVs), and also the levels of terpenoids in carrot leaves, following the inoculation of the seeds. These volatiles are known herbivore-induced plant volatiles (HIPV). Thus, we expected that infection by these endophytes could affect the behavior of some arthropod pests and natural enemies. In a preliminary study, infection by these endophytes reduced the number of spider mites on Shiso (*Perilla frutescens*). In this study, we tested the effects of endophyte infection on the density and behaviour of two spider mite species, *Tetranychus urticae* and *T. kanzawai* (Acari: Tetranychidae). In laboratory experiments using leaf discs of cucumber and eggplant, we tested their preference and fecundity. On cucumber, spider mites tended to prefer un-infested leaves to infested ones, and laid fewer eggs on infested leaves. However, no difference was observed on eggplant. These results imply that the effects of endophytes differ, depending on the combination of species of endophyte, spider mite and plant.

Keywords: Endophyte, spider mites, preference, fecundity, plant volatiles

Do spider mites evolve antagonistic traits against cytoplasmic incompatibility induced by *Wolbachia*?

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Cytoplasmic incompatibility (CI) inducing bacteria are among the most common endosymbionts of arthropods. CI leads to increased embryonic mortality of the offspring from infected male and uninfected female hosts. Consequently, CI indirectly benefits infected females (the transmitting sex) but is detrimental for uninfected females and infected males. This generates sex-specific hostparasite conflicts that may result in the evolution of several host CI-antagonistic traits. Indeed, infected males may (i) avoid uninfected females by mating preferentially with infected ones, (ii) increase mating rates to increase the likelihood of siring offspring, and/or (iii) reduce the level of CI they cause when mating with uninfected females. Similarly, uninfected females may (i) avoid infected males, and/or (ii) compensate the cost of CI by mating multiply. However, whether such antagonistic traits evolve in response to CI remains an open question. To test this, we performed experimental evolution of spider-mite (Tetranychus urticae) populations at different Wolbachia infection frequencies. After 20 generations of exposure to CI, mate choice of uninfected females did not change but they evolved the ability to compensate the cost of CI by mating multiply. Conversely, antagonistic traits did not evolve in infected males but, instead, they evolved to mate preferentially with uninfected females and the level of CI they induced increased, probably due to an increase of Wolbachia manipulation. However, these evolved traits, in both females and males, did not affect the spread of Wolbachia. Still, our results highlight the important role played by endosymbionts on the evolution of their host mating systems.

Keywords: Experimental evolution, maternally inherited symbiont, reproductive manipulation, reproductive behaviour, sex-ratio



2-8 September 2018, Antalya - TURKEY

Spider mites on apparent versus unapparent plants: what changes?

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According to 'Spider Mites Web' (last updated 16 October 2017), there are 1,310 recorded spider mite species, with 15,412 host records on 3,808 different plant species. Furthermore, generalist species such as the two-spotted spider mite, Tetranychus urticae, which infests 1,140 plants of 126 families, and the citrus red mite, *Panonychus citri*, which infests 108 plants of 37 families, are major agricultural pests. *Tetranychus urticae* prefers unapparent plants (short-lived) while *P. citri* prefers apparent plants (long-lived). Both mites can feed on "non-preferred" apparent or unapparent plants under certain conditions. Here, we used these two generalist species as examples to study their population performance on soybean (Glycine max) as an example of an unapparent plant host versus orange (Citrus sinensis) as an example of an apparent plant. Our results showed that: i) both T. urticae and P. citri had higher fecundity, faster growth rate and smaller body size on soybean than on orange; ii) both species showed increased longevity on their preferred host, i.e., T. urticae on soybean and P. citri on orange; and iii) these observations were independent of adapted or non-adapted mite strains. In conclusion, the preference of spider mites for apparent or unapparent hosts seems to be associated with their population performance, especially in reproduction and longevity. Further studies are required to elucidate the trigger for this trade-off (reproduction and longevity) in spider mites during their transfer between apparent and unapparent hosts.

Keywords: Tetranychus urticae, Panonychus citri, life table, host transfer, population performance

New types of attacking behaviors against predators inside and outside nests of Schizotetranychus brevisetosus Ehara (Acari: Tetranychidae) on blue Japanese oak

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Several spider mite species (Acari: Tetranychidae) make dense web nests in the depressions on the surface of host leaves, and multiple generations live together in the same nests. They are called web-nest [WN] species and they frequently show anti-predator behaviors. The adults of several Stigmaeopsis species drive out and even kill phytoseiid mites that intrude into their nests. It is considered that such behaviors increase the survival of relatives. These altruistic behaviors of WN species may evolve because of high relatedness within a nest. Such behaviors have not been reported in other species. In this study, novel types of attacking behaviors on organisms and substances placed outside the nests of Schizotetranychus brevisetosus Ehara, which live on the evergreen, blue Japanese oak, are reported. Adult females attacked a larva of the predatory fly Feltiella sp. searching for prey outside a nest, and sucked its body fluids until it died, although two females were killed in the process. Individuals of S. brevisetosus also «attacked» tiny glass beads and a Parafilm strip. Adult females, nymphs and larvae participated in the attack on the Parafilm. Moreover, an adult female was observed counter-attacking a phytoseiid mite that invaded a nest, as is known in Stigmaeopsis species. Because S. brevisetosus is phylogenetically distant from Stigmaeopsis species, anti-predatory behaviors appear to have independently evolved more than once in WN species.

Keywords: Anti-predator strategy, communal sociality, counterattack behavior, *Stigmaeopsis*, social behavior



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How opilioacarids (Parasitiformes: Opilioacarida) live, love and take care of their offspring

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Mites in the order or suborder Opilioacarida form a relatively small lineage, currently containing 9 genera and about 24 species. A few studies have addressed feeding modes or defensive behaviors but only a few anecdotal reports exist on egg deposition, and none on mating behavior. In this study, most specimens were hand collected from under moss and lichens on large, standing, live pine trees. Three pairs of one male and one female were each placed in small jars with a moistened layer of activated carbon and plaster of Paris. Behavioral observations were made 1-2 times daily for 30 minutes using a Zeiss Stemi 2000-e dissecting microscope. Recordings were made using a digital video camera. Specimens were offered a range of food options, from pollen grains to crushed insects. Occasionally, the mites started feeding on the hard pollen cuticle. Co-feeding on single anthers was repeatedly observed, with no signs of aggression. Specimens remained alive for periods of 5-8 months. During that period two pairs reproduced, resulting in eggs, larvae, protonymphs and deutonymphs. Larvae were not observed to feed, consistent with previous hypotheses. Earlier observations suggested that females coat their eggs, a hypothesis confirmed during the current study. A major question regarding Opilioacarida concerns their mating behavior and specifically their method of sperm transfer. We were not able to observe the latter but can provide observations on some aspects of pre-mating behavior. There are some indications of basic parental care.

Keywords: Neocarus, development, feeding behavior, diet, Central America

Changes in the amplitude of temperature affect the biological parameters of Tetranychus macfarlanei and Oligonychus biharensis

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Tetranychus macfarlanei and Oligonychus biharensis (Acari: Tetranychidae) are two important spider mites with wide distribution on a variety of host plants in Bangladesh. Correctly characterizing the population dynamics related to the amplitudes of temperature is crucial for predicting the timing of outbreaks of T. macfarlanei and O. biharensis, as well as formulating efficient management strategies against these species. In this study, we compared the biological parameters of T. macfarlanei and O. biharensis with empirical values obtained from life-table experiments conducted at an average temperature of 22.5 °C, with a daily fluctuation of \pm 0, ± 2.5 or ± 5 °C. The fluctuation of temperature, species and sex significantly affected the egg to adult development of both species. The egg to female adult development of O. biharensis was not significantly different between the treatments in which the temperature fluctuated and the constant 22.5 °C but T. macfarlanei developed faster at both fluctuating temperatures. The higher fluctuation favored the oviposition period and fecundity of O. biharensis whereas fecundity increased in *T. macfarlanei* at the higher fluctuation. The net reproductive rate of both species was lowest at the constant temperature. The intrinsic rate of natural increase (r_m) of O. biharensis was not significantly different among treatments but the r_m values of T. macfarlanei were higher at both fluctuating temperatures compared with the constant temperature of 22.5 °C. It can be concluded that higher adaptability to fluctuating temperatures was observed in T. macfarlanei than in O. biharensis.

Keywords: Temperature amplitude, spider mite, population dynamics, adaptability, life table parameters



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Friday, 7 September
Kanuni Sultan Süleyman Hall
Section 1. Biological control

Phytoseiid mites (Acari: Phytoseiidae) of Turkey: from past to present

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Phytoseiids are important biological control agents of various pests, including spider mites, thrips and whiteflies. In 1954, Paraseiulus soleiger (Ribaga) was the first phytoseiid mite recorded in Turkey, followed by Kampimodromus aberrans (Oudemans) and Iphiseius degenerans (Berlese) in 1963. The number of known species increased from 35 in 1990 to 62 in 2011. However, in recent years the number has increased dramatically, with detailed surveys carried out mostly by present authors. The phytoseiid fauna of Turkey currently comprises 95 species belonging to 21 genera. Among them, native populations of commercially available species that are widely used for biological control, such as *Amblyseius swirskii* Athias-Henriot, *Iphiseius degenerans* (Berlese), Phytoseiulus persimilis Athias-Henriot, Neoseiulus californicus (McGregor), Neoseiulus cucumeris (Oudemans), are present in Turkey. Among the 33 species reported over the last five years, seven species, Eharius denizliensis, Neoseiulella kazaki, Neoseiulus sekeroglui, Phytoseius ibrahimi, Typhlodromus (Anthoseius) karaisaliensis, T. (Typhlodromus) antakyaensis and T. (T.) papadoulisi, were described as new species for science. New species were found on uncultivated hosts, except T. (T.) antakyaensis, which was on beans. As the new species were found in association with various economically important pests such as thrips and spider mites, they may be possible candidates for biological control, and their effectiveness should be clarified in further studies. These recent surveys have clearly indicated that Turkey has high potential to provide considerably more new species of phytoseiid mites. This may be explained by geographical position of Turkey (bridge between Asia and Europe), including the highest plant species richness ($\approx 10,000$ species) and the highest endemism rate among European countries (\approx 3000 endemic species), and relatively well preserved natural areas. It is possible that the actual number of species may be much higher than already reported. Furthermore, detailed surveys will likely contribute to the discovery of more endemic phytoseiid mite species in Turkey.

Keywords: Checklist, predatory mites, native populations, biological control, Turkey

The effect of birch pollen on the biological control of the two spotted spider mite, *Tetranychus urticae*, by the predatory mite, *Kampimodromus aberrans*

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This study examined the contribution of birch (Betula pendula) pollen to the efficacy of the predatory mite, Kampimodromus aberrans (Oudemans) (Acari: Phytoseiidae) as a biological control agent of the two spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae). The experiments were conducted in a nursery of the Golden Delicious apple cultivar at 1:5, 1:15 and 1:30 predator:prey release ratios at 25 ± 2 °C, $65\pm10\%$ RH and 16:8 photoperiod. In experiments using T. urticae+birch pollen together, the predator was also offered pollen grains daily (0.5-0.10 mg/leaf). At 1:5 predator:prey ratios, significant reductions in *T. urticae* populations were observed one week after the release of K. aberrans, and populations remained at low levels thereafter, especially in the plots in which birch pollen was added. The highest mean numbers of *T. urticae* were found in the third week with 4,700 mites per leaf and 4,922 mites/leaf in the pollen application and nonpollen application plots, respectively, in a control group with no predators. The highest population density of K. aberrans was determined in weeks 3 and 5 with 2.5 mites/leaf at 1:5 predator:prey release ratios in pollen application plots. This study demonstrated the potential of K. aberrans to be an effective biological control agent of *T. urticae* under controlled conditions at 1:5, 1:15 and 1:30 predator:prey release ratios during a three week period, especially at 1:5 predator:prey release ratios. Furthermore, K. aberrans was able to more successfully control T. urticae when birch pollen was added.

Keywords: Biological control, birch pollen, *Kampimodromus aberrans*, predator:prey ratio, *Tetranychus urticae*



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The determination of some biological parameters of the predatory mite Kampimodromus aberrans on Tetranychus urticae

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The two spotted spider mite, *Tetranychus urticae* Koch (Acari: Tetranychidae), is one of the most important pests of crops worldwide. The predatory mite, *Kampimodromus aberrans* (Oudemans) (Acari: Phytoseiidae), was tested as a potential biological control agent of *T. urticae* eggs, nymphs and adults, although it is not a natural predator of *T. urticae* in the field. Although *K. aberrans* is very common in Turkey, there is limited information on its biology and effectiveness. Therefore, the biological parameters of a natural population collected from apple orchards near Ankara were determined in a laboratory study with daily observations under laboratory conditions (25±1 °C, 70±5%, 16:8 L: D). Daily and total fecundities were 1.45 \pm 0.41 and 13.00 \pm 3.33, respectively. The development times were 2.05 ± 0.17 days to egg hatching, 1.00 ± 0.0 days for the larval stage, 1.13 ± 0.09 days for the protonymph stage, and 1.18 ± 0.095 days for the deutonymph stage, with the total development period being 5.35 ± 0.39 days. Female longevity was 13.44 ± 3.28 days, and the preoviposition, oviposition and postoviposition periods were 3.88 ± 0.61 days, 5.188 ± 0.932 days and 2.25 ± 041 days, respectively. The intrinsic rate of increase (r_m) was 0.23 females/female/ day, net reproduction capacity (R_0) was 12.69 females/female, and the generation period was (T_0) 6.05 days. However, the efficacy of K. aberrans certainly needs be confirmed with field tests under natural conditions.

Keywords: Development, fecundity, *Kampimodromus aberrans*, life table, Phytoseiidae

Acknowledgement: This work was supported by the University of Ankara through the Coordination of Scientific Research Projects (BAP-12B4347011).

Use of the predatory mite *Phytoseiulus persimilis* (Acari: Phytoseiidae) in the control of the two-spotted spider mite (*Tetranychus urticae* Koch, Acari: Tetranychidae) in greenhouse cucumber production in Tokat Province, Turkey

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In this study, the effectiveness of the predatory mite, *Phytoseiulus persimilis* Athias-Henriot (Acari: Phytoseidae), as a suppressive agent of the two-spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae), was evaluated on greenhouse cucumbers at predator:prey release ratios of 1:5, 1:15, and 1:30. Releases at each predator:prey ratio were made at 30 T. urticae per leaf. Evaluations were initiated 4 days after the release. The eggs and active forms of *T. urticae* and *P.* persimilis on the underside of leaves selected randomly from the lower, middle and upper parts of the plants in each treatment were counted with a 10X hand magnifier. In the control treatments without predatory mite and acaricide application, the population of *T. urticae* constantly increased and reached 140 active forms/leaf in August but decreased when the plants died. At the ratio of 1:5, P. persimilis reached 8 active forms/leaf while T. urticae populations reached 11 active forms/leaf. At the ratio of 1:15, the *P. persimilis* population increased (3.4 forms active forms/leaf) and the T. urticae population decreased (1.6 active forms/leaf) in September and were kept at low levels after that. In addition, plant damage was significantly reduced at these densities. Separately, the P persimilis population decreased when the T. urticae population decreased. Our work demonstrated the potential of P. persimili, to provide effective control of T. urticae on greenhouse-grown cucumbers at a moderately low predator:prey ratio of 1:15 in Tokat Province, Turkey.

Keywords: Phytoseiulus persimilis, Tetranychus, predatory mite, biological control, cucumber



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Observations of sperm and the sperm transfer process in *Phytoseiulus* persimilis (Acari: Phytoseiidae)

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Phytoseiidae mites produce both female and male offspring from fertilized eggs, while females are diploid and males develop into haploid adults. This genetic system is known as pseudoarrhenotoky or paternal genome elimination. It has been reported that male offspring have paternally derived chromosomes heterochromatinized and eliminated during early egg development. However, limited evidence has been produced regarding the precise timing of the start of paternal genome heterochromatinization and elimination. Both the processes of sperm transfer and embryo development, and the mechanisms of this reproduction system, are not clear. In the present study, detailed descriptions that will deepen understandings of the ultrastructure of male and female reproductive systems of *Phytoseiulus persimilis* were produced, and the process of spermatophore formation and sperm transfer in this species are also described, based on observations with scanning electron microscope and transmission electron microscope. In addition, spermatophores were separated and dissected, with the form and quantity of sperm within each spermatophore at different mating times observed. Phytoseiulus persimilis is one of the Phytoseiidae species with its biology best studied. The results of this study help to form a good foundation for further studies on the timing, process and mechanisms of chromosome heterochromatinization and elimination in P. persimilis male offspring embryos or even in the earlier stages, including sperm.

Keywords: Phytoseiidae, spermatodactyl, spermatophore, heterochromatinization, transmission electron microscope

Biology and potential of the predatory mite, *Amblyseius swirskii* Athias-Henriot (Acari: Phytoseiidae), for controlling thrips in Thailand

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A cohort of the predaceous mite, Amblyseius swirskii, from the Netherlands was introduced to Thailand in May 2016. Laboratory studies were conducted on its life cycle, using the chili thrips, Scirtothrips dorsalis, as food. Its biological attributes were also investigated with life table analysis by using S. dorsalis larvae; the eggs of the rice moth, Corcyra cephalonica; and the pollen of cattail, Typha angustifolia, as food. Its thrips consumption efficiency was determined by using the larvae of: S. dorsalis; bean thrips, Caliothrips phaseoli; and melon thrips, Thrips palmi, as prey. The life cycle study revealed durations of 1.50 ± 0.28 , 0.67 ± 0.04 , 0.88 ± 0.72 and 1.00 ± 0.13 days for the egg, larval, protonymph and deutonymph stages, respectively, and a total of 4.05 ± 1.17 days from egg to adult. Females laid 3.63 ± 0.65 eggs per day, totaling 52.25 ± 5.25 eggs during the oviposition period of 18.19 ± 3.34 days. Its potential when fed on S. dorsalis larvae, eggs of C. cephalonica and pollen of cattail in terms of its biological attributes obtained from life table analysis yielded net reproductive rates of increase (R₂) of 12.54, 20.02 and 4.53 times, respectively; cohort generation times (T) of 14.83, 14.99 and 14.22 days, respectively; capacities for increase (r) of 0.17, 0.19 and 0.10 times, respectively; and finite rates of increase (λ) of 1.18, 1.22 and 1.11 per day, respectively. The study on thrips consumption efficiency, using S. dorsalis, C. phaseoli and T. palmi larvae as prey, showed that during its life span the highest consumption observed was 66.50 \pm 5.54 larvae of *T. palmi* per day which was significantly different (P<0.05) from the 60.80 ± 4.16 and 58.40 ± 4.81 larvae of S. dorsalis and C. phaseoli per day, respectively.

Keywords: Predaceous mite, *Amblyseius swirskii*, food sources, biological attributes, thrips consumption efficiency



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Are predatory mites efficient vectors for entomopathogenic fungi: a comparative study?

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Recent studies have demonstrated that predatory mites can be loaded with entomopathogenic fungal conidia in order to increase infection rates in prey/pest populations. However, there is no strong experimental evidence showing that predatory mites can actively deliver pathogens to prey patches. The objective of our study was to determine and compare the capacity of two phytoseiid mite species, Amblyseius swirskii and Neoseiulus cucumeris, to deliver the entomopathogenic fungus Beauveria bassiana to their prey, Frankliniella occidentalis, the western flower thrips. Predatory mites were loaded with B. bassiana conidia and released on plants that were previously infested with first instar thrips clustered together on single kidney bean leaf. After the predatory mites unloaded all their conidia, we examined each plant section (6 leaves and 3 stem sections) to assess the number of conidia, the number of prey and the presence of conidia on each prey. Our results showed that A. swirskii, but not N. cucumeris, induced a higher spatial overlap between B. bassiana and thrips populations, thereby increasing the proportion of thrips that came into contact with conidia. This pattern likely arises from the different levels of foraging activity between the species. For instance, A. swirskii stayed longer on the plants and had a higher predation rate than N. cucumeris. Our study suggests that loading certain predatory mite species such as A. swirskii with conidia can increase their ability to suppress thrips populations by combining predation and the vectoring entomopathogenic fungi.

Keywords: Amblyseius swirskii, Neoseiulus cucumeris, vector, Frankliniella occidentalis, Beauveria bassiana

Section 2. Biological control

Improvement of biocontrol with releases of astigmatid mites

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Improving the establishment and development of populations of phytoseiid mites is the keystone to guaranteeing the successful biological control of pests inmany crops. This is especially true in the case of crops which do not produce pollen or when the pest threshold is very low, e.g., cut flowers and cucumbers. A strategy based on releases of astigmatid mites on the top of the plant canopy, as an in-crop food source, has been developed by Agrobío, based on 4 years of research. After the selection and evaluation of different astigmatid species as food for several phytoseiid species, which was followed by the testing of different ratios and releasing systems, a program was developed for different crops Specific machineries were developed for releases in high technology greenhouses. In this presentation, a summary of the completed trials and the programs commercially adopted for cucumbers, strawberries and chrysanthemums, is presented. For chrysanthemums, the program is based on 4 releases of Transeius montdorensis, in combination with 6 releases of the prey mite, Suidasia medanensis. Based on 2 years of counts on 4 commercial crops, a mean number of 61.4 predatory mites/plant was counted on 22 plots of 1,000 m², which provided a good control of thrips, with the mean number of thrips being less than 0.3 individuals/plant. However, still cases of some damage were documented when high thrip populations were already established on seedlings coming directly from the nursery. Two trials have been performed in 2018 with complementary releases of insect predators, together with some complementary foods in the early stages. An improved method that combines both strategies is discussed. In addition, the first results are presented for a new release system which is specifically designed for releasing mites and other foods on ornamental plants and vegetables, and particularly convenient for use in low technology greenhouses.

Keywords: Biocontrol, Phytoseiidae, astigmatid, chrysanthemums, cucumbers



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Screening of potential predators for the control of tomato russet mite, *Aculops* lycopersici

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Tomato russet mite (TRM), *Aculops lycopersici* (Tryon) is a key pest in cultivated tomato crops worldwide. Growers are forced to use chemicals due to the lack of commercially available natural enemies, thereby seriously interfering with integrated pest management strategies. Several laboratory studies have demonstrated that phytoseiid predatory mites have potential as biocontrol agents of TRM. Although they are capable of feeding and reproducing on TRM, establishment of those predators on whole tomato plants is usually impeded by the presence of glandular trichomes. TRM, on the other hand, is protected from predation by seeking refuge in between the trichomes. In the present study, we screened some predatory mite species for their establishment on tomato plants using food supplements. Our results show that some of the selected predatory mites indeed demonstrated an increased establishment of tomato as compared to commercially available predatory mites. As compared to a predator-only release, pollen supplementation resulted in a seven-fold increase in population size over 8 weeks. When achieving such high densities, the predator population was capable of controlling artificial infections of TRM. We will discuss the potential of the tested predatory mite species with regard to their biocontrol function, and how to best achieve pre-establishment using different food supplements.

Keywords: Tomato russet mite, biological control, predatory mites, pre-establishment, pollen

Phenotypic plasticity of a predatory mite under high temperatures and its application in Chongqing, China

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The biological control efficiency of spider mites using phytoseiid predators is frequently being disrupted by high temperatures which results in an important and urgent research topic. We hypothesised that this scenario could be ameliorated if the thermotolerance of a certain phytoseiid predator is enhanced. Therefore, a high temperature adapted strain (HTAS) of the predatory mite Neoseiulus barkeri (Hughes) was selected from its conventional strain (CS) via long-term heat acclimation and frequent heat hardenings for multiple generations. As expected, CS N. barkeri were more susceptible to heat stress events than HTAS individuals, as seen in their their higher mortality, prolonged pre-oviposition period and reduced fecundity and longevity. However, the high temperature acclimatory response could affect sex ratio by reducing the female proportion in the HTAS population. We also examined the activities of antioxidant enzymes of N. barkeri, including catalase (CAT), superoxide dismutase (SOD), peroxidase (POX), glutathione S-transferases (GSTs), and total antioxidant capacity (T-AOC), under thermal stress conditions. We also cloned and characterized the cDNA of four heat protein genes, NbHsp40, NbHsp60, NbHsp70, NbHsp90, and examined changes in their expressions due to short-term heat exposure in both strains. Field trials using HTAS N. barkeri were conducted in orange orchards and vegetable greenhouses in Chongqing. Our research results suggest that HTAS N. barkeri is a promising biological control agent and is predicted to increase local biological control services in these high temperature areas.

Keywords: *Neoseiulus barkeri*, acclimatory response, thermotolerance, intraspecific variations, biological control



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Plant feeding by two *Euseius* species (Acari: Phytoseiidae): there is more to it than meets the eye!

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Euseius alstoniae and E. finlandicus, which are commonly found on a wide range of plants in Bengaluru, India, showed peculiar attributes in their ability to feed, develop, reproduce and survive on plants. *In situ* observations and experiments in August 2017 (mean temperature: 25 °C; humidity: 76%; pressure: 1.011 bar) and September 2017 (25 °C; 80%; 1.012 bar) indicated that not only adults but deutonymphs of these two phytoseiids can also feed on Magnolia champaca (champak; Magnoliaceae) and Spathodea campanulata (African tulip tree; Bignoniaceae). Similarly, E. alstoniae adults were observed to pierce Morus indica (mulberry; Moraceae) leaves in nature. Although feeding scars were evident on these plants, no economic damage was apparent, probably because of low population densities (not more than five adults per 100 sq.cm) and the absence of congregation. Neither E. alstoniae nor E. finlandicus was found to take in plant sap from Markhamia lutea (Nile tulip) or Tabebuia rosea (pink trumpet tree), though the mites were naturally found on these two bignoniaceous plants. In the laboratory, neither plant-fed mite could consume the acarid, Tyrophagus putrescentiae, or the phytophagous tetranychid, Tetranychus urticae. Both plant-fed mites did not prefer *Ricinus communis* (castor bean; Euphorbiaceae) pollen. Molecular methods as well as analytical techniques like GC–MS (gas chromatography–mass spectrometry) and LC-MS (liquid chromatography-mass spectrometry) are now being used to examine whether the two Euseius species can depend wholly on plant sap drawn from their preferred hosts for their survival. This is the first report of E. alstoniae as a plant feeder. This is also the first report of plant feeding by any phytoseiid in India.

Keywords: Biological control, Euseius alstoniae, Euseius finlandicus, lifestyle, Phytoseiidae

Comparative biology of *Tetranychus urticae* Koch (Prostigmata: Tetranychidae) and its native predator, *Neoseiulus longispinosus* (Evans) (Mesostigmata: Phytoseiidae) on cucumber

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Tetranychus urticae is a notorious pest of cucumber under protected cultivation in Kerala, India. A native strain of the predatory mite, Neoseiulus longispinosus, collected from spider mite infested okra plants, is being maintained for the evaluation of its biocontrol potential against the mite on cucumber. A laboratory experiment was conducted during 2014 on the biology of *T. urticae* and *N*. longispinosus on cucumber leaves via the leaf disc method. Neoseiulus longispinosus had shorter developmental periods for males and females of 3.91 and 4.27 days, respectively, than T. urticae for which the developmental periods for males and females were 6.75 and 7.15 days, respectively. The adult predator lived longer, with mean longevities of 19.66 days for males and 22.75 days for females compared to its prey which had mean longevities of 8.95, 11.59 and 13.04 days for males, mated females and unmated females, respectively. The predator on average laid 31.33 eggs, of which 89.83% were viable. Tetranychus urticae had fecundities of 47.91 and 36.08 eggs, and egg viabilities of 92.55 and 90.23%, for mated and unmated females, respectively. Both prey (1:4.6) and predator (1: 3.31) had a female-biased sex ratio. In contrast to *T. urticae*, parthenogenesis was not recorded in the predator. The shorter life cycle, longer life span and female-biased sex ratio of N. longispinosus are desirable traits in an efficient predator which suggests that it as an ideal candidate for the biological control of *T. urticae*.

Keywords: *Tetranychus urticae*, *Neoseiulus longispinosus*, predator, biology, biocontrol



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Bionomics of the predatory mite, *Neoseiulus californicus*, as affected by feeding on *Tetranychus urticae* inhabiting three different rose cultivars, with and without the mycelia of *Podosphaera pannosa* var. *rosae*

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The impact of infestation by the fungus, *Podosphaera pannosa* var. *rosae* (Wallr.: Fr.) de Bary (Erysiphales: Erysiphaceae), on the biological characteristics of *Neoseiulus californicus* McGregor (Acari: Phytoseiidae) when fed on *Tetranychus urticae* Koch (Acari: Tetranychidae) reared on the leaves of the exotic rose cultivars, White Teneky, Red Dallas and Yellow Bebion, was studied at 20 °C and 30 °C. The effect of *P. pannosa* was almost neutral throughout the adult phytoseiid female's life span, regardless of temperature. The female life span ranged from 44.9 days to 45.8 days and from 43.5 days to 45.4 days at 30 °C, without and with the fungal mycelia, respectively, on the three rose cultivars. In contrast, the life span of the female mite at 20 °C averaged 76.25 days and 77.92 days, without and with the fungal mycelia, respectively. Adult female egg laying ranged from 72.5 to 78.8 and 47.6 to 63.7 eggs at 20 and 30 °C, respectively. The effect of infestation with *P. pannosa* was not neutral regarding prey consumption over the female lifespan, i.e., rose cultivar significantly influenced prey consumption over the same period. In addition, total egg laying was significantly reduced by the presence of *P. pannosa*. Separately, feeding by starved females of *N. californicus* on *S. pannosa* was not recorded. Other findings on the phytoseiid mite's feeding are discussed.

Keywords: Mite, rose, pathogen, biological control, interaction



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Poster Presentations



A newly recorded mite species from Turkey: *Eutogenes frater* Volgin (Acari: Cheyletidae)

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Three female mite specimens collected from litter and soil under silverberry (*Elaeagnus angustifolia*) in Elazığ Province, Turkey were identified as *Eutogenes frater* Volgin (Cheyletidae). This species shows distinct differences from other species in the genus, namely dorsal idiosoma covered by two shields, surface of the shields with papilliform granules, all dorsal setae fan-like, propodosomal shield bearing 10 pairs of setae and hysterosoma with 12 pairs of dorsal body setae. *Eutogenes frater* has been reported before from the type locality, Bulgaria, and was later recorded from Algeria, Hungary and Iran. This species has also been reported from Giza, Burg Al Arab and the north of the Nile Delta in the former United Arab Republic because *E. africanus* Wafa and Soliman was given as a synonym of *E. frater* by Fain and Bochkov (2001). A description of this species is provided here, and illustrations and measurements were done. This is the first reported occurrence of the genus *Eutogenes* in Turkey.

Keywords: Elazığ Province, *Eutogenes*, occurrence, predatory mite, Turkey



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Mites living in the galleries of the almond bark beetle, *Scolytus amygdali* Guerin-Meneville (Coleoptera: Curculionidae: Scolytinae), attacking almond trees in southern Taleghan, Oazvin Province, Iran

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In recent years, the almond bark beetle, Scolytus amygdali, has been observed as a destructive xylophagous pest of pome and stone fruit trees in some parts of Iran, causing substantial damage to almond trees in plantations and gardens in southern Taleghan, Qazvin Province. This research was performed in order to determine the mite species living in bark beetle galleries in almond trees, as one of the most cultivated trees in the region. Samples of mites were collected from infested trees during 23 months of surveys from September 2014 to July 2016. Infested branches were cut into pieces 15-20 cm long, placed in plastic bags and transferred to the laboratory. The bark was then removed from the wood. Mite specimens were extracted by using a Berlese-Tullgren funnel, preserved in 70% ethanol, cleared with lactophenol or Nesbitt's fluid, and finally mounted in Hoyer's medium. A total of 13 species belonging to 13 genera, seven families and three orders were collected and identified as follows (the developmental stages and altitudes are shown in the parentheses, respectively): Phytoseiidae: Paraseiulus sp. (9, 1843), Typhlodromus (Anthoseius) sp. (2, 1892); Acaridae: Tyrophagus putrescentiae (Schrank, 1781) (2, 1892); Winterschmidtiidae: Winterschmidtia hamadryas (Vitzthum, 1923) (all developmental stages, 1779–1986); Bdellidae: Spinibdella sp. (9, 1796); Iolinidae: Homeopronematus sp. (9, 1791-1892), Proctotydaeus sp. (9, 1791-1892)1892), Pronematulus sp. (2, 1892-1986); Pygmephoridae: Bakerdania sp. (2, 1919), Pediculaster sp. (9, 1887); Tydeidae: *Melissotydeus* sp. (9, 1919), *Paralorryia* sp. (9, 1791), *Lorryia* sp. (9, 1887); 1769). Winterschmidtia hamadryas was the dominant species (92.9%) associated with S. amygdali in the region. This species has a complex life history with two generations, one of which feeds on bark beetle eggs. The specimens are deposited in the mite collection of the Department of Plant Protection, Science and Research Branch, Islamic Azad University, Tehran, Iran.

Keywords: Acari, scolytine, subcortical beetle, arboreal, predation

Mortality effect of vermiwash extracted from cow manure on *Tetranychus urticae*

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The two-spotted spider mite, *Tetranychus urticae*, is distributed across most regions of the world and is arguably the most important pest. Vermiwash, which is extracted from vermicompost, contains macro- and micro-nutrition elements and herbal growth hormones, such as auxin and cytokinin. In the present study, the mortality effect of vermiwash produced from cow manure was evaluated on *T. urticae*. The experiment was conducted with a completely randomized block design at 25±1 °C, 65±5% of humidity and 16:8 h L:D conditions. The initial population of the two-spotted spider mite was from the Research Institute of Plant Protection, Tehran, Iran. Five pairs were placed on a leaf of the Alamoot variety of the kidney bean (*Phaseolus vulgaris*) in each Petri dish. Five concentrations of vermiwash from 100 to 10,000 ppm were prepared. In each replicate, the five pairs of mites in each Petri dish were exposed to one of the five different concentrations of vermiwash. Spider mite mortality was evaluated after one, three and five day periods. The mortality percentage was then estimated with the Henderson-Tilton formula. The results showed that 10,000 ppm of vermiwash caused the highest mortality of *T. urticae* on the 5th day.

Keywords: Vermiwash, cow manure, two-spotted spider mite, biopesticide, biological control



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A species being worthy of its name: Intraspecific variations on the gnathosomal characters in topotypic heteromorphic males of *Cheylostigmaeus variatus* (Acari: Stigmaeidae)

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Distinguishing characters of the species in the genus *Cheylostigmaeus* Willmann (Acari: Stigmaeidae) such as the structure of the gnathosoma are mainly based on males. In this genus, the gnathosoma may show sexual dimorphism unlike other members of the family. Polymorphism may occur in males of this genus. The homeomorphic males resemble the females in the absence of lamellae on subcapitulum. The lamellae and/or the palpal apophyses are characteristic of heteromorphic males. In the present work, morphological variations in distinguishing characters in five topotypic male specimens were identified in *C. variatus* Doğan, Dilkaraoğlu & Fan. The variations in the shapes of lamellar projections, verrucae on the dorsal surfaces of chelicerae and structures of apophyses on palpal segments in these specimens were noted. We consider that the differences in the specimens were intraspecific variations and that there was not enough evidence to justify a new species. This hypothesis may be supported by the rearing of a population of *C. variatus* or molecular evidence.

Keywords: Gnathosoma, heteromorphic, intraspecific, mite, morphology, variation

First record of *Cheletonella* (Acariformes, Cheyletidae) in Poland, with comments on other members of the genus

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Members of the family Cheyletidae are mainly free-living predators and they have a worldwide distribution. A total of 15 species of this family have been recorded from Poland. The genus *Cheletonella* Womersley is distinguished within the family Cheyletidae by its ovoid body, absence of eyes, presence of a single shield on the propodosoma, palp tarsus with two comb-like setae and two, sickle-like setae, palp claw with basal teeth, and all legs having claws. The genus comprises three species, including *Cheletonella vespertilionis* Womersley. Here we present the first record of *Cheletonella* and *C. vespertilionis* for the fauna of Poland. We also consider *Cheletonella summersi* Chatterjee & Gupta, a *species inquirenda*.

Keywords: Cheletonella, fauna, mite, predator, species inquirenda



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Testing the interplay between specialization and dispersal in the invasive wheat curl mite, *Aceria tosichella* (Acariformes: Eriophyidae)

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Predicting species range shifts and the spread of potentially invasive organisms is a key to managing pest outbreaks and maintaining ecosystem health. Many plant-feeding mites of economic importance are increasing their host range and there is a need to explain mechanisms behind this expansion. Our goal was to understand the successful spread of the invasive wheat curl mite (WCM), Aceria tosichella, to cereal-producing regions worldwide, which has challenged researchers and cereal growers for decades. WCM is a species complex comprising several genetic lineages. The aim of this presentation is to propose an empirical test of the evolutionary interplay between host specialization and dispersal in the most polyphagous and invasive lineage of the complex, MT-1. This approach may help explain its colonization success. The WCM MT-1 stock colony was established from populations collected in various localities in Poland and was checked for the presence of Wolbachia and other endosymbionts. The MT-1 lineage is being experimentally manipulated in the following treatments replicated in 10 independent trials: (i) experimental evolution of MT-1 in two environments: one favouring specialists (S) and the other favouring generalists (G); and (ii) artificial selection of S and G lines for higher and lower dispersal. Selected lines will be tested for the fitness consequences in different environments. The results of this approach may answer the question of whether WCM MT1 high dispersal ability influences local adaptation to different hosts and thus the likelihood of host shift and rapid range expansion.

Keywords: *Aceria tosichella*, colonization, Eriophyidae, dispersal, host specialization, wheat curl mite

Acknowledgement: The study is being funded by National Science Centre grant no. 2016/21/B/NZ8/00786.

Eriophyid mite species on olive orchards and their distribution in Hatay Province of Turkey

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Olive (*Olea europeae* L.) is one of the earliest cultivated plants. Its fruit is highly valued and is important for the agricultural sector of Mediterranean countries. Hatay Province has 6.3% of Turkey's olive production areas and is in sixth place among the provinces. There have been no detailed studies of harmful mites in olive plantations in Hatay Province. The aim of the current study was to determine the eriophyid mite species and their distribution in olive plantations in Hatay Province. A survey was conducted in 12 districts of Hatay Province (Antakya, Altınözü, Kırıkhan, Samandağ, Erzin, Arsuz, Yayladağ, Dörtyol, Defne, İskenderun, Belen and Hassa) between April and October, 2017. In each sampled orchard, according to the phenological period of the plant, 25-30 cm long shoot samples containing buds, flowers or fruits were taken from the four sides of ten trees. Thirty nine of 58 sampled orchards were infested with eriophyid mites at different levels. The prevalence rates of two species, *Aceria oleae* and *Tegolophus hassani*, were 67.24% and 24.13%, respectively. Furthermore, Antakya and Hassa were the most infested districts. There was no mite infestation of the samples from Yayladağ district and Erzin was the next least infested district. These data are the results of the first year of a two-year study, with the second year of the study underway.

Keywords: Hatay, Turkey, Eriophyidae, olive, distribution

Acknowledgement: This study was supported by Mustafa Kemal University, Hatay, Turkey (BAP-16640).



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Contact toxicity to spirodiclofen resistant and susceptible *Tetranychus urticae* Koch (Acari: Tetranychidae) populations of some essential oils

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The two-spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae), is a harmful species that causes considerable losses in agricultural production areas due to its wide host range and high reproductive rate. It also rapidly develops resistance to the acaricides used in its control. Therefore, alternative methods of control of *T. urticae* have gained importance. In this study, the contact toxicities of pine, daphne and juniper essential oils to 296 fold spirodiclofen resistant and susceptible T. urticae populations were investigated during different life stages. Applications to the adult and larval stages were made with the leaf disc-spray tower method using concentrations of 1, 5, 10 and 20 ml/l of the essential oils. Water containing a 0.3% tween 20 solution was used as the control. The essential oil solutions were sprayed on the leaf surface at a pressure of 1 bar at the spray tower to apply 1.2-1.6 mg/cm² of leaf area. The experiments were carried out with 15 individuals and 3 replicates for each treatment. Counts of dead and live larvae and adults were made at 24, 48 and 96 h. The highest mortality effects of essential oils on larvae and adults for both of the *T. urticae* populations were obtained at 20 ml/l and 96 h. The highest effects on the adults were 100% for pine oil, 98% for daphne oil and 100% for juniper oil in the susceptible population; and 59.46% for pine oil, 58% for daphne oil and 51% for juniper oil in the spirodiclofen resistant population. Highest effects on the larvae were 81.58% for pine oil, 95.24% for daphne oil and 95.65% for juniper oil in the susceptible population; and 50% for pine oil, 56.25% for daphne oil and 58% for juniper oil in the spirodiclofen resistant population. The contact effect of all three essential oils was higher for the susceptible population than for the spirodiclofen resistant population.

Keywords: Tetranychus urticae, pine, daphne, juniper, essential oil

The effects of milbemectin resistance on some biological parameters and life table of *Phytoseiulus persimilis* A.-H. (Acari: Phytoseiidae)

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Phytoseiulus persimilis A.-H. (Acari:Phytoseiidae) is one of the effective predatory mites used in the biological control of Tetranychus urticae Koch (Acari: Tetranychidae) in agricultural production areas. In this study, a susceptible population of P. persimilis was selected 5 times with milbemectin under laboratory conditions to obtain a 31-fold resistant P5 population. The leaf discspray tower method was used for the selections. Furthermore, the pre-oviposition, oviposition and post-oviposition periods, adult lifespan, total number of eggs laid per female, net reproductive rate (R_o), intrinsic rate of increase (r_m), doubling time (DT) and mean generation time (T_o) of the milbemectin-resistant P5 and susceptible P. persimilis populations were compared and life tables were created. The oviposition period, mean number of eggs/female, adult lifespan, net reproductive rate (R_o) and intrinsic rate of increase (r_m) values were statistically different between the P5 and susceptible populations (P < 0.05). In the P5 and susceptible populations, respectively, oviposition periods were 21.24 and 14 days; total number of eggs laid per female were 56.88 and 33.48; adult lifespans were 23.76 and 17.84 days; net reproduction rates (R_o) were 35.80 and 20.02 (females/ female/generation) and intrinsic rates of increase (r_m) were 0.30 and 0.24 (females/female/day). In conclusion, milbemectin resistance in P. persimilis may have positive effects on some of its biological parameters and its life table.

Keywords: *Phytoseiulus persimilis*, milbemectin, resistance, biological parameters, life table



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Spirodiclofen resistance levels in *Tetranychus urticae* Koch (Acari: Tetranychidae) populations on eggplant in Turkey

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The two spotted spider mite, Tetranychus urticae Koch (Acari:Tetranychidae), is a harmful that causes considerable economic losses in greenhouse and open vegetable production areas. In this study, the aim was to determine the spirodiclofen resistance levels of nine *T. urticae* populations collected from eggplant production fields in Serik district of Antalya Province, Turkey. The populations were named S1, S2, S3, S4, S5, S6, S7, S8 and S9. In the bioassay experiments, the spray tower-leaf disc method was used. Spirodiclofen was dissolved in pure water and the appropriate doses were prepared. The acaricide concentrations were prepared to be 1 control + 7 doses, and 3 replicates, with 50% dilution following the first dose prepared. Twenty-five adult female individuals were transferred under a binocular microscope to a leaf disc with a softtipped brush. Two mL of each of the pesticide preparations at all concentrations were sprayed under 1 atm pressure at the spray tower onto the leaves in the Petri dishes. Only pure water was applied to the control. Dead-live counts were done on the 7th day and the LC₅₀ values for the nine spider mite populations were calculated with the POLO computer program. Resistance ratios were calculated by comparing the LC₅₀ ratios of the resistant *T. urticae* populations with the LC₅₀ ratio of susceptible populations. The highest resistance level against spirodiclofen in the eggplant populations was 168.94 fold in the S1 population and the lowest resistance level was 42.09 fold in the S5 population.

Keywords: Tetranychus urticae, spirodiclofen, resistance, LC₅₀, eggplant

Demographic response of the two-spotted spider mite (Acari: Tetranychidae) to egg treatment with biopesticides

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The effects of biopesticide products based on oxymatrine, azadirachtin and Beauveria bassiana on the life table parameters of the two-spotted spider mite, *Tetranychus urticae* Koch, were evaluated in laboratory bioassays at 27±2 °C, 50-70% RH and 16/8h light/dark photoperiod. The biopesticides were applied to bean leaf discs (30 mm) with a Potter Tower tower (2 mL liquid, 100 kPa pressure, 2.7 mg/cm² water deposit). To assess the effects on demographic parameters, life tables were constructed for two cohorts of mites sprayed at the egg stage: 1) with distilled water (control) and 2) with the biopesticide (treatment). Eggs up to 24 h old were treated with one of the following concentrations: 50 µl/l (oxymatrine-based product), 0.075% (azadirachtin-based product) and 0.3% (B. bassiana-based product). These concentrations were within the 95% confidence limits of the LC₅₀s estimated in previous acute toxicity bioassays. The mites that hatched from treated eggs completed their juvenile development on the same leaf discs. When the surviving females entered the preovipositional period, cohorts of 40 control and treated females were transferred to untreated leaf discs (1 female per disc). The biopesticide treatments caused significant reductions in the intrinsic rate of increase (r_m) and other life table parameters. In the bioassays with the oxymatrineand azadiraachtin-based products, the r_m values were reduced by 22% and 16%, respectively, due to reduced survival and fertility, as well as extension of juvenile developmental time of the females from treated eggs, compared to the controls. In the bioassay with the B. bassiana-based product, the r_{m} fell by 7%, mostly due to the reduced survival level of females from treated eggs.

Keywords: Tetranychus urticae, oxymatrine, azadirachtin, Beauveria bassiana, life tables



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A tool of pollution estimation: Soil mites and other microarthropod groups

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The objective of this study was to estimate the ecological status of forest ecosystems under the influence of Copsa Mică pollutant emissions. În 1990 Copsa Mică was known as one of the most polluted areas in Europe. This was due to emissions of a large amount of carbon black, sulfur dioxide and particulate matter containing heavy metals and other pollutants. The research was carried out through a quantitative and qualitative analysis of the edaphic mesofauna on the whole and by systematic and trophic groups. Series of samples of litter and soil were taken from every considered forest stand. The fauna was extracted from the soil samples by the selective method of Tullgren – Berlese modified by Balogh. The assessment was carried out comparatively, including by choosing control ecosystems located at a large distance from the pollution source and also by comparison between two periods, one affected by high noxious emissions (1986) and the other affected by less pollutant emissions (2010). The comparison between the two periods showed that in the polluted forests the total density of edaphic mesofauna increased. The recovery trend was more pronounced in summer when the recorded densities were 1.9-4 times higher than in the previous similar period. The ratio of Oribatida / Collembola was predominantly supra-unit which indicates the predominance of humification in relation to mineralization in the process of biodegradation of vegetal necromass. The improved quality of the edaphic environment was also highlighted by the presence of some groups (mites belonging to Labidostommatidae and Uropodina) more sensitive to altered living conditions, as well as the proliferation of groups more efficient in the decomposition of organic matter. The restoration of edaphic, micro-arthropod communities is a lengthy process that is premised on maintaining the levels of emissions of pollutants as low as possible.

Keywords: Industrial pollution, forests, edaphic mesofauna, bioindicators

Compatibility of *Beauveria bassiana* and *Phytoseiulus persimilis* against *Tetranychus urticae* on potted bean plants

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The two-spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae), causes severe damage in both greenhouse and field crops. The entomopathogenic fungus Beauveria bassiana (Balsamo) Vuillemin and the predatory mite Phytoseiulus persimilis Athias-Henriot are both biocontrol agents against *T. urticae*. In this study, we assessed the compatibility of both biocontrol agents against T. urticae on potted bean plants with the following treatments: i) a low release rate of P. persimilis (10 prey:1 predator), ii) a high release rate of P. persimilis (5 prey:1 predator), iii) a single application of B. bassiana (1×10^8 spores/ml), iv) a single application of B. bassiana after a low release rate of *P. persimilis*, and v) a non-treatment control (no application of either *B*. bassiana or P. persimilis). The single application of B. bassiana reduced the T. urticae population just after application but the mite population rebounded again after few days. The low release rate of *P. persimilis* could not completely eliminate the pest population but the high release rate could eliminate T. urticae within a short period. The combined application of B. bassiana and low release rate of *P. persimilis* could successfully reduce the *T. urticae* population which trended to zero within 6 days after application. The density of the *P. persimilis* population after release became significantly different over time among the treatments but the number fell at the end of the treatment at the high release rate due to lack of hosts. In leaf damage analysis, the single application of B. bassiana in combination with the low release rate of P. persimilis achieved the lowest level of leaf damage. Therefore, B. bassiana can be used to control T. urticae without affecting the benefits of *P. persimilis*.

Keywords: Entomopathogenic fungus, phytoseiid, spider mite, compatibility, biological control



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Phytoseiid species (Acari: Mesostigmata) in Bursa Province, Turkey, with their original illustrations

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The climate of Bursa Province, Turkey is characterized by temperate and humid conditions which support a diversity of predatory mite species on many cultivated plants and weeds. Among these predators, the Phytoseiidae family is the one of the most effective predator groups against small arthropods, insects and many mite species. During the past two decades, many phytoseiid species have been collected from various vegetables, fruit trees and weeds in Bursa Province. These species were *Amblyseius andersoni*, *Amlyseius swirskii*, *Amblyseius setosa*, *Euseius finlandicus*, *Kampimodromus aberrans*, *Neoseiulus alpinus*, *Neoseiulus bicaudus*, *Neoseiulus barkeri*, *Neoseiulus californicus*, *Paraseiulus triporus*, *Phytoseius echinus*, *Phytoseius finitimus*, *Proprioseiopsis messor*, *Typhlodromus* (*Anthoseius*) recki, *Typhlodromus* (*Typhlodromus*) athiasae and *Typhlodromus* (*Typhlodromus*) tiliae. In addition, *Amlyseius swirskii* collected from olive trees in 2016 was first recorded in this study. In this presentation, original, handmade illustrations of each species are exhibited. In the illustrations, important morphological characters, e.g. dorsal integument pattern, solenostome positions, shapes of sternal, genital and anal plates and shapes of spermatheca, spermadactyl, dorsal/ventral setae, macrosetae and peritreme, are shown. Besides a checklist of these species, the habitat of each species are also listed.

Keywords: Phytoseiidae, habitat, checklist, illustration, Bursa Province

Intraguild aggressiveness between an alien and a native predatory mite

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The predatory mite, Amblydromalus limonicus, non-native to Europe, can be used legally in several European countries as a greenhouse biocontrol agent against thrips species. The first record of the unintended occurrence of A. limonicus in apple orchards in Europe came from Catalonia, Spain, where it has been well established alongside the native predatory mite community since 2011. The dominant species in the community is Amblyseius andersoni, which has a similar lifestyle to A. limonicus, a large, aggressive predator with a broad diet range, making intraguild (IG) interactions between the two predators likely. Thus, we tested the IG aggressiveness of native and alien female predators when provided with IG prey (larvae). The alien A. limonicus females proved to be highly aggressive IG predators against larvae of the native A. andersoni, which were attacked more frequently and earlier than alien larvae were attacked by the native predator. Nearly all attacks by the alien predator resulted in the death of native IG prey whereas about 20% of the alien IG prey escaped the attacks of the native predator. Additionally, native IG prey is smaller than alien prey, which should facilitate the overwhelming of the native by the alien predator. We argue that the strongly aggressive IG behavior of A. limonicus has contributed to its successful establishment alongside the native predatory mite community.

Keywords: Biological control, exotic species, intraguild predation, Phytoseiidae



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New host and country records for the genus *Imparipes* (Acari: Scutacaridae)

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In order to disperse, adults and nymphs of some mites are transported on insects and other arthropods. This transportation is termed phoresy and the transported organism is termed phoretic. The purpose of this study was to contribute to the knowledge of phoretic mites associated with insects. The family Scutacaridae (Acari) is the most abundant and cosmopolitan in the superfamily Pygmephoroidea. Many scutacarid mites are phoretic on different insects. The family Staphylinidae (rove beetles) is one of the largest Coleoptera (beetle) families known. Members of the genus *Lucifotychus* within this family have been found in leaf litter, often wet areas with mosses. In this study, five phoretic mite specimens of *Imparipes* sp. (Scutacaridae) were collected from a specimen of *Lucifotychus* during a survey of the mite fauna in Erzincan Province, Turkey. The host insect was extracted by Berlese funnel with other soil arthropods from soil and litter under *Populus* sp. and *Salix* sp. Mite specimens were cleared in 60% lactic acid and mounted on microscope slides in Hoyer's medium under a stereomicroscope. The mite specimens and their host were examined and photographed with Olympus Corporation BX3-CBH DIC and Nikon Corporation SMZ25 stereomicroscopes. This is a first report of the genus *Imparipes* in Turkey and the genus *Lucifotychus* is a new host record for *Imparipes*.

Keywords: Insect, mite, phoresy, Scutacaridae, transportation

Mesostigmatic mites (Acari) of the mangrove forests in southern Iran

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The Mesostigmata (Acari) is a large, diverse, cosmopolitan assemblage of the superorder Parasitiformes, most of which are free-living predators. To date, 390 species from this order of mites (excluding the family Phytoseiidae) has been reported from Iran. The mangrove or hara forests of Qeshm in the northern area of the Persian Gulf are protected areas that are predominantly comprised of *Avicennia marina*. The mite fauna of these forests in southern Iran is almost unknown. A survey of edaphic, mesostigmatic mites of the mangrove forests of Qeshm Island and Khamir Port was conducted in 2017-2018. For that purpose, samplings were done on different soil substrates, including soil and litter, mud and crushed cockleshells. Mites were extracted from the samples using Berlese-Tullgren funnels, cleared in Nesbitt's fluid and then mounted in Hoyer's medium on microscope slides. Specimens belonging to the families Laelapidae, Uropodidae, Ologamasidae, Blattisociidae, Pachylaelapidae, Parholaspididae and Rhodacaridae were collected, of which one genus and species, *Dendrouropoda schulzi* Willmann, 1959, are new reports for the Iranian mite fauna. Adult female and male specimens of *D. schulzi* were collected in soil and crushed cockleshells.

Keywords: Hara forest, fauna, Dendrouropoda schulzi, Persian Gulf, mangrove



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Two new records of Mesostigmata (Acari) from Turkey

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The Mesostigmata is a large, cosmopolitan group of mites of which the majority of species are free-living predators. Although mites of the family Ascidae are relatively well-known in Turkey, the Ologamasidae mites of the country are poorly known. The Turkish fauna of both families need more investigation because the country is large and has many different ecosystems and habitats. In a survey of edaphic Mesostigmata in Turkey from 2008 to 2014, soil samples were collected in Bayburt, Giresun, Gümüşhane, Sivas and Tokat Provinces and the mite specimens were extracted by using Berlese-Tullgren funnels. Mite specimens were cleared in Nesbitt's fluid or lactic acid and then mounted in Hoyer's medium on microscope slides. Some specimens from the families Ascidae and Ologamasidae were identified. In this research, some specimens of *Neojordensia levis* (Oudemans & Voigtz, 1904) and also an unidentified species of the genus *Sessiluncus* Canestrini were collected and identified. Herein, *N. levis* is reported for the first time from Turkey. Also, this is the first report of a species belonging to the genus *Sessiluncus* from Turkey.

Keywords: Ascidae, Ologamasidae, soil-dwelling mites, *Neojordensia*, *Sessiluncus*

Metabolomic changes in a model system of gallogenesis induced by eriophyoid mites

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Greatly miniaturized and morphologically simplified mites of the superfamily Eriophyoidea are capable of inducing a variety of colored, shaped and localized galls on higher plants. We studied for the first time the metabolomic changes in plant tissues during growth of the pouch leaf galls caused by an eriophyoid mite, Fragariocoptes setiger (Phytoptidae), on strawberry, Fragaria viridis (Rosaceae). A series of ten plant samples were collected from May to August between 2016 and 2017 from the same wild strawberry population in north-west Russia. Each of the plant parts collected were analyzed separately: galls, remnants of the leaf blades from which the galls were cut, whole infected leaves bearing galls, and whole leaves collected from healthy plants with no galls and mites. Metabolic profiles for all samples were obtained through gas chromatography. Among 107 identified metabolites, four chemical compounds, which are potential biomarkers of gallogenesis in strawberry, were detected. They were two phenolic metabolites (4-hydroxyphenylethanol, 4-hydroxybenzoate), glycerol 3-phosphate and quinic acid. Analyses of the metabolic matrix showed that the differences in the correlation structure of the metabolic network of galls and leaves from which they were removed gradually decrease from the earliest date (May) to the latest (August), so that by August differences between the galls and the leaf blades bearing them are almost undetectable. That means that by the end of the growing season, at the metabolite level, the leaf infected by gall-mites turns into a single pathological structure, like a large gall. This result suggests that instead of viewing the gallogenesis induced by eriophyoids as a local process, i. e., the growth of a small tubercle on the leaf blade in the case of F. setiger, we should shift to a new interpretation of this phenomenon and consider gallogenesis in the studied model as a systemic plant disease.

Keywords: Metabolomics, gallogenesis, galls, strawberry, plant pest

Acknowledgements: This study was supported by the Russian Foundation for Basic Research (RFBR grant 16-04-01292) and the Russian Science Foundation (RSF grant 16-16-10011).



2-8 September 2018, Antalya - TURKEY

Alterations in leaf developmental program and expression of regulatory genes in a model system of gallogenesis induced by eriophyoid mites

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Gall-parasite interactions are complex processes involving the regulatory genes of both the pest and host plant which change the phytohormone balance in plant tissues to create habitat inside the plants. This leads to local changes in the expression of genes controlling morphogenesis and results in the formation of a new organ, the gall. Acariform mites of superfamily Eriophyoidea are an understudied group of microscopic phytoparasites that are capable of inducing gallogenesis on higher plants. We used the mite Fragariocoptes setiger and its strawberry host plant, Fragaria viridis, as our model to identify the genetic mechanisms of gall formation since this species of mite elicits a strong host plant response, resulting in the formation of red, hairy, pouch galls on leaves. The histological structure of the gall and the alteration of gene expression by F. viridis during gall formation were studied. For histological purposes, gall formation was split into four stages with an analysis of specific changes that occurred during each stage. A dramatic change of adaxial-abaxial polarity of the lamina throughout the four stages was observed. We analyzed the expression of genes encoding meristem-specific transcription factors (KNOX and WOX families), genes responsible for leaf development (HD-ZIPIII, KANADY, YABBY, LBD, AS1, AS2, CUC, ANT), genes encoding components of CLAVATA systems (CLE10, 41, 45, 46), genes of primary response to auxin and cytokinin (RR-A, Aux/IAA), and cell cycle genes (CycB1, CycD3). Some of the studied genes showed significant alterations in their expression levels, allowing us to hypothesize their role in the development of *F. setiger*-induced galls.

Keywords: Strawberry, gall, gene expression, phytohormone, adaxial–abaxial polarity

Acknowledgements: This study was supported by the Russian Foundation for Basic Research (RFBR grant 16-04-01292) and the Russian Science Foundation (RSF grant 16-16-10011).

South-East Asia, the biodiversity hotspot of the Uropodina mites (Acari: Mesostigmata)

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Uropodina is a widely distributed group of Mesostigmata that inhabits soil, moss and leaf litter but can also be found under the bark of trees and in the nests of ants, mammals and birds. The group consists of more than 1,500 valid species worldwide; however, the faunas of some large regions are still largely unexplored. Recently, 25 important "biodiversity hotspots" were nominated for having a high number of endemic species. Most are endangered by human impacts. Four of these hotspots are in South-East Asia (SEA), namely Indo-Burma (Myanmar, Laos, Cambodia, Thailand and Vietnam), Sundaland (Brunei, Malaysia and western part of Indonesia), Wallacea (eastern part of Indonesia) and the Philippines. Some other genera occurring in SEA (e.g. *Deraiophorus* and *Macrodinychus*) are more widely distributed, especially in the other areas of the former Gondwanaland and Laurasia (e.g. *Trachytes, Dinychus*) but the region has numerous endemic genera like *Hutufeideria, Phymatodiscus, Editella, Depressorotunda, Didepressorotunda, Sumatrella* and *Trachyibana*, together with numerous indigenous species. Despite this high level of endemism, the uropodine fauna of SEA remains scarcely investigated and the discovery of numerous new taxa is expected in the future from the poorly investigated parts of this region.

Keywords: Turtle-mites, endemism, zoogeography, biodiversity, indigenous species



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Alien, non-indigenous spider mites and flat mites (Acari: Tetranychidae and Tenuipalpidae) in Hungary

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A revised check-list of the Hungarian tetranychid and tenuipalpid mites comprises 37 spider mite and 19 flat mite species. The majority of the listed species are widely distributed and well-known pest species, including alien, non-indigenous mites, with very few of the species endemic. Due to recent intensive studies on the Hungarian fauna, six alien species were recorded. Two species are flat mites [Tenuipalpus pacificus Baker, 1945 and Brevipalpus californicus (Banks, 1904)], which were collected in greenhouses, namely T. pacificus on Phalenopsis orchids and B. californicus on palms. These two species live in the warmer/hotter parts of America; therefore, they can survive only in greenhouses in Hungary and can cause damage in these habitats. Two of the four alien spider mites are pests of planted bamboos [Schizotetranychus bambusae Reck, 1941 and Stigmaeopsis nanjingensis Ma & Yuan, 1980)]; the other two are pests of conifers [Eotetranychus thujae (McGregor, 1950) and Eotetranychus libocedri (McGregor, 1936)]. The two bamboo-inhabiting species (S. bambusae and S. nanjingensis) arrived from South-East Asia via the transport of their host plants. On the other hand, the two *Eotetranychus* species arrived from North America by the transport of conifer plants and they have infested the conifers of the urban parks in the larger cities of Hungary. We expect that other non-indigenous species will be found in Hungary due to the intensive global trading of ornamental plants.

Keywords: Pest mites, introduced, invasive species, incursions, Hungary

Redescription of six feather mite species of the genus *Proterothrix* Gaud, 1968 (Analgoidea: Proctophyllodidae: Pterodectinae) from the "Edouard Louis Trouessart" Collection

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Feather mites are ectosymbionts commonly found on birds and spend their entire life on the host. The genus Proterothrix Gaud, 1968 includes 30 species of feather mites, of which 28 are included in three species groups: megacaula (three species), schizothyra (four species) and wolffi (21 species). Representatives of the schizothyra group are restricted to kingfishers (Coraciiformes: Alcedinidae), those of the wolffi group are distributed on species of several passerine families of the infraorders Corvida (Acanthizidae, Dicruridae, Meliphagidae, Monarchidae, Paradisaeidae, Ptilonorhynchidae and Rhipiduridae) and Passerida (Leiothrichidae, Muscicapidae, Paradoxornithidae, and Pellorneidae), while those of the megacaula group are known from hosts of the infraorder Passerida (Muscicapidae). Six species of this feather mite genus were discovered and briefly described, without being drawn, by Edouard Louis Trouessart, at the end of the 19th century. Fortunately, the type material used to describe these species is still preserved in the Muséum National d'Histoire Naturelle in Paris, France. All the acarological material (mites mounted on slides) used in the present study was loaned from the "Edouard Louis Trouessart" Collection from that museum. Many slides from this old and fabulous collection of feather mites were in a poor condition, with the Faure medium crystallized, but they were re-examined in the 1980's by Prof. Warren T. Atyeo (University of Georgia, Athens, USA), who remounted some of this material. The detailed redescriptions and illustrations are given, according to the current format used for species of pterodectine mites, for the following six species: Proterothrix diminuta (Trouessart, 1899), P. modesta (Trouessart, 1899) and P. phyllura (Trouessart, 1899), all from Manucodia ater (Lesson) (Corvida: Paradisaeidae); P. emarginata (Trouessart, 1899) from M. chalybatus (J. R. Forster) (Corvida: Paradisaeidae); P. paradisiaca (Trouessart, 1885) from Paradisaea minor Shaw (Corvida: Paradisaeidae) and Sericulus chrysocephalus (Lewin) (Corvida: Ptilonorhynchidae); and P. xiphiura (Trouessart, 1885) from Psarisomus dalhousiae (Jameson) (Tyranni: Eurylaimidae).

Keywords: Feather mites, ectosymbionts, "Edouard Louis Trouessart" Collection, *Protherotrix*, systematics



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New data on the genus *Dissorhina* Hull, 1916 (Acari, Oribatida, Oppiidae), based on a review of species from the Romanian fauna

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Within the family Oppiidae, one of the largest and diverse families of oribatid mites, the genus Dissorhina Hull, 1916 currently includes 12 species and 4 subspecies with semi-cosmopolitan distribution (mainly Holarctic but also in Ethiopian and Neotropical regions). More than half of the extant species have been described from south-eastern Europe, and moreover, two fossil species have been discovered in Tertiary Period sediments from the same region. These data, which support the hypothesis of a possible speciation centre for *Dissorhina* in this region, were also the premise for the present study. A rich source of material available in the institute collection was used for this study. Samples (litter, soil, moss, decaying wood) have been collected over the past 2-3 decades from various types of ecosystems in almost all regions of Romania. Dissorhina specimens were preserved in 70% ethanol and then cleared in lactic acid for the microscopic study. The main morphological and biometrical characters were analyzed in the light of the original descriptions of the species, and subsequent re-descriptions or additional data available in the literature were also considered. Six known species were confirmed or identified, namely Dissorhina ornata (Oudemans, 1900), D. carpatica (Gordeeva and Melamud, 1991), D. longispina Mahunka, 2006, D. shqipetarica Mahunka and Mahunka-Papp, 2008, D. signata (Schwalbe, 1989) and D. tricarinatoides (Dubinina, 1966). Dissorhina shqipetarica was recorded now for the first time in Romania. In addition, two other species have been identified, to be described as new species. A comparative morphological analysis, illustrations, data on local distribution and ecology of each species are given, and an identification key is proposed.

Keywords: Dissorhina, morphology, biometry, new species, south-eastern Europe

Registered acaricides in Turkey

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Phytophagous mites can cause significant yield losses in various kind of plants such as ornamentals, fruits and vegetables. Especially under hot climatic conditions, they can become serious pests. Because of favorable conditions, including hot climate and the availability of plants throughout the year, the southern part of Turkey, which also has vast majority of greenhouses, has more mite problems than other parts of Turkey. Although biological control agents are widely used in greenhouses, their control is still based on acaricides or insecticide/acaricides, especially when high population densities occur. However, the intensive use of these chemicals causes the rapid development of resistance. Therefore, using the appropriate chemicals when necessary is vitally important in terms of managing and delaying resistance development. In Turkey, there are more than 15 different registered synthetic acaricides and insecticide/acaricides which target nerves and muscles, respiration and growth and development. This diversity of chemicals allows for proper resistance management, if growers use them appropriately. In this study, the chemicals which are used against phytophagous mite species in Turkey, their registration dates and formulation types will be reviewed. In the light of this information, the possible futures of these chemicals in Turkey will be discussed.

Keywords: Acaricides, resistance management, phytophagous mites, Tetranychidae



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Do females evolve to avoid incompatible crosses?

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Wolbachia is a widespread, endosymbiotic bacteria commonly found in populations of the spider mite Tetranychus urticae. These bacteria often induce cytoplasmic incompatibility (CI) whereby a cross between an uninfected female and an infected male yields a reduced number of fertile offspring. As crosses leading to CI are costly for uninfected females they may avoid mating with Wolbachia-infected males. To address this possibility, we investigated whether antibiotic-treated (uninfected) females from 6 naturally Wolbachia-infected T. urticae populations discriminate between infected and uninfected males. Females showed no preference. However, female choice is expected to evolve only in populations with intermediate infection levels, as choice is only possible in those populations. To test this, we merged the populations previously tested and let them evolve with: i) full Wolbachia infection (positive control), ii) absence of infection (negative control) or iii) absence of infection in females but intermediate infection level in males (i.e. Wolbachia-uninfected females were given the choice between infected and uninfected males in each generation). After 20 generations of selection, both selected and control, uninfected females mated more often with infected than uninfected males, suggesting higher competitive ability of the former but no selection for more choosy females under mixed infection. However, uninfected males and females from the mixed infection regime had shorter latency to mate and longer mating duration than control individuals. Therefore, although evolving under mixed infection did not affect the host mating choice, it did affect their mating behaviour. These results constitute the first experimental evidence that the evolution of CI-antagonist strategies is possible.

Keywords: Experimental evolution, maternally-transmitted symbiont, reproductive manipulation, reproductive behaviour, assortative mating

Mite communities (Acari) of salt marshes in the Russian Arctic: taxonomic structure and spatial organization

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Seashore mite assemblages have been explored in detail only in northern and western Europe. No research has hitherto concerned the littoral and saltmarsh mites in the Arctic zone. During the last few years, we have studied the organization of saltmarsh mite communities in different sectors of the Russian Arctic, i.e. the coasts of the Barents Sea, Pechora Sea, Kara Sea, Bering Sea and the Sea of Okhotsk. Standard series of soil samples were collected everywhere at several hypsometric levels, all marked by characteristic vegetation types. The acarofauna of salt marshes contains a significant proportion of widely distributed polyzonal species (about 42%) yet the geographical ranges of 20% of species are restricted to the Arctic. Low marsh levels are populated by specialized halobiontic mites but mainly by hydrophilous species that inhabit various wet, saltfree meadows as well. Clear geographical vicariance for species of some genera (Vulgarogamasus, Thinoseius, Halolalaeps) is revealed between the Pacific and other littoral faunas studied. Both species diversity and total mite abundance grow with increasing hypsometric level. Even species dwelling at several marsh levels show a clearly preferred elevation zone. Some of the species dominate at low levels and others have a clear maximum abundance at the middle levels or in high marshes. Numerous species are sporadically recorded only in the highest marsh zone and are obviously dwellers of adjacent tundras. Peculiarities of species distributions along the marsh profile are indicative of the existence of three different types of mite community: (1) assemblages of low marshes, (2) assemblages of high marshes, and (3) intermediate communities formed at mid-levels of the profile. The species compositions of low marshes in all regions studied, even rather distant ones, are much more similar than those at high marsh levels.

Keywords: Mesostigmata, Oribatida, halobiont, littoral, area



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Relationships between columbiform birds (pigeons and doves) and quill mites of the genus *Gunabopicobia* (Acariformes: Syringophilidae: Picobiinae)

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The subfamily Picobiinae is taxonomically diverse group of obligate, permanent and highly specialized parasitic mites. All picobiines exclusively occupy quills of the contour feathers of neognathous birds belonging to ten orders. The avian order Columbiformes has its own and unique picobiine fauna belonging to the poorly investigated genus *Gunabopicobia*. In our study, we tried to explain some of ecological and evolutionary host-parasite relationships. We examined 98 species of columbiform hosts (31% of the world fauna) from all zoogeographical regions inhabited by these birds. In the mite material, we recorded seven Gunabopicobia species (incl. five new species) associated with 23 host species belonging to 12 genera. For all these mite species, we established two morphologically distinct groups. Members of both groups are mono- (3 species), oligo- (1) and mesostenoxenous parasites (3). The quite high index of prevalence of 20-100% in comparison to other examined wild bird hosts of picobiine mites probably corresponds with the social life of the examined pigeons and doves. In addition, based on the host distributions, we classified representatives of *Gunabopicobia* into three zoogeographical groups: Afro-Eurasian group (1 species), New World group (4 species) and Australo-Indonesian group (2 species). We also hypothesize that because representatives of the Gunabopicobia occupy a broad spectrum of the hosts belonging to all main clades of Columbiformes (Columbinae, Raphinae, and Claravinae), these mites may have parasitized the common ancestor of these birds.

Keywords: Acari, Columbiformes, ectoparasites, pigeon, doves

Acknowledgement: Financial support was provided by the Polish National Science Centre (NCN2014/15/B/NZ8/00208).

The host-parasite relationships in the system composed of quill mites of the subfamily Syringophilinae (Acariformes: Syringophilidae) and parrots (Aves: Psittaciformes)

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The subfamily Syringophilinae includes permanently quill inhabiting parasites of birds. Although they are known from almost all recent orders of birds, Psittaciformes remains one of the least known groups of hosts for quill mites. Due to their usually narrow host specificity, the Syringophilinae are a good model for the study of ecological and evolutionary host-parasite relationships. In our study, we analyzed 72 species of parrots (21% of the world fauna) from the Australian, Oriental, Neotropical and Afrotropical regions. We recorded 27 species grouped in six genera of syringophilines associated with 38 host species belonging to 20 genera. The examination of host specificity showed that Syringophilinae parasitizing parrots were mainly monoxenous (67%), and the rest of them were oligoxenous (26%) and mesostenoxenous (7%). We also report: a) two species of syringophilines occurred on hosts from two families and from different zoogeographical regions; b) the co-occurrence of two quill mite species belonging to different genera on seven host species; these species always occupied different microhabitats in the plumage of their hosts; c) the genera *Neoaulobia* and *Megasyringophilus* were associated with the Cacatuidae, Psittacidae and Psittaculidae families; d) *Castosyringophilus* and *Terratosyringophilus* were found on New- and Old World parrots; and e) the genus *Psittaciphilus* occurred exclusively on Neotropical parrots.

Keywords: Acari, host specificity, parrots, Syringophilinae, zoogeographic distribution

Acknowledgement: Financial support was provided by the Polish National Science Centre (NCN2014/15/B/NZ8/00208).



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Are r and K genetically correlated?

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Per-capita growth rate at low population density and equilibrium population size are often assumed to be traded off with each other. Inspired by the classical equation for logistic growth, arguably the simplest population dynamic model accounting for density dependence, this is known as the r vs K-selection paradigm. However, other models suggest that r and K should actually be positively correlated through shared underlying individual-level traits. Here, we aimed to investigate this question empirically. Through the use of 19 isogenic lines of a species of spider-mite, Tetranychus urticae, we are currently measuring 4 traits crucial to population dynamics: 1) the intrinsic growth rate (r), measured as the number of viable females produced from a single female; 2) the resource use (u), i.e., the quantity of resource consumed by a single individual, measured through the amount of damage caused to a piece of leaf; 3) the carrying capacity (K), which is the density at which the number of offspring produced equals the number of parents, determined by exposing the same amount of resource to increasing densities and then measuring the offspring produced by these individuals; and 4) the degree of intraspecific competition (c) measured by how the presence of individuals negatively affects consumption by conspecifics. We will then test whether r can be predicted from u, and K from c, by measuring the correlation between these traits. Subsequently, we will test whether r and K are correlated, and if so, whether this correlation is negative or positive.

Keywords: Carrying capacity, population growth rate, competition, resource use, individual and population traits

Does an increased male mating rate evolve in response to *Wolbachia*-induced cytoplasmic incompatibility?

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Wolbachia is a genus of maternally inherited, endosymbiotic bacteria that manipulates the reproduction of many arthropod species. In the spider mite, Tetranychus urticae, it can cause cytoplasmic incompatibility (CI), which leads to the embryonic death of fertilized eggs from crosses between infected males and uninfected females. Thus, while CI indirectly benefits infected females (the transmitting sex), it is detrimental to infected males, which suffer reduced fertility when mating with uninfected females. This generates a conflict Wolbachia-male, which may lead to the evolution of an increased mating rate in infected males, compared to uninfected ones, to increase their reproductive success. However, this should evolve only under the selection pressure of CI, which is expressed only at intermediate Wolbachia infection prevalence, i.e., when both infected and uninfected hosts coexist in a population. To test this, T. urticae populations were allowed to evolve under three different selection regimes: (i) in the absence of Wolbachia (0% infection), (ii) when totally infected by Wolbachia (100% infection), and (iii) at intermediate Wolbachia infection frequency (50% infected mites). After 20 generations of evolution, the mating frequency, copulation duration and offspring sex ratio of males from the different selection regimes and matings with infected females were measured. Although we found that the males' reproductive success is strongly positively correlated with their mating rate, the proportion of mated males, mating rate and copulation duration did not differ significantly among selection regimes. However, infected males that evolved under intermediate Wolbachia prevalence tend (albeit non-significantly) to produce more daughters than uninfected males. Therefore, although evolving under mixed Wolbachia infection did not affect male mating frequency, our results suggest that CI might constitute a selective force for the evolution of spider mite reproduction.

Keywords: Experimental evolution, reproductive behaviour, sexual selection, multiple mating, fitness compensation



2-8 September 2018, Antalya - TURKEY

Dispersal factors of the shiso rust mite, *Shevtchenkella* sp. (Acari: Eriophyidae)

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Shiso (*Perilla frutescens* L.) is a herbaceous plant whose green leaves are extensively used in Japanese cuisine. The shiso rust mite (*Shevtchenkella* sp.) is a serious pest in Japanese shiso cultivation, causing rust damage on the leaves and transmitting the Perilla mosaic virus. To control this species, it is important to elucidate its ecology, especially its dispersal behavior. This mite was captured by aerial sticky traps in shiso fields in an earlier study. In this study, we investigated the influence of wind velocity and mite density on aerial dispersion by using wind tunnel equipment and determined whether mites disperse by any phoresy in shiso fields. In the wind tunnel experiment, the removal rate from the shiso leaves was inversely related to the wind velocity between 0.5 m/s and 2.5 m/s, with the maximum removal rate being 43% at the minimum wind velocity of 0.5 m/s. There was no relationship between the removal rate and the changing of wind velocity from strong to weak. In addition, there was no difference in the removal rate for mite numbers of 100 and 150 on a leaf. A total of 103 insects, mites and spiders hosting phoretic species were captured in the shiso fields but no shiso rust mites were found on these organisms. Therefore, the dispersion of the mite by phoresy is considered unlikely.

Keywords: Eriophyidae, *Shevetchenkella*, wind dispersion, phoresy, mite density

Searching for the sister-group of Eriophyoidea based on rDNA sequence data

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The Eriophyoidea is one of the most species-rich and specialized phytophagous mite groups. In the most widely accepted current classification, this superfamily belongs to the order Trombidiformes. However, the most recent morphology-based parsimony analysis calls into question this relationship. Similarly, some older morphological analyses pointed to Tydeoida as a sister group of Eriophyoidea but molecular data suggest as the sister-group the eupodoid clade, including Tydeoidea, or the endeostigmatid family Nematalycidae, or even place the superfamily outside Trombidiformes. We show results concerning the phylogenetic position of eriophyoids using standard rDNA markers. Our sampling aimed to include representatives of all eriophyoid families and a large contribution of the other major acariform lineages. Phylogenetic analysis of ssu rDNA data, conducted using maximum likelihood and Bayesian inference methods, clearly supports one of the earlier hypotheses, namely that Eriophyoidea is the sister group of Tydeoidea within the Eupodides clade, with the latter defined in a narrow sense without Bdelloidea, Halacaroidea and Rhagididae. We suggest that the inconsistency between our analyses and previous molecular analyses arises from the more intense sampling of eupodoid mites, especially eriophyoids and tydeoids, and a different alignment strategy, without the removal of hypervariable sites or/and long insertions.

Keywords: Eriophyoidea, Tydeoidea, molecular phylogeny, rDNA, Acariformes



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The diversity of oribatid mites (Acari: Oribatida) in arid and semi-arid ecosystems of eastern Georgia

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In order to characterize the oribatid mite communities of disturbed and natural arid and semiarid ecosystems of eastern Georgia, field samplings were performed in November 2017, and in April and June of 2018. Seven types of ecosystems were defined (strong and medium erosion in arable lands, heavily and moderately overgrazed pastures, strong and medium natural (geological) erosion and natural steppe) in three geographical units (Shiraqi Plain, Eldari lowland and Gareji Range). The area of the sampling sites in each ecosystem was 50 m² and at each site three soil samples of 10×10 cm area and a depth of 10-12 cm were taken. Oribatid mites were extracted with a modified Berlese apparatus. More than 50 species were identified and Ceratozetes bulanovae is a new record for Georgia. Simkinia tianschanica, Oribatula (Z) exarata and Oribatula (Z) terricola are the characteristic species of arid and semi-arid ecosystems. The highest and lowest indices of diversity were found in natural steppe and eroded arable sites, respectively. Naturally eroded and steppe sites were dominated by *Punctoribates* spp. and *Scheloribates* spp.; on arable sites, Punctoribates punctum and P. meridianus dominated, and in pastures, Scheloribates laevegatus, Scheloribates latipes, S. tianschanica, O. (Z) exarata and O. (Z) terricola dominated. Punctoribates punctum and Scheloribates species are known to be stress tolerant and can exist in disturbed ecosystems. Oribatid mite communities from arable sites were structurally different from pastures and steppes. Tillage that leads to soil destruction has more negative effects on oribatid mite fauna than overgrazing.

Keywords: Arid and semi-arid ecosystems, oribatid mites, biodiversity, erosion, anthropogenic impacts

Dispersal strategies in cereal-feeding eriophyoid mites

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Because of their minute size and lack of wings, the majority of mites accomplish long-distance dispersal through passive means. For specialized phytophagous mites, finding the proper host plant is crucial and therefore directed dispersal would be expected. However, it is not clear how passively dispersing species increase the probability of successful dispersal given that they cannot control the direction of their movement. We tested whether two agriculturally important species of plant-parasitic eriophyids, wheat curl mite (WCM), Aceria tosichella, and cereal rust mite (CRM), Abacarus hystrix, display behaviours indicating their readiness to depart in the presence of dispersal cues: wind, vectors and fresh plants. We also aimed to assess the efficiency of dispersal by counting mites that successfully colonised new plants. We hypothesized that: (i) in the presence of dispersal cues, mites display behaviours indicating dispersal propensity; (ii) mites should achieve their highest dispersal efficiency when using wind as a dispersal agent; and (iii) both species of eriophyids would respond similarly to the cues. We found a surprisingly low proportion of mites exhibiting dispersal behaviours, which may suggest the existence of predisposed dispersers and residents in the population. Wind was the most important cue influencing the mites' behaviour, and wind dispersal was the most efficient mode of movement. WCM was more active than CRM, which may be one reason for WCM's high invasive potential.

Keywords: Eriophyoidea, phytophagous mites, dispersal, wheat parasites, plant-parasitic eriophyids

Acknowledgement: This study was funded by National Science Centre (Grant no. 2016/21/B/NZ8/00786).



2-8 September 2018, Antalya - TURKEY

Status of insecticide resistance and associated mutations in two spotted spider mite, *Tetranychus urticae*, from China

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The two-spotted spider mite, *Tetranychus urticae* Koch, is one of most damaging agricultural pests in the world and its control mainly depends on insecticides. In order to evaluate the development of resistance in *T. urticae*, the susceptibilities to various pesticides of 7 field populations collected in China were determined using leaf-dip bioassays. The mutation frequencies of the insecticide resistance-related genes were also determined. The results showed that the *T. urticae* populations exhibited varying levels of resistance to the different tested insecticides. All the 7 field populations had developed high resistance to abamectin whereas the resistance to bifenthrin and bifenazate was low. The mutation frequencies of G314D (*GluCl*1) and G326E (*GluCl*3) which correlated to abamectin resistance ranged from 28.33% to 63.64%, and 0% to 95%, respectively. The Miyun and Haidian populations in Beijing had the highest mutation frequencies for G314D and G326E among all the tested populations. For F1538I (*kdr*) mutations, a range of 3.33% to 100% was observed and it reached 100% in the Shunyi population collected from Beijing. However, no mutations of the bifenazate resistance-related genes were detected. These results may be helpful for the development of an efficient resistance management strategy for *T. urticae* in China.

Keywords: *Tetranychus urticae*, insecticides, resistance, mutation, China

Natural acarofauna in intensive greenhouse horticultural crops in Almeria, Spain

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After the implementation of biological pest control measures in greenhouses in Almeria in the south-east of the Iberian Peninsula in Spain, many different groups of mites associated with these crops have newly appeared. The samples studied here were collected using pitfall traps in 3 greenhouses harvesting peppers in the 2013; in addition, samples containing mite pest species were submitted by farmers to the Plant Production and Vegetable Health Laboratory in La Mojonera, Almeria for identification between 2006 and 2017 were also analyzed in this study. These samples showed a great diversity of mites, especially of predatory mites; predators were well dispersed in all the crops analyzed, in the aerial part of the plant as well as the soil. During the current 2018 season, replicates of these sampling efforts are being carried out in 4 greenhouses harvesting peppers, with two collection dates during the crop cycle. A total 19 species grouped in 13 families have been identified. One of the species is detritivorous (Carpoglyphidae), two are phytophagous (Tetranychidae); 2 are fungivorous (Eupodidae, Eupodes sp., Penthalolidae, Penthalodes ovalis) and the other fourteen are predators (Parasitidae, Parasitus sp.; Phytoseiidae, Amblyseius swirskii and A. barkeri; Ameroseiidae, Ameroseius sp.; Laelapidae, with two species; Bdellidae, with 3 species of the genus Bdellodes; Anystidae, Anystis baccarum; Erythraeidae, Balaustium hernandezi; Trombidiidae, Allotrobium sp.; Cheyletidae, one species). We are expecting the number of species to increase after the material that is currently being collected is identified. The high number of species reported shows that these crops are being managed using less types and amounts of pesticides and with techniques that improve the biodiversity and abundance of mite species. Therefore, it is recommended that that the current type of managements on these crops is maintained and that this acarofauna is maintained and promoted.

Keywords: Acarofauna, predators, horticultural crops, greenhouse, Almeria



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Biodiversity of mites in caves in south Spain

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The diversity of the mite community present in caves in Spain has not been widely studied or its knowledge is limited to certain caves or groups of mites. In the Andalusia region in southern Spain, 102 caves were seasonally sampled during the years 1994 and 2013. These studies, which were subsidized by different agencies, aimed to characterize the cave arthropod communities in order to protect endemic and threatened species in the south of the Spain. The number of mites varied widely among caves. In the drier ones no specimens were captured, and in those that had mites, they represented 1.7% with less than 50 to which 50% of the arthropods are mites with more than ten thousand specimens. In this work, we identified the mite fraction of arthropods captured in those field trips. Acari were captured using pitfall traps filled with a preservative solution or directly hand-captured using a small brush. Approximately 25,000 mites were collected and identified to genus and species level when possible. The most abundant groups of mites were Mesostigmata, Oribatida and prostigmatid Labidostommatoidea, Eupodoidea and Trombidioidea, among others. The diversity of the mite community found in different caves was also compared. This analysis revealed that there is a group of species only present in certain caves, while other species are widely distributed, appearing in many of the caves sampled. This is the first comprehensive study of the mite community present in caves of the Iberian Peninsula.

Keywords: Biodiversity, mites, caves, Andalusia, Spain

First report of parasitic mites from the colluvial mesovoid shallow substratum

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This study was conducted in the Sierra de Guadarrama National Park in Central Spain. The traps were installed in the colluvial, mesovoid shallow substratum (MSS). The sampling was performed mainly by using subterranean sampling devices (SSDs) consisting of a 1m long PVC cylinder with numerous perforations in its lower half. A pitfall trap filled with 1,2-propanediol and cheese (bait) was slid inside using a nylon cord. Our samples contained several adult specimens of *Laemostenus* (Eucryptotrichus) pinicola (Graells, 1851) parasitized by tens of mites of the genus Beronium Southcott 1986 (Parasitengonina, Eutrombidiinae). The parasites were found along the entire body of the beetles. Three species have been described in the genus Beronium: Beronium coiffaiti (Beron, 1973) from Jebel El Ouad cave in Morocco, Beronium veronicae Haitlinger, 1994 from Tenerife in the Canary Islands, and Beronium laemostenis Mayoral and Barranco, 2005, described from the Cueva Larga cave in Almería, Spain. The first two species have been reported only from their type localities but B. laemostenis has been recently reported from 6 additional caves in Andalusia, expanding the distribution of this species to all of the south of Spain. Beronium coiffaiti and B. laemostenis have been reported only from caves but B. veronicae was found on an epigean ground beetle and has never been found in caves. The specimens of Beronium presented in this work and captured in Guadarrama resemble B. laemostenis and B. veronicae. However, they show some morphometric differences to those two species. The host, L. (E.) pinicola, belongs to the same genus as the host of the species, B. laemostenis and B. coiffaiti. There seems to be a preference for Beronium spp. to parasitize ground beetles of the tribe Sphodrini Laporte, 1834. To the best of our knowledge, this is the first report of mites parasitizing arthropods in the MSS.

Keywords: Beronium, cave, parasites, Laemostenus, MSS



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The efficacy of soft soap and garlic bulb extracts in controlling Polyphagotarsonemus latus (Prostigmata: Tarsonemidae) on Barbunia bean (Phaseolus vulgaris L. cv. 'Barbunia')

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Polyphagotarsonemus latus (Banks) (Prostigmata: Tarsonemidae) is a serious pest of a variety of agricultural crops worldwide. In most agricultural crops, the use of synthetic pesticides is the main control method for managing *P. latus*. However, the use of synthetic pesticides has harmful effects on the environment, non-target organisms and human health. Therefore, there is need to develop non-toxic natural products that have the potential to replace synthetic pesticides for controlling this pest. Plant extracts and soft soap are among the non-chemical control options. In this study, the efficacy of soft soap (10%) and water-based garlic bulb extract (10%) in controlling P. latus on Barbunia bean (Phaseolus vulgaris L. cv. 'Barbunia') was investigated in a climate controlled room at 25°C± 2, 70-80% relative humidity and a photoperiod of 16L:8D (Light: Dark). There were four treatments; unsprayed control, sprayed control, garlic bulb extract and soft soap. Abamectin 18 g 1-1 was used on the sprayed, control plants. Each treatment included five replicates with six plants per replicate. The mite populations were evaluated weekly by sampling young leaves from the top of the plant for four weeks. When the *P. latus* density (all stages except egg) was above an average of 4 mites leaf¹, spraying was done. The results showed that there was no statistically significant difference among the effects of the garlic bulb extract, soft soap and abamectin treatments on P. latus. However, further investigation is needed to assess the efficacy of the garlic extract and soft soap under greenhouse and field conditions.

Keywords: Broad mite, garlic bulb extract, pest control, *Polyphagotarsonemus latus*, potassium soap

Effect of cold storage on the survival and fecundity of the predatory mite Neoseiulus californicus (McGregor) (Acari: Phytoseiidae)

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Neoseiulus californicus (McGregor) (Mesostigmata: Phytoseiidae) is a predatory mite which primarily attacks spider mites but it can also survive on other mites, small insects and even pollen. It is an effective natural enemy species that is produced commercially and distributed for biological control by many companies. The success of biological control is dependent on the quality, including fecundity and longevity, of the natural enemies before their release. Storage techniques after rearing must ensure the availability of quality natural enemies. Therefore, the influence of cold storage on the survival and fecundity of N. californicus was investigated under controlled conditions in growth chambers. Newly-emerged (1–2 days old), mated, adult females were used in the experiment. The females were stored for 5 days at 10 ± 0.4 °C and RH of $50\pm$ 5% under continuous darkness. They were fed with mixed stages of Tetranychus urticae Koch (Prostigmata: Tetranychidae), as needed. The females from the control group were held at 25 ± 1 $^{\circ}$ C, RH of $70 \pm 5\%$ and a photoperiod of L:D 16:8 h. After storage, the number of eggs deposited by the females, and female mortality, were recorded daily until seven days or she died, whichever occurred first. The results indicated that the stored female survival rate was equivalent to unstored females, i.e., no effect on the survival of the stored adults was observed. However, the unstored females of N. californicus had a higher fecundity than the stored females. The impacts of longer storage periods at lower storage temperatures on post-storage biological traits also need to be investigated.

Keywords: Neoseiulus californicus, biological control, cold storage, fecundity, longevity



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First insight into quill mite (Prostigmata: Syringophilidae) microbiomes

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The microbiome is an integral component of every animal species, providing them with numerous benefits, affecting their behavior and role in the ecological system. In this context, permanent parasites, such as quill mites (Syringophilidae), deserve special attention. These obligatory bird ectoparasites occupy quills of feathers and feed on the host bird's subcutaneous tissues. Most of the known species have a strongly unbalanced, female biased sex ratio. Since quill mites are tightly associated with a specific habitat (quills), they can be considered as a part of a tripartite system (bird-mite-microbiome) in which different levels of biological organization can affect each other. Thus, this system enables testing predictions about microbial transmission and about microbiome-mite-bird cophylogeny. Also, the quill mite feeding regime makes this group interesting in terms of potential transmission of pathogens between bird hosts. Moreover, it is assumed that the reproductive disorders observed in most mite species are caused by reproductive parasites, such as Wolbachia and Spiroplasma. Here, we investigated the microbiota of 67 mite specimens representing 4 species parasitizing passeriform birds in Poland. We sequenced the V4 region of 16S SSU rRNA on an Ion Torrent. Altogether, 1,609,920 sequences were obtained and they were assigned to 4,325 amplicon sequence variants (ASVs). In addition to Wolbachia, which we documented earlier in quill mites, the mites harboured diverse, heterogeneous bacterial communities. These data represent a first step in deciphering the interactions of microbiota, quill mites and birds.

Keywords: Quill mites, ectoparasites, Syringophilidae, birds, microbiomes

Interaction between two-spotted spider mite (*Tetranychus urticae* Koch, Acari: Tetranychidae) density and the leaf chlorophyll content of different strawberry varieties

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Six different strawberry varieties (Ottoman, Karacilek, Hairy, Camarosa, Kabarla and Sweet Charlie) were used in this study which was carried out in the greenhouses at Gaziosmanpaşa University, Tokat in the summer of 2017. A randomized block design with 5 replications was used. Ten adult, two-spotted spider mites (Tetranychus urticae Koch) were released onto three leaflets of each potted strawberry plant. No spider mites were released on the control treatments. Chlorophyll content was measured on the three leaflets of each pot, once a month, 1 week after exposure. The amount of chlorophyll (Chlorophyll Concentration Index: CCI) in the control treatments was highest in August with 42.5 in Ottoman, followed by Camarosa (40.2), Karaçilek (37.5), Sweet Charlie (37.4), Kabarla (36.9) and Hairy (30.6). In September, the amount of chlorophyll was again measured, with the highest in Ottoman (46.2), followed by Camarosa (45), Karaçilek (42), Sweet Charlie (41.8), Kabarla (40.7) and Hairy (35.7). From August to September, the chlorophyll content in all varieties was highest and stayed constant or declined in all but 2 varieties (Hairy and Sweet Charlie) after September. The amount of chlorophyll in the leaflets exposed to *Tetranychus* urticae was highest in August with a maximum of 35.5 in Kabarla, followed by Camarosa (32.3), Karaçilek (30.4), Hairy (29.9), Ottoman (29.8) and Sweet Charlie (23.6). In September, the amount of chlorophyll was highest in Kabarla, followed by Camarosa (27.6), Ottoman (26.8), Hairy and Karaçilek (26.3) and Sweet Charlie (20.1). Overall, Tetranychus urticae caused a gradual decline in the chlorophyll content of the leaves from August to November. The reduction of leaf chlorophyll content caused by T. urticae feeding is likely to have a negative effect on the development and yield of strawberry plants.

Keywords: *Tetranychus*, chlorophyll, strawberry, leaf, yield



2-8 September 2018, Antalya - TURKEY

Some phytophagous mite species (Acarina: Trombidiformes: Prostigmata) on stone fruits in Ordu Province, Turkey

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A large number of mite species are harmful to fruit cultivation and mite damage to fruits is a worldwide problem. In this study, we determined the phytophagous mite species and their distribution on stone fruits in Ordu Province on the Black Sea coast of Turkey during 2016 and 2017. Surveys were carried out in eleven different districts (Altınordu, Akkuş, Ünye, Fatsa, Ulubey, Kumru, Perşembe, Gülyalı, Kabadüz, Çaybaşı and İkizce) of Ordu Province on five different stone fruits, namely cherry, cornelian cherry, peach, plum and sour cherry. Leaf samples were collected weekly during two growing seasons, i.e., from late April through early October of each year. At each sampling date, leaves were taken from different parts of the tree canopy, i.e., lower, middle and upper canopy. During the surveys, a total of nine plant parasitic mite species belonging to three families, Tetranychidae, Eriophyidae and Diptilomiopidae, were collected. *Tetranychus urticae* Koch and *Amphitetranychus viennensis* Zacher (Trombidiformes: Prostigmata: Tetranychidae) were the most common species.

Keywords: Phytophagous mite, stone fruit, canopy, Ordu Province, Turkey

Acknowledgement: This research is a part of corresponding author's Masters thesis and was supported by the Ordu University Scientific Research Project Coordination Unit (ODUBAP; Project No, TF-1622).

Morphological variations observed in the cosmopolitan mite species Eustigmaeus segnis (Koch) (Acari: Stigmaeidae)

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Eustigmaeus segnis (Koch) is one of the most widespread and abundant species of the genus which is in the family Stigmaeidae. In the present work, 2 larvae, 8 protonymphs, 23 deutonymphs, 105 females and 19 male specimens of E. segnis from Erzincan, Harşit Valley and Örümcek Forests in Turkey were examined, and their morphological features are herein compared with other, known Turkish specimens. Structural variations on the intercoxal area of the specimens in the deutonymph stage, location of their aggenital setae and different setation on leg genu III were observed. Different location of aggenital setae and different setation on genu II and coxa II in the protonymph stage were noted. Different forms of some dorsal setae in both female and male specimens of the species were detected. In addition, one specimen of each of the two nymph stages had asymmetric variations in the number of setae on their genua II and IV. However, differences in morphological features of the larvae were not evident. Intraspecific variation is a problem for species identification and may lead to taxonomic confusion. The aim of this study was to understand variations in the morphological features of E. segnis on the basis of the Turkish specimens.

Keywords: Asymmetry, intraspecific, mite, morphology, variation

Acknowledgement: A part of this study is based on the mite material obtained in a research project (No.113Z094) that was supported by the Scientific and Technological Research Council of Turkey (TÜBİTAK).



2-8 September 2018, Antalya - TURKEY

Trombidiid mites (Acari: Trombidiidae) of park and garden areas of Erzincan Province, Turkey

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Mites are almost everywhere, which means that finding mite habitats is a relatively simple matter. Prostigmata is one of the cosmopolitan groups in the mite world. Prostigmatid mites prefer grassy areas, soil, lichens, moss and litter habitats as living environments. The species living in urban areas occupy different habitats such as forested areas, stream banks, arable fields, and open spaces such as gardens, parks and tree groves. The world's population is increasing rapidly and green areas are decreasing. Rapid urbanization and industrialization across the world has caused the loss off natural habitats, and as a consequence, the biodiversity in urban areas, including mites, has been negatively affected. In this study, we compared the number of both species and specimens collected from urban and rural areas in Erzincan Province which is located in the eastern Anatolia Region of Turkey, with high mountains and plateaus. The mite samples (soil, litter and moss) were collected from the gardens of homes, public institutions, green areas, parks and the wall sides in Erzincan between April and November in 2016. The mites were extracted by using Berlese funnels. The collected materials were preserved in 70% ethyl alcohol and cleared in 9% KOH. Specimens for light microscope studies were mounted on the slides in Hoyer's medium. As a result of this study, eight species belonging to three families were diagnosed. In conclusion, the number of both species and specimens collected from the districts surrounding Erzincan was higher than from the city center.

Keywords: Acari, fauna, Erzincan, Trombidiidae, Turkey

A review of the erythraeoid mites (Acari: Prostigmata) of Turkey

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The Parasitengona (Acari: Prostigmata) constitutes one of the most diverse taxa among the Acari with respect to species richness and inhabited biotopes. This study is aimed to combine all the data available for erythraeoid mites from the different provinces of Turkey. Turkey is very rich in terms of biodiversity but the number of identified erythraeoid species is very low compared to other countries. Approximately 855 species belonging to 74 genera have been reported worldwide, whereas only 24 species belonging to 11 genera have been reported from Turkey. Fifteen of these 24 erythraeoid species (63%) are known to be present only in Turkey. Another remarkable point is that these data were mostly obtained as a result of informal field studies done by foreign scientists while holidaying in Turkey. Since Turkey has various topography, habitats and climatic conditions, more comprehensive investigations involving in all of the provinces of Turkey would very likely substantially increase the number of species.

Keywords: Acari, Erythraeoidea, fauna, Parasitengona, Turkey



2-8 September 2018, Antalya - TURKEY

Leptus (Trombidiformes: Erythraeidae) larvae parasitizing Odonata – a case study of terrestrial parasitengones associated with dragonflies in Zambia

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The genus Leptus comprises about 280 species, the vast majority (225) of which are known exclusively from the larvae. Thirty five species, including 33 known exclusively from larvae and two known only from active postlarval forms, have been described from the Afrotropics. Despite the increasing interest in host-parasite interactions, the knowledge of host spectrum still remains poor due to the deficiency of ecological studies focused on particular species. The majority of terrestrial Parasitengona species are known from a few specimens only, which limits inference on intraspecific variation and constitutes the main obstacle to determining host specificity. Terrestrial Parasitengona, in contrast to aquatic ones (Hydrachnidia), rarely have been reported to parasitize dragonflies. The records to date apply to the representatives of two erythraeid genera, Charletonia and *Leptus*. In the course of studies on the dragonfly fauna of Zambia, carried out in 2013–2015, the non-incidental parasitism of Leptus larvae on dragonflies was observed. Ectoparasitic larvae were discovered on four species representing two suborders and four distinct families of Odonata. The substantial material collected during the survey allowed the analysis of parasite taxonomy, including intraspecific variation of morphological and molecular traits, and is supported by data on ecology and host-parasite interactions. The taxonomic affiliation of parasitic larvae confirms the earlier hypotheses on limited host selectivity observed for *Leptus* spp.

Keywords: *Leptus*, taxonomy, ecology, host-parasite interactions, Odonata

Determination of resistance, inheritance and some detoxification enzymes in a *Panonychus ulmi* Koch (Acari: Tetranychidae) population selected with milbemectin

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In this study, the development of resistance, resistance inheritance and biochemical resistance mechanisms to milbemectin in *Panonychus ulmi* (Koch) were investigated. For that aim, the susceptible population HS was selected with milbemectin. Firstly, the LC₅₀ and LC ₇₀ values for milbemectin in the HS population were determined firstly. For the first selection dose, the LC₇₀ value was used. Subsequent selection doses were increased 1.5-fold each time. At the end of the fifth selection, resistance inheritance studies and biochemical studies were carried out in the resistant populations. For the susceptible *Panonychus ulmi* (HS) population, the LC₅₀ and LC ₇₀ doses of milbemectin were 0.117 and 0.264 µl / 100 ml water, respectively. At the result of the five selections in the HS population, the LC₅₀ value increased to 0.870 µl / 100 ml water and the resistance rate increased 7.43 fold. In the resistance inheritance studies, in the F1 females obtained from M5 $\stackrel{\wedge}{\circ}$ X GSS $\stackrel{\hookrightarrow}{\circ}$ and GSS $\stackrel{\wedge}{\circ}$ X M5 $\stackrel{\hookrightarrow}{\circ}$ reciprocal crossing, D = 0.56 and D = 0.06, respectively. In the biochemical studies, enzymes of esterase, glutathione S-transferase (GST) and cytochrome P450 (P450) were identified by α -naphthyl acetate, 1-chloro-2,4-dinitrobenzene (CDNB) and 7-ethoxycoumarin (7-EC) substrates. In the selected population (M5), esterase, GST and P450 enzymes increased by 1.67, 0.57 and 2.09 fold, respectively, compared to the parental population.

Keywords: Panonychus ulmi, milbemectin, resistance, esterase, GST

Acknowledgement: This research was supported by Süleyman Demirel University in Isparta, Turkey as a BAP project (4528-YL1-15) and is a part of the first author's Master's thesis.



2-8 September 2018, Antalya - TURKEY

Monitoring of abamectin resistance in *Tetranychus urticae* Koch (Acarina: Tetranychidae) populations collected-from cut flower greenhouses in Antalya, Turkey

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The two-spotted spider mite *Tetranychus urticae*, one of the most economically important pests in greenhouse and field crop production, damages annual and perennial crops such as vegetables, fruits and ornamental plants. Farmers generally use pesticides to control mites. Tetranychus urticae has developed resistance to many different classes of acaricides when they are heavily used. Abamectin, a chloride channel activator, is a widely used insecticide and acaricide in Turkey. In this study, the resistance levels to abamectin of eight different *T. urticae* populations collected from six clove and two gerbera greenhouses in Antalya were determined with the spray tower-leaf disc method. Mortalities were determined 24 h after treatment, and mites were considered dead if appendages did not move when prodded with a soft brush. Resistance levels to abamectin were determined by comparing the samples with a standard susceptible strain, GSS. Resistance levels to abamectin were 234 -fold for the SV-1, 215 -fold for the SV-2, 851 -fold for the AO-1, 741 -fold for the AO-2, 1.6 -fold for the AO-3, 197 -fold for the AO-4, 254 -fold for the AO-5 and 232 -fold for the AO-6 populations. All populations, except AO-3, were highly resistant to abamectin. To prevent resistance, acaricides having different mechanisms of action should be integrated with compatible biological control agents in *T. urticae* control programs.

Keywords: *Tetranychus urticae*, resistance, abamectin, bioassay, greenhouse

Acknowledgement: This research was supported by Süleyman Demirel University BAP project (5079-YL1-17), Turkey and is a part of the first author's Master's thesis

Metabolism of xenobiotics in mites

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Phytophagous arthropods are regarded as one of the most successful groups of organisms, having co-evolved with plants for many millions of years. During this extremely long period, plants have developed defence mechanisms against herbivory. Among the best known mechanisms is the production of allelochemicals. However, arthropods have counter defence mechanisms, including a detoxification system to metabolize the secondary metabolites of plants. When plants get attacked by herbivores/phytophages, they immediately start to increase their secondary metabolite production. Correspondingly, phytophagous arthropods utilise their detoxification systems, with enzymes produced to metabolize all kinds of xenobiotics. The most striking example of a plantherbivorous relationship is provided by the two spotted spider mite (TSSM) (Tetranychus urticae Koch), which can feed on more than 1,000 plant species; because of its high innate detoxification ability, TSSM also has a great ability to develop resistance to acaricides. Plant hormones such as jasmonic acids and salicylic acid play important roles in the defence systems of plants. Increases in the levels of these hormones can cause disruptions in both the reproductive and dispersal behaviours of phytophagous mites. Last but not least, trichomes provide both chemical and physical barriers against mites in plant defence systems. In this study, plant defence systems against phytophagous mites and the strategies of mites for overcoming plant defences are reviewed. With better understanding of plant-mite interactions, novel mite management strategies can be developed.

Keywords: Xenobiotic, trichomes, detoxification, plant hormones, two spotted spider mite



2-8 September 2018, Antalya - TURKEY

Genome and transcriptome sequencing of *Phytoseiidae persimilis* (Acari: Phytoseiidae) and comparative analyses of potential sex-determination genes

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Phytoseiulus persimilis is one of the most important biological control agents of spider mites. However, no reference genome of this species has been published. In this study, we sequenced its genome using 10X Genomics linked-read sequencing. Our results showed that the N50 contig length was 195.42 Kb, and a total 706 scaffolds were assembled, among which 320 scaffolds had a length of more than 10 Kb. Furthermore, the N50 scaffold length was up to 2.45 Mb and the longest scaffold was 7.44 Mb. The total size of the assembled genome was 197.23 Mb which was close to the 210.41 Mb estimated by our previous genome survey sequencing. This genome is larger than that of *Metaseiulus occidentalis* (151.7 Mb), the only species in Phytoseiidae with its genome published. A total of 23,670 high confidence genes were predicted, including 23,168 protein coding genes and 502 tRNA genes. Candidate genes involved in *P. persimilis* reproduction and sex determination were identified on the basis of orthologous genes in M. occidentalis and in other arthropods. Expressions of these genes were compared between mated and unmated P. persimilis males and females based on transcriptome sequencing data, and phylogenetic analyses were also conducted to infer the molecular relationships between *P. persimilis* and other arthropods. The results of this study enriched genomic information on the Phytoseiidae and the Acari, and provided a basis for further studies on the molecular mechanisms responsible for paternal genome elimination in the Phytoseiidae.

Keywords: Phytoseiidae, genome assembly, transcriptome, phylogenetic analyses, sex determination

A new locality record and distribution of *Enemothrombium bifoliosum* (Canestrini, 1884) (Acari: Microtrombidiidae) from Turkey

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Microtrombidiid mites are cosmopolitan, predatory mites that are found in soil and decomposing organic matter. The family includes 115 genera and about 427 species worldwide but the fauna of Turkey has been poorly investigated, with only about 15 species reported. The genus *Enemothrombium* is distributed in Europe and contains five species. Two of them (*Enemothrombium culicoidium, Enemothrombium wohltmanni*) are known from the larval forms and two of them (*Enemothrombium bipapillatum, Enemothrombium dartevellei*) are known from the postlarval forms, while only one of them (*Enemothrombium bifoliosum*) is known from both the larval and postlarval forms. In the present work, specimens of *E. bifoliosum* collected from Çanakkale Province were evaluated. Short descriptions of these species and their global distributions are given.

Keywords: Canakkale Province, microtrombidiid, predatory, Prostigmata, Trombidiformes



2-8 September 2018, Antalya - TURKEY

Evaluation of skins of trombidiid mites (Actinedida: Trombidiformes) changed during their transformation from larval to deutonymphal phase

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The terrestrial Parasitengona go through seven life stages, namely egg, prelarva, larva, protonymph, deutonymph, tritonymph and adult, with different morphologies. The larval stage is usually parasitic but they are predatory in the deutonymph and adult stages. Although these two stages are similar, the deutonymph body is smaller than the adult. A very large number of trombidioid species identified so far are only described from the larval or postlarval stage. This situation has caused considerable misinformation and confusion in this group. Currently, great emphasis is placed on the diagnosis of both the larval and postlarval stages in the identification of species. Thus, more accurate diagnoses are being made. Mites collected alive by hand and by trapping are put into plaster+charcoal filled bottles for rearing. Factors such as the appropriate temperature and humidity required by mites for maturation can be provided in the laboratory environment. Sometimes a small number of engorged larvae collected from the host are also placed in the rearing bottles. Since the larva is engorged, it passes to the deutonymphal stage after a certain period, changing its skin during the transition process. The skin left in the rearing bottle is collected and a permanent preparation is made for measurement purposes. Other underfed larvae collected from the host are stored in alcohol before preparations are made. When the engorged parasitic larvae are put into the rearing bottle, the number of samples of the larval stage and the total number of characters measured are reduced. The purpose of this study was to increase the number of data for the larval stages by taking measurements of the skins left behind while they transition to the postlarval stage. For this purpose, the skins of six engorged larvae obtained from deutonymphs belonging to three species were prepared as permanent slides and measurements of important characters were recorded.

Keywords: Acari, biology, life cycle, Prostigmata, Trombidioidea

Acknowledgement: A part of this study was supported by The Scientific and Technological Research Council of Turkey (TÜBİTAK-Project No. 217Z184).

First report on soil-inhabiting mites of the cohort Gamasina (Acari: Mesostigmata) in the Kashan region, Isfahan Province, Iran

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Kashan is located in the north of Isfahan Province in the center of Iran. It has a hot and dry climate. During research conducted from the spring to the winter of the years 2015 and 2016 in this region, a total of 20 species belonging to 13 genera and six families of Gamasina were collected from different sites. They were identified as follows; among them, one species marked with an asterisk is new to science (items given in parentheses are in the respective order of sex, region, specific site and altitude [m a.s.l.], separated with a semicolon): Ameroseiidae: Ameroseius lidiae Bregetova, 1977 (♀; Hanjan, Qamsar; almond, rose; 1545–1550); Digamasellidae: Dendrolaelaps spp.1 & 2 $(\mathcal{L}, \mathcal{L})$; Hanjan, Jowshaqan, Niyasar; pomegranate, riverbank, roadside; 1400–1700); Laelapidae: Androlaelaps aegypticus Willmann, 1959 (\$\times\$; Niyasar, Qamsar; pussy willow, roadside; 1557— 1700); A. shealsi Costa, 1968 (♀, ♂; Jowshagan, Kashan, Mashhad Ardehal, Niyasar, Qamsar; almond, pussy willow, turnip, vineyard, roadside; 1530–2370); Cosmolaelaps claviger (Berlese, 1883)(\bigcirc ; Niyasar; water-spring soil; 1700); *C. rectangularis* Sheals, 1962(\bigcirc ; Hanjan; pomegranate; 1550); Euandrolaelaps karawaiewi (Berlese, 1903) (♀; Niyasar; poplar; 1700); E. sardoa Berlese, 1911 (\updownarrow ; Hanjan; riverbank; 1550); Gaeolaelaps aculeifer (Canestrini, 1884) (\updownarrow ; Niyasar; rose, water-fall soil; 1620–1700); G. angustiscutatus (Willmann, 1951) (♀; Hanjan; water-spring soil; 1550); G. arabicus Hafez and Naser Elbadry, 1982 (♀; Niyasar, Qamsar; almond, pussy willow; 1584–1880); Gaeolaelaps n. sp.* (♀; Kashan; olive; 1000); Haemolaelaps casalis (Berlese, 1887) (♀; Kashan, Qamsar; pussy willow, roadside; 1050–1550); Hypoaspis (s. lat.) asperatus (Berlese, 1904) (\(\sigma\); Hanjan, Jowshagan, Kashan, Niyasar; almond, fava-bean, persimmon, turnip, riverbank, water-fall soil; 1066–1740); *Pseudoparasitus missouriensis* (Ewing, 1909) (\(\times\); Hanjan; riverbank; 1550); Melicharidae: *Proctolaelaps pygmaeus* (Müller, 1859) (♀; Niyasar; rose, under lumber soil, water-spring soil; 1700–2000); Ologamasidae: Gamasiphis sp. (♀; Hanjan, Kashan; vineyard, roadside; 1000–1550); Rhodacaridae: Multidentorhodacarus sp. (♀; Niyasar; rose; 1558); Rhodacarellus sp. nr. subterraneus Willmann, 1935 (♀; Kashan; fava-bean; 1000).

Keywords: Mesostigmata, Gamasina, soil mite, altitude, Iran



2-8 September 2018, Antalya - TURKEY

New quarantine mite detections in South Africa

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With the continuous high rate of international agricultural trade, there is an increasing likelihood that mite pests will be inadvertently introduced to new regions. South Africa is no exception, and recently a number of new mite pests have been detected for the first time. Here we list the four most recent new mite pests recorded: *Acalitus vaccinii* (Keifer) (Eriophyidae) from blueberries in 2012; *Acalitus essigi* (Hassan) (Eriophyidae) from blackberry in 2014; *Brevipalpus lewisi* McGregor (Tenuipalpidae) from grape vines in 2015; and *Raoiella indica* Hirst (Tenuipalpidae) from date palms in 2016. These mites were listed quarantine pests, meaning that agricultural authorities were aware of the risk and on the look-out for them in imported goods, but they still managed to pass through border biosecurity. Preventing the accidental introduction of mites, detecting new incursions and responding to them presents a number of challenges. Due to their small size, mites are difficult to detect, making them highly likely to pass through biosecurity undetected and for a new incursion to remain unrecognized for an extended period. Responses to reports of new mite pests in a country need to take this situation into account. The detection and subsequent phytosanitary responses to each of these new pests in South Africa are discussed. We examine possible routes of entry, their economic impact and the possibilities for control.

Keywords: Agriculture, incursion, quarantine, pest, Acari

Spatio-temporal distribution of *Oligonychus afrasiaticus* on date palm fruits: a step towards early detection and establishment of a sampling program

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The Old World date mite (OWDM), Oligonychus afrasiaticus (McGregor) (Acari: Tetranychidae), is a serious spider mite pest that attacks date palm fruits. The present work is the first study aiming to investigate the spatial distribution patterns of OWDM populations, as well as population dynamics on fruits, as a first step towards establishing a comprehensive sampling program. The fruit strand was considered as a sampling unit to estimate mite density. Data was collected from two sampling sites (Riyadh and Dammam Provinces) for four years (2011, 2012, 2014 and 2016). Total and average numbers of mites were taken from two stages (Kimri and Khlal) of date fruits through collecting fruit strands from four different directions (east, north, west, south) on bunches and three strand positions (outer, middle, inner) in each bunch. Our results showed higher populations at the end of the Kimri stage followed by a significant decline after changing to Khlal. The OWDMs showed a clumped distribution pattern during both the Kimri and Khlal stages. A generalized linear model (GLM) was fitted to the first three weeks data compiled in each year to assess the differences in mite population density between and among bunch direction and strand position. Variations in mite densities were non-significant between and among different bunch directions and strand positions. The non-significant differences in mite density for bunch direction and strand position may direct us to focus on other parts of date palm trees, like fronds, for mite detection at the early stage of infestation. The present study may also provide vital steps toward establishing a sampling program for effective pest monitoring and management.

Keywords: Population dynamics, date palm strands, date palm mite, IPM, Saudi Arabia



2-8 September 2018, Antalya - TURKEY

The genus *Oligonychus* Berlese (Prostigmata: Tetranychidae) from Saudi Arabia; new records and some morphological and webbing behavioral variations between *Oligonychus ephamnus* and *Oligonychus afrasiaticus*

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Two species, Oligonychus (Reckiella) ephamnus Beard and Walter and O. (R.) orthius Rimando, are recorded for the first time from Saudi Arabia from grasses (Poaceae) under the date palm, Phoenix dactylifera L., and Washingtonia sp. (Arecacae), in association with the date palm mite, O. (R.) afrasiaticus (McGregor). The Oligonychus species, especially those belonging to the subgenus Reckiella Tuttle and Baker, are very difficult to identify through the morphological characters of adult females and usually are distinguished by the shape of the male aedeagus. Some morphological and webbing structural variations between adult females of O. (R.) ephamnus and O. (R.) afrasiaticus, were observed and studied in the present research work. The females of these two species are morphologically similar, except for differences in comparative length of leg empodia and proximo-ventral hairs, and the characteristics of web structure. All leg empodia are 1.6 to 1.8 times longer than proximo-ventral hairs in O. afrasiaticus, compared to all empodia almost equal in length to the proximo-ventral hairs in O. ephannus. Moreover, O. afrasiaticus deposited its fecal pellets on the leaf surface of the date palm and Washingtonia sp., and the eggs were laid in the middle of an irregular, complicated web structure whereas in O. (R.) ephamnus, both the fecal pellets and eggs were scattered throughout the regular, complicated web structure. Webbing structure behavior may also be used to distinguish other closely related Oligonychus species. An illustrated key of males and females of all known Oligonychus species from Saudi Arabia is provided.

Keywords: Date palm, mite, fecal pellets, webbing structures, taxonomy

A new species of *Cosmolaelaps* (Mesostigmata: Laelapidae) of rose greenhouses in The Netherlands with potential to control the edaphic phases of thrips

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A mite species with potential as a biological control agent of Frankliniella occidentalis (Thysanoptera: Thripidae) was collected from the litter and remains of plant material in the soil in different rose greenhouses in The Netherlands. In order to identify this species and test its potential as a thrips control agent, a morphological characterization was carried out, as well as experiments on consumption and oviposition in the laboratory. Specimens from a laboratory colony initiated with specimens collected in greenhouses were analyzed morphologically, by means of the measurement of structures and determination of the main morphological characteristics and the quetotaxy of the leg segments. Oviposition experiments were conducted using three different diets: Carpoglyphus lactis, F. occidentalis and a combination of both. In the consumption experiments the quantity of F. occidentalis and C. lactis consumed was evaluated. Specimens of the mite were identified as a new species which is most similar to Cosmolaelaps brevipedestra (Karg, 1985) and Cosmolaelaps hortensis (Ishikawa, 1986); however, these species are smaller (difference of about 20% in the average length) and with different relative length of setae, among other characteristics. The oviposition of the new species was greater when consuming F. occidentalis, and a combination of F. occidentalis and C. lactis, than when it consumed only C. lactis. The consumption of F. occidentalis per female per day was 1.3 ± 0.2 and of C. lactis it was 8.2 ± 0.3 . The discovery of this new species and its potential as a predator of thrips showed that there are several options that can be explored for its practical use in agriculture.

Keywords: Edaphic mites, biological control, morphology, oviposition, consumption



2-8 September 2018, Antalya - TURKEY

Increasing biological control by providing alternative food for the litterinhabiting predator, *Cosmolaelaps* n. sp. (Mesostigmata: Laelapidae)

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Biological control using generalist predators is successful in many crops. Such predators feed on pests and food or alternative prey that do not cause economic damage to the crop. Adding food for predators to a crop has a positive effect on their numerical response. Thus, more predators are available to potentially attack the pest, reducing its density (apparent competition). However, in the short term, the addition of alternative food may decrease the number of attacks on pests, if the predators are satiated or preferentially feed on the alternative food (apparent mutualism). The positive effects of alternative food on pest densities may occur repeatedly when populations of pests or of alternative food fluctuate. We investigated whether providing generalist, litter-inhabiting predators with alternative prey in the litter could increase control of the thrips, Frankliniella occidentalis. The larvae of this pest feed on above-ground plant parts, causing significant damage, but the prepupae and pupae live in the litter layer. Densities of thrips and damage to above-ground plant parts were significantly reduced by supplying litter-inhabiting predators, predominantly Cosmolaelaps n.sp., with alternative food. Subsequently, Cosmolaelaps n. sp. was tested separately; this species alone also reduced thrips densities and damage significantly when it was supplied with alternative food. In conclusion, litter-inhabiting predators can significantly reduce above-ground plant damage when supplied with alternative food in the litter layer.

Keywords: Apparent competition, biological control, *Frankliniella occidentalis*, below-ground interactions, above-ground interactions

Detection of endosymbiont bacteria in *Tetranychus urticae* collected from cutflower greenhouses

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Tetranychus urticae, one of the major global pests, causes major economic losses in vegetable, fruit and ornamental crops. This pest rapidly reaches high population densities due to its short life cycle, high reproductive capacity and arrhenotoky in reproduction. Producers generally use chemical control to keep populations under control in greenhouses. The sustained use of acaricides has inevitably led to the development of resistance in field populations of this pest. Different mechanisms of resistance to acaricides have been reported for spider mites. Among others, the presence of certain endosymbiotic microorganisms may be associated with acaricide resistance in spider mites. In this study, the presence of seven different endosymbionts (Arsenophonus, Cardinium, Fritschea, Hamiltonella, Portiera Rickettsia and Wolbachia) was investigated in eight abamectin resistant (1.6 to 851 fold resistance) populations of T. urticae collected from cutflower greenhouses, and in a susceptible laboratory strain (GSS), with the PCR method. Only the bacterium Wolbachia was detected in all the T. urticae populations collected. However, Wolbachia and Fritschea were both present in the susceptible GSS strain. Because Fritschea was consistently associated with the GSS strain of T. urticae, the possible involvement of this endosymbyont in acaricide sensitivity should be examined in more detail.

Keywords: Acaricide, arrhenotoky, resistance, sensitivity, susceptible



2-8 September 2018, Antalya - TURKEY

An unusual species of *Eharius* Tuttle & Muma (Acari: Phytoseiidae) from Turkey: *Eharius* sp. nov.

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Eharius Tuttle & Muma is a genus in the sub-family Amblyseiinae (Acari: Phytoseiidae) and is characterized by having a dorsal setal pattern 10A:8C (setae S4 absent). It can be separated from the closely related genus *Kampimodromus* by the absence of the ventral seta, ZV3. Other characteristics are longitudinal reticulation running parallel to the dorsal shield, short peritremes, smooth movable digit and cup-shaped calyx of spermatheca. In addition, Eharius species do not have stout, serrated dorsolateral setae but they are rather slender and setiform. Eharius species usually occur on host plants in the family Lamiaceae. In this study, a series of phytoseiid specimens were collected from Phlomis sp. (Lamiaceae) in Isparta Province in south-western Turkey. Preliminarily observations showed that the species belonged to the genus Eharius (absence of setae S4 and ZV3) and to the kuznetzovi species group (presence of JV4). All other morphological characters are identical to the genus (e.g. dorsal reticulation, calyx of spermatheca and smooth, movable digit). However, this species is unusual in having much longer dorsolateral setae (≥ 40 µm). In addition, these longer setae are serrated in the apical-half and knobbed apically. Prior to our study, dorsal setae serrations were observed only on Z5 in almost all known species, and apical knobs were only on Z5 in E. marzhaniani, in this genus. Serration of the dorsal setae occurs in generalist phytoseiid species using the "Type IIIa" feeding habit that live on pubescent leaves. The host plant (Phlomis sp.) on which Eharius sp.nov. was collected also had a high density of trichomes. Setal serrations are understood to help phytoseiids colonize their microhabitats, as well as to protect them from intraguild predation by larger predators. Therefore, Eharius sp. nov. may be a promising candidate for use in biological control on host plants that have a high density of trichomes. *Eharius* sp. nov. is described and illustrated, based on adult females.

Keywords: Eharius, description, taxonomy, setal serration, apical knob

Internal transcribed spacer (ITS) sequences of some *Kampimodromus* (Acari: Phytoseiidae) populations: species status validation of *Kampimodromus ragusai*

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Fifteen nominal species of Kampimodromus Nesbitt (Acari: Phytoseiidae) are known worldwide. Among them, Kampimodromus aberrans (Oudemans) is an effective biological control agent in many cultivated plants, including grapes, hazelnuts and apples, in some parts of the Western Palearctic region. It is the most widely distributed species of the genus. However, possible misidentifications are suspected because of difficulties in confirming some important morphological characteristics, e.g., the number of solenostomes on dorsal shield and cheliceral movable digit (MD) dentition. Kampimodromus ragusai Swirski & Amitai, a closely related species to K. aberrans, has four pairs of solenostomes. It was first described from Israel and was recently recorded from Turkey. The only difference between these two species appears to be presence/absence of a tooth on the MD. In a previous study, K. ragusai was suspected to be a junior synonym of K. aberrans. Therefore, here we isolated DNA from a Turkish population of K. ragusai to confirm whether MD dentition is enough to separate these two species. Populations of other species, such as K. corylosus Kolodochka from Croatia, and K. aberrans and K. langei Wainstein & Arutunjan from Italy, were also included in the molecular analysis. A phylogenetic tree was constructed using the DNA sequences obtained in this study and from a public gene bank database. The genetic distance between K. aberrans and K. ragusai (4%) is higher than the distance between K. ragusai and K. langei (3%). The last two species shared a common character by having one tooth on the MD but can be separated by having four and five pairs of dorsal solenostomes, respectively. In conclusion, the species status of K. ragusai was validated by internal transcribed spacer (ITS) sequences. It was also demonstrated that MD dentition and the number of dorsal solenostomes are useful in separating K. ragusai from the closely related species, K. aberrans and K. langei, respectively.

Keywords: Taxonomy, predatory mites, ITS, movable digit dentition, dorsal solenostomes



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Amblyseius tamatavensis (Acari: Phytoseiidae), a new record for the United States of America

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Several specimens of a phytoseiid mite (Acari: Mesostigmata) were collected in association with the banded-wing whitefly *Trialeurodes abutiloneus* (Haldeman) (Hemiptera: Aleyrodidae) on Laportea aestuans (Urticaeae) and Solanum americanum (Solanaceae) in southern Florida. A small rearing of the predator was established using *Phaseolus vulgaris* L. and *Ficus benjamina* L. leaves infested with the sweet potato whitefly, *Bemisia tabaci* (Gennadius) and the ficus whitefly, Singhiella simplex (Singh) on water-saturated cotton wool in a plastic tray under laboratory conditions. The predator adapted to these prey and started reproducing in a short period. Slidemounted specimens were identified as Amblyseius tamatavensis Blommers. This is the first report of A. tamavensis in Florida and the United States of America. The two whitefly species used to maintain the predator colony are invasive and major pests of ornamental, vegetable and fruit crops in Florida. Therefore, further efforts to evaluate the biological traits of A. tamatavensis and its potential to be used in biological control are warranted in Florida. The host plant (L. aestuans) from which we first collected this predator has a high density of glandular and stinging trichomes. Many phytoseiid species are unsuccessful at keeping pest populations under economic thresholds due to the high trichome density on host plants. Whether A. tamatavensis can be used to control pests on host plants with glandular trichomes should also be investigated. Amblyseius tamatavensis from Florida was re-described and illustrated, based on female specimens. In addition, the world distribution, collection details, host plants and associated prey, are presented. The Florida population is similar to specimens reported from South Africa in terms of cheliceral dentition.

Keywords: North America, fauna, predatory mite, whitefly, biological control

Population development of the European red mite, *Panonychus ulmi* (Koch) (Acari: Tetranychidae) in apple orchards in Çanakkale Province of Turkey

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The aim of this study was to determine the seasonal population dynamics of the European red mite, *Panonychus ulmi* (Koch) (Acari: Tetranychidae) in apple orchards in Çanakkale Province of Turkey during 2010 and 2011. Surveys were carried out every week from April to November in both years in sprayed and unsprayed apple orchards having the varieties Golden Delicious, Starking Delicious and Granny Smith. The results of the study indicated that the population densities of spider mites generally began to increase in early May, reaching the maximum level from mid-June to late August and persisting to late September in both years. During both years, *P. ulmi* preferred Starking Delicious to Golden Delicious and Granny Smith. The population density of *P. ulmi* reached a maximum of 115.9 and 75.3 mites/per leaf on Starking Delicious in sprayed orchards in 2010 and 2011, respectively. In unsprayed orchards, spider mite numbers remained at very low levels because of the presence of *Typhlodromus athiasae* Porath and Swirski (Acari: Phytoseiidae) which was the only predator of spider mites collected. In sprayed orchards, *Stethorus punctillum* (Coleoptera: Coccinellidae) and *Zetzellia mali* (Acari: Stigmaeidae) were the most abundant predators of spider mites but they could not control the spider mites on the three apple cultivars in both years.

Keywords: Biological control, coccinellids, population dynamics, spider mites, predatory mites



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Two potential targets for RNAi-based pest mite management

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Phytophagous mites have caused great economic losses in recent years in China. There is an urgent need to develop effective and safe new alternatives for the management of pest mites. As a new molecular biology technique, RNAi could inhibit the expression of functional genes by gene silencing, resulting in pest malformations or death, so as to achieve the purpose of pest control. In this study, two important functional genes, arginine kinase (AK) and chitin synthase (CHS) genes, were cloned and the effects of their dsRNA on Tetranychus turkestani were determined. The main results were as follows: the toxicity assays for AK dsRNA synthesised in vitro showed that it has lethal effects on both the females and eggs of *T. turkestani*. Furthermore, the LC₅₀ was 21.214ng/µL. TtAK dsRNA was sub-cloned into RNase III-deficient HT115 (DE3) E. coli bacteria and the mortality reached 54.0% at 120h. dsRNA was also applied against the chitin synthase gene (TtCHS1-3) of T. turkestani by the same method used earlier. The mortality of T. turkestani fed with TtCHS1-3 dsRNA bacteria was up to 50% and much higher than the control group, and the hatching rate of eggs of the F₁ generation was only 48%, which was much lower than the control group (93%). Furthermore, dsRNA towards the AK-CHS1-3 fusion gene was constructed and subcloned into HT115 cells. The mortality caused by dsAK-CHS1-3 synthesised in vitro was 92% and the LC_{50} was 12.986ng/ μ L. The mortality caused by feeding on bacteria containing dsAK-CHS1-3 was 61.7%. AK-CHS1-3 dsRNA suppressed the egg hatchability of F₁ generation of T. turkestani but has less damaging effects on the larvae and nymphs. The results of this study showed that RNAi targeting AK-CHS is a new, potential tool for the environmentally sound control of mites.

Keywords: Arginine kinase gene, chitin synthase gene, dsRNA, RNAi, Tetranychidae

Hazelnut big bud mites in Georgia and an innovative method for their PCR analysis

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Hazelnut is one of the leading agricultural crops in Georgia which is the fifth highest producer internationally. It is cultivated on 8% of the arable area in Georgia and is of great economic importance. Therefore, it is important to protect hazelnut plants from pests in order to produce high quality nuts and minimize losses. In recent years, the big bud mites, *Phytoptus avellanae* Nal. and Cecidophyopsis vermiformis (Nal.) (Acari: Eriophyoidea), have become major pests of hazelnut orchards in Georgia. Their timely detection and diagnostics will assist the implementation of effective control measures. For this study, 20 orchards in the western Georgia regions of Guria, Samegrelo and Adjara were selected. Shoots 20-30 cm long with big buds were collected randomly from 30 branches in each orchard. The big buds were checked under a binocular microscope and slides were prepared for identification of the big bud mite species collected. Three species, namely P. avellanae, a vagrant cryptic species associated with P. avellanae, and C. vermiformis, were found. For DNA analysis of the mites, individuals were removed from the buds and leaves with a fine needle and placed in 99.8% ethyl-alcohol for PCR analysis. The DNA was extracted with a DNA-extraction kit (DNeasy Blood & Tissue Kit Qiagen), with the lysis time increased to 24 hours. The DNA purity was 2.0 (A_{260}/A_{280}) and its concentration was 200 ng/ μ l. Increasing the period of cell lysis increased the amount of lysis products, including DNA.

Keywords: *Phytoptus avellanae*, *Cecidophyopsis vermiformis*, hazelnut, big bud mites, molecular analysis

Acknowledgement: This study was funded by Shota Rustaveli National Science Foundation of Georgia (Project number: YS- 2016-53).



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Laboratory evaluation of predators of the Citrus leprosis virus vector, *Brevipalpus yothersi* (Acari: Tenuipalpidae)

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Citrus leprosis (CiLV) is one of the most important diseases of citrus crops in the Americas. CILV is a disease complex caused by several viruses transmitted by mites belonging to genus *Brevipalpus* (Acari: Tenuiplapidae). Brevipaplus vothersi Baker is associated with the most damaging virus (CiLV-C) in Brazil, Colombia and Mexico. The disease may cause defoliation, blemishing, fruit drop and dieback if not controlled. All regions recently infected with CiLV had non-virulent B. yothersi prior to the emergence of the disease. The control of CiLV has been mostly carried out with acaricidal applications against its vector. However, recent surveys indicated that three phytoseiid species, namely Amblyseius largoensis (Muma), Neoseiulus chilenensis (Dosse) and Neoseiulus longispinosus (Evans), and a cheyletid species (Hemicheyletia bakeri (Ehara), may be potential biological control agents of B. yothersi in southern Florida. We determined their effectiveness in feeding on different stages (egg, larva, nymph and adult females) of B. yothersi under laboratory conditions. Our results indicate that the three phytoseiid species can feed on all developmental stages of B. yothersi but prefer the eggs and immature stages, whereas H. bakeri prefers to feed on motile stages. On-going field and laboratory experiments are being conducted to identify more natural enemies associated with *Brevipalpus* in citrus crops and determine their potential for use in biological control.

Keywords: Citrus leprosis, Brevipalpus, Phytoseiidae, Cheyletidae, biological control

Repellent and mortality effects of different essential oils on *Tetranychus urticae* (Acari: Tetranychidae)

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In this study, the repellency and lethality of seven essential oils to adults of Tetranychus urticae (Acari: Tetranychidae), which is a serious, polyphagous pest of vegetables in open fields and greenhouses, were evaluated under laboratory conditions. Tetranychus urticae individuals were reared under climate controlled conditions at 25±1 °C, 60±5% RH and 16:8 (light: dark) in 50 x 50 x 50 cm in plexiglass containers covered with netting. A cotton wool ball containing 5 ml of an essential oil (1%) was placed at the edge of a 10 cm diameter Petri dish. The direction of movement of adult mites released at the center of the dish was observed and recorded. The experiments were replicated five times with 10 mites per replication. In addition, the fumigant effects of the same oils were tested. Petri dishes of 10 cm diameter were again used. A cotton wool ball containing 0.5 ml of essential oil (0.2%) was placed at the edge of the dish. Five mite individuals were then transferred to the dish which contained a bean leaf. After that, the dish was completely sealed. Experiments were replicated 4 times. After one hour and 24 hours, both living and dead individuals were counted. The repellency efficacy of the seven oils, namely rosemary, pine needle, ginger, lavandin, cinnamon, oregano and eucalyptus, were 82, 78, 76, 76, 68, 52 and 48%, respectively. Regarding their fumigant effects, the mortality rates caused by the oils (in the same order as above) were 21.05, 7.14, 0.00, 7.69, 42.85, 58.33 and 0.00% after one hour and 23.52, 30.76, 38.46, 8.33, 50.00, 100.00 and 10.00% after 24 hours. Utilization of the repellent effects of rosemary, pine needle, ginger and lavandin oil may complement the current IPM methods. With respect to its lethality, it appears that oregano oil could complement the existing IPM control methods.

Keywords: Mite, rosemary, pine needle, ginger, lavandin.



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Role of house dust mite and CD14 (C-159T) polymorphism in the development of asthma among the West Bengal population, India

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House dust mites play an important role in causing various allergic disorders. Many factors, such as temperature and humidity, as well as different microclimatic conditions, may influence mite growth. India is the home to around 15-20 million asthmatics and asthma prevalence is increasing in Indian metropolitan areas, including Kolkata, West Bengal. Complex interactions of genetic and environmental factors are involved in asthma. A genome-wide search for susceptible loci regulating the IgE response (atopy) has identified a candidate gene, CD14, which may be important in the context of allergic responses of respiratory system. The present study aimed to investigate the role of house dust and house dust mites in the development of bronchial asthma and explore the possible association of the candidate gene CD14 with disease manifestation among the Kolkata patient population. The skin-prick test was done on 950 asthmatic patients for 8 aeroallergens, including house dust and house dust mites, and total serum IgE and allergen specific IgE were measured. PCR-RFLP was done for patients and a non-asthmatic control (n=255 in each) to characterize a functional polymorphism, C(-159)T of CD14, a positional candidate gene for allergy. We identified house dust as the most common aeroallergen sensitizer among atopic patients in Kolkata, followed by Dermatophagoides pteronyssinus and D. farinae mites. Patients' sera contained a significantly higher IgE level than that of the controls. The allergen specific IgE antibody test revealed that 76.4% patients had specific IgE antibody against D. pteronyssinus. There was a significant difference of allele and genotype distribution for CD14 polymorphism with increase of disease severity. In Kolkata, the house dust mite is a common aeroallergen and D. pteronyssinus is predominant among mites. The present study also revealed that bronchial asthma has a genetic background.

Keywords: House dust mite, allergy, asthma, CD14, genetic polymorphism

Contribution to the fauna of chigger mites (Acariformes: Trombiculidae & Leeuwenhoekiidae) parasitizing small mammals in Iran

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Chigger mites (Acariformes: Trombiculidae & Leeuwenhoekiidae) are a large group of more than 2,000 species of temporary parasites and vectors attacking terrestrial vertebrates, including humans and domestic animals. Up to the present, 84 chigger species have been recorded in Iran. During our survey of chiggers parasitizing small mammals in the north Iranian provinces of Alborz, Tehran, Gilan, Mazandaran, Golestan and North Khorasan, 20 sampling sites were investigated in June-July and October 2017. The collection of chiggers at altitudes higher than 3,000 m was performed in Iran for the first time. A total of 76 rodents and soricomorphs belonging to 11 species were captured and 51 of them were infested by chiggers. Identification of more than 350 chigger specimens revealed 22 species from 11 genera. One species from high mountain localities (Neotrombicula aff. kermani) was new for science and 11 species were recorded in Iran for the first time. Among these species, 4 are usual elements of the Middle Asian chigger fauna (Leptotrombidium raropinne, Neotrombicula lubrica, Schoutedenichia angusta and Shunsennia oudemansi); 4 species were previously known from their type localities in Turkmenistan only (Kepkatrombicula brevis, Kepkatrombicula magnus, Leptotrombidium noxium and Neotrombicula aideriensis); one species (Miyatrombicula ramitensis) was described from Tadjikistan; and 2 species (Brunehaldia lucida and Hirsutiella alpina) are elements of the chigger fauna characteristic of the Caucasus, Transcaucasia and Asia Minor. Ten species, namely Brunehaldia silvatica, Cheladonta firdousii, Euschoengastia meshhedensis, Hirsutiella llogorensis, Leptotrombidium silvaticum, Leptotrombidium subsilvaticum, Multisetosa persicus, Neotrombicula delijani, Neotrombicula talmiensis and Neotrombicula vulgaris, which were previously known from Iran, were recorded in new localities In general, the chigger fauna of the north Iranian highlands does not significantly differ from that of the lowlands and includes mainly the usual species for central Asia.

Keywords: Chigger mites, ectoparasites, Iran, small mammal, Trombiculidae



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Prevalence and body distribution of the poultry red mite (*Dermanyssus gallinae*) in layer farms in Western Azerbaijan Province of Iran

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The aim of this study was to determine the abundance and distribution on the body of *Dermanyssus gallinae*, the poultry red mite (PRM), on laying hens in layer farms in Urmia, Iran. A total of 1,100 randomly selected laying hens were examined from January to August, 2017. Twelve (71%) of the layer farms and 19% of the laying hens were infested with *D. gallinae*. There was a significant correlation between mite prevalence and climatic conditions of the region. The most common site for *D. gallinae* infestation was the cloacal region (52.7%), which was significantly higher than for the other sites, and the highest mixed infestation rate was 10.9% for the wing-breast and cloacabreast combination. It was concluded that the overall level of *D. gallinae* infestation was relatively low and that the favoured infestation sites may affect egg laying capacity.

Keywords: Dermanyssus gallinae, laying hens, infestation, red poultry mite, Urmia

DNA barcoding and phylogenetics of neotropical *Amblyomma* (Acari: Ixodideae) from the ICMT collection, Colombia

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The tick genus Amblyomma includes approximately 130 species, 57 of which have been reported in the Neotropics. In order to understand the evolution of the genus, it is necessary to gain a better understanding of the relationships between taxa. Additionally, several Amblyomma species have been reported as vectors of parasites which are of medical and/or veterinary importance. Therefore, it is important for control and surveillance programs that individual ticks be accurately identified to the species level. The tick collection of the Instituto Colombiano de Medicina Tropical (ICMT) in Colombia has 47 species of *Amblyomma* species without barcoding information. In this study we amplified and sequenced the COI and 12S genes for 30 neotropical species of the genus Amblyomma available in the collection. Samples were 50 to 100 years old and had been kept in 70% ethanol. Several extraction protocols were tested, including Bioline, Oiagen and Epicentre kits. The Epicentre (Masterpure DNA purification kit) gave the best results. For the amplification and sequencing of the COI gene we initially used the standard invertebrate primers, LCO1490 and HCO2198. However, not all the samples amplified. New COI Amblyomma specific primers were designed to amplify a shorter fragment of 400bp. 12S gene specific Amblyomma primers were also designed in the lab to amplify a 500pb fragment. Our sequences and other Amblyomma sequences downloaded from GenBank were aligned and analyzed using Bayesian and Maximum likelihood phylogenetic analyses considering the best substitution models for each region. We confirmed the utility of the COI gene as a barcoding marker in the genus Amblyomma and generated original and validated data useful for the molecular identification of larvae and nymphs of *Amblyomma* species.

Keywords: Amblyomma, COI, 12S, systematics, vectors



2-8 September 2018, Antalya - TURKEY

Ticks and tick-borne pathogens in Sudan

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Ticks are important ectoparasites and vectors of pathogens of human and veterinary medical importance. Currently, limited information about ticks in Sudan and their exact geographical distribution is available. In the present study, ticks collected from livestock (cattle, sheep, goats, horses, camels and dogs) in the Sudanese states of West Darfur, River Nile and Al-Jazeera in 2017 were morphologically identified to stage and species level. A total of 1,612 ticks were collected, belonging to the genera Amblyomma, Hyalomma and Rhipicephalus, totaling 16 species. Among them are Amblyomma (A.) lepidum (57 ticks), A. variegatum (4 ticks), Hyalomma (H.) anatolicum (850 ticks), H. dromedarii (30 ticks), H. impeltatum (3 ticks), H. rufipes (128 ticks), H. truncatum (3 ticks), Rhipicephalus annulatus (one tick), Rh. bequaerti (7 ticks), Rh. bergeoni (118 ticks), Rh. decoloratus (30 ticks), Rh. evertsi (328 ticks), Rh. guilhoni (2 ticks), Rh. muhsamae (one tick), Rh. praetextatus (35 ticks) and Rh. senegalensis (13 ticks). Two ticks could not be reliably identified morphologically. The level of infestation on individual farm animals varied from a single specimen to more than one hundred ticks. The large number of ticks in the investigated region indicates that these species are of great importance to Sudanese agriculture. All ticks were screened for *Rickettsia* spp. and 77/1,612 (4.7%) samples tested positive in panRick PCR. They were comprised of 50/128 (39%) H. rufipes, 8/30 (26.6%) H. dromedarii, 12/57 (21%) A. lepidum, 2/4 (50%) A. variegatum, 2/30 (6.6%) Rh. decoloratus, 2/328 (0.6%) Rh. evertsi and 1/13 (7.6%) Rh. senegalensis. Furthermore, all Hyalomma spp. tested negative for the Crimea Congo hemorrhagic fever virus. Hyalomma rufipes and H. dromedarii carried R. aeschlimannii and A. *lepidum* carried R. africae. These findings indicate that Rickettsia spp. may be borne by a number of Sudanese tick species, most importantly A. lepidum, H. rufipes and H. dromedarii.

Keywords: Tick, vector, Rhipicephalus, Hyalomma, Rickettsia

Gertrud Theiler Tick Museum - Standing on the shoulders of giants

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The Gertrud Theiler Tick Museum was started by Gerald Bedford in 1912. Since that time, several prominent scientists have made contributions to the collection in both specimen depositions and scientific study. This has elevated the collection to stand as the largest to house African ticks globally, containing 55 type specimens and 375 identified species. The value of museums in 21st century biology is a topic of important discussion in light of the biodiversity crisis and climate change. Moreover, museums may come of age once they acquire an adequate number of specimens and species that capture a considerable degree of natural variation. Study of this variation may be used to answer important questions regarding public health, agriculture, biodiversity and evolutionary processes. Of course, these are all underpinned by the relentless pursuit of the main function of museum collections – systematics. The Gertrud Theiler Tick Museum is poised to realise this vision, having come of age by presenting the most complete collection of hard-earned African ticks. The raw data preserved in each specimen, comprising its species designation, morphology and collection data, in combination with modern methods of data capturing, analysis and dissemination, will serve to elevate the museum further toward a crucial position in a developing continent.

Keywords: Tick, collection, natural history, systematics, taxonomy



2-8 September 2018, Antalya - TURKEY

To sequence or not to sequence: Comparison of high-throughput sequencing and quantitative PCR for detection of pathogen prevalence in *Ixodes* ticks

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Ixodes (Ixodidae) ticks are recognised as important vectors of numerous severe pathogens in humans. Currently, the most common practice to screen pathogens is to use real-time quantitative PCR (qPCR) with known markers for certain pathogens. There are many advantages in this method including sensitivity to the smallest amounts of bacterial or viral material in the template and the potential for relative or absolute quantification. However, recent studies have shown ticks as carriers of several previously unrecognised pathogens, some of which are conceivably dangerous to humans. Thus, there is an urgent need for more efficient ways to analyse for multiple pathogens in parallel, both known and unknown. High-throughput sequencing (HTS) is a modern tool, used for microbial profiling in soil, ecological dietary studies and massive parallel DNA barcoding, to name a few. HTS has high potential to reveal rare pathogens and it seems to be an efficient way to analyse multiple samples. In this study, we tested both methods (qPCR and HTS) to analyse the prevalence of the most important bacterial and eukaryotic pathogens and also to reveal potential, previously unidentified microorganisms in Ixodes ticks. Our samples were collected from a much studied site in south-western Finland as part of the nationwide Turku University Tick Research project. We simulated the impact of HTS sequencing depth on the results and validated the findings using qPCR analysis. Our results highlight the advantages of both methods, and we give cost estimates, recommendations and preliminary guidelines for when and how to use each approach. As a novel aspect, we propose the use of HTS to analyse tick population dynamics in parallel with pathogen patterns. Our study adds to the expanding toolbox of molecular methods to explore both micro- and macroecosystems.

Keywords: *Ixodes*, pathogens, real-time quantitative PCR, high-throughput sequencing, DNA barcoding

The exploration of the cold response genes of *Dermacentor silvarum* and functional analysis of its important genes

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The tick, *Dermacentor silvarum*, is generally recognized as an important vector of many pathogens in China. The current study analyzed the differential gene expression of D. silvarum before and after cold acclimation (4), using high-throughput transcriptomic sequencing. A total of 136,740 unigenes were assembled, and 2,196 differentially expressed genes were explored before and after cold acclimation, with 745 up-regulated and 1,451 down-regulated. Through GO analysis, the differential genes were mainly focused on cell composition, catalysis and metabolic processes. Gene COG classification results showed that the differential genes were mainly involved in the control of amino acid, carbohydrate and lipid transport and metabolism. Based on the differentially expressed genes of D. silvarum before and after acclimation, three genes, namely Hsp90, Hsp70 and Tubulin, were further analyzed for their open reading frames, and compared for sequence homology, predicted protein secondary structure and tertiary structure. Finally, RNAi was used to verify their functions during the cold response of ticks. Results showed that when the Hsp70 and Tubulin genes were knocked out, the mortality of ticks significantly increased after cold treatment (P<0.05), which indicates that the Hsp70 and Tubulin genes play an important role in the cold tolerance of D. silvarum, whereas the regulation of the Hsp90 gene was relatively weak. These results provide a base for in-depth study of the molecular regulation mechanisms of the cold response of ticks and also generated fundamental information that can be applied to the integrated control of ticks and to the prevention of tick-borne diseases.

Keywords: Dermancentor silvarum, cold tolerance, transcriptome, HSP, Tubulin

Acknowledgement: Funding was provided by the National Natural Science Foundation of Hebei Province (C2015205124) and the Natural Science Research Programs of the Educational Department of Hebei Province (BJ2016032)



2-8 September 2018, Antalya - TURKEY

Attachment sites of the tick *Hyalomma aegyptium* on the *Mediterranean spurthighed* tortoise, *Testudo graeca* in Nevsehir, Cappadocia in central Anatolia, Turkey

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Hyalomma aegyptium in its adult stage feeds on Testudo tortoises and the distribution of this tick is limited to the distribution of the principal host, Testudo graeca. It is known to be a carrier of numerous zoonotic agents such as Theileria, Rickettsia, Anaplasma, Ehrlichia, Coxiella and Borrelia, and even the Crimean-Congo haemorrhagic fever virus. A tortoise habitat located in Nevsehir, Cappadocia in central Anatolia, Turkey was selected as the study area. Tortoises were captured by hand in opportunistic encounters while walking between April and September of 2012–2014. All body surfaces of the tortoises were thoroughly checked for the presence of ticks. Tortoises were individually marked with unique codes. Five different attachment sites on the posterior part, anterior part and shell of the tortoises were characterized. Ticks were collected in labelled tubes containing 70% ethanol and were identified to species by using morphological keys. Three parasitological indicators were quantified according to the body regions of the tortoises, namely host sex, tick developmental stage and tick sex. A total of 497 ticks removed from 111 tortoises were identified as Hyalomma aegyptium. The overall infestation prevalence was 90% and the infestation intensity ranged from 1 to 52. Adult ticks represented 64% of all ticks and nymphs represented 73% of the immature ticks. There was a significant difference in tick burdens between adult and sub-adult tortoises. In addition, tortoises were significantly more infested by male ticks than females (M/F: 4:3). There was a weak, positive correlation between the number of ticks and the size of the tortoise. Immature ticks preferred the anterior parts of the body but both female and male adult ticks preferred the posterior parts. There was no relationship between the numbers of female and male ticks and body region of the host and there was no relationship between the numbers of adults and immature ticks.

Keywords: *Hyalomma aegyptium, Testudo graeca*, Nevsehir, Cappadocia, infestation prevalence

Molecular detection and characterization of tick-borne encephalitis virus in ixodid ticks in Lithuania

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Tick-borne encephalitis (TBE), which is one of the most dangerous human infections, affects the central nervous system and can occur in people of all ages. During the last few decades the incidence of the disease has been increasing and it is a growing health problem in almost all European and Asian countries where it is endemic. Lithuania is one of the countries with the highest number of reported TBE cases, with an average of 450 cases of TBE reported yearly. The main vectors of the TBE virus (TBEV) in Euro-Asia region are ticks from the Ixodidae family, mainly Ixodes ricinus and Ixodes persulcatus. The aim of this study was to investigate the current prevalence of TBE virus in different species of ticks and genetically characterize the strains of virus distributed in Lithuania. In March-September 2017, 1,884 ticks were collected from eight Lithuanian counties in 18 regions. The collected ticks were identified as *I. ricinus* (n=1,351) and D. reticulatus (n=533). For RNA extraction, the ticks were grouped in 267 pools according to species, sampling site, development stage and sex. For the detection of TBEV, quantitative realtime reverse transcription-PCR (RT-PCR) was performed. Samples found positive by real-time PCR were used for one step RT-PCR and for nested PCR for future sequencing of the partial E protein and NS3 genes. The minimum infection rate (MIR) of TBEV in the analyzed ticks was 1.52% (8/524) (1.86% I. ricinus and 5.6% D. reticulatus). TBEV was detected in adult ticks. The TBEV prevalence in males and females of each species was not significantly different. The phylogenetic analysis of NS3 and E gene sequences showed that the detected strains belong to the European subtype and are specific to Lithuania. In addition, this is the first detection of TBEV in D. reticulatus ticks in Lithuania.

Keywords: Tick-borne encephalitis, ticks, Ixodes ricinus, Dermacentor reticulatus, Lithuania



2-8 September 2018, Antalya - TURKEY

The genetic diversity of *Anaplasma marginale* isolates in the Moscow region of Russia

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Anaplasma marginale (Rickettsiales: Anaplasmataceae) is a tick-borne pathogen of cattle that causes the disease bovine anaplasmosis throughout the world. Both cattle and ticks become persistently infected with A. marginale and thus serve as reservoirs. These obligate intracellular organisms replicate in bovine erythrocytes or tick cells. Major surface proteins (MSPs) are involved in host-pathogen and tick-pathogen interactions and have been used as markers for the genetic characterization of A. marginale. MSP1a is involved in the adhesion and transmission of A. marginale by ticks and varies among strains in the number and sequence of amino-terminal tandem repeats. The aim of this study was to determine the prevalence and genetic diversity of A. marginale strains in cattle from the Moscow region of Russia. In 2015-2016, blood samples from 42 cattle were collected and screened for the occurrence of A. marginale by rtPCR targeting the msp4 gene. The partial msp1a gene containing tandem repeat sequences was amplified from msp4 positive samples, cloned into pJet vector and sequenced. The genetic diversity of A. marginale strains was analyzed based on the Msp1a tandem repeats structure. A. marginale DNA was detected in 24 cattle (57.1%). Eleven new genotypes were found in 15 isolates. Eight new tandem repeats are described for the first time. The number of repeats differed between 1 and 6 across the isolates. The MSP1a microsatellite analysis identified three genotypes. The tandem repeat and microsatellite analyses of the mspal gene showed high diversity among the isolates. This is the first report of the genetic diversity of A. marginale strains in cattle in Russia.

Keywords: *Anaplasma marginale*, major surface proteins, genetic diversity, bovine anaplasmosis, Russia

An investigation of *Dermacentor reticulatus* genetic diversity using the *12S* rRNA marker

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The ornate meadow tick, *Dermacentor reticulatus* (Fabricius, 1794) is an important tick-borne disease vector in Europe. It transmits bacterial and viral diseases dangerous to humans, livestock and wild animals. The expansion of the range of *D. reticulatus* to new areas has been observed in central and northern Europe and is explained by climate change. The distribution range of this tick is discontinuous, with an existing gap in central Poland. In order to investigate the origin of the emerging foci and already established areas, we used the *12S rRNA* mitochondrial marker. Ticks were collected by using the flagging method in a timeline of 2012 and 2017 from most of the distribution range in Europe, including Great Britain, Spain, France, Germany, Poland, Slovakia, Serbia, Croatia, Lithuania, Latvia and several sites in Ukraine and Kazakhstan. *12S rRNA* gene fragments were amplified and sequenced using specific PCR and Sanger sequencing. In total, we sequenced 60 individuals from the localities mentioned above and included sequences derived from the Genbank database. Analysis of the obtained sequences showed sufficient polymorphism to analyse the distribution of haplotypes and phylogenetics of *D. reticulatus*. The data identified a haplotype structure within the western parts of Europe, with individuals from Slovakia, Poland and Latvia forming a separate cluster, which is in accordance with the separation in Central Poland.

Keywords: Dermacentor reticulatus, tick-borne disease, variability, phylogenetics, vector



2-8 September 2018, Antalya - TURKEY

Genetic diversity of *Ehrlichia canis* in dogs from Turkey inferred by TRP36 sequence analysis and phylogeny

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Canine monocytic ehrlichiosis is a tick-borne rickettsial disease causing serious and fatal infections in dogs in subtropical and tropical regions. The Tandem Repeat Protein (TRP36/gp36) gene, which encodes for a major immunoreactive protein, is a useful marker for genotyping Ehrlichia canis isolates. The aim of this study was to assess the genetic diversity of E. canis, and to determine the phylogenetic relationship between E. canis isolates from Turkey and strains found worldwide. A total of 167 archived blood samples randomly collected from dogs in municipal shelters in three distinct geographic regions were analysed, of which 10 (5.98%) were positive in nested PCR for E. canis. Three tandem repeat forms (TEDSVSAPA, ASVVPEAE and EASVVPAAEAPQPAQQTEDEFFSDGIEA) were found in the analyzed isolates, indicating high genetic diversity in Turkish E. canis strains. In addition, two novel repetitions, EAPAAEAPQPAQQTEDEFFSDGIEA and EAPAAEAPQPAQQTEDEFFSDGIEA, in the tandem repeat region of the E. canis gp36 sequences were also identified. Maximum likelihood analysis based on the gp36 amino acid sequences showed that the isolates identified in this study fell into four well-defined phylogenetic clusters among geographically dispersed E. canis strains from America, South Africa, Asia, Europe and the Middle East. This study revealed that dogs in Turkey could be infected with at least four distinct E. canis genogroups, based on tandem repeat amino acid sequencing of the gp36 protein.

Keywords: Ehrlichia canis, TRP36 (gp36) gene, tandem repeat, genogroup, dog

Molecular evidence for a novel species of *Babesia* in unfed *Rhipicephalus* sanguineus sensu lato

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This study reports a novel species of *Babesia* in unfed *Rhipicephalus sanguineus sensu lato* and its phylogenetic relationship to other species. One hundred and forty DNA samples extracted from tick pools comprising 5,403 unfed *R. sanguineus s.l.* ticks were screened for *Babesia*. Overall, *Babesia* infection was detected in female, male and nymph pools, with infection rate maximum likelihood estimates (MLE) of 1.98 (CI 0.65-4.74), 0.50 (CI 0.03-2.40), and 0.07 (CI 0.01-0.21), respectively. Three adult female tick pools (MLE 1.44, CI 0.38-3.88) and one adult male pool (MLE 0.50, CI 0.03-2.40) hybridized with the catchall and *Babesia* genus probes but did not hybridize with any species-specific probe tested, suggesting the presence of an unidentified *Babesia* species. Phylogenetic analysis and sequencing revealed that the newly detected *Babesia* isolate formed a clade distinct from fully identified canine, bovine, equine and ovine *Babesia* species, with a range of 88.6 to 92.9% nucleotide identity.

Keywords: Novel *Babesia*, *Babesia ovis*, *Rhipicephalus sanguineus sensu lato*, clade, maximum likelihood estimates



2-8 September 2018, Antalya - TURKEY

A survey of canine haemoprotozoan parasites from Turkey, including molecular evidence of an unnamed *Babesia*

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Canine, tick-borne, apicomplexan parasites have emerged in recent years, showing a wider geographic distribution and increased global prevalence. A reverse line blot assay was performed on 219 blood samples collected from domestic dogs for simultaneous detection of all named canine piroplasm species, as well as Hepatozoon canis. Ten samples hybridized to the Theileria/Babesia and Babesia catchall probes but did not hybridize to any species-specific probe tested, suggesting the presence of an unrecognized *Babesia* species or genotype. Sequencing results showed 91.5%, 91.9%, 92.4%, 92.4% and 89.2% similarity to B. canis, B. vogeli, B. rossi, B. gibsoni and B. conradae, respectively. The highest homology (98.1-98.5%) was observed in unnamed Babesia sp. isolates (Ludhiana and Malbazar) described in dogs, *Babesia* sp. of buffalo origin, *Babesia* sp. Kashi 2, and Babesia orientalis, along with Babesia occultans of cattle origin. The partial cox1 sequence indicated that this isolate was most similar to *Babesia* sp. 1 HG-2012, with an identity of 86.5%. The survey revealed a high prevalence of haemoprotozoans in domestic dogs (57.5%, CI 50.7-64.2), with Hepatozoon canis the most prevalent (54.3%, CI 47.5-61.117%), followed by Babesia sp. (4.6%, CI 2.2-8.2), B. vogeli (1.4%; CI 0.3-3.9), and B. canis (0.4%, CI 0-2.5). Combined infection with *Hepatozoon canis* and *Babesia* sp. was detected in five dogs (2.3%, CI 0.7-5.2) samples and of *H. canis* and *B. vogeli* in two dogs (0.9%, CI 0.1-3.2). The study provides an insight into the distribution and phylogenetic diversity of canine piroplasms in Turkey.

Keywords: Babesia vogeli, Babesia sp., dog, Hepatozoon canis, RLB

Eriophyoid mites on weeds in three families in wheat fields in the Central Anatolian Region of Turkey

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Eriophyoid mite species infest crops worldwide. Many are serious pests that cause considerable production losses, including species capable of transmitting plant viruses. However, other species of eriophyoid mites have generated considerable interest in their potential use as biological control agents of weeds. This study investigated eriophyoid mites on weeds in wheat fields in Ankara and Nevşehir Provinces, Turkey between April and July in the period 2010 to 2015. A quadrat sampling method was employed to sample weeds in the selected fields, with twenty five shoots and fifty leaves collected from each field. The samples included two, four and three weed species belonging to Convolvulaceae, Fabaceae and Lamiaceae, respectively. Initially, the eriophyoid mites were counted in a 4 cm² area of both the upper and lower surfaces of the 50 leaves to determine the population density of each species. The mites were then removed with a fine brush under a stereomicroscope, mounted on slides and identified. Three species belonging to Eriophyidae were found on four weed species, namely Aceria onychius (Nalepa) on Phlomis pungens Willd. (Lamiaceae), Aculus acraspis (Nalepa) on Medicago sativa L. (Fabaceae), and Aceria convolvuli (Nalepa) on Convolvulus arvensis L. and Convolvulus althaeoides L. (Convolvulaceae). Aceria onychius, A. acraspis and A. convolvuli were found on P. pungens, M. sativa and C. althaeoides, respectively, for the first time worldwide. Aceria convolvuli was also found for the first time on C. arvensis in Turkey. Aceria onychius on P. pungens, and A. convolvuli on C. arvensis, had the highest and lowest population densities, respectively.

Keywords: Acari, Eriophyidae, weed, biological control, wheat

Acknowledgement: This study, which is a part of the Ph.D. thesis of the first author, was funded by the Scientific Research Foundation of Ondokuz Mayis University (Project number: PYO. ZRT.1904.10.020) and the Ministry of Agriculture and Forestry of Turkey (Project number: TAGEM-BS-11 / 07-01 / 01-09).



2-8 September 2018, Antalya - TURKEY

Mite species on wild mushrooms on the campus of Ondokuz Mayis University in Samsun, Turkey

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Mushrooms, which have been consumed as food for many hundreds of years, have a high nutritional value that includes essential amino acids. The nutraceutical properties of mushrooms are also of considerable importance. Samsun Province, located in the centre of the Black Sea Region in Turkey, is rich in terms of the diversity of its macrofungi due its warm, temperate climate and habitat diversity that includes various forest types. Edible wild mushrooms of various species have been collected and consumed by the people of Samsun for centuries. These mushrooms are also sold at local markets. The main pests of mushrooms are flies, mites and nematodes. There are fungivorous, saprophagous and predatory mites living on mushrooms. The predatory mites feed on small insects and mites, and the other species feed on fungi, bacteria and decaying organic materials. The aim of this study was to determine the mite species on wild mushrooms on the 600 ha campus of Ondokuz Mayis University in Samsun, Turkey. A hundred and thirty five mushroom samples were collected from 14 different habitats such as forest, creek side and bush in 2016 and 2017. The collected mushroom samples were observed under a stereomicroscope and then processed through Berlese funnels to extract the mites. All of the mite specimens were preserved in 70% ethyl-alcohol before clearing in lacto-phenol and mounting in Hoyer's medium for identification. A total of six species belonging to four families were found. They were *Paracarpais* (*Eteocarpais*) lunulata Müller, Pergamasus laetus Juvara-Bals, Pergamasus sp. (Parasitidae); Phytoseius finitimus Ribaga (Phytoseiidae); Allothrombium subtile Daniel (Trombidiidae) and Zerconopsis sp. (Ascidae). Three of them, *P. lunulata*, *P. laetus* and *A. subtile*, are first records for Turkey.

Keywords: Acari, mite, wild mushroom, edible mushroom, Turkey

Acknowledgements: This study is a part of the M.Sc. thesis of the first author and was funded by the Scientific Research Foundation of Ondokuz Mayis University (Project Number: PYO. ZRT.1904.17.008).

Mite species associated with cultivated mushrooms in Samsun Province, Turkey

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Mushrooms have been consumed as food for many hundreds of years. More recently, the growing of mushrooms has become an important agricultural industry worldwide, and especially over the last three decades it has become one of the most dynamically developing fields of agriculture in Turkey. The white button mushroom, Agaricus bisporus (J.E. Lange), accounts for the highest proportion of total mushroom production, followed by *Pleurotus* spp., *Lentinula edodes* (Berk.), Ganoderma lucidum (Curtis) and others. The main pests of cultivated mushrooms are flies, mites and nematodes. The large amounts of organic matter, constant temperature and high humidity required for the commercial growing of mushrooms provide ideal conditions for the proliferation of fungivorous, saprophagous and predatory mite species. Some of these species can damage mushrooms, reducing both quality and yield. The aim of this study was to determine the mite species on cultivated mushrooms in Samsun Province in Turkey where the cultivation of mushrooms in small growing facilities is common. A total of 77 mushroom and compost samples were collected from 10 different mushroom farms throughout 2017. The collected samples were observed under a stereomicroscope and then processed through Berlese funnels to extract the mites. All of the mite specimens were preserved in 70% ethyl-alcohol before clearing in lacto-phenol and mounting in Hoyer's medium for identification. Only one quarter of the samples (26%) were infested by mites, which probably reflects the widespread use of pesticides to control fungivorous species. A total of six species belonging to three families were collected. They are *Arctoseius semiscissus* (Berlese) (Ascidae); Parasitus americanus Berlese (=P. bituberosus Karg), Parasitus sp., Vulgarogamasus sp. (Parasitidae); Pediculaster mesembrinae (Canestrini) and Pediculaster muscarius (Martin) (Pygmephoridae). Two species, *P. mesembrinae* and *P. muscarius*, are first records for Turkey.

Keywords: Acari, mite, Pediculaster, cultivated mushroom, Turkey

Acknowledgements: This study, which is a part of the M.Sc. thesis of the first author, was funded by the Scientific Research Foundation of Ondokuz Mayis University (Project number: PYO. ZRT.1904.17.040).



2-8 September 2018, Antalya - TURKEY

Efficacy of some endophytic fungi against *Tetranychus urticae* Koch

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The two spotted spider mite, *Tetranychus urticae*, is a polyphagous pest found worldwide. It feeds on more than 150 species of host plants, including most deciduous fruit trees and vegetables, causing major financial losses. The extensive use of pesticides has led to the development of pesticide resistance, environmental pollution, toxicity to non-target organisms and harm to human health. The aim of this laboratory study was to determine the acaricidal and ovicidal effects of some endophytic fungi against *T. urticae*. The experiment was conducted in a completely randomized design under laboratory conditions at 23 °C and 46% R.H., with two *Acremonium* sp. isolates, and one isolate of each of *Chaetomium* sp., *Cladosporium* sp., *Fusarium* sp., *Trichoderma* sp. applied, and NeemAzal applied as the standard pesticide and distilled water as the control. Each treatment was replicated ten times, with the spray application applied to each replicate which consisted of five newly emerged, copulated females on a bean leaf disc in a Petri dish. Observations were made daily for ten days. One way ANOVA and Duncan's multiple range test were used for statistical analyses. The efficacy of each treatment was determined with the Abbott formula. The efficacies of the endophytic fungi ranged between 34.5% and 95.5%. These endophytes appear to be potential biological control agents of *T. urticae*.

Keywords: Acari, *Tetranychus urticae*, fungi, endophyte, acaricidal effect

Efficacy of Tagetes minuta L. extracts against Tetranychus urticae Koch

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The acaricidal, ovicidal and repellent effects of *Tagetes minuta* L. extracts against *Tetranychus urticae* Koch (Acarina: Tetranychidae) reared on bean (*Phaseolus vulgaris* L.) were investigated in this study. The experiment was conducted in a completely randomized design with 10 replications and ten mites in each replicate under laboratory conditions at 24 °C and 55% R.H. Essential oil and hydrolate from floral and leaf extracts of *T. minuta* were used at seven concentrations, namely 0.09%, 0.18%, 0.37%, 0.75%, 1.5%, 3%, 6%, and three concentrations, 1.5%, 3%, 6%, respectively. Distilled water was used as the control. The spray application was applied to newly emerged, copulated females on a bean leaf disc in a Petri dish. Counts of dead mites were started on the first day after the treatments were applied and continued daily for five days. The living adults were removed after 5 days and then the hatching of eggs was recorded. The Abbott's formula and one-way ANOVA followed by Duncan's multiple range test were used for the statistical analyses. The efficacies of the essential oil ranged from 20% to 54% and efficacies of the hydrolates ranged from 2.27% to 43.47%. The results of this study indicated that extracts from *T. minuta* grown in Samsun Province, Turkey had low efficacy in causing mortality of *T. urticae*.

Keywords: Plant extracts, essential oil, *Tagetes minuta*, two spotted spider mite, *Tetranychus urticae*



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Addenda Oral Presentations



Mites associated with Ambrosia beetles (Curculionidae: Scolytinae) on avocado orchards in Michoacan, Mexico

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Avocado is one of the most important crops in Mexico which is the biggest producer in the world. Given its importance, the study of mites and insects associated with this tree is important. Three study sites with different management and crop conditions were selected in the State of Michoacan in 2017. Orchards were searched for trunks infested with ambrosia beetles. In the laboratory, the infested avocado tree trunks that had been collected were placed in emergence chambers; the insects and mites that emerged were collected, mounted and identified. In the present study, four species of Scolytinae were found associated with avocado, comprising three ambrosia beetles, namely *Monarthrum exornatum*, *M. frimbriaticorne* and *Drycoetes capucinus*, and one species of bark beetle, *Phloeocleptus plagiatus*. The bark beetle had been previously reported associated with avocado but ambrosia beetles are poorly known in these orchards in Mexico. *Monarthrum fimbriaticorne* was found at all three sites in the present study. The seven mite species collected belonged to 5 genera, namely *Proctolaelaps, Tricouropoda, Mexecheles, Eutogenes* and *Elattoma*. *Proctolaelaps bicleyi* was the most abundant and frequent species collected in this study. These results represent the first record in Mexico of mites associated with Ambrosia beetles in avocado orchards.

Keywords: Persea americana, mite associations, avocado, Ambrosia beetles, Mexico



2-8 September 2018, Antalya - TURKEY

Ticks (Acari: Ixodidae) and laelapid mites (Acari: Mesostigmata: Laelapidae) on small rodents in Lithuania

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From the human health perspective, rodent-ectoparasite associations are hugely important in most ecosystems. Climatic changes have caused the spread of ectoparasites into new regions and increased their abundance. They also have had indirect effects on host ecology and abundance, causing the emergence of vector-borne diseases. Rodents are important hosts of the immature stages of the tick *Ixodes ricinus* which has expanded its range in recent decades, and its population density has increased within known endemic areas in Europe. Laelapidae mites are ecologically diverse and are frequently associated with small rodents. These mites are a medically important group worldwide. However, there is a lack of knowledge on the distribution and host associations of ticks and mites in Baltic countries. The aim of this study was to investigate ticks and mites parasitizing small rodents and estimate their infestation patterns on different rodent species inhabiting the Curonian Spit in western Lithuania. Small mammals were captured in different locations in the Curonian Spit during 2013–2016. A total of 565 small rodents representing 7 species were trapped, namely Apodemus flavicollis, A. agrarius, Myodes glareolus, Micromys minutus, Microtus oeconomus, M. arvalis and M. agrestis. The captured rodents harboured I. ricinus ticks (n = 1,250) and 5 species of parasitic mites from the family Laelapidae (n = 910), namely Laelaps agilis, Hyperlaelaps microti, Haemogamasus nidi, Eulaelaps stabularis and Myonyssus gigas. The dominant species of mite found on rodents was L. agilis (94.9%). Ixodes ricinus and L. agilis had similar overall host infestation prevalence. The values of abundance and mean intensity of infestation for *I. ricinus* and L. agilis varied between species of hosts and in different years, with the highest being for A. flavicollis, followed by M. glareolus, and M. minutus. In the present study we documented new geographical and host records for I. ricinus ticks and gamasine mites on seven rodent species in Lithuania.

Keywords: *Ixodes ricinus*, Laelapidae, rodent, infestation, Lithuania



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Addenda Poster Presentations





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Spider mites of the genus *Oligonychus* Berlese, 1886 (Trombidiformes: Tetranychidae) on coniferous plants in the territory of the former USSR

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An examination of the author's personal spider mite collection and the collections of the Nikitsky Botanical Garden Institute revealed a total of eight mite species of the genus *Oligonychus* (subgenera system is according to Mitrofanov et al. 1987) on coniferous plants in the territory of the former USSR. The species are *O. (Wainsteiniella) brevipilosus* (Zacher, 1932), *O. (Wainsteiniella) karamatus* (Ehara, 1956), *O. (Oligonychus) lagodechii* Livshits and Mitrofanov, 1969, *O. (Wainsteiniella) livschitzi* Mitrofanov and Bossenko, 1975, *O. (Oligonychus) piceae* (Reck, 1953), *O. (Wainsteiniella) pinaceus* Mitrofanov and Bossenko, 1975, *O. (Oligonychus) pini* (Hirst, 1924) and *O. (Oligonychus) ununguis* (Jacobi, 1905). Furthermore, plantings of the genera *Picea, Pinus* and *Larix* most frequently hosted the species *O. ununguis, O. pinaceus* and *O. karamatus*, respectively. In addition, the diagnostic characters of the mites of the subgenera of *Oligonychus* and *Wainsteiniella* occurring on coniferous plants in the former USSR are described.

Keywords: Tetranychidae, *Oligonychus*, conifers, host plant, phytophagous

Development of *Tetranychus evansi* Baker and Pritchard (Acari: Tetranychidae) on *Solanum tuberosum* L. in Tunisia

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Tetranychus evansi Baker and Pritchard (Acari: Tetranychidae), which is considered an invasive species, is a damaging pest of potato and other solanaceous crops. Some biological parameters of females were studied at 30 °C, 65% relative humidity and 16 h light on potato leaves. The maximum longevity of *T. evansi* was 12 days. The mean female longevity was 9.2 days, and the mean pre-oviposition, oviposition and post-oviposition periods were 0.6, 7.8 and 0.8 days, respectively. The intrinsic rate of natural increase (rm) was 0.254 days-1. This value, which is considered high, suggests that the development rate of *T. evansi* is a contributing factor to its pest status

Keywords: *Tetranychus evansi*, *Solanum tuberosum*, longevity, oviposition, intrinsic rate of natural increase



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THANK YOU

Dear colleagues

On behalf of the organising committee, please accept our sincere thanks for participating in XV ICA 2018 in Antalya, Turkey. We greatly appreciate the time and effort you put into attending the congress. Its success was to a large degree due your personal involvement and that of your fellow participants. To you we say a big 'Thank you'. We hope that the photo gallery uploaded at http://www.acarology.org/ica/ica2018/ brings back many wonderful memories for you.

The broad demographic of participants, which ranged from students in their 20s to veterans in their 90s, speaks volumes to the power of ICA to inspire acarologists and bring them together every four years. In total, we were delighted to have 271 participants from 44 countries and 6 continents who gave 188 oral and 91 poster presentations. The program featured 6 keynote speakers, 3 invited speakers, 5 plenary lectures, 4 symposia and 13 regular sections spread over 5 days.

We hope that the congress met all your personal expectations. The positive feedback we have received has complimented the congress venue, program and atmosphere.

We therefore trust that you'll want to experience the ICA environment again and that you're already thinking about XVI ICA 2022 in Auckland.

Very best wishes

On behalf of the Organising Committee Prof. Dr. Sebahat K. Ozman-Sullivan President XV ICA 2018



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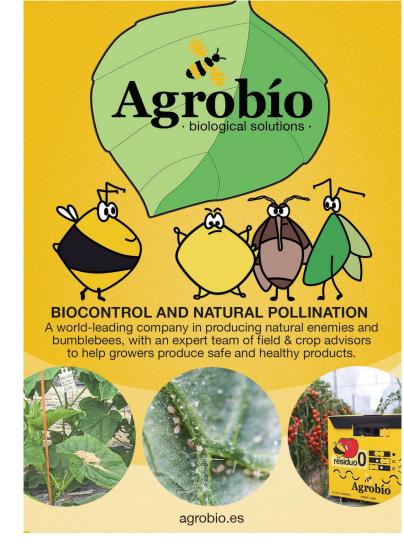
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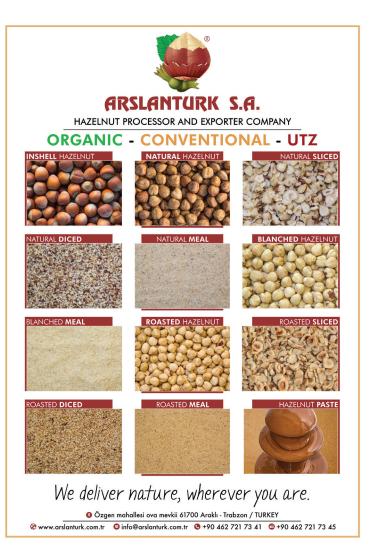
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