THE NEWSLETTER OF THE ORTHOPTERISTS' SOCIETY

Metaleptea

SPECIAL CONFERENCE ISSUE

10th INTERNATIONAL CONGRESS OF ORTHOPTEROLOGY

21-25 June 2009

Antalya, TURKEY

Presented by the Orthopterists' Society and

Akdeniz University

10th INTERNATIONAL CONGRESS OF ORTHOPTEROLOGY

21-25 June 2009
Antalya, TURKEY

Presented by the Orthopterists' Society and
Akdeniz University

CONTENTS

COMMITTEES

ICO-2009 Scientific Committee Members (In alphabetic order)

Charles BOMAR
USA
Ali Nihat BOZCUK
TURKEY
Maria Marta CIGLIANO
ARGENTINA
Battal ÇIPLAK
TURKEY
Theodore COHN
USA
Ali DEMİRSOY
TURKEY
Klaus-Gerhard HELLER
GERMANY
Daniel JOHNSON
CANADA
L. Lacey KNOWLES
USA
Michel LECOQ
FRANCE
Long ZHANG
CHINA
Selahattin SALMAN
TURKEY
Michel SAMWAYS
SOUTH AFRICA
Greg SWORD
AUSTRALIA

Orthopterists' Society Executive Committee

Michel LECOQ
(PRESIDENT)
Maria Marta CIGLIANO
(PRESIDENT ELECTED)
Theodore COHN
(TREASURE)
Charles BOMAR
(EXECUTIVE DIRECTOR)

Local Organising Committee

Battal ÇIPLAK *(CHAIR)*
Akdeniz Univ.
Deniz ŞİRİN
Akdeniz Univ.
M. Sait TAYLAN
Akdeniz Univ.
Sarp KAYA
Akdeniz Univ.
Gürkan SEMİZ
Akdeniz Univ.
Abbas MOL
Ondokuz Mayıs Univ.
Hasan SEVGİLİ
Harran Univ.
Serap MUTUN
Abant İzzet Baysal Univ.

SUNDAY- JUNE 21, 2009

09:00 – 18:00	**Arrival, Registration and Poster Display Registration Desk at Ataturk Conference Hall**

MONDAY- JUNE 22, 2009

Ataturk Conference Hall 09:00 – 10:20	**Opening Ceremony and Plenary Lectures**
Opening speeches (Presenter - Jason HOLDFWORTH)	
Battal Çiplak	Behalf of Organisation Committee
Maria-Marta Cigliano	Behalf of Orthopterists' Society
Prof.Dr. Mehmet Öz	Chair of Biology Department
Prof.Dr. A. Aziz Ergin	Dean of Science Faculty
Prof.Dr. Israfil Kurtcephe	Rector of Akdeniz University
Prof.Dr. Selahattin Salman	Dr. Tevfik Karabağ, a memorial

10:20 – 10:40	**Exhibition**	**Art and Orthoptera**
Exhibition – Art and Orthoptera (ARThoptera): by Yusuf GUVEN, Murat ÇELİK and Ü. Ilgaz TOPCUOĞLU		

10:40 – 11:00	**Break**

11:00 – 11:45	L. Lacey Knowles	Tracing paths of speciation: insights from phylogeography and population genetics
11:45 – 12:30	Maria Marta Cigliano	Taxonomy in Orthoptera: an uncertain future

12:30 – 14:00	**Lunch**

Ataturk Conference Hall	**Organizers Michael Samways & Dan Johnson**	**Symposium Orthoptera and Global changes**
14:00 – 16:30	**(25 min. per talks)**	

	Michael Samways, Dan Johnson	Orthoptera in a changing world
	Anton Kristin, Peter Kanuch, Vladimira Fabriciusova and Vladimir Gavlas	Responses on habitat and global change of some Mediterranean orthopteran species occurring in blown sands in Central Europe
	Corinna Bazelet and Michael Samways	Grasshopper bioindicators in the design and management of large-scale ecological networks
	Axel Hochkirch	Population trends of Orthoptera - what do we really know?
	Klaus Riede	Acoustic profiling of Orthoptera for species monitoring and discovery in a changing world
	Paul B.C. Grant and Michael J. Samways	Application of acoustic profiling of Orthoptera within areas threatened by global changes

16:30 – 17:00	**Break**

17:00 – 17:45	**Poster Session ACH, first floor**
Posters of the all sections will be presented in this session and will be available during four days of meeting.	

Social events		
14:00 - 17:00	**Daily tour**	**A Guided Tour to Antalya/Kurşunlu and Duden waterfalls**
17:45 - 23:30	**Welcome Reception**	**Travel to Side old town, welcome reception at Apollo Temple during sunset and returning to hotels**

TUESDAY- JUNE 23, 2009

Ataturk Conference Hall	**Organizer L. Lacey Knowles**	**Symposium Phylogeography and speciation**
09:00-10:45 (30 min. per talks and 15 for discussion)		
	Battal Çiplak, Klaus-Gerhard Heller, Fer Willemse	Phylogeny and biogeography of the genus *Eupholidoptera* (Orthoptera, Tettigoniidae): the morphological speciation of a Cretan origin in synchrony with geographical evolution of East Mediterranean
	Giuliana Allegrucci	Molecular clocks and Miocene palaeogeography enlighten the evolutionary history of *Dolichopoda* cave crickets in the Mediterranean area

	Marie-Pierre Chapuis	Phylogeography and population genetics of swarming grasshoppers

10:45 – 11:15	**Break**

Ataturk Conference Hall	Chair Hojun Song	Session Biogeography
11:15 – 12:45 (13 min. presentation + 2 min. discussion per talk)		
	Michael G. Sergeev	Biogeography of Orthoptera of the Palaearctic region: relationships between the Mediterranean and steppe territories
	Ertan Mahir Korkmaz, Serdal Arslan, Battal Ciplak and Hasan Hüseyin Başıbüyük	Analyses of cpnl-I nuclear dna sequences from Anatolian populations of the meadow grasshopper *Chorthippus parallelus* (Orthoptera, Acrididae, Gomphocerinae)
	Sarp Kaya, Islam Gunduz and Battal Ciplak	Establishing a phylogeographic analogy between global warming and interglacials for cold demanding refugial taxa: a case study on south-west Anatolian species *Poecilimon birandi*
	Michael G. Sergeev, Jirong, Valentina M. Murav'eva and Nadezhda E. Hudiakova	Diversity and distribution patterns of Orthoptera in the Altay Mountains
	Baudewijn Odé, Roy Kleukers and Luc Willemse	Sharing observations via internet; building a community for faunistic data
	Holger Braun	New and little-known tettigoniids from southeast Ecuador

Posters: Biogeography		
PP01	Deniz Şirin, Abbas MOL and Battal Ciplak	Distribution of endemic Orthoptera species in Anatolia: a statistical approach
PP02	Jaroslav Holusa and Petr Kocarek	Orthoptera and orthopterology in the Czech Republic: current stage of knowledge
PP03	Mohamed Abdallahi Babah Ebbe, Marie Françoise Courel, Alex Franc, Sidi Ould Ely and Jean François Duranton	Biogeographical synthesis of *Schistocerca gregaria* (Forsk., 1775) in Mauritania - 7 acrido mapping regions

PP04	Robert Vlk	Cave-crickets *Troglophilus neglectus* (Krauss, 1879) (Orthoptera: Rhaphidophoridae) in the Czech Republic
PP05	Zina Sofrane, Abboud Harrat	The acridid community of the high plateaus of Setif (Algeria)
PP06	Zoltán Kenyeres, Norbert Bauer, Barnabás Nagy	Distribution and habitats of *Arcyptera microptera* (Fischer Von Waldheim, 1833) in its western area-margin (Central-Europe, Western-Hungary)
PP07	Serap Mutun, David W. Borst	Intraspecific variation and the phylogeography of the lubber grasshopper, *Romalea microptera* (Orthoptera: Acrididae)
PP08	Michael G. Sergeev, Oksana V. Efremova and Olga N. Skalon	Distribution Patterns of Orthopteran Assemblages in urban ecosystems of the south-eastern part of West Siberia

Mediko SKS Hall	**Chair** **Marcos Lhano**	**Session** **Physiology, morphology, development**
11:15 – 12:45 (13 min. presentation + 2 min. discussion, per talk)		
	Glenn K. Morris	Acoustic morphology of ensiferan signal production
	Maja Zorovich and Berthold Hedwig	Cricket brain neurons – song pattern recognition and control of walking
	Amel Ben Hamouda, Mohamed Ammar, Arnold De Loof, Abderrahmen Bouain and Mohamed Habib Ben Hamouda	Comparative study of peptides from the females' accessory glands and oocytes of solitary and gregarious *Schistocerca gregaria*
	Parimalendu Haldar, Chandrik Malakar and Arijit Ganguly	Mercury effects on the development and reproductıon of *Oxya fuscovittata* (marschall)
	Abboud Harrat, Jeanne Raccaud-Schoeller and Daniel Petıt	Development of the subsoephageal body cells and the pericardiac cells during embryogenesis with diapause in *Locusta migratoria* (linnaeus 1758) (Orthoptera: Acrididae)
	Rıffat Sultana, Muhammad Saeed Wagan	Comparative study on the immature stages of three *Hieroglyphus* species (Acrididae: Orthoptera) from Pakistan

Posters: Physiology, morphology, development		
PP09	Fatma Acheuk, Bahia Doumandji-Mitiche, Karima Ait Kaci and Fethia Fazouane	Insecticidal activity of alkaloids of *Pergularia tomentosa* (Asclepiadaceae) on 5th instar nymphs of the migratory locust *Locusta migratoria*

PP10	Ammar Mohamed, Ben Hamouda Amel and Ben Hamouda Med Habib	Leaves action of *Olea europea* (Oleaceae) and *Cestrum parquii* (Solanaceae) on cuticle and brain of desert locust, *Schistocerca gregaria* Forsk. (Orthoptera, Acrididae)
PP11	Fatma Halouane, Fatma Zohra Bissad and Bahia Doumandji-Mitiche	The study of the effect of entomopathogenous *Beauveria bassiana* on cuticle biochimesry and structur of *Schistocerca gregaria*
PP12	Ghania Tail, Patrick Porcheron, Bahia Doumandji-Mitiche and Catherine Blais	Action of diflubenzuron on ecdysteroid levels in ovary and in eggs of the locust *Schistocerca gregaria*
PP13	Marcos Goncalves Lhano and Marinêz Isaac Marques	Can nymphs of *Cornops aquaticum* (Bruner, 1906) (Acrididae, Leptysminae) be determined by their terminalia?

12:45 – 14:15	**Lunch**

Ataturk Conference Hall	**Organizer** **Gregory Sword**	**Symposium** **Orthopteroomics: Unravelling the link between orthopteran genomes and phenotypes**
14:15-16.30 (25 min. per talk)		
	Stephen M Rogers, Heleen Verlinden and Swidbert Ott	The use of desert locust (*Schistocerca gregaria*) transcriptome to analyse to mechanisms of behavioural phase change
	Swidbert Ott and Stephan Rogers	Phase differences in brain size and allometry of brain regions in the desert locust
	Gert Simonet, Liesbeth Badisco, Heleen Verlinden, Elisabeth Marchal, Jurgen Huybrecths and Jozef Vanden Broeck	Locust EST databases: applications in the post genomic era
	Heleen Verlinden, Swidbert Ott, Rut Vleugels, Julie Tobback, Steve Rogers, Malcolm Burrows, Jozef Vanden Broeck	RNA interference in desert locust
	Jurgen Huybrechts, Bart Boerjan, Liliane Schoofs	Proteomics: another approach to tackle locust phase polyphenism.

16:30 – 17:00	**Break**

17:00 – 18:00	Society affairs (OS), Ataturk Conference Hall

Social event
09:00 - 17:00 **Tour to Perge and Side antic towns, and Manavgat waterfall**

WEDNESDAY - JUNE 24, 2009

Ataturk Conference Hall	Chair Klaus-Gerhard Heller & Long Zhang	Symposium Communication and Orthoptera
09:00-10:45 (30 min. per talks and 15 for discussion)		
	Johannes Schul	Acoustic communication in katydids: mechanisms, evolution and evolutionary mechanisms
	Fernando Montealegre-Z	The biophysical basics of tonal sound production in Ensifera
	Long Zhang	Molecular mechanism of chemoreception of locusts
	Torto Baldwyn	Physiological basis of the sub-lethal effects of the desert locust pheromone phenylacetonitrile (PAN)

10:45 – 11:15	Break

Ataturk Conference Hall	Chair Theodore Cohn	Session Evolution
11:15 – 12:45 (15 min. presentation + 3 min. discussion per talk)		
	Andrej V. Gorochov	Late mesozoic and early caenozoic stages in the evolution of Orthoptera
	Elen Oneal and L. Lacey Knowles	Testing for selective divergence in a caribbean cricket (genus *Amphiacusta*)
	Frédéric Legendre, Tony Robillard, Hojun Song, Michael F. Whiting, Laure Desutter-Grandcolas[1]	Ensifera phylogeny: we are not out of the woods yet
	Haruki Tatsuta, Izumi Yao and Shin-ichi Akimoto	Phylogeography and fine-scale genetic structure in *Podisma kanoi*: insights from landscape genetic approaches
	Peter Kaňuch, Frida Holma, Åsa Berggren and Anna Cassel-Lundhagen	Evolution of invasive traits in range margin populations of the roesel's bush cricket (*Metrioptera roeselii*)

Posters: Evolution		
PP14	Alexander Bugrov, Ilyas Jetybayev, Tatiana Karamysheva and Nikolay Rubtsov	Telomeric and rDNA repetitive sequences in karyotypes of Gomphocerinae grasschoppers (Orthoptera: Acrididae)
PP15	Anja Klöpfel, Jan Sradnick, Alexander Hübner and Norbert Elsner	Introgression of genes and morphological characters in a grasshopper hybrid zone on Mt. Tomaros
PP16	Jan Sradnick, Varvara Vedenina, Anja Klöpfel, Sylvia Fähsing and Norbert Elsner	Study of isolation barriers between hybridizing grasshopper species
PP17	Norbert Elsner, Jan Sradnick and Anja Klöpfel	A hybrid zone of two Acridid grasshopper species on Tomaros Mountain in North-West Greece
PP18	Peter Kanuch, Vladimira Fabriciusova and Anton Kristin	On the life history of isolated populations of *Pholidoptera frivaldskyi* (Tettigoniidae) in Central Europe
PP19	Varvara Vedenina	Song evolution and phylogenetic relations between the european species of the *Chorthippus albomarginatus* group (Orthoptera, Acrididae, Gomphocerinae)

12:45 – 14:15	**Lunch**

Ataturk Conference Hall	**Chair Klaus Riede**	**Session Behaviour**
14:15 – 16:30 (14 min. presentation + 2 min. discussion per talk)		
	Kate Umbers, Adam Stow, Greg Holwell and Marie Herberstein	The function of colour change in the chameleon grasshopper (*Kosciuscola tristis*)
	Nataša Stritih	The vibrational startle response of a non-hearing cave cricket (*Troglophilus neglectus*, Rhaphidophoridae) and its neuronal correlates
	Baudewijn Odé	Complex song characters: registration, description and interpretation
	Swati Diwakar and Rohini Balakrishnan	Call diversity and spectro-temporal partitioning in an acoustically communicating Ensiferan assemblage of a tropical evergreen forest
	Klaus-Gerhard Heller, Tim Ostrowski and Claudia Hemp	The function of low frequencies: singing and hearing in aerotegmina (Tettigoniidae: Listroscelidinae)

	Manfred Hartbauer, E. Ofner and Heinrich Römer	Acoustic distance estimation in the European katydid *Metrioptera roeseli roeseli*
	Gerlind U.C. Lehmann	Are male bushcrickets honest signaler?
	Andrew C. Mason, Norman Lee, Damian O. Elias	Phonotaxis in response to multiple sound sources in the acoustic parasitoid fly *Ormia ochracea*

Posters : Behaviour		
PP20	Dirk Berger and Brigitte Gottsberger	"I like to move it, move it!" A detailed analysis of the multimodal courtship repertoire of *Myrmeleotettix antennatus* (Fieber, 1853) (Orthoptera, Caelifera, Gomphocerinae)
PP21	Zoltán Kenyeres and Norbert Bauer	Daily activity of *Poecilimon intermedius* (Fieber, 1853) in a typical steppe habitat of the species (Central-Europe, Hungary)
PP22	Hossein Zamanian, Mehdi Dehghani and Maede Mehdipour	Remote modeling and analyzing of insect sounds by using a computer and microcontroller-based system
PP23	Klaus Riede	Similar songs, distinct species: bioacoustic diversity and vicariance in tropical cricket communities
PP24	Tarai Nacer and Doumandji Salaheddine	Feeding preferences of gregarious nymphs and adults of the desert locust, *Schistocerca gregaria* (Forskäl 1775) (Orthoptera, Cyrtacanthacridinae) in different habitats at biskra oasis, Algeria
PP25	Xinyang Zhang and Long Zhang	An attractant for gregarious nymphs of oriental migratory locust
PP26	Petr Kocarek	Vibrational communication in *Tetrix ceperoi*: description of male and female songs
PP27	Natasha Mhatre, Fernando Montealegre-Z, Rohini Balakrishnan and Daniel Robert	Mechanical response of the tympanal membranes of the tree cricket *Oecanthus henryi*

Mediko SKS Hall	**Chair Alexandre Latchininsky**	**Session Ecology & Evolution**
14:15 – 16:30 (16 min. presentation + 3 min. discussion per talk)		
	Leila Benfekih and Daniel Petit	Do graminivores Caelifera consume the Poaceae according to their relative abundance?

	Elodie Blanchet, Ange-Marie Risterucci, Claire Billot, Marie-Pierre Chapuis , Laurence Blondin, Ronan Rivallan , Christine Pages, Antoine Foucart, Jean-Michel Vassal and Michel Lecoq	Development of molecular tools for studies in the *Calliptamus* genus
	Eva Schultner, Elodie Blanchet, Christine Pages, Antoine Foucart, Jean-Michel Vassal and Michel Lecoq	Biology and ecology of *Arcyptera brevipennis vicheti* Brunner, 1861
	Sarah L. Bush and Johannes Schul	Are leader preferences in katydids the outcome of a sensory bias?
	Dirk Berger	The evolution of grasshoppers and their songs: insights from morphology and behaviour
	Brigitte Gottsberger	Consequences of hybridization in two closely related gomphocerine grasshopper species - male songs and female preferences
	Varvara Vedenina, Jan Sradnick, Anja Kloepfel and Norbert Elsner	Song and song preferences in two grasshopper hybrid zones: similar fate of hybrids between the species with complex courtship

16:30 –17:00	**Break**
17:00 – 18:00	Meeting **AAAI (Mediko SKS Hall)**
18:00 – 19:00	**Meeting (Moderator: T. Miller and A. Hilali)**
Biotechnology in locust control (Mediko SKS Hall)	

Social events		
09:00 – 12:00	**Daily tour**	**Walking in the old town of the Ottomans, visit to the Marina and the Antalya Museum**
20:00 – 23:00	**Gala**	**Gala Dinner by the "Society of Social and Applied Gerontology" Beach Park**

THURSDAY - JUNE 25, 2009

Ataturk Conference Hall	Organizer Michel Lecoq	Symposium Integrated pest management for locusts and grasshoppers: are alternatives to chemical pesticides credible
09:00-10:45 (30 min. per talks and 15 for discussion)		
	Dave Hunter	Credibility of an IPM approach for locust and grasshopper control: the Australian example
	Harold van der Valk	Progress of incorporation of *Metarhizium* into IPM preventive control of Desert locust
	Wim Mullié	Does bird predation enhance the impact of Green Muscle for grasshopper control - Experiences from cleared woodland in Central Senegal
	Torto Baldwyn	Pheromonal control of the desert locust: lessons learned and future prospects
10:45 – 11:15	**Break**	

Mediko SKS Hall	Organizer Karim Vahed	Special session Sexual selection in orthopteroid insects
11:15 – 12:45 (15 min. presentation + 3 min. discussion per talk)		
	John Hunt	What is wrong with good genes sexual selection?
	Karim Vahed	Prolonged copulation following spermatophore transfer in bushcrickets is associated with reduced nuptial gift mass and modifications in the form and use of the males' cerci.
	Axel Hochkirch	The interspecific dimension of sexual selection: how reliable are specific mate recognition systems in Orthoptera?
	Gerlind U.C. Lehmann	Titillators in bushcrickets as sexually selected devices
	Will Pitchers and John Hunt	Phenotypic integration as a constraint on call evolution

Ataturk Conference Hall	Chair A. Nihat Bozcuk	Session Ecology
11:15 – 12:45 (15 min. presentation + 3 min. discussion per talk)		
	K. Abbassi, Z. Atay Kadiri and S. Ghaout	Desert Locust and intensive rainfall in Morocco from 1995 to 2008

	Mustapha Bounechada and Fenni Mohamed	Grasshoppers and locusts and climat change in setifian region [North-East of Algeria]
	Alexandre Latchininsky	Gray bird grasshopper *Schistocerca nitens* on a NW Hawaiian Island: a challenge to conservation
	Guendouz Benrima Atika, Jean François Duranton and Bahia Doumandji Mitiche	Food choice of the desert locust *Schistocerca gregaria* (forsk., 1775) (Orthoptera, Cyrthacantacridinae) in its solitary phase in Algeria
	Daniel Petit and Leila Benfekih	Comparison of two Caelifera-rich communities in the semi-arid stage of North Algeria

Posters: Ecology		
PP28	Arijit Ganguly, Chandrik Malakar and Parimalendu Haldar	Study on the nutritional ecology of *Oxya fuscovittata* to obtain a suitable food plant for their successful rearing
PP29	Jaroslav Holusa, Petr Kocarek, Pavel Drozd and Robert Vlk	Analysis of population trend in *Saga pedo* (Orthoptera: Tettigoniidae) on the edge of its range: more abundant or more intensively studied?
PP30	Malik Laamari	Influence of the drought on the food behavior of the moroccan locust *Dociostaurus maroccanus*
PP31	Petr Kocarek, Sarka Grucmanova, Zuzana Filipcova, Lenka Bradova, Vitezslav Plasek and Pavel Drozd	Food composition of two European groundhoppers (Orthoptera: Tetrigidae: *Tetrix tenuicornis*, *Tetrix ceperoi*): bryophagy or detritophagy?
PP32	Idrissa Maiga, Michel Lecoq and Serge Morand	Egg survival strategies of the senegalese grasshopper during the dry season in the African sahel
PP33	Lecoq Michel, Chamouine Abdou and Luong-Skovmand My-Hanh	Red locust phasis in Madagascar

12:45 – 14:30	**Lunch**

Ataturk Conference Hall	**Chair** **David Hunter**	**Session** **Pest Management**
14:15 – 16:30 (14 min. presentation + 3 min. discussion per talk)		

	Alexandre Latchininsky and Ramesh Sivanpillai	Mapping potential Italian locust (*Calliptamus italicus*) habitats in NE Kazakhstan with satellite imager
	David H. Branson and Lance T. Vermeire	Effects of fire and post-fire grazing intensity on grasshopper assemblages in a northern North American grassland vary between years
	Annie Monard	Towards better locust management in Caucasus and Central Asia
	Sidi Ould Ely, Magzoub Omer Bashir, Harry Bottenberg, Mohamed Abdallahi Babah Ebbe and Ahmed Hassanali	Toward a simulation model for desert locust gregarisation
	Eleonora Abashidze, Stefan Jeronski, Rami Horowitz, Alex Latchininsky and Gvantsa Aduashvili	Evaluation of entomopathogenic fungi for locust control in Georgia
	Pierre Mineau and Paul Story	Post-spray pesticide residues in Orthopterans and the risk assessment process for gorge-feeding birds and mammals
	Wail Haroon, Abdalla Mohamed Abdalla, M. Lecoq and My Hanh Luong-Skovmand	Efficacy of metarhizium *Anisopliae var. acridum* against the tree locust, *Anacridium melanorhodon melanorhodon*
	Rakesh K. Gupta, Stefan T. Jaronski, K. Srivastava and K. Bali	First record on epizootics of *Entomophthora grylli*, on grasshoppers, *Oxya velox* in Indian subcontinent

Posters: Pest management		
PP34	Abdelghani Bouaichi, Jamal Chihrane, Lajcen Idrissi Raji and Ahmed Mouhim	Evaluation of dose-effect of spinosad® (125 g/l ulv) on Acridoïdea's species and assessment of their side effect on non-target fauna under field conditions in high Atlas mountain, Morocco
PP35	Ahmed Amin, Idris Salam	Impacts of the entomopathogenic fungus *Beauveria bassiana* (balsamo) vuillemin as biological control approach of mole crickets, *Gryllotalpa gryllotalpa* (Orthoptera: Gryllotalpidae)
PP36	Mamadou Abdou , Ahmed Mazih, Said Ghaout, Inezdane Alzouma, Abderrahim Hormatallah	Impact study of the pesticides used to control desert locust (*Schistocerca gregaria* Forskål 1775) (Acrididae: Orthoptera) on two species of *Prionyx* (Hymenoptera, Sphecidae) in Aïr (Niger)
PP37	Badderdine Guennouni, Abdelghani Bouaichi and Ahmed Mazih	Predation and parasitism : an evaluation of their impact on Acridoidea's population dynamics in high Atlas mountain, Morocco

PP38	Furkat Gapparov, Utapov Nemat, I. Hamraev and B. Eshchanov	Modern technologies for locust control in Uzbekistan
PP39	Lajcen Idrissi Raji, Abdelghani Bouaichi, Abderrahim Hormatallah, Mohamed Sarehane	Impact of malathion and deltamethrin applied in ULV formulation on the honey bees *Apis mellifera*, under semi-field condition
PP40	Michel Lecoq, Emmanuel Gay Pierre and My-Hanh Luong-Skovmand	Red locust in Southern Madagascar: suitable conditions for outbreaks and gregarious areas
PP41	Seema Rathour, A.K. Karnatak and D.C. Karnatak	Biotechnological approaches in pest management programmes
PP42	Wail Haroon, Jean Vassal, Abdalla Mohamed Abdalla, Michel Lecoq and My Hanh Luong-Skovmand[2]	In vitro compatibility between metarhizium *Anisopliae var acridum* and neem seed oil
PP43	Ying Yan, Fang Yu and Long Zhang	The fine structure of the Entomopathogenic fungus *Metarhizium anisopliae* infecting *Locusta migratoria* (Orthoptera:Acrididae)
PP44	Peter A. Spurgin, H. McRae, A. Monard	Use of the biopesticide Green Guard® containing the entomopathogenic fungus *Metarhizium anisopliae* var. *acridum*, to control an outbreak of Migratory Locust, *Locusta migratoria*, in Timor Leste
PP45	Aalya Mohamed Ibrahim Shomo	Locusts and grasshoppers as human being food

Mediko SKS Hall	**Chair** **Charles BOMAR**	**Session** **Systematics and Phylogeny**
14:15 – 16:30 (16 min. presentation + 3 min. discussion per talk)		
	Olivier Béthoux	Evidence for a unique origin of the stridulatory file in ensiferans
	Claudia Hemp	Climatic fluctuations as motor for speciation processes in flightless saltatoria (Insecta: Orthoptera)
	Dragan Chobanov and Beata Grzywacz	Phylogeny and systematics of the *Isophya modesta* group (Phaneropteridae: Barbitistinae)
	Hojun Song, Matthew J. Moulton, Kevin Hiatt and Michael F. Whiting	Phylogeny of *Schistocerca* revisited: locust biogeography inferred from molecular fossils

	Karine Berthier, Marie-Pierre Chapuis, Seyed Mojtaba Moosavi, Donya Tohidi-Esfahani and Gregory A. Sword	Mitochondrial pseudogenes plague locust nuclear genomes
	Mohammad Kamil Usmani	Significance of male and female genitalia in the classification of Indian Acridoidea (Orthoptera)
	Hasan Sevgili, Selim Çağlar, Ismail K. Saglam	Bioacoustics, systematics and distribution of the *Phonochorion* genus (Orthoptera: Tettigoniidae: Phaneropterinae)

Posters: Systematics and Phylogeny		
PP46	Andrej V. Gorochov	Evolution of the copulatory apparatus in Ensifera (Orthoptera): introduction
PP47	Balázs Kolics , Zoltan Acs , Dragan Petrov Chobanov, Shun Qiang Lo , Balázs Kovács, Deniz Sirin , János Taller, András Speciár, László Orbán, Tamás Muller	Phylogeny of the European Saginae
PP48	Olivier Béthoux	Merits of nomenclatural procedures
PP49	Charles R. Bomar and Stephen C. Nold	Grasshopper phylogeny: bringing exploration to science education
PP50	David C. Eades	Species file software and the Orthoptera species file
PP51	Deniz Şirin and Battal Ciplak	Taxonomy of *Chorthippus biguttulus* group (Orthoptera, Acrididae, Gomphocerinae) in Anatolia: morphometry support song based taxonomy
PP52	Marcos Gonçalves Lhano	Is the tribe Tetrataeniini (Acrididae, Leptyminae) a monophyletic group?
PP53	Massa Bruno	Supraspecific systematics of groups currently belonging to *Platycleis* Fieber, 1852 and *Metrioptera* Wesmael, 1838 (Orthoptera: Tettigoniidae)
PP54	Mauro Rampini, Claudio Di Russo , Francesca Pavesi and Marina Cobolli	The Rhaphidophoridae cave crickets of the Eastern Mediterranean area: a checklist of species from the Balkans, Greece and Turkey
PP55	Mehmet Sait Taylan, Deniz Sirin and Battal Ciplak	Paternal characteristics of song in *Anterastes* (Orthoptera, Tettigoniidae): is there any evolutionary sign

PP56	Roy Kleukers[1], Baudewijn Odé [1], Luc Willemse [1] and Klaus-Gerhard Heller [2]	A website on European Orthoptera
PP57	Asu Aytac, Pınar Konu, Zehra Boztepe, Sarp Kaya and Battal Ciplak	Morphometry for taxonomy of *Anterastes*: partly congruent qualitative and quantitative morphologies
PP58	Josefina Silvia Alberghina, Maria Marta Cigliano, Elio Castillo, Dardo Marti, Carlos Lange and Viviana Andrea Confalonieri	A phylogeographic study of *Ronderosia bergi* (Orthoptera: Acrididae) morphotypes
PP59	Pablo Adrián Dinghi, Viviana Andrea Confalonieri and Maria Marta Cigliano	A phylogenetic analysis of the "paranaense-pampeano" assembly of species (Orthoptera: Acrididae: Melanoplinae) based on morphological and molecular characters: testing the monophyly of this informal group
PP60	Viktoria Dzyubenko, Alexander Bugrov, Tatiana Karamysheva and Nikolay Rubtsov	Molecular composition of supernumerary (B) chromosomes from eastern populations of the grasshopper *Eyprepocnemis plorans*
PP61	Elzbieta Warchalowska-Sliwa, Beata Grzywacz, Anna Maryanska-Nadachowska and Dragan P. Chobanov	Comparative analysis of rDNA and tDNA locations in the genus Isophya (Orthoptera, Phaneropterinae)
PP62	A.G. Bugrov, O.S. Novikova, A. V. Gorochov, A.G. Blinov	Using DNA sequences of two mitochondrial genes (*COI* and *COII*) for taxonomy and phylogeny of Tettigoniidae
PP63	Matthew J. Moulton, Hojun Song, and Michael F. Whiting	Assessing the effects of primer specificity on eliminating numt coamplification in DNA barcoding
PP64	*Gu Junjie, Ren Dong and Shih ChungKun*	Jurassic-Cretaceous fossil Hagloidea from China

16:30 –17:00	**Break**	
17:30 – 18:30	**Ataturk Conference Hall**	**Evaluation and Closing**

ABSTRACT CONTENT

Exhibition

Art and Orthoptera (ARThoptera): A pirate presentation to ICO2009

Yusuf Güven[1], Murat Çelik[1], Ilgaz Topçuoğlu[2]

[1]*Faculty of Fine Arts, Mersin University Mersin, Turkey*

[2]*Faculty of Fine Arts, Akdeniz University Antalya, Turkey*

The '**ARThoptera**' project is inspired from the image 'grasshopper' corresponding 'life', 'word' and 'action' in daily life. In this context, the image 'grasshopper' is not considered as a scientific matter but 'as a purified part of daily life'. Although the project based on the principles to combine sounds and pictures, its relation to the congress is use of the image 'grasshopper'.

Scientists may have great knowledge on every aspect of grasshoppers but the project informs scientists about another aspect. The main question of the project is neither the cause of existence of grasshopper nor their mode of reproduction or feeding or sheltering of grasshoppers. The main object of the project is to 'explain grasshoppers to the orthopterists'. Thus, an ironic exposition takes place.

We know that the grasshopper has been illuminated under the light of science like many other subjects. The **ARThoptera** can be considered the dark side of this illumination process. This dark side–to perceive it–it is necessary to look from outside without considering scientific principle and process. If so, 'there is noting' at dark!

The **ARThoptera** project is neither an extension of an idea of contemporary or past art nor an innovation. It may be considered as 'pirate presentation' of 10th International Congress of Orthopterology.

PLENARY LECTURES

Ataturk Conference Hall (09:00 – 10:30 / June 22, 2009)

Prof.Dr. Tevfik Karabağ, a memorial

Selahattin Salman[1]

[1]*Ahi Evran University Kırşehir, Turkey*

Tevfik Karabağ was born in 1911, in Kars. In 1934, he graduated from Faculty of Agriculture at High Agriculture Institute in Ankara (Ziraat Fakültesi, Yüksek Ziraat Enstitüsü). He finished his PhD in 1944 in the Faculty of Sciences at the same institute (Tabii İlimler Fakültesi, Yüksek Ziraat Enstitüsü). He started working as associate professor and then full professor, in 1948 and 1953 respectively, at the same faculty in Ankara.

Karabağ carried out researches in the British Museum (The Natural History Museum, London) between 1949-1951. He was elected as Dean of Science Faculty (Ankara University) for twice, first in 1957 and second in 1966. He chaired the department of Systematic Zoology in the same faculty during 1961-1977. During the period of 1977-1983 he has conducted mission of the General Secretariat of TUBITAK (Scientific and Research Council of Turkey). He loaned an active role in the establishment of Dicle University in Diyarbakır.

Tevfik Karabağ was among the members of "Royal Entomological Society of London". He published several worldwide known papers/books. He introduced several new species or genera to scientific world and now he is the author of 5 generic and 77 species/subspecies names. He was awarded by the highest award of TUBITAK (TUBITAK-Hizmet Ödülü in 1977). Prof. Dr. Tevfik Karabağ is not among us since 2003.

Tracing paths of speciation: insights from phylogeography and population genetics

L. Lacey Knowles

University of Michigan, Museum Zool., Dept. Ecol. & Evolutionary Biol., 1109 Geddes Ave, Ann Arbor, MI 48109 USA

For decades, phylogeographic studies have sought to understand the processes that have influenced the spatial distribution of genetic variation within species and among closely related taxa. The increased prospect of achieving such goals owe to developments at the molecular level, as well as computational advances that include the forging of diverse approaches. While much of the appeal and insights of phylogeographic study can be traced to its character as a unified eclectic field, at times this diversity has also created an aura of an uncertain future. As the field moves to overcome the inherent conflicts that can emerge as new concepts and ideas are integrated into its purview, the true virtues of phylogeography are becoming realized. These include not only unprecedented details about the demographic past, but this increased resolution also provides a critical backdrop for addressing questions that extend beyond the phylogeographic history of species, such as interpreting patterns of species diversity and phenotypic divergence.

Taxonomy of Orthoptera: an uncertain future?

Maria Marta Cigliano[1]

[1]*CCT La Plata CONICET-CEPAVE, Museo de La Plata, La Plata, Argentina*

The global imperative for the conservation of biodiversity has brought into focus the needs for taxonomic research. However, the crisis facing the conservation of biodiversity is reflected in a parallel crisis in taxonomy. On the other hand, molecular information is having an increasingly important impact on the evidential basis for delimiting species and it is likely to result in greater scientific debate and controversy. Revisionary taxonomy is frequently dismissed as merely descriptive and lacking a hypothesis driven nature. Phylogenetic classifications are optimal for storing and predicting information, but phylogeny divorced from taxonomy is unrealizable. Taxonomy, systematics, and phylogeny are interwoven, hypothesis-driven sciences with a theoretical base. Taxonomic knowledge remains essential to credible biological research and is made urgent by the biodiversity crisis. An easy accessible taxonomic knowledge base is critical for all biodiversity-related sciences. Taxonomy, like academia in general, needs to prepare to take advantage of new information technology capabilities. Full synonymic and taxonomic information for the more than 24,000 valid species of Orthoptera, information at the specimen level data, images of type specimens and of specific diagnostic characters, and keys to several taxa are already available on the Web as part of the Orthoptera Species File online. The rapid advances in bioinformatics have provided unprecedented opportunities to conduct taxonomic research more efficiently; cybertaxonomy is emerging as an exciting new branch of taxonomy. The potential of using OSF as a tool for monograph and revisionary studies of Orthoptera is herein presented, as well as a way of integrating many of the most recent cybertaxonomic tools with species descriptions and demonstrating the utility of international standards for biodiversity informatics, in order to engage both the specialist taxonomic community and a wider public in gathering taxonomic knowledge and deepening understanding of it.

SYMPOSIA

ORHOPTERA and GLOBAL CHANGES

Organizers: Michael Samways & Dan Johnson
Ataturk Conference Hall (14:00 – 16:30 / June 22, 2009)

Orthoptera in a changing world

Michael J. Samways[1] and Dan L. Johnson[2]
[1]*Department of Conservation Ecology and Entomology, Stellenbosch University, P/Bag X1, Matieland, South Africa*
[2]*Environmental Science Program, Department of Geography, University of Lethbridge, 4401 University West Drive, T1K 3M4, Lethbridge, Alberta, Canada*

Orthoptera are among the most conspicuous of all invertebrates – acoustically, if not visually. They fulfill many feeding functional roles and are adapted to a wide range of ecosystem types. While they are diverse and abundant across many landscapes, many are also very sensitive to the anthropogenic changes that are currently taking place, with one species only scientifically described after it had become extinct. Conservation awareness of orthopteran species is now coming of age, with a focus on their being the subjects of conservation, as well as contributors to the conservation of biodiversity in general. We are proposing here that us Orthopterists open up our expertise to assisting the conservation cause, bearing in mind that estimates are that a third of all insect species will go extinct in the next few decades. As many orthopteran species are such good indicators of landscape change, let us mainstream our beloved animals into global conservation. This includes threatened endemic species in conservation assessments and action, as well as deploying the more widespread and abundant species as indicators of change. In this symposium, we will explore some of the challenges and opportunities facing Orthopterology in the near future.

Responses on habitat and global change of some Mediterranean Orthopteran species occurring in blown sands in Central Europe

Anton Kristin[1], Peter Kanuch[1], Vladimira Fabriciusova[1] and Vladimir Gavlas[1]
[1]*Institute of Forest Ecology SAS*

Blown sands together with their grasslands belong to the European high priority habitats. Animal communities of these habitats belong to the most thermophilous in Central Europe (Slovakia). Are they profiting from the global warming? What is the response of model pseudo-psammophilous orthopterans to the changing land use and to the global climate change? We have analyzed local population size, distribution, phenology and the accompanying assemblages in four model species at northern limit of their area. Three of the studied species are of Mediterranean origin: *Acrida ungarica*, *Oedaleus decorus* and *Acrotylus insubricus*; the distribution range of the fourth, *Myrmeleotettix antennatus*, has not been specified distinctly yet (Ponto-Mediterranean?). The analysis of distribution data from the periods 1897-1962 and 1999-2008 revealed a considerable decrease in number of the recognized localities – in spite of systematic control – for the first three species (*A. ungarica* 20/7, *O. decorus* 15/2, *A. insubricus* 4/0). But in case of *M. antennatus*, the situation is intricate (6/9). Similar trend was also observed in data on abundance – frequently being on survival limit for the local populations. All these species have mating period shifted towards the end of season. Hence, these species are expected to profit from warm season prolonged thank to the global warming. Despite that and high dispersal ability of all studied species,

their distribution over the northern parts of the area is getting more and more scattered. The hypothesis about their potential northern expansion and increasing abundance has not been corroborated yet. Therefore, in conclusion we call for saving the last refuges in the preserved blown sands in Central Europe.

Grasshopper bioindicators in the design and management of large-scale ecological networks

Corinna Bazelet[1] and Michael Samways[1]
[1]*Stellenbosch University, South Africa*

Ecological networks (ENs) are interconnected nodes and corridors of remnant or restored natural habitat, which are intended to mitigate the effects of landscape-scale habitat loss. Extensive and well-established ENs of remnant grassland associated with production timber plantations in South Africa, provide a unique opportunity to empirically evaluate the conservation value of ENs. Grasshoppers (Orthoptera: Acrdidae) are an effective indicator taxon in the region and species assemblages were compared across ENs to address the following questions: (1) How are grasshopper species assemblages dispersed throughout ENs? (2) What are the main environmental factors contributing to this dispersion? (3) What management principles can be identified using grasshopper species assemblages as bioindicators? Three categories of environmental variables were compared with the species assemblages: vegetation structure, landscape, and management variables. Results indicate that management of ENs has a greater impact in determining the grasshopper species composition than landscape or vegetation structure variables. Furthermore, grasshoppers are an effective practical tool for quantifying the conservation success of ENs.

Population trends of Orthoptera - what do we really know?

Axel Hochkirch[1]
[1]*University of Trier, Germany*

The loss of biodiversity is a major problem of modern times. Red lists have become an important instrument to document species declines and extinctions. They are necessary to make public the dramatic loss of diversity and prioritize species for which conservation management needs to be implemented. Red lists also provide important arguments for reserve planning. It is, therefore, of crucial importance to obtain the relevant information to assess the red list status of species. The IUCN red list is the leading instrument for assessing this status. However, there is a strong bias in the data. Most taxa in the IUCN red list are vertebrates for which better data is available than for insects. In many European countries, red lists for Orthoptera have been published, but the data behind these assessments rarely fulfills the strict criteria formulated by the IUCN. In fact, these criteria is rarely available for any insect species, except for the range size. The range size, on the other hand, is probably not too important for an insect. Using range sizes alone, many island endemics would be red-listed although they may be common in their habitats. The population trend is the most

important criterion for red list assessments, but the data on population trends is scarce, even in countries where Orthoptera have been studied for a long time. Recent activities in Europe have focused on documenting the current distribution of Orthoptera in several atlas projects. It is now important to document also the changes in the distribution. We studied both, Orthoptera decline and range expansions in northern Germany. In 2005, we repeated an Orthoptera mapping project, which had been performed in 1986. 150 study sites were monitored for changes in Orthoptera assemblages. Our results show that rare species are still declining, while some common species have spread, leading to a convergence of Orthoptera assemblages across study sites. The major causes for these changes were habitat loss due to changes in land use, eutrophication and succession. Positive population trends of rare species were found only in nature reserves. We also analyzed the current range expansion in *Metrioptera roeselii* and found that this species was able to expand its range by ca. 20 km in one year. Furthermore, we managed and monitored a field cricket population for ca. 20 years and were able to successfully perform a translocation project.

Acoustic profiling of Orthoptera for species monitoring and discovery in a changing world

Klaus Riede[1]
[1]*Research Museum Alexander Koenig, Bonn, Germany*

Bioacoustic monitoring and classification of animal communication signals has developed into a powerful tool for measuring and monitoring species diversity within complex communities and habitats. The high number of stridulating species among Orthoptera allows their detection and classification in a non-invasive and economic way, particularly in habitats where visual observations are difficult or even impossible, such as tropical rainforests. Using data from my bioacoustics monitoring work, particularly in Ecuadorian Amazon rainforest, I will demonstrate the potential of the method, but also challenges and bottlenecks impeding further progress. A major problem is time-consuming data analysis of recordings. Computer-aided identification software has been successfully developed and applied for cricket and grasshopper song classification, but these tools are still far from practical field application. Another bottleneck is insect song databases: the DORSA database (www.dorsa.de) contains thousands of Orthoptera songs, but lacks tools for automatic or manual song analysis. Therefore, an efficient system for acoustic profiling of Orthoptera should consist of the following components: (1) Protocols for standardized acoustic sampling, at species and community level, and including acoustic data loggers for autonomous long-term recordings. (2) Open access to and efficient management of song data and voucher specimens, involving the Orthoptera Species File (OSF) and Global Species Information Facility (GBIF) (3) an infrastructure for automatised analysis and song classification for on-the ground and web-based analysis, including web2.0 applications for user communities. (4) A strategic framework for future inventorying and monitoring by acoustic profiling. Monitoring should concentrate on endangered species and habitats threatened by global change, such as alpine areas, tropical mountain forests and areas under severe anthropogenic pressure. Inventorying should concentrate on species discovery in hitherto under-sampled areas, some of which will be identified here by GIS-analysis.

Application of acoustic profiling of Orthoptera within areas threatened by global changes

Paul B.C. Grant[1] and Michael J. Samways[1]
[1]*University of Stellenbosch, Stellenbosch, South Africa*

Current human activity has had a resounding impact on biodiversity across the globe and increased pressure on remaining habitats. Therefore priority should be given to monitoring biodiversity within habitats threatened by global change. Acoustic profiling provides a useful, non-invasive tool for monitoring Orthoptera diversity in habitats under threat, including tropical forests which, due to their architectural complexity, render traditional detection methods unfeasible. The application of acoustic profiling has been implemented along elevational gradients in tropical forests of Brunei, an area under enormous anthropogenic pressure and threatened by global climate change. Acoustic profiling in this region allowed assessment of cryptic species, and even provided background for comparing similar elevational gradients within the Western Cape, South Africa. These results show that acoustic profiling is a valuable tool for studying the composition and distribution of orthopteran assemblages. The collective song profile of the whole acoustic assemblage also gives a very good indication of threats to Orthoptera and the state of the habitat, whether in terms of deterioration, or in restoration. Within South Africa, acoustic profiling was applied to various ecosystems under various levels of impact. Preliminary results indicate that, with further bioacoustic surveys, acoustic profiling could provide a valuable, practical tool for assessing habitat quality. Among these is assessment of large-scale ecological networks, which are remnant corridors and nodes which act as a mitigation measure for plantation forestry. First results suggest that acoustic profiling makes a major contribution to the design of these networks.

PHYLOGEOGRAPHY and SPECIATION

Organizer: L. Lacey Knowles
Ataturk Conference Hall (09:00-10:45 / June 23, 2009)

Phylogeny and biogeography of the genus *Eupholidoptera* (Orthoptera, Tettigoniidae): the morphological speciation of a Cretan origin in synchrony with geographical evolution of East Mediterranean

Battal Ciplak[1]
[1]*Department of Biology, Faculty of Art & Science, Antalya, Turkey*

Recently the systematics and biogeography of Mediterranean lineages have received a lot of attention. This paper deals with Eupholidoptera, an example of Mediterranean lineages found Orthoptera, Tettigoniidae. The genus is restricted to the northern and eastern basin of Mediterranean with a significant number of species found on islands. To produce a phylogeny and use it in making assumptions about the historical biogeography of Eupholidoptera, material of 46 species from several collections were studied. A phylogenetic analysis based mainly on morphological characters suggested two lineages in the genus: the E. chabrieri and the E. prasina groups. Based on the consistency between historic geographical events and branching events on the phylogenetic tree, Eupholidoptera is assumed to have evolved from an ancestor present in the Aegeid plate in Mid Miocene around 16–15 Myr BP. The fact that basal branches of each species group are represented in Crete, indicate that the southern parts of the Aegeid plate including Crete were part of the range of the ancestor. The division of the Aegeid plate into Anatolia and Greece in Tortonian, the reoccurrence of terrestrial corridors between these mainlands in the Messinian, the regression of Aegean area in Pliocene and sea level changes in Pleistocene are assumed to have been the main paleogeographical events directing the speciation in Eupholidoptera. As most of the species are allopatric, vicariance is suggested to be main pattern. By combining the nature of the characters used in phylogenetic analysis, the phylogenetic tree produced and the biogeographic assumptions suggested four tentative conclusions can be made: 1) Radiation in the genus is a result of divergence in morphology. 2) Since the main character source is male genitalia possibly there has been an intensive sexual selection which leads to a morphological speciation. 3) As difference in temporal parameters of the song is prominent in sympatric/parapatric sp ecies pairs, co-occurrence is suggested to be the main reason driving divergence in the song. 4) There seems to be a negative correlation between the size of the distribution range and the evolutionary rate in speciation; this may be the reason why the E. prasina group (restricted to a small part of the generic range) is more diverse than the E. chabrieri group which is distributed over the entire generic range.

Molecular clocks and Miocene palaeogeography enlighten the evolutionary history of *Dolichopoda* cave crickets in the Mediterranean area

Giuliana Allegrucci[1] **and Valerio Sbordoni**[1]
[1]*Department of Biology – University of Rome Tor Vergata- Rome, Italy*

Molecular phylogenetic divergence and historical biogeography of cave crickets belonging to the genus *Dolichopoda* (Orthoptera, Rhaphidophoridae) have been investigated by partly sequencing three mitochondrial and one nuclear genes. In particular, we sequenced 1967 base pairs of mitochondrial DNA, representing three fragments of the small and large subunit of ribosomal RNA (16S and 12S rRNA) and the subunit I of cytochrome oxidase (COI). We also included 581 base pairs of nuclear DNA representing a fragment of the large subunit of

ribosomal RNA (28S rRNA). Forty five species (i.e. most of the known *Dolichopoda* species occurring from Pyrenees to Caucasus Mountains) collected across the entire range of the genus were analyzed.

The present study revealed a rather well resolved phylogeny at species level, identifying a number of clades that represent long separated lineages and diverse evolutionary histories within the genus *Dolichopoda*. Four main clades were revealed within the genus, one identifying the western Mediterranean species, two the Hellenic–Aegean species, and one the most eastern species. The two Hellenic-Aegean clades included a north-western and a south-eastern species group. Based on Bayesian analysis, we applied a relaxed molecular clock to estimate the divergence times between the lineages. The results revealed that the origins of eastern Mediterranean lineages are much older than those of western Mediterranean *Dolichopoda*. Tests of alternative biogeographic hypotheses showed that a double colonization of the Hellenic Peninsula, following separate continental and trans-Aegean routes during the Messinian stage, best accounts for the present distribution of Greek *Dolichopoda* species. In particular, the southern lineage probably arose from a trans-Aegean colonization during the Messinian salinity crisis (5.96–5.33 Ma). The northern lineage could be the result of dispersal from the north through the Balkan Peninsula. The opening of the Mid-Aegean trench could have promoted an initial diversification within the uprising Anatolian plateau, while the Messinian marine regression offered the conditions for a rapid dispersal through the whole Aegean–Hellenic region. In addition, climatic events during the Plio-Pleistocene may have been responsible for the speciation within each of the different phylogeographic units, principally attributable to vicariance events.

Phylogeography and population genetics of swarming grasshoppers

Marie-Pierre Chapius[1]
[1]*School of Biological Sciences, University of Sydney, The Macleay Building A12 Sydney, NSW 2006, Australia*

Population studies focusing on neutral sequence variation are recurrently cited as promising candidates to assess the population structure and dynamics of outbreaking insect populations. These questions remain, however, largely unstudied in locusts, in part because of the difficulty of getting suitable molecular markers at both phylogeography and population genetics levels. Undetected intra-individual variation in mitochondrial DNA (as well as in nuclear ITS) sequence data is particularly common in grasshoppers and can confound phylogeographic analyses. The popular and versatile microsatellite loci are prone to both (i) multiple banding amplification patterns due to high similarity between their flanking regions and (ii) high prevalence of null alleles in Orthopteran species. In order to better develop operational microsatellite markers in locusts, we studied the distribution patterns and the molecular evolution of the similar microsatellite-containing sequences repeated within the genome both within and among species of the Orthoptera. In order to comprehensively describe the genetic variation within and among populations of locusts, we assessed null allele effects on statistics and methods traditionally used to analyse microsatellite variation and, in some cases, developed adapted statistical tools for genotype analysis. These works enabled us to build a comprehensive picture of the population genetic structure of two major locust species, the cosmopolitan *Locusta migratoria*, and the Australian-endemic *Chortoicetes terminifera*. Firstly, we assessed the role of the propensity to outbreak in shaping the

worldwide and regional patterns of population genetic variation in *L. migratoria*. Secondly, we showed an absence of genetic differentiation between *C. terminifera* populations from Western Australia and the four Eastern states of Australia, which have been monitored independently, largely assuming low connectivity between populations from both sides of the continent. We used computer simulations and literature survey with the aim to better consider the implications of our molecular genetics findings with respect to spatial population dynamics and management of locusts.

ORTHOPTEROOMICS: Unravelling the link between Orthopteran genomes and phenotypes

Organizer: Gregory Sword
Ataturk Conference Hall (14:15-16.30 / June 23, 2009)

The use of the Desert locust (*Schistocerca gregaria*) transcriptome to analyse to mechanisms of behavioural phase change

Stephen M. Rogers[1], Heleen Verlinden[2] and Swidbert R. Ott[1]
[1]*University of Cambridge, UK*
[2]*Katholieke Universiteit Leuven, Belgium*

The radical transformation between solitarious and gregarious phases in the desert locusts (*Schistocerca gregaria*) encompasses extensive changes in behaviour, physiology, and morphology, underpinned by changes in gene expression. A major challenge in understanding phase change is linking the plethora of genetic changes revealed by emerging genomic technologies to the cascade of cellular and molecular processes that occur during transformation. Our recent work has concentrated on the process of behavioural gregarization, the first and quickest step in the process of swarm formation. A broad sweep analysis of changes in neurochemistry during the entire process of phase change, whilst underlining the extensive changes between phases, revealed that serotonin increased dramatically in the window during which gregarization is established. We have since shown that serotonin is sufficient and necessary to cause behavioural gregarization. We are now collaborating with colleagues at the University of Leuven using EST data, microarray analysis and double stranded RNA constructs to trace how this initial serotonin-mediated stage of gregarization leads to sustained changes in behaviour and physiology. Our initial efforts have concentrated on Protein Kinase A (PKA) known to be a downstream effector of serotonin and Protein Kinase G (PKG), implicated in behavioural plasticity in many other animals. We have used a combination of classic pharmacological intervention and RNA interference to demonstrate that PKA is indeed critical to the acquisition of gregarious behaviour. We found no evidence that PKG has any role in these early stages of gregarization. Long-term gregarious locusts do however contain significantly more PKG in their brains than do solitarious locusts. These data show how the wide scope of genomic analysis can be brought to bear on specific mechanisms underlying physiological change.

Phase differences in brain size and allometry of brain regions in the desert locust

Swidbert R. Ott[1] and Stephen M. Rogers[1]
[1]*University of Cambridge, UK*

Desert Locusts (*Schistocerca gregaria*) show extreme phenotypic plasticity in response to changes in population density, transforming between a solitarious phase that avoids other locusts and a gregarious phase that forms cohesive groups. We investigated whether these very different life styles are reflected in the size of the brains and the relative proportion of neuropile regions of known function within it. Neuropile volumes were measured in brains of male locusts, immunofluorescence-stained against synapsin and optically sectioned by wholemount confocal microscopy. Allometry between neuropile regions was analysed using reduced major axis regression. The total brain neuropile was 1.27x larger in gregarious males, whereas their body weight was only 0.79x that of solitarious males. The phases showed pronounced differences in brain proportions. These arose in part from allometric growth in brain size but there were some marked departures from allometric expectation in some regions. Allometry resulted in a 0.89x smaller optic lobe: midbrain ratio in gregarious locusts. The

medulla however was 1.16x larger than in solitarious animals of corresponding lamina size, and there was an allometry-driven 1.07x expansion in lobula per unit medulla. There was an extreme phase difference in the olfactory neuropiles, with gregarious locusts having a 1.41x larger primary calyx: antennal lobe ratio. Their antennal lobe: brain ratio was 0.87x lower due to a departure from allometric expectation, whereas their primary calyx: brain ratio was 1.22x higher but largely in line with allometric expectation. The accessory calyx and central complex both showed a non-allometric expansion in gregarious brains. Our results demonstrate phenotypic plasticity in absolute and relative investment into (metabolically costly) brain tissue. Solitarious locusts have smaller brains and invest relatively more into low-level sensory processing, possibly to gain sensitivity. Gregarious locusts have larger brains and prioritise higher integration, possibly reflecting the greater complexity of their environment.

Locust EST databases: applications in the post genomic era

Gert Simonet[1], Liesbeth Badisco[1], Heleen Verlinden[1], Elisabeth Marchal[1], Jurgen Huybrechts[1] and Jozef Vanden Broeck[1]
[1]K.U.Leuven

While locusts are particularly well-known as swarm-forming pest insects, their considerable scientific merits as useful research models for the study of insect endocrinology, neurobiology and phenotypic plasticity tend to be underweighted. Locust plasticity is typically characterized by the occurrence of two opposite phenotypes; the solitary, harmless phase and a gregarious swarming phase. Intrigued by this phenomenon, scientists have purified nearly 100 biologically active regulatory peptides from locusts. However, in spite of these efforts, the molecular and physiological events underlying the process of locust phase transition still remain elusive. Moreover, novel molecular strategies to complement previous studies on locust physiology were hindered by the lack of sequence data. Therefore, in order to compensate for the absence of locust genome data, an EST (‘Expressed Sequence Tags') database representing transcripts (mRNA/cDNA) from the central nervous system of *Schistocerca gregaria* was produced in a collaborative effort with the W.M. Keck Center for Comparative and Functional Genomics. Data management and annotation of this high-throughput EST sequencing project was achieved by a specifically designed web-application (ESTIMA), generating a collection of 12,774 unique, high quality sequences. This database complements a previous EST database from *Locusta migratoria*, which was based on whole body transcripts. As a result, a large data set, covering 20746 unique locust transcript sequences, is now at our disposal. This sequence information allows for modern proteomics and (high-throughput) transcriptomic approaches, enabling a large-scale molecular dissection of (phase-related changes in) physiological processes. Custom microarrays, incorporating the full set of unique transcripts from *S. gregaria* and *L. migratoria*, have been designed (eArray platform, Agilent) and an initial study of the genes that are differentially expressed between gregarious an d solitary adult locusts is currently under investigation. In addition, the use of dsRNA-mediated gene silencing was found to be a powerful complementary methodology, facilitating a more detailed functional characterization of locust genes.

RNA interference in desert locusts

Heleen Verlinden[1], Swidbert Ott[2], Rut Vleugels[1], Julie Tobback[1], Steve Rogers[2], Malcolm Burrows[2] and Jozef Vanden Broeck[1]
[1]*K.U. Leuven*
[2]*University Of Cambridge*

The desert locust, *Schistocerca gregaria*, can undergo a density-dependent phase transition between a cryptic solitarious and a swarming gregarious phase that differ in many aspects of behaviour, physiology and morphology. The first characteristic that changes during phase transition is behaviour. The gregarious behaviour is triggered within the first two hours of forced crowding. This reflects conditions in nature where they come together because sources have become rare, and thus the gregarious phase is necessary to migrate to more favourable places. During this period in which the behavioural changes occur, a substantial but transient rise in the amount of serotonin can be measured in the thoracic ganglia (Rogers et al. 2004). This rise was shown to be necessary as well as sufficient to induce the behavioural change (Anstey et al. 2009). Serotonin is a biogenic amine that plays a prominent role in influencing multiple physiological events. It exerts its effects by binding to specific proteins that among others belong to the superfamily of G protein-coupled receptors (GPCRs) and share the structural motif of seven transmembrane domains. Most of these GPCRs transmit the signal to protein kinases, which phosphorylate other effector proteins. We picked up partial sequences of a serotonin receptor (putative 5-HTR-1A) and two protein kinases (PKA and PKG) with degenerated primers. We also found the sequence of the regulatory subunit of PKA-C1 in the EST-database of *S. gregaria*. We studied the expression pattern of these factors in the solitarious and the gregarious phase and during phase transition in *S. gregaria* using qRT-PCR. We also looked at the possible effects of RNAi of these factors on the behavioural phase change.

Proteomics: another approach to tackle locust phase polyphenism

Jurgen Huybrechts[1], Bar Boerjan t[1] and Liliane Schoofs [1]
[1]*K.U. Leuven, Belgium*

Locust phase polyphenism is an intriguing example of phenotypic plasticity. It is subject to profound studies by several research groups for decades. Bit by bit the mechanism is explored but it is still not quit well understood and surrounded with a veil of mystery. Recently it turned out that peptides could trigger responses similar to phase related changes and that a biogenic amine is playing an important role as well. Since phase changes occur at the organismal level we expect to see an impact of phase change on the hemolymph protein content as well. Two dimensional differential gel electrophoresis, 2D-DIGE, is an elegant way to visualize the protein content or the proteoom as it is called from a given tissue or blood sample. Thus far we succeeded in optimizing the protocols for the analysis of both hemolymph and tissue samples of the two phases of the desert locust, *Schistocerca gregaria*. This means that we are able to extract proteins in a quantitative and qualitative manner and produce reproducible gels. The bottleneck however remains the absence of genomic information of the species under study. Indeed, the successful identification of high numbers of protein spots, in *Drosophila melanogaster* for example, basically relies on the available

genomic databases by means of peptide mass fingerprinting (PMF). Using PMF it is sufficient to make a tryptic digest of a protein and measurement of the generated fragments by means of mass spectrometry. Based on the peptide mass pattern it is possible to identify the parent protein. For the locust proteins an additional, time consuming, step is required: amino acid sequencing of the generated tryptic peptides. This can also be done on the mass spectrometric instruments but again the absence of genomic information hamper the sequencing of these peptides. Despite these drawbacks the first proteins are being identified.

COMMUNICATION and ORTHOPTERA

Chair: Klaus-Gerhard Heller & Long Zhang
Ataturk Conference Hall (11:15 – 12:45 / June 24, 2009)

Acoustic communication in katydids: mechanisms, evolution, and evolutionary mechanisms

Johannes Schul[1]
[1]*Biological Sciences, University of Missouri, USA*

The acoustic communication system in the genus *Neoconocephalu*s displays an enormous diversity in male calls and female call recognition mechanisms. We study the evolutionary mechanisms leading to this diversity, focusing on one call trait, the pulse pattern. Among 25 species, five produce calls with a distinct double pulse pattern, with pairs of closing pulses separated by a longer silent interval. Phylogenetic analyses indicate that the double pulse pattern is derived and evolved in *Neoconocephalus* at least 4 times independently from the ancestral single pulse pattern. We comparatively analyzed the call recognition mechanisms of the 5 species with double pulse patterns and of several species with the ancestral pulse pattern. Females of species with single pulse calls evaluate the silent interval between pulses; calls are attractive when the interval is shorter than a species-specific value. In three of the five species with double pulse patterns the novel call pattern is required for call recognition: these species evaluate the rate of the double pulses in male calls. The mechanisms used to evaluate the rate differ among the three species, indicating that they evolved independently from the ancestral state in each species. Females of the other two species with double pulses retain the ancestral call recognition mechanism. The derived call pattern neither increased or decreased the call attractiveness for females, indicating that males may initiate diversification of the acoustic communication system driven by forces other than sexual selection. The encoding of relevant call parameters in the ascending auditory pathway differs among species, as revealed by neurophysiological experiments. Modeling of call recognition in hypothesized brain neurons suggests that even complex temporal selectivities can be generated by intrinsic properties of neurons. The qualitative differences of the call recognition mechanisms among species could be due to small differences in the ion-channel composition of brain neurons.

The biophysical basis of tonal sound production in Ensifera

Fernando Montealegre-Z[1]
[1]*School of Biological Sciences, University of Bristol, UK*

Some ensiferan males (katydids, crickets and mole-crickets) produce advertisement calls by rubbing their forewings or tegmina together. They exhibit two main mechanisms of sound production: resonant and non-resonant. This talk will review the mechanisms of stridulation used to achieve pure-tone songs in the wide range of frequencies exhibited by different species of Ensifera. One part of the talk will address how pure-tone songs made by tegminal stridulation require the integration of wing movements, stridulatory file design and resonant properties of the wing (effected by complex wing morphology). Even when the songs of some Ensifera appear tonally pure, many species exhibit a certain degree of frequency modulation (FM). The mechanisms that lead to FM will also be discussed. From an evolutionary perspective, I will consider scaling effects of the sound generator on song parameters.

Some aspects of cellular and molecular mechanism of locust chemoreception

Long ZHANG[1]
[1]*China Agricultural University, China*.

Like other insects, locust has developed a sophisticated chemoreception in evolution. Through detecting environmental chemical signals locust adapts to various and complex environments. And locust behaviors, such as forage, aggregation, migration and mating are always relating with locust plague outbreaks, and may be caused by chemical information. Studying on chemoreception mechanism is helpful to understand the locust's behavior and to control locust behavior. We found that there are several types of chemosensilla on antenna palp, tarsi and wings of locust, *Locusta migratoria manilensis*. They are *Sensillum chaetica*, *Sensillum basiconica*, *S. trichodea*, *S. ceolconica*, last three belong to olfactory *Sensillum*. All of the four types of *Sensillum* are on antenna, *S. chaetica* and *S. basiconica* on palp, whereas on wings and tarsi only *S. chaetica*, though there are several subtypes of this *Sensillum*. Therefore, antenna is the most important organ for detecting volatile odors. The responsive patterns of S. trichodea have been characterized using single *Sensillum* recording technique. There are at least 5 responsive patterns of *Sensillum trichodea* and indicating that there several functional subtypes of the *Sensillum*. And there are 2-3 neurons in each subtype *Sensillum trichodea*. We first identified an odorant-binding protein (LmigOBP1) from locust in 2003. And the protein has 130 amino acid, its molecule weight is about 14.8 kDa and pI 4.7. This protein starts to express at 0.5 hr before hatching in embryo, and since then it has been expressing for all developmental stages. This protein specifically expresses in *Sensillum trichodea* and *S. basiconica* lymph, implying that the protein plays an important role in olfaction. We have investigated the ligand-binding specificity of LmigOBP1 using 67 volatile odor compounds. Fluorescence assays indicate that LmigOBP1 does not bind fecal volatiles or green leaf odors, but shows high affinity for some linear aliphatic compounds, with pentadecanol and 2-pentadecanone being the strongest binding ligands. A 3-dimensional (3D) model of LmigOBP1 was built by homology modeling. Docking simulations based on this model suggested that Asn74 of LmigOBP1 is a key binding site, and this was validated by site-directed mutagenesis and fluorescence assays. We suggest that, as a general rule, a hydrophilic amino acid at the entrance of the binding cavity participates in initial recognition of ligands, and contributes to ligand-binding specificity of OBPs.

Physiological basis of the sub-lethal effects of the desert locust pheromone phenylacetonitrile (PAN)

Torto Baldwyn [1]
[1]*icipe, Box 30772-00100, Nairobi, Kenya*

Pheromone communication in the desert locust *Schistocerca gregaria*, the most notorious migratory agricultural pest in Africa has been previously studied. Exploitation of sub-lethal concentrations of one of its pheromones, phenylacetonitrile (PAN), as a disruptive agent of grouping in non-PAN producing gregarious juveniles has also been studied, but little is known about the underlying physiological and behavioral effects of PAN on juveniles. Mass spectral analyses show that juveniles exposed to the pheromone absorb it through their cuticle, which causes a marked shift pheromonal titer at its storage site to levels that appear toxic to the

juveniles. While the pheromone is not detected in the haemolymph, mass spectral analyses also indicate there appears to be a hormonal imbalance in the haemolymph due to exposure to the pheromone. Behavioral observations indicate that exposure to the pheromone reduces mobility and feeding in exposed juveniles, strongly indicating that it exerts a toxic effect on juveniles. These results suggest a possible stress effect of the pheromone on juveniles.

INTEGRATED PEST MANAGEMENT for LOCUSTS and GRASSHOPPERS: Are alternatives to chemical pesticides credible?

Organizer: Michel Lecoq
Ataturk Conference Hall (09:00-10:45/ June 24, 2009)

Credibility of an IPM approach for locust and grasshopper control: the Australian example

David Hunter[1]
[1]*125 William Webb Drive, ACT 2617, McKellar, Australia*

The search for alternatives to the widespread use of chemicals to control locusts and grasshoppers in Australia has led to the development of the mycopesticide Green Guard®, which has as its active ingredient the FI-985 isolate of the fungus *Metarhizium anisoplae* var. *acridum*. Green Guard has played an important part in the IPM of locusts and grasshoppers in Australia, and has included use in large scale control operations, with nearly 100,000 ha treated since operational use began in 2000. Most has been applied in environmentally sensitive areas and on properties in locust source areas in inland Australia that produce organic beef for export. There have been some additional uses as part of a desire to reduce chemical residues in commercial products: in vineyards that produce wine for export, generally only biological control of locusts is permitted. However, Green Guard still accounts for less than 10% of the area treated for locust and grasshoppers. Green Guard costs more than chemicals and mortality is slow when temperatures are mild. While Green Guard causes >90% mortality of locusts within 6-10 days when it is very hot (maximum temperatures 37-42 C), mortality is often slightly less (80%) and is slower (2 weeks or so) when it is mild. But a most important factor limiting the uptake of Green Guard is a lack of biological control products for most pests, so that there is still the widespread use of chemicals that results in chemicals being present in most products and in most environments. Perhaps in the future, when biological control products are available for many more pests, Green Guard use will expand to become a substantial part of locust and grasshopper control.

Progress in incorporation of *Metarhizium* into IPM / preventive control

Harold van der Valk[1]
[1]*Independent consultant, Werkendam, The Netherlands*

The entomopathogenic fungus *Metarhizium anisopliae* var. *acridum* (isolate IMI 330189) has been field-tested against the Desert Locust (*Schistocerca gregaria*) since the mid-1990s. These field trials have shown that adequate control is achieved at a dose rate of 2.5 x 1012 conidia/ha (50 g conidia/ha), which appears fairly robust over a range of environmental conditions encountered in Desert Locust control. Although commercial formulations of the biological control agents have been available for some time, operational use of *Metarhizium* against the Desert Locust has been very limited thus far. This is partly due to the lack of regular control targets, but also because of constraints of biological (e.g. temperature limitations), operational (e.g. speed of action, shelf-life, application requirements, cost) and psychological (e.g. limited trust in biological control agents, high political pressure for quick and visible control solutions) nature. The possibilities and limitations of the use of *Metarhizium* for the control of the Desert Locust are discussed, assessing its advantages and constraints in the light of different types of control situations and external environmental or economic requirements. It is concluded that *Metarhizium* is an effective complement to the use of chemical insecticides against the Desert Locust. However, its use is likely to remain

very limited unless regulatory or financial incentives are applied to promote its inclusion in Desert Locust control campaigns.

Does bird predation enhance the impact of Green Muscle for grasshopper control - Experiences from cleared woodland in Central Senegal

Wim Mullie[1]
[1]*Fondation Agri pour l'éducation et la santé, BP 6792, Dakar, Sénégal*

In ornithological literature two hypotheses circulate relating population fluctuations of Palaearctic migrant birds to migratory locusts and to locust control. Both hypotheses will be shown to be unlikely and two alternatives will be proposed: the first is that grasshoppers in adult diapause are both certain and widely available prey in the Sahel, representing annually an important part of the diet of acridivorous bird species. The second is that biopesticides used to control acridids, under certain conditions, attract rather than deter acridivorous birds. The latter may act synergetically with the impact of the biopesticide. A large-scale field trial was conducted in October 2008 in a formerly protected sylvo-pastoral reserve of which 55 400 ha had been cleared between 1991 and 2004 for groundnut production. Two dosages of Green Muscle (*Metarhizium anisopliae* var. *acridum)* were sprayed under experimental conditions on six 400 ha plots, whereas three controls remained unsprayed. The results showed that daily removal rates of grasshoppers from sprayed plots in the first three weeks post-treatment increased ten-fold from 0.01 to 0.1%. In control plots this remained stable at a level of 0.01-0.03%. In the following three months, grasshopper removal rates from all plots increased until they all reached a ceiling of about 1% daily. This remained stable for another two months when observations seized. The increase of grasshopper removal was the result of a reduction in grasshopper availability rather than of an increase of predator numbers. However, it is conceivable that the slow recovery rate of the grasshopper community on treated plots was the result of bird predation, which thereby enhanced the impact of *Metarhizium*. Only by excluding birds from fields their impact can be reliably assessed. White Stork (3500), Cattle Egret (5000), Lesser Kestrel (5000) and Montagu's Harrier (6000), were identified as the main predators during the dry season.

Pheromonal control of the desert locust: lessons learned and future prospects

Torto Baldwyn [1]
[1]*icipe, Box 30772-00100, Nairobi, Kenya*

The effect of the desert locust adult pheromone phenylacetonitrile (PAN) on juveniles of the locust was carried out in field studies in Port Sudan, Sudan, with a view to developing a methodology, so called 'preventive control strategy' for use against small to medium size populations of juveniles. A number of interesting facts were learnt in this study: (1) PAN applied at 10 ml/ha at a volume rate of 2 L/ha is effective in disrupting grouping and promoting cannibalism in treated juveniles, (2) at this dose and volume rate, the pheromone does not alter the viability of the grasshopper biopesticide 'Green Muscle' (GM) when

combined with it, (3) a quarter of the recommended dose of GM +PAN is as effective as the recommended dose of GM used alone, (4) similarly, a quarter of the recommended dose of the insecticide fipronil or Marshal + PAN is also as effective as the recommended dose of either insecticide used alone, and in general (5) predation by natural enemies contributes significantly to the mortality found in treated juveniles. Ecotoxicological studies suggest that these treatments have no significant adverse effects on desert arthropods. Future prospects will look at developing these preventive control strategies for use against other locust species, and their possible integration with climate-based early warning systems into more effective coordinated rapid response systems.

SPECIAL SESSION

SEXUAL SELECTION in ORTHOPTEROID INSECTS

Organizer: Karim Vahed
Mediko SKS Hall (11:15 – 12:45/ June 25, 2009)

What is wrong with good genes sexual selection?

John Hunt
University of Exeter, U.K.

The "good-genes" hypothesis is one of the most widely invoked explanations for the evolution of female mate choice. A more specific form of the good-genes hypothesis, known as the age-based indicator mechanism, posits that females who mate with the oldest male(s) in the population will receive "good-genes" as these males have already proven their viability. Consequently, longevity is often viewed as a signal of genetic quality. Using phenotypic and genetic data from experiments on the native Australian field cricket, *Teleogryllus commodus*, we will demonstrate that this is not always the case. In particular, we will discuss how the acquisition and allocation of resources and genotype-by-environment interactions may obscure the true relationship between longevity and genetic quality. Our findings illustrate that (*i*) issues of genetic quality need to be examined within the appropriate life-history and quantitative genetic framework, (*ii*) more rigid experimental data are needed to test the generality of "good-genes" models of sexual selection and (*iii*) there are unlikely to be any universal signals of genetic quality.

Prolonged copulation following spermatophore transfer in bushcrickets is associated with reduced nuptial gift mass and modifications in the form and use of the males' cerci

Karim Vahed[1]
[1]*University of Derby, U.K.*

Male crickets and bushcrickets (Orthoptera: Ensifera) exhibit a range of behaviours that have been interpreted as functioning to deter the female from interfering with ejaculate transfer. These behaviours include feeding the female a spermatophylax and prolonged copulation following spermatophore transfer (PCFST). The hypothesis that these traits are analogous in function predicts that, across taxa, relative spermatophylax size will be reduced in species with PCFST. The aims of this study were to test this prediction and to examine qualitatively differences in the structure and use of the male's cerci (which are used to grasp the female) between species with and without PCFST. Data on ejaculate (ampulla) mass, spermatophylax mass and the duration of copulation following spermatophore attachment were obtained for a range of species of Tettigoniids. Species regression revealed that, as predicted, relative spermatophylax mass (in relation to ampulla mass) was reduced in species with PCFST. There was also a positive relationship between ejaculate volume and the duration of copulation following spermatophore transfer across species with PCFST. Such species also showed clear modification in the structure and/or the use of the males' cerci. The occurrence of PCFST in a few members of at least seven different Tettigoniid sub-families strongly suggests that this behaviour has evolved independently several times within this family.

The interspecific dimension of sexual selection: how reliable are specific mate recognition systems in Orthoptera?

Axel Hochkirch[1]
[1]*University of Trier, Germany*

The songs of grasshoppers, crickets and katydids are usually thought to act as specific mate recognition systems. Indeed, the taxonomic value of Orthoptera songs is high and a number of morphologically cryptic species have been described based upon their distinctive songs. These songs are often so different that most scientists believe that they represent an effective barrier to hybridization. However, male Orthoptera are often not very choosy and may attempt to copulate with any potential mate. As in most other animal species, the females are thought to be the choosy sex. Nevertheless, even females may choose a wrong male if its receptivity is high or conspecific males are not available. We performed several experiments with different species pairs to test, if interspecific sexual interactions (reproductive interference) between Orthoptera species exist. All tested species pairs engaged in heterospecific interactions although to a different degree. *Tetrix ceperoi* males attempted to mate with *Tetrix subulata* females, but they were usually rejected. This decreased the number of conspecific matings in *Tetrix ceperoi* significantly and also the reproductive success of this species. *Tetrix subulata* males preferred females of *Tetrix undulata* and some heterospecific matings (but no hybridization) have been observed, which decreased the number of conspecific copulations in *Tetrix subulata*. Females of *Chorthippus montanus* clearly preferred conspecific males, but females of *Chorthippus parallelus* were indiscriminate. In this case, heterospecific matings also led to hybridization, which might explain why these two species only rarely co-occur at the same site. Our results show that species boundaries are rather fluent and that the communication behaviour of Orthoptera does not represent a complete barrier. In fact, it is likely that sexual interactions among species strongly determine the local and global distribution of Orthoptera.

Titillators in bushcrickets as sexually selected devices

Gerlind U.C. Lehmann[1]
[1]*Institute of Biology/Zoology, Free University Berlin*

In animal evolution, the general trend for the morphology of male genitalia is rapid divergence compared to other structures. It has been proposed that either sexual selection by cryptic female choice or sexually antagonistic co-evolution might be largely responsible for this pattern. In bushcrickets, grasping of females for copulation is generally achieved by a male's cerci, functioning as non-genital claspers. Internal structures, termed titillators, may function as genital claspers. We compared titillator complexity and mating durations (between coupling and spermatophore transfer) in a large number of European, and to a lesser extent, Australian species from six bushcricket subfamilies. Titillators were present in five of the six subfamilies studied, but not in the Phaneropterinae. Copulation durations from initial coupling to final spermatophore transfer were much longer in species possessing titllators. Family-wise comparison also showed that copula duration and spermatophore size were strongly linked within the titillator possessing Tettigoniinae, but not in the Phaneropterinae. However, no correlation was found between titillator complexity and either copula duration or

spermatophore size within the Tettigoniinae. Our data support the notion, that internal genitalia might be subject to sexual selection as their occurrence is associated with prolonged copula duration. Copula duration in turn is linked to spermatophore size, at least in the Tettigoniinae. Whether copulation duration is primarily under male or female control in the Tettigoniidae remains to be investigated.

Phenotypic integration as a constraint on call evolution

Will Pitchers[1] and John Hunt[1]
[1]*University of Exeter in Cornwall, Falmouth, UK*

Phenotypic integration refers to the patterns of covariance between functionally related traits. Complexes of traits that are strongly integrated expose only certain trait combinations to selection and hence constrain the direction of trait evolution. The question is these intrinsic developmental constraints or the products of genetic architecture? In *Teleogryllus commodus*, a widely distributed field cricket, we found that call traits differ geographically. However, the covariance structure of calls is conserved across populations, despite differing selection regimes measured through female choice experiments. This covariance structure is also conserved across diet regimes, suggesting that the integration is not subject to condition dependence. We crossed populations to measure the relative contributions of additive versus non-additive genetic variation to call traits, and experimentally increased thermal stress during development to measure canalisation.

SESSIONS

BIOGEOGRAPHY

Oral Presentations

Chair: Hojun Song
Ataturk Conference Hall (11:15 – 12:45/ June 24, 2009)

Biogeography of Orthoptera of the Palaearctic region: relationships between the Mediterranean and steppe territories

Michael G. Sergeev[1]
[1]*Novosibirsk State University, Novosibirsk, Russia*

Orthoptera is an important and relatively diverse group in the southern parts of the Palaearctic. These insects can be extremely abundant in the steppes, semi-deserts and deserts. During outbreaks some of them damage local agricultural fields and rangelands. Global warming can result in changes of their distribution and ecological significance. The aim of this presentation is to analyze orthopteran relationships of two wide areas of the Palaearctic, the Mediterranean and Scythian (Steppe) Subregions, with regards to possible changes during global warming. The Mediterranean Subregion is characterized by high levels of orthopteran diversity and endemism. In its western part, there are many endemic katydids and grasshoppers (e.g., see *Amphiestres* Fieber, *Acinipe* Rambur, *Cophopodisma* Dovnar-Zapolskij, et al.). The mountains of the East Mediterranean are also characterized by many endemic forms (see *Ancistura* Uvarov, *Paranocarodes* I. Bolivar, *Oropodisma* Uvarov, et al.). The level of endemism in the Scythian Subregion is relatively low. The list of local endemics and subendemics includes the only genus *Miramella* Uv. and about 40 species. However, the analysis of ecological and geographic distributions allows us to hypothesise that more than 60 species originated from this area. Many subfamilies, tribes and genera are common in the Mediterranean and Scythian Subregions. Almost all of them are widely distributed in the southern parts of the Palaearctic. Several taxa evidently associated with the Mediterranean Subregion extend into the Scythian Subregion. Some genera (mainly gomphocerine grasshoppers) could move from the steppe life zone to the Mediterranean Subregion. The process of species invasions became especially significant during the last decades due to global warming and local human activities. This has resulted in changes of orthopteran diversity, population and assemblage distributions, and in their long-term dynamics. These studies were supported by the RFBR (07-04-00341) and the Russian Federal Education Agency (2.2.3.1/1557).

Analyses of cpnl-I nuclear dna sequences from Anatolian populations of the meadow grasshopper *Chorthippus parallelus* (Orthoptera, Acrididae, Gophocerinae)

Ertan Mahir Korkmaz[1], **Serdal Arslan**[1], **Battal Çıplak**[1] **and Hasan Hüseyin Başıbüyük**[1]
[1]*Department of Molecular Biology & Genetics, Faculty of Science & Literature, Cumhuriyet University, 58140 Sivas, Turkey*
[2]*Department of Biology, Faculty of Science & Literature, Akdeniz University, Antalya, Turkey*
[3]*Department of Biology, Faculty of Science & Literature, Cumhuriyet University, 58140 Sivas, Turkey*

Anatolia is one of the most important refugia of glacial ages and probably a centre for many Palaearctic species. In addition to being a refugium in the Pleistocene glacial ages, Anatolia harbours significant intra- and/or interspecific genetic diversity due to its various topography and climate. Therefore, an investigation on population dynamics of species distributed in Anatolia is very important from the evolutionary point of view. We studied the widely distributed species, *Chorthippus parallelus* (Orthoptera, Acrididae, Gomphocerinae), whose

population structure is relatively well-known in Europe, but data on Anatolian populations is largely absent. In this study, specimens of *C. parallelus* are collected from different localities of Anatolia. Genomic DNA for ten populations was isolated and a non-coding nuclear DNA fragment was amplified. The sequence data was analysed using several population genetics and phylogeny programs. Total haplotype diversity and the average within-population diversity proved high. However, the level of differentiation among populations is low. The most genetically diverse population includes a great number of unique haplotypes. These results suggest presence of high genetic diversity relative to other previously studied refugial populations of Iberia, Italy and Greece. Moreover, it provides a good example to a rear edge population.

Establishing a phylogeographic analogy between global warming and interglacials for cold demanding refugial taxa: a case study on south-west Anatolian species *Poecilimon birandi*

Sarp Kaya[1], Islam Gunduz[2] and Battal Ciplak[1]
[1]*Department of Biology, Faculty of Art & Science, Akdeniz University Antalya, Turkey*
[2]*Department of Biology, Faculty of Art & Science, Ondokuz Mayis University Samsun, Turkey*

One of the main consequences of present warming is population fragmentation. Defining range changes during past interglacials may provide tools to understand fragmentations due to global warming. To test this assumption we studied *Poecilimon birandi*, a species confined to South-west Anatolia that demands cold climate. A 536 bp fragment of 16S rRNA gene was sequenced in 79 specimens from 13 sampling localities; 5 individuals of *Poecilimon luschani* and 4 of *P. tuncayi* (Denizli) were also included in the analyses as outgroups. We found 28 haplotypes (including indels) of *P. birandi* in three main phylogroups (Western, Eastern and Demre). There are no shared haplotype between three phylogroups. Results ofF-statistics suggest strong isolation not only between phylogroups but also between local populations. Although there is strong isolation between phylogroups, each of them nonetheless harbor considerable haplotype diversity. These analyses suggest the following conclusions: (i) there are at least three co-temporal radiations, each of which are probably from an isolated refugial ancestral populations present in lowlands during the last glaciation, (ii) *Poecilimon birandi* harbors considerable genetic diversity that may allow it to survive under a changing climate, (iii) since *P. birandi* is present at both low- and high-lands, but still prefers a similar low temperature, it might have changed its phenology during warming through Holocene, and (iv) although changing climate may threatened present Anatolian biodiversity, past climatic fluctuations appear to have contributed to its species richness.

Diversity and distribution patterns of Orthoptera in the Altay Mountains

Michael G. Sergeev[1], Jirong[3], Valentina M. Murav'eva[4] and Nadezhda E. Hudiakova[4]
[1]*Novosibirsk State University, Novosibirsk, Russia*
[2]*Institute of Systematics and Ecology of Animals, Novosibirsk, Russia*
[3]*Xinjiang Normal University, Urumqi, Xinjiang, China*
[4]*Gorno-Altaisk State University, Gorno-Altaisk, Russia*

The Altay (Altai) Mountains are situated in the central part of Eurasia. This mountain system is a significant geographic and biogeographic barrier that divides both the western and eastern parts of the Palaearctic and its different life zones, such as the forest, steppe, semi-desert and deserts. There are at least 130 species of Orthoptera, 6 of which are endemics to these mountains. An analysis of species distributed in different geographic regions of the Altay Mountains shows that the northern, western and central parts of this region are inhabited by species more or less widely distributed either in the Palaearctic or in the steppe zone. The so-called southern Altay (mainly in Kazakhstan, between the Bukhtarma and Kaba Rivers) and south-eastern Altay are characterized by the occurrence of some semi-desert and desert species associated with the adjacent territories of Kazakhstan (in the southern Altay) or Mongolia (in the south-eastern Altay). The orthopteran insects of the north-eastern Altay are widely distributed in the Palaeartic, especially through its boreal territory. The Mongol Altay (the large southern part of the mountains) is not similar to other regions of the Altay. There are a lot of desert Orthoptera, some of which are found in the upper altitudinal belts. The general distribution of Orthoptera in the Altay Mountains shows that one of the main factors determining the species distribution is the distribution of life zones. Thus, the species distribution through the mountains resembles that of the plain territories. This suggests that global warming may result in spreading of Orthoptera in the Altay Mountains not only to higher elevations, but also northwards. These processes may also influence by well developed mountain slopes and river valleys that may be used as corridors for species spreading. This study was supported by the RFBR (07-04-00341, 08-04-92228) and the Russian Federal Education Agency (2.2.3.1/1557).

Sharing observations via internet; building a community for faunistic data

Baudewijn Odé[1], Roy Kleukers[1] and Luc Willemse[1]
[1]*European Invertebrate Survey, Netherlands*

Many orthopterologists live in areas with a well-known fauna. Data often include recent comprehensive distribution data that are sufficient for example for establishing red list assessments and conservation programmes, as well as being useful for spatial analyses (e.g., in search of the effects of climate change). In those well-researched countries not only are collection-based data often used, but such data are also validated with observation data in national distribution databases. Consequently, many of the faunistic challenges are found in countries without a history of faunistic research, which in Europe include most of the southern and eastern countries. These countries not only need more collections made and collections researched but also more observation data. Several initiatives to collect observation data via internet applications have began, which include field computers with GPS to facilitate data collection in the field. WNPDA in combination with the website observado.org is an application for the Windows Mobile forum. It was used in Turkey in the week preceding the ICCO congress. The type of data collected includes species name, locality (latitude, longitude), date, time, sex, stage and number of individuals, as well as noting whether a specimen is collected. This method of collecting observation data is very useful for species that the observer is already familiar with. For example, distribution data has been collected for species that are easily recognised by their appearance or song, which would otherwise be difficult to catch or are present in many places. After uploading the observations to the central database

they are available via internet along with extra information, such as photos and sound recordings. Although the results are quite good for observations of well-known species, WNPDA is not sufficiently equipped for collecting observation data for species without a properly given name in the field that are only collected for further examination and determination. The described initiative provides an easy way to store ones observations to be edited or extracted where needed. Observation data might be used by others in several ways, such as a kind of excursion planner for a region of interest. This could be of great importance for starting orthopterologists or students. Initiatives should focus on raising data collection initially for the country where the observations have been done. Validation is an issue to be tackled by international species-group specialists or with a growing national knowledge by national specialists that are embedded in a potentially growing community of professional of otherwise skilled orthopterologists.

New and little-known tettigoniids from southeast Ecuador

Holger Braun
Illinois Natural History Survey, University of Illinois

The katydids (Tettigoniidae) fom two recent surveys in the Zamora-Chinchipe province of Ecuador will be presented. The first area, comprising lower-elevation mountain rainforest in 800-1500 m at Maralí (a little upstream of El Pangui in the Río Zamora valley) was visited in January 2009. The second site is located in the upper Río Nangaritza valley in the southeasternmost part of the country and will be visited in April 2009, after the writing of this abstract. In Maralí were found female, male, and tiny nymphs of a new species of colour-polymorphic little walking leaf, belonging to the genus Typophyllum (Pterochrozini, Pseudophyllinae), a new brachypterous genus of Eucocconotini (Pseudophyllinae) with unusual and rarely performed calling song, and two more new species of Pseudophyllinae. In addition *Loja laevis* (Conocephalinae), which has not been reported since its description by Giglio-Tos in 1898, and other interesting and insufficiently studied species were discovered. Faunistic comparisons of the two field sites, separated by 60-70 km, will be briefly considered.

BIOGEOGRAPHY
Poster Presentations

PP01

Distribution of endemic Orthoptera species in Anatolia: a statistical approach

Deniz Şirin[1], Abbas MOL[2] and Battal Çıplak[1]
[1]*Department of Biology, Faculty of Arts and Sciences, Akdeniz University, Antalya, Turkey*
[2]*Department of Biology, Faculty of Arts and Sciences, Ondokuz Mayıs University, Samsun, Turkey*

Endemism of the Orthoptera (Insecta) species of Turkey was evaluated. Our data and related literature about the Orthoptera of Turkey were combined for analysis. Of the 624 Orthoptera species recorded from Turkey 297 (47.5%) are endemic, of which 207 (69.5%) belong to Ensifera and 91 (30.5%) belong to Caelifera. These endemic species were grouped into four different clusters according to their distribution in phytogeographic provinces: Irano-Anatolia (IA), Mediterranean (MD), Euxin (EU) and Mesopotamia (MP). The similarity of provinces based on shared endemic species was evaluated with biodiversity analyses. Results of the analyses suggest that IA is most similar to MD and that IA+MD is more similar to EU than MP. The maximum diversity of species was observed in IA with 140 species, followed by MD with 131 species, and EU with 87 species. The minimum diversity was found for MP with 12 species. The proportion of local endemic species distributed in IA, MD, EU and MP was % 44.5, % 33.5, % 19.9 and % 2.1 respectively. The two provinces with the greatest endemic species diversity are also the areas with the highest number of summits (i.e., points higher than 1000m) with a total of 495 different elevations. These results indicate to two general conclusions. First, IA, EU and MD exhibit a typical Palaearctic fauna, whereas MP has a more Ethiopian composition. Second, the Anatolian fauna, and specifically, the high diversity appear to be related to the highly variable topography of the region.

PP02

Orthoptera and orthopterology in the Czech Republic: current stage of knowledge

Jaroslav Holusa[1] and Petr Kocarek[2]
[1]*Czech University of Life Sciences, Czech Republic*
[2]*University of Ostrava, Czech Republic*

The Czech Republic has a long tradition in entomological research and the research on Orthoptera is not an exception. The first works dealing with Orthoptera were published around the mid of 19th century (Seidl, 1836, Fieber, 1853). Several others works were published by the turn of the 19th and 20th century (e.g., see the works of Krejčí, Haury & Nickerl, Czižek, Zacher). The first comprehensive treatment of orthopteran insects of the Czech Republic was published by Obenberger (1926). Later, Dobšík (1959) treated the order Orthoptera within the series Key to the fauna of Czechoslovakia. A complete list of species found in the Czech and Slovak Republics was compiled by Mařan & Čejchan (1977) and later by Kočárek et al. (1999). The recent comprehensive publication by authors Kočárek, Holuša and Vidlička (2005) summarises the current stage of knowledge and it is the background of extensive mapping project with goal to prepare the first atlas of species distributions. The book is forwarded by regularly actualised web pages (Kočárek, 2005) with current faunistic information, check-list, bibliography, images and sounds database, and above all, an on-line interactive determination keys. Ranging from single records to thorough faunistic treatments of some areas and/or taxonomical groups, faunistic data are scattered in more than 300 papers

(Holuša et al., 1999). Notwithstanding, the faunistic knowledge of Orthoptera is still poor, many bioregions of the Czech Republic are not sufficiently known and we have still many "white places". The reason is especially the absence of amateur entomologists, who are principally collectors of faunistic data – as we can see in other currently well known groups of insects (e.g., Lepidoptera, and Odonata). The knowledge level depends very much on this sampling effort. There was found statistically significant correlation between numbers of new recorded species and number of publications in ten years periods. So far, 98 orthopteran species are known in the Czech Republic. Four of them were newly documented for the fauna since the year 2000. Another five species also very probably occur in the Czech Republic and are awaiting discovery. In contrary, at least nine species are extinct in the Czech Republic and have not been observed more than fifty last years.

PP03

Synthèse biogéographique de Schistocerca gregaria (forsk., 1775) en mauritanie - cartographie de 7 acrido-régions

Mohamed Abdallahi Babah Ebbe[1], Marie Françoise Courel[2], Alex Franc[3], Sidi Ould Ely[1] and Jean François Duranton[3]

[1] *Centre National de Lutte Antiacridienne Nouakchott Mauritanie*

[2]*Ecole Pratique des Hautes Etudes – Paris*

[3]*Cirad-UPR50, Baillarguet, Montpellier, France*

The National Desert Locust Control Center of Mauritania has started the storage of the Desert Locust data available since the 1960s. More than 55,000 records, each corresponding to one surveyed site, are gathered into a chrono- and geo-referenced database, whose structure copies the RAMSES/FAO database. The most important part of the database consists of the records form the last 20 years. The spatial analysis of locust occurrences in relation with phase (i.e., solitarious, transiens, gregarious), phenological stage (hopper, imago), season and global locust situation (i.e., recession, outbreak, upsurge and plague) resulted in the definition of consistent locust areas for the annual achievement of the locust biological cycle, or "Locust eco-regions". These Locust eco-regions reflect the Desert Locust biogeography on the Mauritanian territory: 1. A summer breeding area for solitary (July-September), 2. An intermediate summer-autumn breeding area for solitary (July-September and/or October-December), 3. An autumnal breeding area for solitary (October-December), 4. An autumnal and winter intermediate breeding area for solitary (October-December / January-March), 5. A winter breeding area for solitary (January-March / April-June), 6. A breeding and\or dispersal area for gregarious (all the year), and 7. a hostile area only suitable for migrations, Majabât El-Koubra. It was demonstrated that locust gregarisation can only occur within restricted hot spots and during some specific periods; the Locust eco-regions 3, 4 and 5 appear as essential for the understanding of the initial stages of the gregarisation process. Our spatial results can now direct field surveys operations, improve their performance and reduce their cost.

PP04

"Cave-crickets" *Troglophilus neglectus* (Krauss, 1879) (Orthoptera: Rhaphidophoridae) in the Czech Republic

Robert Vlk[1]

[1]*Department of Biology, Faculty of Education, Masaryk University, Brno, Czech Republic*

"Cave-crickets" of the genus *Troglophilus* were discovered in the Czech Republic for the first time ten years ago (Holuša et al., 1999). The described population is distributed in a small area in the central part of Moravia. Initially, the crickets were misidentified as *Troglophilus cavicola* (Kollar, 1833) although their external identification characters corresponded with those of *T. neglectus*. Afterwards, another population was discovered and correctly identified (Chládek et al., 2000) in the north-western part of Bohemia very close to the border with Germany. In the same year, "cave-crickets" *T. neglectus* were also discovered for the first time in Germany (Zinke, 2000) in the neighbouring localities distributed on the Czech side of the border. Therefore, there are two isolated populations of *T. neglectus* in Czechia, both situated very far away from the northest edge of the continual area of distribution in southern Austria (Carinthia and Styria). *T. cavicola* is also distributed more northwards, where the most nothern population is widespread across many recent localities near south-western suburbs of Vienna. Both aforementioned Czech populations of *T. neglectus*, as well as three other central-european populations discovered in different parts of Germany (published 2000-2001), have some interesting characteristics: (1) they are very isolated, (2) they are parthenogenetic, (3) they do not inhabit karstic areas, but instead landscapes built of different grounds, such as slates or sandstones, with lack of larger underground cavities. The current author's project, based on the analysis of mitochondrial DNA (16S rDNA and COI markers), should be useful in resolving the origin and taxonomical status of these populations. They could represent relict cryptic species (or subspecies), or possibly descendants of some individuals introduced from southern parts of Europe.

PP05
The acridien population of the high plateaus of Setif (Algeria)

Z. Sofrane[1] and A. Harrat [2]
[1] Departement of Biology, Faculty of Sciences, University Ferhat Abbas, Setif, Algeria
[2] Laboratory of biosystematic and ecology of the arthropods, Department of Sciences of nature and the life, Faculty of Science of nature and the life, Mentouri University, Constantine, Algeria.

To have knowledge as complete as possible on acridien diversity motivated this study on the high plateaus of Setif, which are located at the North-East of Algeria and are characterized by a semi-arid climate. This work revealed the presence of three families, Acrididae with 22 species, Pamphagidae with 7 species and the family of Pyrgomorphidae with 3 species. Analysis of the dominance of the acridien species revealed that dominance varied depending on the type of environment. Calculation of the Shannon-Weaver and equitability indices showed that the stations of study represent diversified and well-structured settlements. The study of the type of spatial distribution shows four types characterize the species inventoried: regular, random, uniform, and contagious. This last type is most remarkable. By means of the principal components analysis, we noted that the collected species are distributed according to their ecological affinity.

PP06

Distribution and habitats of *Arcyptera microptera* (Fischer Von Waldheim, 1833) in its western area-margin (Central-Europe, Western-Hungary)

Zoltán Kenyeres[1], Norbert Bauer[3] and Barnabás Nagy[2]
[1]*Acrida Conservational Research L.P., H-8300 Tapolca, Deák F. u. 7., Hungary*
[2]*Plant Protection Institute of the Hungarian Academy of Science, Department of Zoology, H-1525 Budapest, P.O. Box 102., Hungary*
[3]*Hungarian Natural History Museum, Department of Botany, H-1087 Budapest, Könyves K. krt. 40., Hungary*

Arcyptera microptera is a widespread, Eurasian, thermo- and xerophytic locust species. In Russia it is known as a damaging, but non-gregarin steppe species, that sometimes brings agricultural harm to cultivated fields. To the contrary, in Central-Europe and towards the west *Arcyptera microptera* is a rare species with isolated occurrences. In Hungary there were little data before our study on the distribution and occurrences of the species was carried out in the Bakony Region (Western-Hungary). Results showed that habitats of *Arcyptera microptera* are restricted to dry grasslands found in a middle mountain-boundary zone (202–342 metres altitude, mostly on dolomite bedrock and black turf soil). The most robust populations were observed in grasslands characterized by heterogenous vegetation structure (mixture of outcrops, patches of fleet and deep soil etc.). Within this habitat type, the presence of the species was not typical neither in closed grasslands (vegetation cover more than 80%), nor in open grasslands (vegetation cover below 40%). Short-grass steppe grasslands with open soil (deep) surfaces are suitable for the *Arcyptera microptera* to colonize. The requirement of incompact soil is probably due females laying their eggs deeper in the soil than other locusts. Habitats of *Arcyptera microptera* are usually characterized by disturbances (mostly former or current military training areas). Based on these results we were able to considerably increase our knowledge about the distribution of *Arcyptera microptera* in Hungary. Ten new records (average distance of 6.7 kilometres between the localities) from the Bakony Region were explored. Two further previous records were confirmed. We presume that *Arcyptera microptera* occurs in the Wiener Basin–Lower Moravian Plain, foreland of the North- and Eastern-Carpathians and Transylvanian Middle Mountains. Intensive field work in May and June is proposed, because of the early hatching of the species.

PP07

Intraspecific variation and the phylogeography of the lubber grasshopper, *Romalea microptera* (Orthoptera: Acrididae)

Serap Mutun[1] and David W. Borst[2]

[1]*Abant İzzet Baysal University Faculty of Science and Arts Department of Biology Bolu Turkey*
[2] *Department of Biology University of Central Florida 4000 Central Florida Blvd Orlando, FL USA*

The lubber grasshopper, *Romalea microptera (=guttata*), is an endemic species to the southern part of the United States. A 420-bp region of the mitochondrial cytochrome b gene sequence data of 168 individuals collected from 12 sites in the southern United States were

used to explore population genetic structure and gene flow, intraspecific phylogeography, and the effects of the last glacial ice age on the genetic structure of this low mobile species. Analyzed populations contained 49 mtDNA haplotypes. A high level of genetic diversity was observed in these populations (3.8%), most of which was due to variation within populations. The highest genetic variation was found in a northern Florida population (collected at St. Marks, FL) and the lowest was found in a southern Florida population (Copeland, FL). The most divergent mtDNA haplotype were found in the northern Florida, however, the results did not support the hypothesis that this haplotype was not a refuge haplotype; instead it could indicate retained ancestral polymorphism. The statistical analyses related to the estimates of historical and current population sizes also indicated that most of the lubber populations have undergone drastic declines in size at some point in the past. In contrast to previous studies on several other species in this region, statistical results, phylogenetic analyses (PAUP) and haplotype age phylogenies (PHYLIP) indicated that the *R. microptera* populations showed no major geographic structure of the genetic diversity. This may result from the absence of long term barriers for the dispersal of this species. Alternately, the distribution of this species in the past may have been homogeneous, rather than the patchy distribution that is currently observed. Either of these might have contributed to the lack of a genetic structure divided geographically into east-west groupings that is seen in other species from this region.

PP08

Distribution Patterns of Orthopteran Assemblages in urban ecosystems of the south-eastern part of West Siberia

Michael G. Sergeev[1], Oksana V. Efremova[2], Olga N. Skalon[3]
[1]*Novosibirsk State University, Institute of Systematics and Ecology of Animals, Novosibirsk, Russia*
[2]*Novosibirsk State University*
[3]*Kemerovo State University*

Taxonomic diversity of Orthoptera and their assemblages distribution patterns were investigated in the urban ecosystems of several cities in the south-eastern part of West Siberia (Novosibirsk, including Academgorodok), Kemerovo, Novokuznetsk, Leninsk-Kuznetskii) from 1979 until 2008. Most Orthoptera penetrate the urban ecosystems from the adjacent similar habitats. There are two typical ways of formation of orthopteran assemblages in these cities: (1) gradual transformation of the assemblages of natural meadows (meadow steppe > forest-park meadows > lawns of outer spaces of cities > lawns of inner parts of cities), and (2) long-distance migrations. The conditions of the forest-steppes are extremely favorable for the Orthoptera penetration. The outskirts of lawns in this life zone may appear favouring outbreaks of some grasshoppers. Long-term changes in diversity are also described. Local populations of some species (e.g., *Podisma pedestris*) were eliminated, on the contrary, spreading of some species (e.g., *Dociostaurus brevicollis*, *Oedipoda caerulescens*, *Phaneroptera falcata* et al.) are established. This distribution patterns may be explained both by changes in local human activities and by global warming. This studies was supported by the Siberian Branch of the Russian Academy of Sciences (grant No 10), RFBR (07-04-00341, 08-04-92228) and the Russian Federal Education Agency (2.2.3.1/1557).

PHYSIOLOGY, MORHOLOGY, DEVELOPMENT

Oral Presentations

Chair: Marcos Lhano
Mediko SKS Hall (11:15 – 12:45/ June 23, 2009)

Acoustic morphology of Ensiferan signal production

Glenn K. Morris[1]
Department of Biology, University of Toronto at Mississauga, 3359 Mississauga Road Mississauga, ON L5L 1C6 Canada

Some insect cuticle is adapted for transduction of airborne sound. Among Ensifera such structures are nominally part of the tegmina, yet other adjacent body regions are also involved: pronota and thoracic tergites for example. How can one recognize cuticle adapted for making sounds? Size, mass, shape, thickness, flexibility, stiffness, elasticity, surface area etc. are important features of structures effecting adaptive sound radiation. The carrier frequencies of the signals are influenced by the overall size of the insect and by the size of its radiating membranes. Tegminal cells have their mass reduced to transparent speculae and are adaptively loaded by adjacent air masses, defined and delimited by pronotal chambers, tergite recesses, projecting shelf-like wing veins etc. Broadcast fields are affected by pronotal shape, short-circuiting by costal folds. Once one is able to recognize morphology that has been shaped by adaptive sound radiation, it becomes apparent that the diversity of such structural modifications among Tettigoniidae is greatly underestimated. This paper attempts to characterize morphological adaptations for sound production in acoustic Ensifera that point the way for future bioacoustic study.

Cricket brain neurons – song pattern recognition and control of walking

Maja Zorovich[1] **and Berthold Hedwig**[1]
[1]*National Institute of Biology, Ljubljana, Slovenia*
[2]*University of Cambridge, Cambridge, UK*

During auditory communication in crickets, silent females walk towards singing males. Two fundamental processes underlie this behaviour: the female must recognize the song of conspecifics and localize its source in space. Cricket calling song is made up of chirps, which are repeated at 500 ms intervals. It was previously assumed that recognition of the song pattern takes place before localization, but the findings by Hedwig and Poulet (Nature 430, 2004; JEB 208, 2005) have revealed that the females start steering with a latency of 55-60 ms after the onset of the first chirp, which is well before any pattern recognition could have taken place in the brain recognizers. Further behavioural investigations revealed that pattern recognition gates this unselective rapid steering (Poulet and Hedwig, PNAS 102, 2005). We described morphology and functional properties of three types of local auditory neurons that connect left and right sides of the brain and branch in the lateral accessory lobes. Based on their response latencies, filtering characteristics and coding of the temporal pattern, we propose their putative roles in the process of song recognition and localization. We have also developed an apparatus that enabled us to record the activity of single brain neurons in a behaving cricket. Using this set-up, we described several descending auditory neurons that control walking and/or turning.

Comparative study of peptides from the female's accessory glands and oocytes of solitary and gregarious *Schistocerca gregaria*

Amel Ben Hamouda[1], Mohamed Ammar[2], Arnold De Loof[3], Abderrahmen Bouain[1] and Mohamed Habib Ben Hamouda[4]
[1] *Faculty of Sciences of Sfax, Tunisia*
[2]*National Institute of Agronomy of Tunis, Tunisia*
[3] *Zoological Institute, Naamsestraat 59, 3000 Leuven, Belgium*
[4] *Biological Sciences and Plant Protection Department, Agronomics Sciences Institute of Chott Meriam 4042-Sousse, Tunisia*

Peptides content of the female's accessory gland and eggs was studied in crowded (gregarious phase) and isolated (solitary phase) *Schistocerca gregaria* adults using chromatographic and immunological techniques. Quantitative differences were found in the presence of a peptide with a retention time of 37.20 min. Its presence in much higher concentrations in the crowd-reared (gregarious) phase than in the isolated-reared (solitarious) one suggests a role in phase polyphenism. This result was confirmed by immunoelectrophoresis assay; an antiserum was raised against the gregarious and solitarious extract of female's accessory glands shows a supplementary precipitin arc in gregarious phase. An additional western blot analysis was successfully done in gregarious and solitary oocytes shows a supplementary band with 17KD in gregarious oocytes, absent in the solitary ones. This concordance in our results shows that there was a gregarizing factor transmitted from the gregarious *S. gregaria* mothers to their progeny.

Mercury effects on the development and reproduction of *Oxya fuscovittata* (Marschall)

Parimalendu Haldar[1], Chandrik Malakar[1] and Arijit Ganguly[1]
[1]*Entomology Research Unit, Dept. of Zoology, Visva-Bharati University, Santiniketan, West Bengal, India*

Grasshoppers have a great ecological significance as they are the main protein source of many vertebrate animals. Marked effects on ecosystem may be observed if any change occurs in their population dynamics. In the past decade mercury had been increasingly taken up by the plants and transferred further up the food chain especially in the industrial areas. In the present study newly hatched nymphs were fed on foods treated with three sublethal concentrations of $HgCl_2$ (i.e. 3 ppm in green food & 20 ppm in oat or dose 1, 5 ppm in green food & 40 ppm in oat or dose 2 and 8 ppm in green food & 80 ppm in oat or dose 3) until the end of adult life for two consecutive generations (F1 & F2). Toxicological observations were followed in F1 and in the F2 generation derived from mercury fed F1 adults. Total developmental period of F1 generation were longer with the increase of doses. The F2 generation followed similar trends with much more severity. Mortality of nymphs was higher in F2 generation. Fresh body weight of both males and females decreased proportionately with the increase of doses in both generations. Females of the F2 generation fed with highest dose of mercury in food were unable to lay eggs due to shorter adult life span. For both generations number of egg pods laid by females and the number of eggs in each pod decreased with the increase of mercury doses. Here also F2 generation showed more severe results. Youngs hatched from the eggs of F1 parents were higher in number than the young's

from F2 parentrs. The above observations give an idea that mercury has a chronic effect on the development and reproduction of *O. fuscovittata*.

Development of the subsoephageal body cells and the pericardiac cells during embryogenesis with diapause in *Locusta migratoria* (Linnaeus, 1758) (Orthoptera: Acrididae)

Abboud Harrat[1], Jeanne Raccaud-Schoeller[2]and Daniel Petit[3]
[1] *Université Mentouri/Constantine, Faculté des Sciences de la Nature et de la Vie, Département de Biologie Animale, Laboratoire de Bio-systématique et Ecologie des Arthropodes, route d'Aïn-El-Bey, Constantine, Algérie. E-mail: abboud52@yahoo.fr*
[2] *Université Pierre et Marie Curie Paris 6, Laboratoire de Physiologie des Insectes, 4 Place Jussieu 75252, Paris-Cedex 05, France.*
[3] *UMR INRA 1061, Faculté des Sciences et Techniques, Université de Limoges, 123, av. A. Thomas, 87060 Limoges-Cedex, France.*

During *Locusta migratoria* embryogenesis, the yolk is progressively degraded and the resulting metabolites are released in the haemolymph. We researched the organs possibly involved in the uptake of haemolymphatic proteins. Among organs originated from mesoderm, the SOB (suboesophageal bodie) situated in the embryonic head, are remarkable by a very early acquisition of differentiated cytological characters, while most other cells of the embryo are undifferentiated. The SOB quite disappears before hatching. Just before katatrepsis stage, the other organs derived from mesoderm begin to differentiate, including the PC (pericardial cells) which takes over from the SOB. These cells, situated in thorax and abdomen, are developed during the dorsal close of embryo. The development and the ultrastructural changes of the SOB cells and of the PC were studied during an embryogenesis with diapause. The morphology of embryos which enter diapause is comparable with that of a continuous development at the beginning of katatrepsis. However, the cells of SOB and PC cells suffer from remarkable changes not only physiologically but cytologically. At the beginning of diapause, the proteosynthetic activity practically disappears in the SOB cells and the lysis areas appear. Nevertheless, the exchanges between these cells and the haemolymph still remain important. For the period of cold, which is necessary to the resumption of development, the aspect of the SOB cells changes and in particular the areas of lysis become less wide. When the embryo reopens its development, the SOB cells show a proteosynthetic activity and the areas of lysis disappear. The changes of the SOB cells and of the PC cells are regularized during the resumption of the development: the SOB cells which had taken again a normal activity start to regress from the stage VII on, while the PC cells take over.

Comparative study on the immature stages of three *Hieroglyphus* species (Acrididae: Orthoptera) from Pakistan

Rıffat Sultana[1] and Muhammad Saeed Wagan[1]
[1]*Department of Zoology, University of Sindh, Jamshoro Pakistan* 76080

Hieroglyphus Krauss is among the most economically important pest of rice, sugarcane, wheat, maize and minor pest of millets and fodder crops in Pakistan. Presently immature stages of *Hieroglyphus perpolita* (Uvarov), *H. oryzivorus* Carl and *H. nigrorepletus* I. Bolivar were studied under the laboratory conditions during the years 2005-2007 from Pakistan. The first instar hatched in the form of vermiform larva. In both sexes, normally there are six moults and six larval stages the adult being the seventh stage. Hoppers usually emerge during June-July as soon as monsoon begins. Sex ratio was extremely in the favour of females in all the species studied. Inner side of hind femur with tinge of red or orange red colour was reported in *H. perpolita;* on contrary it was light green in *H. nigrorepletus*. Posterior margin of pronotum was recorded almost straight in *H. oryzivorus* while it was obtuse angular in *H. perpolita*. Morphometric studies on the immature stages of these three species showed that there was significant differences in the measurement of different body parts as well as all instars are also slightly differ with each other. The total average developmental period from first instar up to the last instar was recorded 5.964±1.29 days for *H. perpolita,* 7.442±1.51days for *H. oryzivorus* and 5.386±0.88 days for *H. nigrorepletus*. Study of life-history, including life-span, development time, and sex ratio contributes importantly to our understanding of these insect species.

PHYSIOLOGY, MORHOLOGY and DEVELOPMENT

Poster Presentations

PP09

Insecticidal activity of alkaloids of *Pergularia tomentosa* (Asclepiadaceae) on 5th instar nymphs of the migratory locust *Locusta migratoria*

Fatma Acheuk[1], Bahia Doumandji-Mitiche[2], Karima Ait Kaci[1] and Fethia Fazouane[1]
[1]*Université de Boumerdes, Faculté des Sciences, Département de Biologie, Boumerdes, Algérie*
[2]*Institut National Agronomique, El-Harrach, Alger, Algérie*

The migratory locust *Locusta migratoria* in its various gregarious forms is a frightening acridid. The control of grasshoppers in Algeria has been based exclusively on chemical insecticides, however, as these compounds are known to be harmful to the environment, it require to find other alternative methods. Since works by Fraenkel (1959) and by Philogène (1989), it is well-known that the plants rich in secondary metabolits are able to control the harmful populations of insects. Accordingly, the use of extracts of plants equipped with insecticidal activities offers a potentiality in plant protection. Encouraging results were obtained both in laboratory and in natural conditions with botanical substances. The aim of this preliminary study was to investigate the effect of alkaloidic extract of *Pergularia tomentosa* on some biological parameters of the 5th instar larvae of the migratory locust *Locusta migratoria*. The preliminary results indicate that the alkaloids extract of *P. tomentosa* exhibited insecticidal activity when ingested to newly larvaes 5th instar. It is anti appetant, caused weight loss and exerts a similar effect has that of the growth regulators on the cuticle. On the digestif tract, the action was marked on the level of the stomodeum and mesenteron. The results obtained in the present study suggest that it may be possible to use natural substances extracted from local plants to protect grazing areas in the short term, and eventually, this may lead to production of new, more efficient and less noxious control agents.

PP10

Leaves action of *Olea europea* (Oleaceae) and *Cestrum parquii* (Solanaceae) on cuticle and brain of desert locust, *Schistocerca gregaria* Forsk. (Orthoptera, Acrididae)

Ammar Mohamed[1], Ben Hamouda Amel[2] and Ben Hamouda Med Habib[2]
[1]*National Institute of Agronomy of Tunisia, Tunisia*
[2]*High Institute of Agronomy of Schott Mariem Sousse, Tunisia*

Olea europea leaf powder added at 2% in an artificial diet resulted in a partial inhibition of cuticle genesis of desert locust, *Schistocerca gregaria*. This inhibition is expressed by a cuticuline and wax layers narrowing at the epicuticle level which may explain the soft aspect of integument and the persistence of juvenile colour until mature stage. Whereas, the brain structure at this stage, doesn't show apparent modifications due to the olive leaf powder effect. In the case of *Cestrum parquii* leaf powder at 2%, the cuticle structure of 5th instars larvae is highly modified. In the absence of exuvial space, the layers of the new procuticle did not develope entirely and the old cuticle reduced partially. The brain of these larvae has a totally modified structure compared to the control. The neurosecretory cells and the globuli show a highly developed vacuole system and pycnotic nucleus. The brain is flooded by gigantic vacuoles between these cells. These observations indicate toxic effects of *Cestrum* leaf powder.

PP11

The study of the effect of entomopathogenous *Beauveria bassiana* on cuticle biochimesry and structur of *Schistocerca gregaria*

Fatma Halouane[1], Fatma Zohra Bissad[1] and Bahia Doumandji-Mitiche [2]
[1]*Biology Departement, Boumeres University, Bumardas, Algeria*
[3]*Agronomic Institut of Elharrach, Algier, Algeria*

The application of *Beauveria bassiana* on the cuticule of 5th hopper instars and adults of *Schistocerca gregaria* result in a significant reduction in the dry weight of the cuticule as well as in the chitin and proteins contents (respectively from 36.5mg to 32.9mg, 7.4mg to 6.4mg and 29.1mg to 26.5mg for the 5th instars, and from 46.5mg to 42.3mg, 7.4mg to 4.2mg 39.1mg to 37.9 for the adults). The application produce an obvious disruption in the structure of the cuticle. On the 3rd day post treatment one could observe a complete disappearance of the epicuticule and a clear reduction in the exo and endocuticule thickness in comparison with the control. The destructuration of the cuticular layers in the larvae treated is probably the result of a degradation by proteolytic and chitinolytic enzymes from the fungus.

PP12

Action of diflubenzuron on ecdysteroid levels in ovary and in eggs of the locust *Schistocerca gregaria*

Ghania Tail[1], Patrick Porcheron[2], Bahia Doumandji-Mitiche[3] and Catherine Blais[4]
[1]*Département de Biologie, Faculté des Sciences Agro-Vétérinaire, Université Saad Dahleb, 09000 Blida, Algérie*
[2]*UMR 1272 UPMC-INRA- AgroParis Tech Physiologie de l'Insecte, Signalisation et Communication, UPMC, 7, quai Saint Bernard 75005 Paris*
[3]*Département de Zoologie Agricole et Forestière, Institut National Agronomique, 16200 El-Harrach, Alger, Algérie*
[4]*FRE2852 UPMC-CNRS, Groupe Biogenèse des stéroïdes, UPMC, case 29, 7 quai St Bernard 75005 Paris, France*

The insecticide diflubenzuron (DFB), a benzoylphenyl urea, was tested on female of *Schistocerca gregaria*. The objective of this study was firstly to see the action of DFB on ovarian ecdysteroid levels in females after its ingestion for 24h by *Schistocerca gregaria*. The compound reduced ovarian ecdysteroid titres of the first ovarian cycle. DFB action on eggs ecdysteroid levels in females was also evaluated. In laid eggs of *S. gregaria* females, we measured ecdysteroid content before and after enzymatic hydrolysis, to compare free and conjugated ecdysteroids in control eggs and after DFB treatment. DFB significantly ($P< 0.02$) reduced the levels of both free and conjugated ecdysteroids, about three times, compared to the control.

PP13

Can nymphs of *Cornops aquaticum* (Bruner, 1906) (Acrididae, Leptysminae) be determined by their terminalia?

Marcos Gonçalves Lhano[1] and Marinêz Isaac Marques[2]
[1]*Federal University of Reconcavo of Bahia, Center of Agricultural, Environmental and Biological Sciences - Cruz das Almas, BA, Brazil*
[2]*Federal University of Mato Grosso, Institute of Biology - Cuiabá, MT, Brazil*

Cornops aquaticum (Bruner, 1906) (Acrididae: Leptysminae: Tetrataeniini) is a semi-aquatic grasshopper distributed from Northern Mexico (23° N) to Central Argentina and Uruguay (35° S). It is a medium size green grasshopper (2,5 to 3 cm body length) with black and yellow longitudinal lateral stripes on the sides of the body. *Cornops aquaticum* lives on Pontederiaceae, mainly on *Eichhornia* spp., where it develops all its life cycle and feeds on the epidermis of these plants. The waterhyacinth is one of the worst weeds in the world and this grasshopper species is considered a potential agent for biological control of this plant. In general, the species has 5 development instars with blue and red longitudinal stripes along the lateral of the body. Morphological and anatomical diagnosis and drawings to identify each instar and to determine the sex is provided herein. Nymphs from the Brazilian Pantanal (16°18' S, 56°32' W) were studied under a binocular stereomicroscope with a drawing tube and the terminalia of males and females (dorsal, ventral and lateral view) of all instars were drawn.

EVOLUTION

Oral Presentations

Chair: Theodore Cohn
Ataturk Conference Hall (11:15 – 12:45/ June 24, 2009)

Late Mesozoic and early Caenozoic stages in the evolution of Orthoptera

Andrej V. Gorochov[1]
[1]*Zoological Institute, Russian Academy of Sciences, Russia*

Transition from Mesozoic stage of orthopteran evolution to Caenozoic one took long period from Upper Cretaceous to possibly Paleocene. Majority of orthopteran families, characteristic of Early Cretaceous Mesophytic landscapes, are very rare in Upper Cretaceous deposits because development of Caenophytic landscapes with domination of angiosperms around large water reservoirs (dinosaur's pastures). In latter landscapes, only family Gryllidae firstly appeared instead Baissogryllidae characteristic for analogous landscapes without angiosperms in Early Cretaceous. Some other groups of Orthoptera are preserved in Mesophytic forests on watersheds. In Paleocene after disappearance of dinosaur's pastures, they begin to occur in water deposits more often. These groups (primitive Tettigoniidae and Stenopelmatoidea) are not identical to their Jurassic and Cretaceous ancestors, but they have very similar coloration imitating leaves of gymnosperms. Possibly, evolution of these groups had place mainly in forests with domination of gymnosperms. In Eocene and Lower Oligocene deposits, Tettigonioidea and Stenopelmatoidea are very rare again. It may be connected with development of mammal's pastures around large water reservoirs, as in Baltic amber (formed in forests), both these groups are well presented. Mass penetration of Tettigonioidea in grasslands near water reservoirs possibly had place not early than in Middle Oligocene only. Eumastacoidea and Acridoidea penetrated such landscapes somewhat early, in Middle Eocene (first group) and in Early Oligocene (second group). Since Early Oligocene, Eumastacoidea were replaced by Acridoidea in grasslands.

Testing for selective divergence in a caribbean cricket (genus *Amphiacusta*)

Elen Oneal[1] and L. Lacey Knowles[2]
[1]*Duke University, USA*
[2]*University of Michigan, USA*

Species distributed on oceanic islands provide an opportunity to examine the process of radiation and the factors influencing population divergence. One question that remains unanswered is the relative importance of natural and sexual selection, versus stochastic processes such as genetic drift, for population and species divergence. An explicit test for selective divergence can be performed by comparing phenotypic divergence in a quantitative trait to a neutral expectation generated from neutral genetic markers. This test for selective divergence in two ecological traits (body size and mandible shape) and one sexual trait (genitalia shape) was performed with a species of ground cricket, *Amphiacusta sanctaecrucis*, distributed throughout the Virgin Islands. A comparison of phenotypic and neutral genetic variance suggested that selection, rather than drift-induced divergence, has driven differentiation in these traits. The finding that selection has played the dominant role in the divergence of island populations of *Amphiacusta sanctaecrucis* has implications for our understanding of the mechanisms driving diversification of the highly species-rich genus *Amphiacusta throughout* the Caribbean.

Ensifera phylogeny: we are not out of the woods yet

Frédéric Legendre[1], Tony Robillard[1], Hojun Song[2], Michael F. Whiting[2] and Laure Desutter-Grandcolas[1]
[1]*Muséum national d'Histoire naturelle, Dept. Systématique et Evolution, Paris, France*
[2]*Brigham Hugh University, Department of Biology, Provo, USA*

There is a huge emphasis today on phylogeny, because it provides a coherent and refutable hierarchical system which can be used to derive classification systems and test evolutionary hypotheses. Because of this high heuristic and practical value, phylogenetic hypotheses should be carefully evaluated before being used. Current methodology offers two complementary criteria to estimate phylogeny robustness, i.e. support indices (Bremer support, Jackknife) and sensitivity analysis. While considerable progress has been made in phylogenetic systematics for several insect orders, Orthoptera, and especially Ensifera, lags behind in adopting an explicit and robust classification scheme. Very few phylogenetic hypotheses have been built for Ensifera from the analysis of a well-specified data matrix using explicit algorithm. Morphological hypotheses were built for high-level terminals, which monophyly was not always ascertained. Actually the only extended data set assembled up to now to study Ensifera phylogeny is the molecular matrix of Jost (2002) and Jost & Shaw (2006). As evolutionary biologists looking for a phylogenetic frame for classification and evolutionary studies, we reanalyzed Jost and Shaw' data set, to test the robustness of hypothesized relationships. We used both traditional analyses with a static alignment using parsimony and a Bayesian approach, and the Direct Optimization algorithm for tree reconstruction with dynamic alignment procedure. In the latter we designed a sensitivity analysis to evaluate the robustness of the resultant clades and calculated Bremer and Jackknife support values. Our results show that most classically recognized groups have high support values and are stable to variation in parameter costs and/or methods, except those dealing with wetas and Jerusalem crickets. Actually, most were already supported by morphological and behavioural synapomorphies. By contrast, relationships above family level are ill-defined, as the present data set is not informative at this level. Sensitivity analysis is used to evaluate the classificatory systems proposed by several authors for Ensifera.

Phylogeography and fine-scale genetic structure in *Podisma kanoi*: insights from landscape genetic approaches

Haruki Tatsuta[1], Izumi Yao[2] and Shin-ichi Akimoto[2]
[1]*Graduate Schol of Agriculture, University of the Ryukyus, Okinawa, 903-0213, Japan*
[2]*Graduate School of Agriculture, Hokkaido University, Sapporo, 060-8589, Japan*

One way to study gene flow is to identify genetic units and the environmental features that are responsible for the differentiation of these units, hence deducing which features restrict or promote movements of individuals. Recently, the development of Bayesian clustering methods has enabled the detection of genetic units using genotypes of individuals as the sole source of information. Based on the related methods, we aimed to investigate the delimitation of genetic units in the apterous grasshopper, *Podisma kanoi*, which is distributed in Echigo mountain range on Honshu, Japan. Because the distribution of the species is limited to the area of high altitude and its habitat is spatially fragmented, the species is considered a relict of

the glacial epoch. We explored the population genetic structure based on microsatellite genotypes that were detected using six primer combinations. When all samples from seven local populations were pooled, five of six loci showed lower observed heterozygosities than expected, suggesting the incidence of inbreeding due to population fragmentation. Bayesian clustering methods revealed that an easternmost local population was most peculiar in genetic structure compared with other populations. Local polynomial fitting for searching relationship between geographic and genetic distance demonstrated that there was a distinctive cline between localities that are situated 20-50 km apart. Since the degree of genetic differentiation was significantly correlated with geographic distance, the present genetic structure may reflect the history of phylogeographic subdivisions of the species.

Evolution of invasive traits in range margin populations of the roesel's bush cricket (*Metrioptera roeselii*)

Peter Kaňuch[1], Frida Holma[1], Åsa Berggren[1] and Anna Cassel-Lundhagen[1]
[1]*Departmnet of Ecology, Swedish University of Agricultural Sciences, Sweden*

A species capacity to establish and become invasive beyond its current distribution has been shown to depend on the founder genotypes, the size of the founding group and the environment it encounters. Due to an increased threat from invasive species on native biodiversity and since present knowledge is not conclusive regarding the generality of the above mentioned factors, it is highly needed to learn how genetic variation is conserved during founder events and to what extent it correlates with traits believed to be important for species' invasiveness. Roesel's bush cricket (*Metrioptera roeselii*, Ensifera: Tettigoniidae) has a continuous distribution in continental Europe and is expanding rapidly. On the Scandinavian Peninsula and in Denmark it occurs in more or less newly established and isolated populations. The species distribution and biology make it highly suitable to study effects of founder events on invasive traits. We sampled 38 sites (768 individuals) around the Baltic Sea coast from continuous and isolated parts of the species distribution. Using nuclear and mitochondrial genetic markers we are currently identifying colonisation pathways and determine founder sizes for each isolated population. These data are combining with data obtained on phenotypic traits. Analyses of selected morphological characters indicate different correlations with latitude in continuous versus newly established, isolated populations. In the paper we are discussing how dispersal patterns can explain the observed variation in morphology.

EVOLUTION
Poster Presentations

PP14

Telomeric and rDNA repetitive sequences in karyotypes of Gomphocerinae grasschoppers (Orthoptera: Acrididae)

Alexander Bugrov[1], Ilyas Jetybayev[3], Tatiana Karamysheva[3] and Nikolay Rubtsov[3]
[1]*Institute of Systematics and Ecology of Animals, Russian Academy of Sciences, Siberian Branch, Frunze str. 11, Novosibirsk 630091 Russia*
[2]*Novosibirsk State University, Pirogov str., 2, Novosibirsk 630090, Russia*
[3]*Institute of Cytology and Genetics, Russian Academy of Sciences, Siberian Branch, Pr. Lavrentjeva, Novosibirsk 630090, Russia*

Subfamily Gomphocerinae is known not only for very conserved karyotype structure but for highly variable heterochromatic regions in the chromosomes. It suggests that repetitive sequences may contribute to evolution of this group, which is widely spread allover herbaceous landscapes of Old and New Worlds. In this research we used methods of molecular cytogenetics to localization two functionally important repetitive sequences on chromosomes of this group. Flourescence in situ hybridization (FISH) of 18s rDNA probe on the chromosomes of 13 species from Gomphocerinae subfamily revealed common pattern of localization within tribe Gomphocerrini, which is significantly differ from other tribes. Two pairs of metacentric chromosomes of 17 chromosome species had cluster of rDNA genes while it was present in one pair of metacentric and one pair of acrocentric chromosomes in 21 chromosome *Chorthippus hammarstroemi* and two pairs of acrocentric ones in *Mesasippus kozhevnicovi* which has 23 chromosomes. It supports monophylitic origin of species with different number of chromosomes in this subfamily from 23 chromosome ancestor by three centric fusions and indicates homeological chromosomes. FISH with telomeric repeats probe showed strong signal on the ends of chromosomes of all analyzed species. *Aeropus sibiricus* had polymorphic loci enriched with telomeric repeats in small acrocentric chromosome M6, which allows us to indicate inversion of distal region of this chromosome. Absence of telomeric repeats in pericentromeric regions of metacentric chromosomes in majority of 17 chromosome species suggests that loss of this repeats on centromeric end of chromosomes resulted in fixation of metacentric chromosomes after fusion, which determined original evolutionary pathway of karyotypes within Gomphocerinae. This approach gives us new markers of karyotype evolution, which is hard to study due to lack of them. Also they can be as additional characteristic of species. Supported by grant of Russian Foundation for Basic Research No 09-04-00401a (for A. Bugrov)

PP15

Introgression of genes and morphological characters in a grasshopper hybrid zone on Mt. Tomaros

Anja Klöpfel[1], Jan Sradnick[1], Alexander Hübner[1] and Norbert Elsner[1]
[1]*Georg-August-University, Göttingen; Johann-Friedrich-Blumenbach-Institute for Zoology und Anthropology; Berliner Str. 28; 37073 Göttingen ,Germany*

In order to reveal the degree of presumed genetic introgression from *Stenobothrus rubicundus* to *Stenobothrus clavatus* (and vice versa) which hybridize in a small zone on Mt. Tomaros morphometric and genetic studies have been executed. About 2600 individuals were

considered which had been collected at more than 120 sites on the slopes of the mountain as well as on other mountains where either *St. rubicundus* or *St. clavatus* is present exclusively. Gradual shifts of the wing venation and the shape of the antennae were observed, leading away downhill from the hybrid zone on the saddle of Mt. Tomaros. Individuals, close to the hybrid zone, show clear similarities to the respective other species while at greater distance specimen resemble more and more those of allopatric populations. The morphometric data indicate that most of the individuals from the Mt. Tomaros do not correspond in shape and pattern to the "pure" individuals of the respective species on the other mountains. Genetically, we conducted AFLP analysis and we analysed the coding and non-coding DNA markers and microsatellites. The first set of data demonstrates a close relatedness between the two species on Tomaros, whereas the populations being present on the allopatric localities seem to be farther related to each other than the two populations on Mt. Tomaros.

PP16
Study of isolation barriers between hybridizing grasshopper species

Jan Sradnick[1], Varvara Vedenina[2], Anja Klöpfel[1], Sylvia Fähsing[1] and Norbert Elsner[1]
[1]*Georg-August-University, Göttingen; Johann-Friedrich-Blumenbach-Institute for Zoology und Anthropology; Berliner Str. 28; 37073 Göttingen, Germany*
[2]*Institute for Information Transmission Problems, Russian Academy of Sciences; Bolshoy Karetny per. 19, Moscow 127994 Russia*

Courtship behaviour of the males is the most important prezygotic isolation barrier in acridid grasshopper species belonging to the sub-family Gomphocerinae. Nevertheless, such barriers sometimes break, as it happens in the case of *Stenobothrus rubicundus* and *Stenobothrus clavatus* on Mt. Tomaros resulting in a stable hybrid zone. The hybrid songs contain novel elements, which are even more complex than the parental once, thus offering a new target for sexual selection. The question arises why those prezygotic isolation borders are overridden. In order to get an answer we crossed and bred F1 hybrid offspring between *St. rubicundus* and *St. clavatus* from the allopatric localities. The offspring of *St. clavatus* females and *St. rubicundus* males obtained in laboratory was much more numerous than vice versa. Also crossing experiments between F1 hybrids were successful and the F2 generation hatched. The F1 hybrids could be also backcrossed with both parental species. Behavioural experiments have been performed which showed that females of *St. rubicundus* are not able to distinguish between the courtship songs of conspecifics males and those of *St. clavatus.* Further, hybrid females collected in the field and those bred in the laboratory can't distinguish between both parental song types and the hybrid songs. The possible reason for this incorrect choice of the *St. rubicundus* females might be the similarity of songs of *St. rubicundus* and *St. clavatus* although these are produced by completely different organs, i.e. wings and the hind legs, respectively.

PP17

A hybrid zone of two Acridid grasshopper species on Tomaros Mountain in North-West Greece

Norbert Elsner[1], Jan Sradnick[1] and Anja Klöpfel[1]
[1]*Georg-August-University, Göttingen; Johann-Friedrich-Blumenbach-Institute for Zoology und Anthropology; Berliner Str. 28; 37073 Göttingen, Germany*

The two acridid grasshopper species *Stenobothrus rubicundus* and *Stenobothrus clavatus* (sub-family Gomphocerinae) are present on different slopes of Mt. Tomaros near Ioannina in North-West Greece at altitudes between 1400 – 2000 m above sea level. Both species can be clearly distinguished from each other because of the morphology of the antennae, details of the stridulatory file on their hindlegs, numerous characters of the fore and hind wings, and most notably, by the different courtship behaviours of the males. They have evolved highly elaborate sonorous and visual displays. While sound is produced in *St. clavatus* with the hind legs only, being accompanied by non-acoustic movements of the head and the antennae, *St. rubicundus* displays its sounds by using its hind legs as well as both pairs of wings beating the hind wings sonorously against each other. Although such completely different courtship behaviours normally serve as powerful prezygotic isolating mechanisms the two species hybridize in the saddle region where the two populations overlap. More than 95% of the individuals living there present a mixture of parental and novel elements both as far as morphological and behavioural characters are concerned. Comparative studies of the parental populations downhill and allopatric populations of either *St. rubicundus* and *St. clavatus* found separately from each other on different mountains at a distance of ca. 25 km give rise to the assumption of genetic introgression from one species to the other.

PP18

On the life history of isolated populations of *Pholidoptera frivaldskyi* (Tettigoniidae) in Central Europe

Peter Kaňuch[1], Vladimira Fabriciusova[1] and Anton Kristin[1]
[1]*Institute of Forest Ecology, Slovak Academy of Science, Sweden*
[2]*Institute of Ecology, Swedish University of Agricultural Science, Sweden*

Long-term isolation often results in populations exhibiting differences in various traits which can be observed in morphology and genetic structure also. Such variability may produces different behaviour and life strategies. Using a model bush-cricket species *Pholidoptera frivaldskyi* (Tettigoniidae), geographical variability among very isolated populations was investigated. It is an endangered flightless species in central Europe, and it occurs only in three sites of small-size mountainous mesophilous meadows (in Slovakia) and possible contact among recent populations (and also since historical introduction) is not supposed there. Study sites were separated by 73–148 km. Discriminant function analysis based on seven selected morphological traits and comparing of mtDNA sequences (COI) provided preliminary information about possible local patterns. Despite of certain morphological (size and colour) differentiation among populations, sequenced individuals exhibited low genetic variability (only one mutation in one population indicated different haplotype). Suggestion

that these populations were founded by pastoral colonization from Balkan territories during the end of the Middle Ages gives opportunity to interesting study of enigmatic species life history in central Europe.

PP19

Song evolution and phylogenetic relations between the european species of the *Chorthippus albomarginatus* group (Orthoptera, Acrididae, Gomphocerinae)

Varvara Vedenina[1]
[1]*Institute for Information Transmission Problems, Russian Academy of Sciences, Russia*

The five grasshopper species of the *Chorthippus albomarginatus* group found in Europe show an extreme complexity and diversity of the courtship songs. Courtship songs consist of many sound elements accompanied by conspicuous visual display. The close resemblance in both morphology and calling songs found in all European species of the *Ch. albomarginatus* group suggests that they evolved from a common ancestor quite recently, probably during the Pleistocene period. The outstanding courtship song complexity in these species could be explained by a rapid speciation via sexual selection and partly by hybridization that could occur during several interglacial periods. Hybridization experiments conducted with different combinations of species revealed that the hybrid songs between two species (e.g., *Ch. albomarginatus* and *Ch. oschei*) have sometimes the song elements of the third species (e.g., *Ch. karelini*). According to the mitochondrial gene COI sequences, there were no fixed differences between the species of this group. Variability was as great within species as it was among species, which supports the idea of hybridization during periods of grasshopper range expansion since the last glacial maximum.

BEHAVIOUR

Oral Presentations

Chair: Klaus Riede
Ataturk Conference Hall (14:15 – 16:30 / June 24, 2009)

The function of colour change in the chameleon grasshopper (*Kosciuscola tristis*)

Kate Umbers[1], Adam Stow[1], Greg Holwell[2] and Marie Herberstein[1]
[1]*Macquarie University*
[2]*University of Auckland*

Several studies have shown evidence both for and against the importance of colour in temperature regulation. The chameleon grasshopper *Kosciuscola tristis* rapidly changes colour with temperature from black to turquoise. To date Key and Day's hypothesis that their colour change aids in thermoregulation had not been formally tested. Our data suggest that colour is unimportant in thermoregulation of the insect: at both black and turquoise phases the grasshoppers have the same rate of internal temperature change when heated by the sun. Therefore, we propose a sexual selection hypothesis for colour change in *K. tristis*. We provide evidence of male aggregative display and female preference for male brightness.

The vibrational startle response of a non-hearing cave cricket (*Troglophilus neglectus*, Rhaphidophoridae) and its neuronal correlates

Nataša Stritih[1]
[1]*National Institute of Biology, Dept. of entomology, Večna pot 111, 1000 Ljubljana, Slovenia*.

Frequency-intensity characteristics of a vibrational startle response (VSR) and the effect of vibratory prepulses on the startle amplitude were investigated in the cave cricket *Troglophilus neglectus* (Rhaphidophoridae), to find some correlates with responses of the previously investigated vibratory interneurons in the species. The startle response was elicited by vibrational pulses applied to an unrestrained animal sitting on a loudspeaker membrane, and was recorded as a movement of the animal's back via the laser-Doppler vibrometry. The response was stationary, consisting of rapid contraction of the legs and the body, which did not result in an escape jump. It was sharply tuned to 50 Hz vibrations with the lowest threshold at 0.7 m/s2. The response magnitude increased with intensity over the whole measured range of 30 dB, and the response 33 ms. In analogy with the prepulse–latency was in the range between 23 inhibition of the acoustic startle response, the effect of subthreshold vibratory prepulses was tested to potentially reveal the sensitivity of the neuronal pathway mediating the VSR. The preliminary results indicate the perceptual impact of prepulses, and thus thresholds of underlying neuronal elements, at 20-25 dB below the VSR threshold. From a large number of vibratory interneurons, which have been identified in the prothoracic ganglion of the species, a class of low-frequency tuned neurons is presented that are physiologically and anatomically suited to consist the VSR pathway.

Complex song characters: registration, description and interpretation

Baudewijn Odé[1]
[1]*European Invertebrate Survey, Netherlands*

Song plays a crucial role both in taxonomy and in evolution of Orthoptera and gains interest of researchers in both fields. In some groups song characters can be quite complex, especially in Gomphocerine grasshoppers. Complex and independent movement of both legs produces complex song patterns. Usually individual species have well-defined and unique songs, although the same song may arise in different geographical areas in different taxa. In these cases the taxonomic value of song characters is not so great. Yet, morphologically similar taxa with different songs may well be reproductively isolated and thus perform as individual species. In the known cases of hybridisation the clear patterns of parent songs mingle into new, usually less clear patterns. Whereas the clear patterns of the parent songs usually can be consistently described, the songs of their hybrid offspring is usually not easy to describe, as shown in a recent publication on the taxonomy of the Gomphocerine grasshoppers in the Peloponnesus, Greece. Taxonomic value of song characters is especially high if evolutionary pressures are present. The major evolutionary pressure in Gomhocerine grasshoppers is the female choice. If we want to interpret the songs correctly, we need to find the triggers that make females responsive to male song. We are only starting to understand those triggers. In search for a correct taxonomy and evolutionary interpretation of the song of Gomphocerine grasshoppers, we need to standardise registration of the songs and the underlying movements of legs and wings, description of songs and where possible define triggers that females use to select mating partners.

Call diversity and spectro-temporal partitioning in an acoustically communicating Ensiferan assemblage of a tropical evergreen forest

Swati Diwakar[1] **and Rohini Balakrishnan**[1]
[1]*Indian Institute of Science, India*

The call structures of twenty species constituting the nocturnal acoustic community of a tropical evergreen forest in Southern India are described. The multi-species acoustic assemblage consisted of diverse taxa from the superfamilies Grylloidea (ten species), Tettigonioidea (nine species) and Gryllacridoidea (one species). Of the ten gryllid species, eight belonged to the family Gryllidae and two to the family Mogoplistidae. Of the nine tettigoniid species, four belonged to the sub-family Pseudophyllinae, two to the Phaneropterinae and three to the Mecopodinae. The gryllid species had narrow-band calls (bandwidths less than 1 kHz) with dominant frequencies between 3 and 8 kHz. The calls of the tettigoniid species covered a wide frequency range, reaching far into the ultrasound in species of the genus *Mecopoda*. Interestingly, the calls of four of the tettigoniid species were narrow-band and in the audible range. The gryllacridoid species, probably of the genus *Gryllacropsis*, had a low-frequency call with the dominant frequency at 1.6 kHz. There was a high overlap of dominant frequencies of species between 3 and 7 kHz, but the species had distinct and diverse temporal patterns. There was no diel partitioning of calling time between the different ensiferan species, with all species calling between dusk and midnight. There was no evidence for a dawn chorus of crickets in the evergreen forest. Quantitative analyses

revealed that species with high levels of temporal overlap had low spectral overlap and vice versa.

The function of low frequencies: singing and hearing in aerotegmina (Tettigoniidae: Listroscelidinae)

Klaus-Gerhard Heller[1], Tim Ostrowski[2] and Claudia Hemp[3]
[1]*Institut für Zoologie II, Friedrich-Alexander-Universität Erlangen-Nürnberg*
[2]*Abteilung Neurobiologie, Johann-Friedrich-Blumenbach-Institut*
[3]*Department of Animal Ecology II, University of Bayreuth*

The carrier frequency of the calling songs of bush-crickets (Tettigonioidea) is generally negatively correlated with body size: the smaller the species, the higher the frequency. One potential reason lies in the dimensions of the sound producing structures. Small species have small tegmina efficiently usable only for the production of sounds with short wavelengths. However, in the correlation between body size and frequency there is a large variation. Some species do not seem to follow the main trend, but the reasons for these deviations are largely unknown. Of special interest are species which produce sounds "too" low for their body size, because this requires special and - judging from the other species - probably expensive modifications of the tegmina. From morphological studies it is well known that in some groups single species or genera with unusually large tegmina can be found (e.g. *Poecilimon*: *P. tschorochensis*, Phyllomimini: Tympanophyllum, Tettigoniini: *Uvarovites inflatus*). For some of these species the carrier frequency of their song is quite low, but the data on song intensity and hearing sensitivity, which are equally important for the understanding of the communication system, are mostly missing. In our study we present data on the acoustic behaviour of *Aerotegmina kilimandjarica*, a small species (pronotal length 4 mm) with extraordinarily enlarged and inflated tegmina. By combining information about song intensity, spectral composition and hearing sensitivity in this species we achieve a better understanding of the circumstances which favour the evolution of low frequent songs.

Acoustic distance estimation in the European katydid *Metrioptera roeseli roeseli*

Manfred Hartbauer[1], E. Ofner[1] and Heinrich Römer[1]

[1]Department of Zoology, Karl-Franzens Univeristät Graz, Germany

In acoustically communicating insects receivers may extract information about the direction and distance of senders by evaluating certain parameters in the perceived signals. The pattern of spacing of signallers in the field (e.g. Thiele & Bailey 1980) suggests that they estimate the distance to their neighbours either by evaluating the absolute sound pressure level or by comparing the perceived amplitude of high-frequency signal components with the perceived amplitude of low-frequency ones. The latter mechanism relies on a stronger attenuation of high-frequency signal components over distance due to excess attenuation. In the Australian katydid *Mygalopsis marki* this results in a distance specific excitation pattern of auditory

receptors, which is also reflected in the operating range of interneurons (Römer 1987). In the European katydid *Metrioptera roeselii* advertisement songs consist of two rapidly alternated song hemi-syllables: a faint ultrasound signal (30-50 kHz) and a loud broadband signal (13-50 kHz). In order to investigate a possible frequency-based distance estimation in this species, a typical male song was transmitted either in dense grass (max. height: 40 cm) or in a transect where grass was sparse. Perceived signals recorded at different distances from the speaker 25 cm was used as playback and broadcast to insect preparations while recording the spiking activity of an auditory neuron (omega cell). Results showed that ultrasound hemi-syllables completely attenuated within 2 – 3 m from the speaker in dense grass (4 – 5 m in sparse vegetation). However, steady-state omega cell activity was quite irregular and revealed a strong masking of ultrasonic hemi-syllables caused by the loud broadband hemi-syllables. A frequency-based distance estimation appears to be possible only in a short period after song initiation. References Thiele, D. & Bailey, W.J. Australian J Ecol 5, 275-286 (1980) Römer H. J Comp Physiol A 161: 33-42 (1987)

Are male bushcrickets honest signaler?

Gerlind U.C. Lehmann[1]
[1]*Institute of Biology/Zoology, Free University Berlin*

Bushcricket spermatophores transferred during mating are costly for males to produce. Females receive several benefits from these nuptial gifts, including boosting their muscle mass with nitrogen. Furthermore, they can fuel their metabolism within three hours by feeding on the male derived nutritious spermatophores. Thus, spermatophore size should be subject to sexual selection via female choice. New data from the bushcricket genus Poecilimon show that spermatophore size depends upon a range of factors. Parasitism and mating history can influence the condition of the male and longer intervals between matings leads to larger spermatophores. For any test of the sexual selection hypothesis, it is essential to control for a number of factors influencing spermatophore investment. A failure to do so might be the reason for mixed results, accumulated over the last two decades, pertaining to whether bushcricket males honestly signal females their spermatophore investment capacity in their songs. Controlling for body size and mating history, I have shown that females choose the heavier male of two competitors for mating. They also prefer males who have not mated recently over others. Consequently, a female is expected to mate with the male who will give her the largest spermatophore. Intriguingly, females only exhibit choice when males are singing, both in phonotactic choice experiments and in close contact. The large male advantage disappears in mute males, indicating the importance of male singing for female choice. I am currently analyzing song characteristics likely to be connected to male condition and spermatophore investment.

Phonotaxis in response to multiple sound sources in the acoustic parasitoid fly *Ormia ochracea*

Andrew C. Mason[1], Norman Lee[1] and Damian O. Elias[1]
Biological Sciences, University of Toronto Scarborough, 1265 Military Tr

The fly, *Ormia ochracea*, is an acoustic parasitoid that must reproduce by placing parasitic larvae on cricket hosts. Female flies obtain hosts by localizing the calls of singing male crickets. Under controlled acoustic conditions, flies localize individual sound sources with great precision using a pair of ears that are exquisitely sensitive to sound direction. In nature, however, flies must deal with chorusing cricket populations in which multiple attractive sound sources may overlap in time and space, potentially masking temporal information necessary for localization. In field experiments, we show that simultaneous sources can disrupt the accuracy of fly phonotaxis. Laboratory experiments under controlled acoustic conditions reliably elicit 'phantom-source localization' in which flies orient to a location intermediate to a pair of attractive sources. With varied temporal overlap, small time differences between two sources allow flies to selectively localize the leading over lagging sources when temporal disparities fall within the duration of a pulse. In addition, selective localization only occurs to leading sources located closer to the midline axis (forward direction) than more laterally located lagging sources. Thus source segregation depends on both the relative timing and location of competing sound sources suggesting that the chorus structure of host populations may be a factor in host exploitation by *Ormia*.

BEHAVIOUR
Poster Presentations

PP20

"I like to move it, move it!"

A detailed analysis of the multimodal courtship repertoire of *Myrmeleotettix antennatus* (Fieber, 1853) (Orthoptera, Caelifera, Gomphocerinae)

Dirk Berger[1] and Brigitte Gottsberger[2]

[1] *Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde, Königsbrücker Landstraße 159, 01109 Dresden, Germany*

[2] *Department für Populationsökologie, Fakultät für Lebenswissenschaften, Universität Wien, Rennweg14, 1030 Vienna, Austria*

Calling and courtship songs of gomphocerine grasshoppers play an important role in pre-mating reproductive isolation, because females discriminate strictly the specific amplitudes and temporal song patterns of the male songs. There is a strong evolutionary pressure on this sender-receiver system as it serves as the main species recognition, mate finding and mate choice mechanism in singing grasshopper species. A high diversity of acoustic signals could have contributed to a fast radiation in this group. In several species amazing courtship repertoires evolved, especially when males combined different song elements with additional visual elements. The visual elements arise through the movement of different parts of the body in specific repeated rhythms. About the function and the origin of such multimodal courtship displays in grasshoppers not much is known yet. We analysed the complex courtship display of *Myrmeleotettix antennatus*, which contains acoustic as well as visual components. The songs and the sound generating leg movements were simultaneously recorded by an opto-electronic device. Additionally, we installed a video camera to the setup to record the full behavioural spectrum. The courtship song consists of three distinct song elements. The first element is a series of gentle pulses produced by one leg. It preludes the courtship and is produced later during courtship in alternation with the other two elements. The other two elements are of conspicuously higher intensity and complexity, and are produced by both hind legs always moved jointly. This duet is repeated 3 to 4 times until the male switches back to produce the first element or tries to mount the female. The visual component of the courtship repertoire of *M. antennatus* consists of a stroke by the antenna that is unique within grasshoppers. Firstly –during the pulse series– the male presents the antennae to the female. Then, while singing the antenna are slowly moved backwards to then be suddenly jerked to the female 3 to 4 times during each courtship sequence. In contrast to several other grasshopper species showing visual display with antennae, the strokes of *M. antennatus* are not accompanied by any leg stroke. The courtship display of *M. antennatus* will be compared to other complex courting grasshopper species. Additionally the detailed analysis of the leg movement patterns of song elements reveal insights into the neurophysiologic basis of the song of *M. antennatus*, which allows us to get first ideas on the origin and function of courtship elements within gomphocerine grasshoppers.

PP21

Daily activity of *Poecilimon intermedius* (Fieber, 1853) in a typical steppe habitat of the species (Central-Europe, Hungary)

Zoltán Kenyeres[1] and Norbert Bauer[2]
[1]*Acrida Conservational Research L.P., H-8300 Tapolca, Deák F. u. 7., Hungary*
[2]*Hungarian Natural History Museum, Department of Botany, H-1087 Budapest, Könyves K. krt. 40., Hungary*

Poecilimon intermedius reproduces parthenogenetically in a larger area than sexual *Poecilimon* species. The Eurasian-Continental forest steppe species occurs from the Czech-Moravian-Hills through the Carpathian Basin and the Russian steppes to the Angara table-land. Habitat requirements and daily activity of the species was studied in Western-Hungary (Mezőföld: Berhida). Based on the results the specimens of the species covered 668 cm during a day (creeping and skipping together). Movements bigger than 1 cm during 10-minute intervals were between 1 and 91 cm. The average cover was 17.5 cm within a 10-minute interval. There were two activity peaks: 11:30–12:30 and 16:50–18:30. These two peaks concurred with the phase showing two same temperature and humidity correlation on the climate diagram (~27°C temperature, 80% humidity). During nutrition the animal consumed the following plants and parts of plant in 98%: *Euphorbia pannonica* Host. (different parts of the inflorescence), *Carduus acanthoides* L. (leaf, spear), *Chamaecytisus austriacus* L. (epipetalous, leaf), *Salvia nemorosa* L. (flower, leaf, spear), *Eryngium campestre* L. (leaf). The intensity of nutrition and the frequency of defecation revealed contradictory tendency. Defecation generally took place in the morning period, and the intensive nutrition mainly occurred in the afternoon. In the studied area *Poecilimon intermedius* usually inhabits in the patches of closed loess grassland association (*Salvio nemorosae-Festucetum rupicolae*). Typical population size, fragmented occurrences, habitat-preferences and daily activity of *Poecilimon intermedius* show that it is a specialist, sensitive species. Considering the natural status the insect is one of the most important indicator species of Eastern European steppe habitats.

PP22

Remote modeling and analyzing of insect sounds by using a computer and microcontroller-based system

Hossein Zamanian[1], Mehdi Dehghani[2]and Maede Mehdipour[2]
[1]*Young research club, Islamic Azad university, Yazd, Iran*
[2]*Young research club, Islamic Azad university, Babol, Iran*

Communication establishment through sound is a kind of mechanical communication which includes specific and very delicate messages for intra-species and interspecies communications. Studying the relation between the sounds produced by insects and environmental parameters such as temperature, humidity, and light is necessary in studying their behaviors. The Remote Modeling and Analyzing of Insect Sounds by Using a Computer and Microcontroller-Based System collects data such as insect sounds, temperature, and humidity in a given environment and sends them wirelessly to a computer to enable sound analysis based on temperature and humidity, and record a precise analysis then. This device in

composed of three different parts: 1) Temperature, humidity and frequency data transmitter, 2) Sensors\' data receiver and transmitter to computers, 3) Computer software. In order to use this device, we should find insects in the environment and put the device near them. In this situation, the system records the data and sends it immediately to the receiver. The receiver receives the data and shows it as graphs. The results of processed data in computer can be presented as 2-D or 3-D charts showing the changes of insect sound rhythm according to effective parameters such as light, humidity, temperature and etc. Moreover, the resulting data can be stored as database in the memory of the computer for further statistical processing. There is no need for the entomologist to specify parameters at close range; instead, he can carry out the sampling more precisely and in more times by using this system. In fact, one of the major problems in studying insect behaviors is that the entomologist should be present in the environment himself to collect and record data; otherwise, taking samples is difficult because there is a large number of samples and parameters. (This invention is granted patent number 44165)

PP23

Similar songs, distinct species: bioacoustic diversity and vicariance in tropical cricket communities

Klaus Riede[1]
[1]*Institut f. Zoologie, Graz, Austria*

Species-specific characteristics of song structure have often been used by taxonomists to differentiate between morphologically similar, “cryptic” species. In crickets, song parameters such as carrier frequency and pulse rate evolved and diverged, often rapidly, along contact zones or during radiation of species swarms. However, when comparing the parameter space of frequency and pulse rate with the actual, hitherto unsufficiently known diversity of tropical crickets, it becomes evident that parameter space is limited. Even adding secondary and tertiary features of pulses and chirps could not provide sufficient possibilities to avoid convergence among songs of appr. 5000 known cricket species. Similar songs are described here for two vicariant species of the diurnally active trigoniid *Phyllopalpus*: *P. amoenus* and *P. cicindeloides*, from Argentina and Panama, respectively. Further examples are presented from two neotropical trigoniid cricket communities from Panama and Ecuador, particularly for the speciose genus *Anaxipha*. The results indicate that bioacoustic cricket identification and taxonomic separation is only possible on a local scale. In addition, extensive monitoring at one site in Panama (Barro Colorado Island) indicates strong seasonal changes, thus amplifying niche space for the entire community. The regional overlap and range of bioacoustic communities is hitherto unknown, but can be inferred from well-studied species complexes and vicariance patterns. A better understanding of the structure and geographic scale of cricket communities could provide better estimates of global cricket diversity, and accelerate species discovery.

PP24

Feeding preferences of gregarious nymphs and adults of the desert locust, *Schistocerca gregaria* (Forskäl 1775) (Orthoptera, Cyrtacanthacridinae) in different habitats at biskra oasis, Algeria

Tarai Nacer [1] and Doumandji Salaheddine[1]
[1]*Departement of Agriculture, University Mohamed Khider, Biskra, Algeria.*
[2]*Institut national Agronomique, El-Harrach, Alger, Algeria*

The Desert locust *Schistocerca gregaria* is generally recognized as a polyphytophagous acridid that commonly causes substantial damage to pastures and crops. During the recent Desert locust upsurge in 2004, the opportunity was taken, at Biskra oasis in Algeria, to identify the types of plants preferentially eaten by gregarious Desert locusts by examining the plant types in their faeces. The plant parts seen in faeces of young nymphs were mainly grasses, especially *Cynodon dactylon* even when shrubs and trees were present. Older nymphs had less grasses in their faeces and more broad leaf crops, shrubs or trees. The faeces of adults contained very little grass remnants, and when broad leaf crops were present, there was a preference for water melon *Cittrullus lanatus* var. *caffer* and melon *Cucumis melo* (Cucurbitaceae) and shrubs (young seedlings) of the common fig *Ficus carica* (Moraceae) and apricot *Prunus armeniaca* (Rosaceae). At the site trees were present, *Casuarina torulosa* was most commonly eaten whereas nearby *Cupressus sempervirens* was not consumed at all. These feeding preferences not only reflect what plants are damaged at different stages of the life cycle but also have important consequences for survey for, and treatment of, the Desert locust.

PP25

An attractant for gregarious nymphs of oriental migratory locust

Xinyang Zhang[1] and Long Zhang[1]
[1]*College of Biology, China Agricultural University*
[2]*Key Lab for Biological Control of the Ministry of Agriculture, China Agricultural University*

The Oriental Migratory Locust (*Locusta migratoria manilensis*) is a very important pest in China, and its semiochemicals play a key role in regulation of its behaviors, such as aggregation, feeding and oviposition behaviour which are related tightly with locust plague, however was not studied deeply. Our electroantennogram (EAG) experiment with the components of the Oriental Migratory Locust fecal volatiles indicates that the antenna of 4th instar nymphs of locust strongly responded to 2,5 dimethylpyrazine one of at low concentration, weakly at higher, while nonanal and cyclohexanol evoke very week. Tested with a Y-type olfactometer system, 4th or 5th instar gregarious nymphs and adults were significantly attracted to the volatiles from juice of wheat leaves compared with control, indicating the system suitable for detecting attracting behavior of locust. The behavior test with the three compounds, 2,5 dimethylpyrazine, nonanal and cyclohexanol showed that 4th and 5th instar gregarious locust nymphs are significantly attracted by 2,5-dimethylpyrazine at 0.1 to 1µl/ml (v/v, 2,5-dimethylpyrazine/mineral oil), but adult andnd the 4th and 5th instar gregarious nymphs responded depending on the concentration. In contrast, nonanal and cyclohexanol did not cause any attractant behavior of gregarious locust nymphs at 4th, 5th nymphs and adults at any concentration.

PP26
Vibrational communication in *Tetrix ceperoi*: description of male and female songs

Petr Kocarek[1]
[1]*University of Ostrava*

Traditionally, Tetrigidae have been considered to be voiceless orthopteroids. Recently, vibrational signals in the genus *Tetrix* were for the first time found by Benediktov (1998). The vibrations (produced as rhythmic contractions of muscles) are transmitted to the substrate through middle legs. The presented study describes the vibratory signalisation in the species *Tetrix ceperoi* (Bolívar, 1887). The observed vibrational signals consist of more or less distinct pulses united into rhythmically repeated groups. Males of *T. ceperoi* produce signals of three functional types: calling, aggressive and courtship. (1) The calling signal is produced by males in order to attract conspecific females and it consists of simple irregularly repeated pulses (duration of pulse 100±10ms, frequency 0.05-0.8kHz; temp. 25-27°C is valid for all the mentioned measurements). (2) The courtship signal is produced by males only in close proximity to a female and it is used for inducing females to mate. Production of this signal is accompanied by specific visual communication behaviour (movements of hind legs, pronotum and wings). This signal is quieter and consists of more regularly and quickly repeated pulses (duration 85±15ms, interpulse intervals 260±50ms, carrier frequency 0.3-0.5kHz). (3) The aggressive signal is the most complicated one because it consists of two different parts and each part can be used separately or in the complex. These signals are produced by males usually during close contact with other conspecific male. The first part of the signal consists of 3-30 regularly repeated pulses (duration 95±20ms, interpulse intervals 125±80ms); the second part consists of 20-135 regularly repeated pulses (duration 18±3ms, interpulse intervals 40±25ms; carrier frequencies of both parts 0.05-0.3kHz). Females of *T. ceperoi* are also able to produce vibrations, which are similar to male's calling vibration and are produced irregularly during contacts with other intra- or interspecific individuals (duration 90±10ms, frequency 0.05-0.3kHz). This study was supported by grant No. 206/07/0811 of the Czech Science Foundation.

PP27
Mechanical response of the tympanal membranes of the tree cricket *Oecanthus henryi*

Natasha Mhatre[1], **Fernando Montealegre-Z**[2], **Rohini Balakrishnan**[1] **and Daniel Robert**[2]
[1]*Centre for Ecological Sciences, Indian Institute of Science, Bangalore, 560012, India*
[2]*School of Biological Sciences, University of Bristol, Woodland Road, Bristol, BS8 1UG, UK*

Crickets (Orthoptera: Gryllidae) have two tympanal membranes on the tibiae of each foreleg. Among several field cricket species of the genus *Gryllus* (Gryllidae: Gryllinae), the posterior tympanal membrane (PTM) is significantly larger than the anterior membrane (ATM). Laser Doppler vibrometric measurements have shown that the smaller ATM does not respond as much as the PTM to acoustic stimulation. Hence the PTM has been suggested to be the principal tympanal acoustic input to the auditory organ of field crickets. The tympanal membranes of tree crickets (Gryllidae: Oecanthinae) do not show a large size difference; in effect, the ATM is slightly larger than the PTM. Interestingly, both TMs are structurally more complex than expected, presenting a series of transverse microscale folds on their distal area. The mechanical response of the TMs to acoustic stimulation was investigated using

microscanning laser Doppler vibrometry in controlled acoustic conditions. Remarkably, only a small portion of the membrane surface area was found to deflect in response to sound. The PTM and ATM were found to have very similar frequency responses, and move out of phase with each other, thus generating compressions and rarefactions of the tracheal volume backing the tympanal system. These results suggest that, unlike in field crickets, tree crickets might have four instead of two functional tympanal membranes. This is interesting in the context of the outstanding question of the role of spiracular inputs in the auditory system of tree crickets. We thank the UK-India Education Research Initiative (UKIERI) and the Human Frontier Science Program for financial support.

ECOLOGY and EVOLUTION

Oral Presentations

Chair: Alexandre Latchininsky
Mediko SKS Hall (14:15 – 16:30/ June 24, 2009)

Do graminivores Caelifera consume the Poaceae according to their relative abundance?

Leila Benfekih [1] and Daniel Petit [2]
[1]*Département d'agronomie, faculté agrovétérinaire, Université Saad Dahleb, Blida,* Algérie
[2]*UMR INRA 1061, Université de Limoges*

We studied the diet of larvae and adults of two graminivore Acrididae during field experiments in Algeria. The first species, *Dociostaurus maroccanus* comes from a short-height herbaceous station in the semi-arid stage, and only the larvae are strictly graminivores. The second species, *Locusta migratoria cinerascens* comes from irrigated cereal perimeters located in the Central Sahara. For *Dociostaurus maroccanus*, the correlation between the plant cover on the ground and their frequency of consumption (all plant families included) increases from the L1 stage until the adult. In parallel, there is a progressive increasing in the diversity of the consumed plants. Concerning Poaceae, no correlation between their covering and their frequency of consumption is noted: some are consumed as of the first larval stage whereas others are not consumed before the adult stage. For *Locusta migratoria cinerascens*, the correlation between the covering of Poaceae on the ground and their frequency of consumption is always significant whatever the stage. In the adults in particular, this correlation is all the stronger as the covering of Poaceae is important. The diet of L4, L5 and adults does not overlap, possibly in relation with different places of food supply. Calculations of regression residues make it possible to classify the plant species from the most repellent as *Triticum durum* and *Phragmites communis*, to the less ones, as *Lolium multiflorum* and *Sorghum vulgare*.

Development of molecular tools for studies in the *Calliptamus* genus

Elodie Blanchet[1], Ange-Marie Risterucci[2], Claire Billot[2], Marie-Pierre Chapuis[1], Laurence Blondin[1], Ronan Rivallan[2], Christine Pages[1], Antoine Foucart[1], Jean-Michel Vassal[1] and Michel Lecoq[1]
[1]*CIRAD Acridologie, France*
[2]*CIRAD, Development and Adaptation of Plants, France*

The genus *Calliptamus* (Orthoptera, Acrididae) includes locusts and grasshoppers, spread mainly throughout the Mediterranean Basin and as far as the southern part of Siberia. Some species are of substantial economic importance, such as *C. italicus* (Linné, 1758). Despite many studies on their taxonomy and biology, the identification of many species remains difficult, particularly for females and nymphs. Furthermore, in spite of their economic importance, dispersion capabilities which could have an impact in outbreak as demonstrated for other locusts - are not well understood. In order to clarify both aspects – identification and dispersion capabilities - we tried to develop molecular tools for various species of this genus distributed in Southern France. We focused our studies on *C. italicus*, *C. barbarus* (Costa, 1836) and *C. wattenwylianus* (Pantel, 1896). In order to facilitate the identification process, we developed a multiplex PCR assays to discriminate - quickly and inexpensively - any specimen collected in the field at the species level. Then, we developed new microsatellite markers to be used for further studies on dispersion capabilities. Seven markers were obtained for *C. barbarus*, six for *C. italicus*, three of them cross amplified on *C. wattenwylianus*. Genetic analyses were performed on two sampling seasons, at different geographic scales: the

first study at an individual level (on two sites of 72 km² and 40 km apart, in Southern France), the second at a population level at different localities throughout the Mediterranean Basin. Analyses are in progress and results will be provided during the congress.

Biology and ecology of *Arcyptera brevipennis vicheti* Brunner, 1861

Eva Schultner[1], Elodie Blanchet [1], Christine Pages[1], Antoine Foucart[1], Jean-Michel Vassal [1] and Michel Lecoq[1]
[1]CIRAD Acridologie, France

Arcyptera brevipennis vicheti Brunner, 1861 (Acrididae, Orthoptera) is a remarkable grasshopper, native of Mediterranean grassland habitats in Southern France and North-East Spain. Modifications in land use are endangering the survival of *A. b. vicheti*. In this study, we describe aspects of this species' life-cycle for the first time. Morphology and development were studied by rearing hoppers in the laboratory. Population ecology and dynamics were studied by bi-weekly population counts on two experimental sites on the Causse d'Aumelas in the Hérault department (France) during the spring season 2008. We recorded the temporal evolution of vegetation and habitat structure in order to establish relationships between environmental factors and the species' life-cycle. Feeding preferences were studied by analysing the faecal contents and reproductive capacity by examining the egg-pods and dissecting of female ovaries. Development of *A. b. vicheti* passes through five stages and is closely associated with the Mediterranean spring season. Hatchlings are prompted by the rise in temperature and humidity mid-April and may continue until mid-May. By mid-June, all individuals in the field are adult, resulting in a mean development time of 42 days. Females lay 16 eggs on average and deposit two clutches in their lifetime; the resulting population fecundity lies at approx. 7 eggs per imago. Our results revealed that *A. b. vicheti* is a true ecological specialist whose survival depends on the conservation of grassland habitats.

Are leader preferences in katydids the outcome of a sensory bias?

Sarah L. Bush[1] and Johannes Schul[1]
[1]Biological Sciences, University of Missouri, Columbia, USA

Males of several *Neoconocephalus* species produce discontinuous calls with regularly repeated verses (or echemes). Durations of verses range from a few tens of ms (e.g. *N. spiza*) to longer than 1 s (*N. nebrascensis*) and verse repetition rates from 0.3 Hz to 5 Hz. Discontinuous calls are limited to one monophyletic clade of the *Neoconocephalus* phylogeny ('discontinuous clade'), which also includes several species with continuous calls. Males of these species synchronize their verses with those of neighboring males. In one species, (*N. spiza*) such call synchrony is the consequence of female preference for leading calls. Here we test the previously proposed hypothesis that this leader preference arises from a sensory bias of the katydid hearing system. This hypothesis predicts that species with continuous calls (the

ancestral state in *Neoconocephalus*) should exhibit a preference for leading calls when responding to synchronized discontinuous calls, i.e. that species with continuous calls possess a hidden leader preference. We tested female preferences during phonotaxis on a walking compensator in *N. nebrascensis*, a species with discontinuous calls, and in two species with continuous calls: *N. bivocatus*, which is sibling species to *N. nebrascensis* and thus within the 'discontinuous clade' and *N. retusus*, which branches off in the phylogeny basally to the 'continuous clade'. We found that females of none of the three species had a preference for leading calls. When two overlapping calls were presented synchronously, females tracked the midline of the two loudspeakers for any delay tested. These results indicate that the female preference for leading calls is most likely not a preexisting sensory bias, but evolved in *N. spiza* following the evolution of discontinuous calls. Because some species with discontinuous calls have a leader preference while others do not, there are most likely two evolutionary trajectories leading to call synchrony in this group.

The evolution of grasshoppers and their songs: insights from morphology and behaviour

Dirk Berger[1]
[1]*Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde, Dresden, Germany*

The crucial factor for the origin of biological species is the development of reproductive isolation. Gomphocerinae produce the most elaborate calling and courtship songs that can be found within grasshoppers. The songs are assumed to play a central role in reproductive isolation between species, whereas differences in genitalia apertures, which could isolate species mechanically, are not well developed. This leads to the assumption that the radiation in this group is closely connected to the evolution of acoustic signals. Thus, analyses of songs are of special interest to answer systematic and evolutionary questions for this group. The focuses of my study are the evolution of song patterns in Gomphocerinae and the intra-specific phenotypic differentiation in geographically separated grasshopper populations. I chose *Stenobothrus* because this genus contains species that produce songs of different complexity levels. To reconstruct the evolution of this taxon a phylogenetic analysis of a combined dataset including behavioural (calling song, courtship song, corresponding leg movement pattern and visual courtship displays) and morphological characters of members of this genus from Europe and Anatolia was made. In addition, some *Omocestus* species were included because prior studies revealed that they have a common ancestor with some of the *Stenobothrus*-species. On the basis of my phylogenetic reconstruction the evolution from simple calling songs to complex multi-element courtship songs within the genus *Stenobothrus* is discussed. In the plesiomorphic stage songs consist of simple structured phrases divided by pauses. These phrases are composed of homogenous syllables, which are produced by straight up and stepped down stroke movements of the two hind legs. Increasing complexity of leg movements leads to distinct substructures within phrases. Highly complex songs evolve, when males combine different song elements within one song and when visual elements are added during courtship. This includes for example rapid movements of the antennae and the hind legs. During this study distinct differences in the songs between geographical isolated populations were found in various species. One example, the subgenus *Stenobothrodes* Tarbinskij, 1948, was studied in more detail. The populations of this taxon are restricted to

small geographically separated populations throughout Eastern Europe and Anatolia. Some of them were described as distinct subspecies. All forms are morphologically rather similar and were supposed to be one highly variable species. According to the analysis of song production leg movements of calling and courtship songs, there are at least two lineages within *Stenobothrodes*. The degree of differentiation between populations within each lineage was studied by analyses of temporal song parameters and by morphometric measurements.

Consequences of hybridization in two closely related gomphocerine grasshopper species - male songs and female preferences

Brigitte Gottsberger[1]
[1]*Department of Population Ecology, Faculty Centre of Biodiversity, University of Vienna, Rennweg 14, 1030 Vienna, Austria.*

The breakdown of species boundaries due to hybridisation is a major problem in speciation. Within the genus *Chorthippus* hybridisation is a frequent phenomenon. I studied the consequences of hybridization between the closely related sympatric grasshopper species *Chorthippus biguttulus* and *C. brunneus* (Gomphocerinae) by hybridisation experiments. I wanted to find out how species identities remain distinct despite hybridisation. Male song parameters and female preferences for songs of the pure species and interspecific laboratory hybrids were investigated. Songs of hybrid males were intermediate between those of both parental species in terms of phrase number and duration. In contrast, species-specific syllable structure within phrases was largely lost in hybrids. As females of gomphocerine grasshopper respond to species-specific male calling songs with reply songs I could conduct playback experiments to access female preferences. The parameters phrase duration and syllable structures were experimentally varied from *biguttulus* to *brunneus* like songs. For *C. biguttulus* females the syllable pattern of songs is the crucial character, whereas for *C. brunneus* females phrase duration is the most important parameter. Hybrid females accepted a wide range of phrase durations from *brunneus* phrase durations up to the longest phrases tested. However, concerning preferences for syllable pattern hybrid females clearly behaved like *C. biguttulus* females. Therefore preference for phrase duration was inherited intermediately while preference for syllable patterns was inherited dominantly.Consequently, as songs of hybrid males between *C. biguttulus* and *C. brunneus* lack a correct syllable structure, females will not choose them as mating partners. If hybrids between the two species occur in nature, then females will rather cross back to *biguttulus*, than to hybrids or *brunneus* males. Thus the dominant expression of the syllable pattern strengthens the isolating barrier between the two sympatric species and helps to maintain species boundaries despite introgression.

Song and song preferences in two grasshopper hybrid zones: similar fate of hybrids between the species with complex courtship

Varvara Vedenina[1], Jan Sradnick[2], Anja Kloepfel[2] and Norbert Elsner[2]
[1]*Institute for Information Transmission Problems, Russian Academy of Sciences, Moscow, Russia*
[2]*Johann-Friedrich-Blumenbach-Institute of Zoology and Anthropology, Georg-August-University, Goettingen, Germany*

Natural hybrids between singing, closely related species of Orthoptera were found in different genera of bushcrickets (e.g., *Ephippiger*, *Orchelimum*), crickets (e.g., *Laupala, Gryllus, Allonemobius*), and grasshoppers (e.g., *Chorthippus*). In most cases the songs of hybrid males were shown to be intermediate between parental species. In mate choice experiments, the hybrid songs were unattractive to females of either parental species; hybrid females preferred either hybrid or the parental songs. These results often demonstrate strong selection against hybrids and thus, have substantial implications for models of speciation by reinforcement. Two hybrid zones between the grasshopper species with complex courtship strikingly differ from the examples mentioned above. *Chorthippus albomarginatus* and *Ch. oschei* hybridize in a broad contact zone of about 200 km wide on the territory of Ukraine and Moldova. They are similar in morphology and the calling songs, however, extremely different in their elaborate courtship songs that consist of many sound elements with different and complex temporal patterns. All courtship song elements were shown to be homologous in these species. Other two species, *Stenobothrus rubicundulus* and *S. clavatus*, hybridizing in a very narrow contact zone of about 500 m wide at the Mt. Tomaros in Greece, are remarkably different in several morphological characters, e.g. antennae shape and wing venation. They differ both in the calling and courtship songs, and some parameters of the complex courtship songs were shown to be non-homologous in two species. Despite many differences between the two hybrid zones, courtship song analysis showed similar results. In either hybrid zones, some parameters of the hybrid songs were intermediate between parental species, whereas others comprised the novel elements that are absent in the parental songs. Thus, hybrid songs may offer potential material for sexual selection by female choice. Analysis of the female preferences showed similarity between two hybrid zones as well. In behavioural experiments, females of the parental species showed unequal selectivity, but they sometimes did not distinguish between hybrid and conspecific males. Hybrid females were unselective, responding almost equally often to the hybrid songs and the songs of the parental species. Since hybrids can compete with the parentals for attracting mates, we suggest no or weak exogenous selection against hybrids in either hybrid zones. Moreover, a hybrid speciation is very plausible in both groups of these grasshopper species with complex courtship.

ECOLOGY

Oral Presenatations

Chair: A. Nihat Bozcuk
Ataturk Conference Hall (11:15 – 12:45/ June 25, 2009)

Desert Locust and intensive rainfall in Morocco from 1995 to 2008

K. Abbassi [1], Z. Atay Kadiri [1] and S. Ghaout [2]
[1]*Laboratoire de Zoologie et de Biologie générale, Faculté des Sciences, Rabat-Agdal, Morocco*
[2]*Centre National de lutte antiacridienne*

Morocco is invaded periodically by Desert Locust. After a calm period that followed the catastrophic invasion of 1986-1989, the plague threaten this country again in 2003, originated from summer breeding area in Mauritania, concerned by intensive rainfall in June 2003. The large mature swarms of Desert Locust invade South Morocco, regions side of the Atlas Mountains and Northeastern Morocco. In all these areas, conditions were favourable for winter-spring breeding and survival of the locust, a consequence of heavy autumnal rainfall followed by abundant spring rains. Furthermore, Desert Locust population dynamics during the 2003-2004 invasion highlighted the role of Saharan provinces as biotopes during winter breeding and Northeastern Morocco for spring reproduction. Drâa valley and Tafilelt present a higher ecologic potential for the autochthonous and allochthonous Desert locust populations. Breeding in the Saharan provinces, Souss valley and Northeastern Morocco characterize major invasions. In addition, a good spatio-temporal distribution of rainfall between Saharan provinces, regions side of Atlas Mountains and Northeastern Morocco have been source of the evolution of the 2003-2004 Desert locust invasion. From January 2005, cold and drought together with intense control operations caused a decline of the invasion. The same situation was observed in 1989. However, the initial phase of the 2003-2004 invasion increased very rapidly. On the contrary, the major phase of the 1986-1989 invasion was preceded by a minor event in 1986 where conditions were favourable for spring reproduction, followed by a second phase in 1987-1988 when conditions were better for winter and spring breeding. In Morocco, Desert locust situation from 1995 to 2008 revealed a continuous presence of solitary populations in South of Drâa valley, Tafilelt and Bouârfa. From 2008 up to now, the Desert locust situation remain calm in Morocco and neighbouring countries.

Grasshoppers and locusts and climat change in setifian region [North-East of Algeria]

Mustapha Bounechada[1] and Fenni Mohamed[2]
[1]*University Ferhat abbas, Faculty of Scineces, Dpt of Biology, Setif, Algeria*
[2]*University Ferhat abbas, Faculty of Scineces, Dpt of Agronomy, Setif, Algeria*

The effects of climate change on our planet are beginning to be measured and assessed. Insects have proven to be particularly good indicators of these changes. The different work done on the Orthoptera species in the region of Setif [1991-1999] make it possible to determine whether species distributions, abundances, and phenologies have changed and to what degree they have done so. The effects of climate change on the grasshoppers and locusts, they may also help us understand why some species are more impacted than others. Results showed that the weather is the most significant factor that affects fluctuations in population abundance of the Orthoptera species.

Gray bird grasshopper *Schistocerca nitens* on a NW Hawaiian Island: a challenge to conservation

Alexandre Latchininsky[1]
[1]*University of Wyoming, Dept. 3354 - Renewable Resources, USA*

Gray bird grasshopper *Schistocerca nitens* (Orthoptera: Acrididae, Cyrtacanthacridinae) has occurred on the main Hawaiian Islands since 1964. It was first reported from the tiny (63 ha) and uninhabited Nihoa Island situated 250 km NW of Kauai in 1977. The island's known terrestrial biota include 26 vascular plants, 27 birds, and 243 arthropods; approximately half of the species are endemic to Nihoa or indigenous to Hawaii. Four plant species and two resident bird species are federally listed as threatened or endangered species. In 2002–2004, the grasshopper produced an outbreak that severely denuded Nihoa's vegetation. Potential threats to the island's biota, in particular, for the endangered insectivorous Millerbirds, are discussed. The case of *S. nitens*' establishment on the island of Nihoa presents a challenge for conservation biologists with respect to the justification for human efforts to extirpate the insect.

Food choice of the desert locust *Schistocerca gregaria* (forsk., 1775) (Orthoptera, Cyrthacantacridinae) in its solitary phase in Algeria

Guendouz Benrima Atika[1], **Duranton Jean François**[2] **and Doumandji Mitiche Bahia**[3]
[1]*1 Université Saad Dahleb, Département d'Agronomie, B.P. 270, Blida, Algérie*
[2]*2 CIRAD Acridologie, F-34032 Montpellier, France*
[3]*3 Institut National Agronomique, El Harrach, Alger, Algérie*

The gregarious phase of the Desert Locust, *Schistocerca gregaria* (Forsk., 1775), is known for a long time for its great polyphagia and the broad variety of crops attacked. Polyphagia seems more limited in the solitary phase whose diet is largely unknown. This work, conducted in the Algerian Sahara, deals with the qualitative and quantitative assessment of the diet of solitarious Desert Locust. The qualitative assessment of the diet was made by comparing the range of plant species in the locust biotopes with plant species identified in the faeces. The quantitative assessment was realized by comparing the frequencies of plant species observed in the faeces with their abundances in the field. The frequency of plant species consumed could be estimated by the ratio of imagos which have consumed the plant species on the number of imagos present in the biotope. The discrepancy observed between the plant species eaten and their abundances in the habitats shows a strict food selection. It appears that the diet of the Desert Locust depends on both the floristic composition of the vegetation and of the choices he made in his search for food. The food spectrum of the adult is extended to the species not very abundant and far from abundant. The adult displacement increases the probability of a widened choice. In general, the plants appreciated by the Desert Locust are those which allow the best development and reproduction.

Comparison of two Caelifera-rich communities in the semi-arid stage of North Algeria

Daniel Petit [1] and Leila Benfekih [2]
[1]*INRA-UMR 1061, Université de Limoges*
[2]*Département d'agronomie, Univ. Saad Dahleb, Blida, Algérie*

Monthly samplings of Caelifera were conducted during two years in the area of Ain Boucif (150 km in the western south of Algiers) in two herbaceous stations located in the semi-arid Mediterranean stage. Station 1 presents approximately 20% of bare ground with 27 Caelifera species and a Shannon index of 3.11 and with 61 plant species. Station 2 on the other hand has a total richness of 22 Caelifera species with a Shannon index of 2.71, and 66 plant species. A correspondence analysis of the two communities, followed by a cluster analysis, highlighted 3 sub-communities. The summer community is the most diversified, and was revealed identical in both stations, while the spring and autumn communities differ significantly, the one on station 1 being more diversified. A weekly survey of the biological stages of *Dociostaurus maroccanus* and *Ocneridia volxemi* was carried out. We hypothesize that the higher larval mortality of both species in station 1 would be due to a stronger predation pressure, in particular by larvae of the *Mantid Rivetina fasciata* and by Ensifera species that develop early in the season, as *Odontura algerica*.

ECOLOGY
Poster Presentations

PP28

Study on the nutritional ecology of *Oxya fuscovittata* to obtain a suitable food plant for their successful rearing

Arijit Ganguly[1], Chandrik Malakar[1] and Parimalendu Haldar[1]
[1]*Dept of Zoology, Visva-Bharati University*

Oxya fuscovittata is a widely distributed acridid in the grassland habitats of India. Experiments revealed that it is easy to culture this species in laboratory condition; hence it can be used as a model species for various ecological experiments on grasshoppers. For this, a continuous rearing is essential in the insectariums. The aim of the present study was to find out a suitable plant species that may be a better food plant for laboratory *O. fuscovittata* culture than *Cynodon dactylon* which is usually fed to them in the insectariums. Newly hatched nymphs of *O. fuscovittata* were reared on four selected food plants in the laboratory until they matured and died after completion of their life cycle. The food plants included: *C. dactylon*, *Sorghum halepense, Oryza sativa* and *Triticum aestivum*. Survival was highest (96.67%) and nymphal duration was shortest when rearing was on *S. halepense* (37 days in average, compared to nearly 48, 44 and 57 days for *C. dactylon, T. aestivum* and *O. sativa* respectively). Growth parameters (i.e. growth rate, specific growth rate, percent weight gain and average daily growth) showed that *S. halepense* is the most suitable host plant that results highest growth of the grasshopper, however, adult body weight did not vary significantly among the individuals fed with the selected food plants. Adult life span, number of egg pods laid per female and eggs hatched per pod were also observed. Results revealed that the females fed with *S. halepense* and C. dactylon gave the best results. It is concluded that *S. halepense* is the most suitable food plant, because the individuals fed on this plant grew faster than the others, adults lived a longer life and gave birth to a considerable amount of offspring.

PP29

Analysis of population trend in *Saga pedo* (Orthoptera: Tettigoniidae) on the edge of its range: more abundant or more intensively studied?

Jaroslav Holusa[1], Petr Kocarek[2], Pavel Drozd[2] and Robert Vlk[3]
[1]*Czech University of Life Sciences, Prague, Czech Republic*
[2]*University of Ostrava, Ostrava, Czech Republic*
[3]*Masaryk University, Brno, Czech Republic*

Long-term monitoring studies of animal population development in extent of decades are very scarce. Principal problem of the analyses is the lack of a reliable quantitative data, because a sampling period of existing systematic surveys rarely exceed a few years. Therefore we have only rare opportunity to observe long-term changes in abundance of populations, that allow to assess an influence of various environmental factor (e.g. global climate changes, extensive changes associated with changes of landscape structure, methods of land management etc). In the Czech Republic, *Saga pedo* reaches the northest edge of its range. The species occupy only one small area (the Pavlovské vrchy hills) in the long term and it has never been systematicaly monitored there till 2006. Since the first finding in 1922, *Saga pedo* has been recorded only several times and almost all findings have been published and the specimens preserved in museum collections. They have represented casual findings in all cases, with

only several exceptions carried out by entomologist specialized in different insects taxa, by vertebrate zoologists, by botanists or photographers of the nature. On the contrary, the species was recorded from many localities and its occurrence was relatively abundant during an intensive research carried out in 2005-2008. Based on increasing frequency of findings during last decades we could expect that the population size is increasing. However, this very simplifying view is biased due to unequal sampling effort during last 70 years. Therefore total number of papers concerning terrestrial fauna of the Pavlovské vrchy hills for each year was used as the weight (covariate) of the sampling effort. Based on the modified available data we asked if the population size of *Saga pedo* in the area of the Pavlovské vrchy hills has increasing trend, or if the trend only reflects an increasing probability of findings due to more intensive study of local nature. We found significant relationship between "sampling effort" and number of occasional records of *Saga pedo*. Consequently linear model with "sampling effort" as a covariate confirmed significant increasment of population size.

PP30

Influence of the drought on the food behavior of the moroccan locust *Dociostaurus maroccanus*

Malik Laamari[1]
[1]*Département d\'Agronomie, Faculté des Sciences, Université de Batna, Algeria*

The survey carries on the food regime of the moroccan locust *Dociostaurus maroccanus* (Thunberg, 1815) in the Aures region (Algeria) during 1993 and 1994. By the method of the stools analysis, the plants consumed by the different stages are identified and are quantified. In 1993, the wealth of the plant covering the ground let this locust to express its food preferences. While in 1994, the very precocious drought of the natural plant carpet obliged this acridien to widen its food specter. Effectively, a plant like *Peganum harmala*, poisonous to animals, as well as some wing fragments, paws, antennas, buccal pieces and even of whole individuals of aphids *Sitobion fragariae* and *Brachyunguis harmalae* are consumed extensively by the different stages.

PP31

Food composition of two European groundhoppers (Orthoptera: Tetrigidae: *Tetrix tenuicornis*, *Tetrix ceperoi*): bryophagy or detritophagy?

Petr Kocarek[1], **Sarka Grucmanova**[1], **Zuzana Filipcova**[1], **Lenka Bradova**[1], **Vitezslav Plasek**[1] **and Pavel Drozd**[1]
[1]*University of Ostrava*

Tetrigidae are known to feed on algae, mosses, small plants and detritus, but there is a lack of data about proportion of the above mentioned food types. There still remains a question what is the main food component of their diet. We studied food composition of the species *Tetrix ceperoi* (Bolivar, 1887) and *T. tenuicornis* (Sahlberg, 1893) by means of dissections and analysis of their gut contents. The percentage of food components within the gut content was

determined from microphotographs of the microscopic preparations. A dominant component of the diet of both species at each micro-locality was detritus (soil with unidentified decomposed organic matter). On average, it comprised 79.4% of the total amount of the food in *T. tenuicornis* and 89.9% in *T. ceperoi*. Females of both species consumed significantly larger amount of food, as well as more detritus and more mosses particularly; but the rate of detritus vs. mosses consumption was constant in both sexes and both species. Four moss species were found in the diet of *T. ceperoi* and five moss species in *T. tenuicornis*. The most frequent moss in the gut of both species was identified as *Bryum caespiticium*, which was the dominant moss species in the locality with relative coverage of 80%. Altogether, the presence of at least one fragment of one moss species was detected in 90% of *T. ceperoi* specimens and 97% of *T. tenuicornis* specimens. Besides mosses and organic detritus, some fragments of vascular plants (grasses), pollen grains, algae, hyphae of *Basidiomycetes*, and rarely also fragments of arthropods (Arachnida, Insecta) and *Tardigrada* were found. The total portion of these components in the food was not higher than 1.0% in particular species. This study was supported by grant No. 206/07/0811 of the Czech Science Foundation.

PP32

Egg survival strategies of the senegalese grasshopper during the dry season in the African sahel

Idrissa Maiga[2], Michel Lecoq[1] and Serge Morand[3]
[1] *Direction de la Protection des Végétaux, Niamey, Niger*
[2] *CIRAD Acridologie, F-34398 Montpellier, France*
[3] *CNRS, Institut des Sciences de l'Evolution, F-34095 Montpellier, France*

The Senegalese grasshopper is an important pest for the Sahelian crops in Africa. It develops 3 generations per year and undergoes an embryonic diapause during the long dry season that can last up to 7-8 months. Egg-pods, collected at the end of the rainy season, from mid-August to the end of September (period for diapause induction), were placed in incubation (in semi-natural conditions) and were humidified on various dates from November to August of the following year. Results show that the survival strategy of the Senegalese grasshopper during the dry season is more complex than previously supposed and does not rely merely on a simple embryonic diapause. The strategy combines several components. The embryonic diapause during the dry season allows a global adaptation to the regular seasonal variation in rainfall. The other components constituted the adaptations of the species to the various risks related to different irregularities in rainfall pattern. The high number of hatchlings within a short period at the end of the rainy season, for egg-pods laid before the end of August and without diapause, allowed an adaptation to the frequently abrupt end of rainfall. The possibility of embryonic quiescence can allow the eggs to survive for up to one year without diapause and constitutes an adaptation to a reduced rainy season (end before diapause induction). Lastly, the staggering of hatchlings for diapausing eggs over a lengthy period at the beginning of the rainy season, constitutes an adaptation to the progressive set in of the rains and to frequent long interspersed periods of drought following the first rains that trigger hatchlings.

PP33
Red locust phasis in Madagascar

Michel Lecoq [1], Abdou Chamouine[2] and My-Hanh Luong-Skovman[1]
[1]*CIRAD Acridologie*
[2]*Université de Tuléar, Madagascar*
[3]*CIRAD Acridologie*

The Red locust, *Nomadacris septemfasciata* Serville, is an important pest for various crops in Madagascar. The species is regularly surveyed and controlled by the National Antilocust Center. Studies on some field survey archives, from 2001 to 2007, highlighted that information on the phase statuses (gregarious vs solitarious) was lacking and that the criteria used were unsuitable, in particular for hoppers. During two consecutive rainy seasons, samples of hoppers were collected in the field within populations of very diverse densities, from less than 1 to several hundreds of hoppers per square meter. 1,147 hoppers were described on the basis of their pigmentation, including the general colour of the individual and the various black spots distributed over the entire body. The precise criteria making it possible to describe the phase status of a larva and that of a population as a whole were selected. A clear typology was established and about fifteen pigmentary classes were distinguished. Within a population, the respective percentages of each class, from the more solitary to the more gregarious, evolve in relation to the population density. From a practical point of view, 4 phase states were recognized (solitary, solitaro-transient, transient and gregarious). The threshold for phase transformation (hopper instars 4 and 5 mainly) was estimated at around 10 larvae per square meter. In lower density populations, only larvae belonging to the various solitary classes were observed. Beyond that level, the first manifestations of gregarism were noted with the appearance of larvae of the solitaro-transient and transient categories. The gregarious larvae started to appear in populations with around 60 larvae per square meter.

PEST MANAGEMENT

Oral presentations

Chair: David Hunter
Ataturk Conference Hall (14:15 – 16:30/ June 25, 2009)

Mapping potential Italian locust (*Calliptamus italicus*) habitats in NE Kazakhstan with satellite imagery

Alexandre Latchininsky[1] and Ramesh Sivanpillai[2]
[1]*University of Wyoming, Dept. of Renewable Resources, USA*
[2]*University of Wyoming, WyGIS Center / Botany, USA*

Abandoned croplands (fallows) with weedy vegetation dominated by sagebrush (*Artemisia* spp.) are the primary egg-laying habitats of the Italian locust (*Calliptamus italicus* L.) in NE Kazakhstan. From these breeding habitats locusts migrate to agricultural fields and destroy crops (grain, buckwheat, sunflower etc.) vital to the region's economy. Since 1990, more than 750,000 ha of croplands have become fallow in NE Kazakhstan, thus increasing the area of suitable habitats for the Italian locust. Plant protection service personnel monitor locust populations, forecast the infestation risk, and apply insecticide treatments to infested areas which exceed 1 million ha during outbreaks. Given the vast area (up to 6 million ha) that needs to be surveyed every year, traditional ground survey methods are inefficient and unreliable. We used the Indian Remote Sensing AWiFS data to map current Artemisia spp. shrublands and other vegetation in NE Kazakhstan. Spatial distribution of fallows was mapped using 1989-90 Landsat TM data on then active agricultural lands. These data were combined with vegetation map derived from IRS-AWiFS data to generate the potential locust habitat map. Plant protection specialists can incorporate this information in their future surveys. The spatial (56 m) and spectral resolution of the AWiFS data (4 bands) was sufficient to distinguish features such as riparian zones, water bodies and bare ground. However there was some overlap between the active and inactive croplands, and sparsely vegetated shrublands and bare ground. The large swath width provided by the AWiFS data (740 km) was helpful to map the entire region using an image acquired on the same day/time.

Effects of fire and post-fire grazing intensity on grasshopper assemblages in a northern North American grassland vary between years

David H. Branson[1] and Lance T. Vermeire[1]
[1]*United States Department of Agriculture, Agricultural Research Service, USA*

Grasshoppers are highly responsive to altered habitat structure, providing significant opportunities for managing populations and reducing outbreaks through habitat manipulation. Both burning and livestock grazing have been shown to influence grasshopper population density and community composition in multiple ecosystems. Responses of grasshoppers to late summer fire and post-fire grazing intensity were examined in a field experiment in eastern Montana, United States. The study was designed to examine how late summer fire or post-fire grazing intensity affects grasshopper densities and species composition. Treatments included no fire and 0% utilization, and fire with 0%, 17% and 50% utilization. The experiment was replicated at adjacent sites burned in consecutive years to encompass a wider range of climate conditions. Grazing plots were stocked with sheep in the summer following burning. Grasshopper population density and species composition were assessed before the fire and for two years following the fire. Following the first years fire, grasshopper abundance was 74% lower in burned plots in the 1st year post-fire and 51% lower in the 2nd year post-fire. In

contrast, burning in the second year of the experiment did not significantly reduce grasshopper population densities or affect species composition. The effects of burning on grasshopper populations were influenced by drought effects on fuel load at the time of burning. Burning when biomass is abundant appears effective in reducing some, but not all, grasshopper species. Post-fire grazing did not affect grasshoppers following the first fire. After grazing was initiated in the plots burned in the second year, grasshopper population densities were significantly lower in 50% utilization plots compared to ungrazed plots. Additional investigation is needed to examine if results differ when grasshopper densities are higher.

Towards better locust management in Caucasus and Central Asia

Annie Monard[1]
[1]*FAO, Italy*

Locusts and grasshoppers are the most important threat to agriculture in the Caucasus and Central Asia. The three main locust pests jeopardize food security and livelihood in both regions as well as in adjacent areas of Afghanistan and the Russian Federation. The most affected populations are often the most vulnerable communities living in the concerned rural areas, whose health and environment can moreover suffer from negative impacts of locusts control operations. Locusts are migrant and transboundary pests; in the Caucasus and Central Asia, the context is largely complicated by countries' geographical configuration. Any long-term solution to these locust issues can only result, in addition to adequate preparation by each single country, from concerted joint efforts by all countries. Against this background and following requests of assistance from the countries, FAO approved a 2-year regional project on 27/02/2009. Its long term strategic objective is to reduce occurrence and intensity of locust outbreaks in the Caucasus and Central Asia and thus preventing damage to crops and rangeland and impact on food security and livelihood of the most vulnerable rural communities; the immediate objective is to improve national and regional locust management in Caucasus and Central Asia and launch regional cooperation. Nine countries are concerned: Afghanistan, Armenia, Azerbaijan, Georgia, Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan and Uzbekistan. The expected outputs are the following: overview of locust situations and management in the 9 countries; definition of the common platform on which to build up regional cooperation; development of a technical network for exchange of information and experience; regular use of survey & control standard forms and issuance of national bulletins; improved and safer control strategies & techniques; increased visibility of locust issues, including a Website in English and Russian.

Toward a simulation model for desert locust gregarisation

Sidi Ould Ely[1], Magzoub Omer Bashir[2], Harry Bottenberg[3], Mohamed Abdallahi Babah Ebbe[4] and Ahmed Hassanali[1]
[1]*International Centre of Insect Physiology and Ecology, P.O. Box 30772, Nairobi, Kenya*
[2]*ICIPE Field Station, P.O. Box 1213, Port Sudan, Sudan*
[3]*USAID/West Africa, Accra, Ghana*
[4]*Centre National de Lutte Antiacridienne, B.P. 665, Nouakchott, Mauritanie*

Previously, we proposed a conceptual kinetic model for desert locust gregarisation based on our current understanding of the mechanisms associated with crowd formation in primary breeding areas of solitarious locusts and multiple interactions between gregarising groups and solitary individuals. We proposed that because of the heterogeneity of typical breeding areas and divergent behaviours of the two phases of the insect, a dynamic interplay between forces of crowd formation and dispersal (leading to a series of equilibria) can be expected depending upon distribution pattern of vegetation pattern and locust numbers. As part of a process of generating quantitative data on the relationship between these parameters, we studied phase shifts in solitarious nymphs that hatched from different numbers of egg pods in field arena with different densities of host plants (Heliotropium spp. and bulrush millet). Large variation in the pace of development of gregarious traits was found, depending on hopper and plant densities. Further arena studies involving different compositions of preferred and un-preferred plants (for oviposition, feeding and roosting by the solitarious locusts) are planned to shed further light on phase shifts under different plant configurations. These will be complemented by ground surveys in successive breeding seasons in selected habitats. These studies are expected to form a basis of a more accurate characterization of biotopes prone to gregarisation and construction of an area-wide locust outbreak model, which could facilitate the development of an early warning system critical for a preventive intervention strategy.

Evaluation of entomopathogenic fungi for locust control in Georgia

Eleonora Abashidze[1], Stefan Jeronski[1], Rami Horowitz[1], Alexander Latchininsky[1] and Gvantsa Aduashvili[5]
[1]*Plant Protection Institute, Tbilisi -0162, Georgia*
[2]*USDA ARS NPARL, Sidney MT USA*
[3]*The Volcani Center, ARO, Gilat Research Center, Israel*
[4]*Dept. of Renewable Resources, University of Wyoming, Laramie WY USA*
[5]*Tbilisi State University, Tbilisi, Georgia*

Orthoptera, esp. *Calliptamus italicus* L., *Dociostaurus maroccanus* Thunb.and *Locusta migratoria migratoria* L. , represent frequent, severe sources of crop loss in the Caucasus. Last 12 consecutive years Georgia has experienced heavy locust outbreaks because of significant agricultural changes, and there is a need to identify indigenous entomopathogenic fungi for locust control as alternatives to chemical pesticides. As part of an effort to build insect pathology infrastructure within the Plant Protection Institute in Georgia, a program was conducted to identify potentially useful fungi for locust control. Seven isolates of *Beauveria bassiana* and eight isolates of *Metarhizium anisopliae* (including five that may belong to the variety *acridum*) were made from georgian Orthoptera. These isolates were evaluated in terms

of conidial production in a pilot-scale, biphasic solid-substrate fermentation system, vegetative growth under constant temperatures of 10, 15, 20, 25, 30, 35, and 37° C. and also transient 39 and 41° C., mimicking periods of behavioral fever in host insects, and bioassay efficacy against *Melanoplus sanguinipes* and/or *Schistocerca americana*. Six of eight *Metarhizium* isolates produced >40 g conidia/kg substrate. All of the *B. bassiana* isolates were very poor conidia producers (<2 g conidia/kg substrate), however, tending towards extensive mycelial growth rather than conidiation, ruling them out for commercial development. There was considerable variability among the isolates in their tolerance to temperatures <15° C. and >30° C., as measured by radial growth on agar media. After 3-9 hr of transient exposure to 39 or 41° C. many showed a 1-2 day lag before resuming normal growth upon return to 28° C. All of the isolates were virulent for either of the two acridids. Several of the *M. anisopliae* isolates have potential for operational use as mycoinsecticides against Georgian Orthoptera. This research was funded by US Agency for International Developme nt grant TA-MOU-03-CA23-022.

Post-spray pesticide residues in Orthopterans and the risk assessment process for gorge-feeding birds and mammals

Pierre Mineau[1] and Paul Story[2]
[1]*Science and Technology Branch, Environment Canada*
[2]*Australian Plague Locust Commission, Department of Agriculture, Fisheries and Forestry*

The risk of massive pesticide exposure to gorging species of birds and mammals has been well documented following grasshopper and locust control operations. Despite increasing evidence that dermal exposure to pesticides is very important in assessing the risk to vertebrate wildlife, gorge feeding on recently sprayed grasshoppers and/or locusts needs to be carefully assessed in order to minimise the non-target impacts of spraying. Regulators in North America and Europe have long struggled with the prediction of residue levels in sprayed insects. Early attempts used relative surface to volume ratios (i.e. insect size) to set standard contamination levels. More recently, a wealth of empirical data from European farming conditions has led to proposed values that differentiate between foliar and soil dwelling species. However, a comparison of these proposed values with residue values measured on orthopterans in the course of control operations suggests that orthoptera-specific procedures need to be developed for risk assessment. In this presentation, we will review data available on residue levels in orthopteran species subject to control applications, assess the need to correct for ingested residues in the case of slow-acting insecticides and provide a road map for assessing the risk of pesticides to gorging species.

Efficacy of metarhizium *Anisopliae var. acridum* against the tree locust, *Anacridium melanorhodon melanorhodon*

Wail Haroon[1], Abdalla Mohamed Abdalla[1], M. Lecoq[2] and My Hanh Luong-Skovmand[2]
[1]*Department of Plant Protection, University of Kordofan, P O Box 160, El Obeid, Sudan*
[2]*CIRAD Acridologie, 34398 Montpellier, France*

The Tree Locust, *Anacridium melanorhodon melanorhodon* (Walker 1870) (Orthoptera: Acrididae) is a serious pest of gum Arabic tree, *Acacia senegal* in Sudan and elsewhere in Africa. Efficacy of *Metarhizium anisopliae* var. *acridum*, strain IMI 330189 alone and its mixture with Neem oil was investigated for two seasons (2006/07 and 2007/08) against the Tree Locust in the North Kordofan State of Sudan. The locust nymphs (4th instars) were treated with *Metarhizium*, *Metarhizium*/Neem mixture, Neem, and Malathion used as standard synthetic locusticide. The nymphs were directly sprayed in the field (50 x 50 m plots) with the test materials in a plantation of *Acacia senegal* using a hand-held micro-ulva sprayer. Nymphs samples were taken 24 hours after application from each treatment, placed in cages and observed for mortality. For the two seasons, respectively, mortality equivalent to 74.2% and 94.8% was obtained in locusts treated with the *Metarhizium*/Neem mixture in contrast to 64.2% and 81.5% mortality obtained in those treated with *Metarhizium* alone, respecting the previous season's order, during a three week period. These findings clearly reveal that mixing *Metarhizium* with Neem could enhance locust mortality and accelerate killing capacity compared to either *Metarhizium* or Neem when used alone. Among the treated plots, in comparison to the control, an obvious reduction in locust density was observed from the 3rd day after application in plots treated with Malathion (83.18%). The reduction in locust density in *Metarhizium* plots was similar to that observed in Malathion plots 12 days after application and this trend continued until day 16, while the efficacy decreased in Malathion plots. The study concluded that the use of Neem oil as a mixture with *Metarhizium* in the field boosts the killing speed.

First record on epizootics of *Entomophthora grylli*, on grasshoppers, *Oxya velox* in Indian subcontinent

Rakesh K. Gupta[1], Stefan T. Jaronski[2], K Srivastava[3] and K. Bali[3]
[1]*3Biocontrol Laboratory, Division of Entomology, SK University of Agricultural Sciences and Technology, Jammu, FOA, Main Campus, Chatha-Jammu (J&K) India- 1800*
[2]*1Laboratory of zoophysiology, Gent university, Gent, Belgium, 9000*
[3]*2USDA, ARS Northern Plains Agricultural Research Laboratory, Sidney, MT59720*

Grasshoppers are host to a wide range of micro-organisms that cause disease. Of these, entomopathogenic fungi have the greatest probability of exploitation as microbial control agents for managing grasshopper populations. The most promising candidates are found among the *Beauveria* spp., *Metarhizium* spp., as their conidia, or spores (the infective entity), are easily produced on commercially available solid substrates or in fermentation processes and can be formulated and applied similarly to other contact chemical pesticides. Nevertheless, ecologically obligate parasite *Entomophthora grylli* Fresenius (Batko) which is highly pathogenic and could cause spectacular field epizootics in many countries, has attracted interest as insect control agents, in both classical and augmentative biological control of Orthopteran. A naturally-occurring fungus called *Entomophthora grylli* was first time isolated from two species of grasshopper *Oxya velox* and *Oxya vicinia* in Jammu and Kashmir, India. The pathogen was widely distributed in command belt while the epizootic was confined along Indo –Pak border between 74 degree 24' and 75 degree 18', East longitude and 32 degree 50' and 33 degree 30' North latitude. On the basis of the available literature this seems to be the first record from the Indian sub-continent. The natural mortality was significantly influenced by the population density and number of pear shape conidia/cadavar. The percent infection

increased from 26.00 to 73.60 over the period of epizootics. Microscopic examination on the diseased insect over the period of study revealed the presence of germinating conidia from August to starting October. While, many infected grasshoppers apparently produced neither conidia nor resting spores, the cadavers were found full of hyphal bodies and resting spores towards the end of epizootics. These resting spore or their germ tubes were not invasive as such but if sprayed on wet tissue papers with around 90 % humidity they start germinating resulting in germ conidia which were able to induce dermal pathogencity. Further, it was observed that, the disease could not be transmitted to healthy individuals by ingestion However, intra-haemocoel infectivity of fresh resting spores, germinated resting spores, and germ conidia proved highly pathogenic as it could result in 81.4 to cent percent mortality of grasshopper. Since, *E. grylli* is fastidious it can only be propagated either in vivo in their orthopteran hosts. Although, it can be multiplied on large scale as protoplasts which are infective upon injection in their hosts but the lack of cell wall renders them very fragile, and they are neither infective upon application to the insect's cuticle nor upon ingestion. Since, in the present study, the resting spores remained viable for 2 years at -20°C a novel method on delivery of pathogen through "sticky molasses pan trap" was developed for inducing infection in grasshopper in paddy nursery.

PEST MANAGEMENT
Poster Presentations

PP34

Evaluation of dose-effect of spinosad® (125 g/l ulv) on Acridoïdea's species and assessment of their side effect on non-target fauna under field conditions in high Atlas mountain, Morocco

Abdelghani Bouaichi[1], Jamal Chihrane[1], Lajcen Idrissi Raji[1] and Ahmed Mouhim[1]
[1]*Centre National de Lutte Antiacridienne Ait Melloul, Maroc*

The biological activity of three doses of Spinosad 125 g/l (12, 25 and 45 g a.i./ha) on moroccan locust and grasshopper and their impact on non-target fauna were evaluated under the natural conditions in comparison with those of a conventional insecticide commonly used in locust control, Malathion, and an IGR's, Diflubenzuron. The dose-effects on locust were evaluated on the basis of density's population. The impact on non-target fauna was assessed on the basis of natural enemies trapped by Pitfall, yellow plate or mowing net. Results obtained showed a highly significant reduction of locust's densities, second day after treatment in the plots treated with Malathion 600 g a.i./ha, with Spinosad 45 g a.i./ha and Spinosad 25 g a.i./ha. In the untreated plots and the ones treated with Diflubenzuron 29 g a.i./ha and Spinosad 12 g a.i./ha, the decreases of locust's number, second day after treatment were not significant. These is however a gradual dose-effect of Spinosad. The Spinosad at the dose of 45 g a.i./ha has a double biological effectiveness with a high speed of action similar to those of Malathion and with a long persistence comparable to Diflubenzuron. The tested doses of Spinosad had no impact on coleopterans species mainly represented by Meloidae (*Mylabris spp*) and Tenebrionidae. The order of Hymenopterans represented essentially by bees of the genus *Apis* was significantly affected by Malathion and Spinosad 45 g a.i./ha, second day after treatment. However, ants of the genus *Formica* were not affected. The order of Dipterans represented by the two families of Bombylidae and Asilidae have either not been affected.

PP35

Impacts of the entomopathogenic fungus *Beauveria bassiana* (balsamo) vuillemin as biological control approach of mole crickets, *Gryllotalpa gryllotalpa* (Orthoptera: Gryllotalpidae)

Ahmed Amin[1] and Idris Salam[1]
[1]*Plant Protection Res. Institute, ARC, Egypt*

Mole crickets are one of the most destructive groups of vegetables, field crops, turf and pasture grass pests in Egypt and world wide countries based on the damage they cause and the high cost of control. The use of conventional insecticides in field crops and vegetables fields often exposes environmentally sensitive areas such as irrigation lakes, residential homes, and wildlife to the possible deleterious effects of chemicals. A more environmentally friendly control agent is the entomopathogenic soil fungus, *Beauveria bassiana*. The present work aims to evaluate the efficacy of using the biological agents *Beauveria bassiana* in controlling the mole cricket, *Gryllotalpa* sp. Field studies were conducted during 2005 and 2006 to study and evaluate the biologically based management program of cotton key pests in Bani Sweif Governorate located 150 km south Cairo, Middle Egypt Region. Results showed that the total number of the dead insects after seven days was 509 in the treatment of Hostathion - H 40 % in 2005 and 334 in 2006 followed by Biosect (6.4 X1010), Biosect (4.8 X1010), Biosect (4

X1010) and Biosect (3.2X X1010), respectively in both the two seasons. Also, the area of the new surface tunnels produced was significant with mean values for each set of replications varying from a low of 26.608 cm² in the Biosect (6.4 X1010)treatments in 2006 to a high of 281.869 cm2 in the control treatments in 2005 tests.

PP36

Impact study of the pesticides used to control desert locust (*Schistocerca gregaria* Forskål 1775) (Acrididae: Orthoptera) on two species of *Prionyx* (Hymenoptera, Sphecidae) in Aïr (Niger)

Mamadou Abdou[2], Ahmed Mazih[1], Said Ghaout[3], Inezdane Alzouma[2] and Abderrahim Hormatallah[1]
[1]*Institut Agronomique et Vétérinaire Hassan II, Morocco*
[2]*Centre National de Lutte Antiacridienne, Niger*
[3]*Centre National de Lutte Antiacridienne, Morocco*

A study of the biological efficacy of chlorpyrifos ethyl and fenitrothion - organophosphate pesticides used to control locusts and grasshoppers - on two species of *Prionyx* (Hymenoptera, Sphecidae) was conducted from July to December 2004 in the valley of Tafidet (Aïr), Niger, a summer breeding area of the Desert Locust (*Schistocerca gregaria* Förskal, 1775) (Acrididae: Orthoptera). The main objective was to evaluate the harmful effects of these pesticides on these two species of *Prionyx*, which are predators of grasshoppers, by using the method of the yellow traps fixed at 80 cm height, perpendicularly with the direction of the prevailing wind (270°). The experimental device used is the plan in complete random block. The experimental units are squares of 9 ha (300 m x 300 m). We had three blocks therefore three treatments. A treatment carried out with the chlorpyrifos ethyl at 225 g a.i/ha, a fenitrothion treatment at 450 g a.i/ha and a third treatment was the control where no chemical was applied. The blocks are distant between them 1000 m and the experimental units of 500 m between them. The treatments were carried out using a MicroUlva® sprayer. In each experimental unit, 40 yellow traps - distant of 5 m - were laid out (20 traps/diagonal). To facilitate interpretation of the results, the period post treatment was divided into three intervals of time: 1, 2 and 3 (respectively 1-12 / 16-24 / 28-60 days post treatment). The results showed that the chlorpyrifos ethyl and the fenitrothion had a reducing effect on the captures of insects in the treated plots, whereas the population of *Prionyx niveatus* and *Prionyx sp* increased in the pilot plots. In the first interval of time, the reduction in the captures varied from 59% to 80% with the chlorpyrifos ethyl, and from 34% to 74% with fenitrothion, respectively with *Prionyx sp* and *Prionyx niveatus*. During this first period no significant difference was noticed between the two treatments. At periods 2 and 3, the reduction of the captures of the two species of *Prionyx* was low (< 25%).

PP37

Predation and parasitism: an evaluation of their impact on Acridoidea's population dynamics in high Atlas mountain, Morocco

Badderdine Guennouni [1] Abdelghani Bouaichi [2] and Ahmed Mazih[3]
[1] Institut Agronomique et Vétérinaire Hassan II, CHA Agadir
[2] Centre National de Lutte Antiacridienne Ait Melloul, Maroc
3Institut Agronomique et Vétérinaire Hassan II, Morocco

The present study was carried in order to underline the relationship between locusts's dynamic and their natural enemies aiming at understanding the *Orthopteroïdea* population regulation in order to constrain the biological effect of some harmful locust's species such as the Moroccan Locust. The study was carried on the western north foothills of the High Atlas Mountain in Morocco, known as one of the Moroccan Locust's breeding area. The evidence of interaction between locust and their natural enemies has been accomplished by monitoring the population dynamics using method of density assessment. The evaluation of the relative abundance of some natural enemies has been achieved using trapping method such as "Yellow Trap" and "Pitfall". Field observations on behavior of locust and their natural enemies were conducted as an additional feedback to populations dynamic. The results show that egg's predation is two times higher than larvae and adult locust's predation overall. The Meloïdae's (Coleopterans) and Bombyliidae's (Dipterans) species seem to be the most egg-pod's destruction agent. An interaction between locusts populations and their predators has been somewhat established but it is insignificant because of the low densities of natural enemies. The important destruction caused by some vertebrates such as reptiles and birds predators at the end of the season has been nevertheless very crucial in controlling locust's population. In conclusion, predator's and parasite's populations ″cohabit″ with each other in harmony and sustained a natural equilibrium of locust populations to an acceptable threshold. This equilibrium is very fragile and depends sensitively on the external factors.

PP38

Modern technologies for locust control in Uzbekistan

Furkat Gapparov[1], Utapov Nemat[1], I. Hamraev[1] and B. Eshchanov[1]
[1]Scientific research Institute of plant protection of the republic of Uzbekistan

Over the ages one occasionally faces mass propagations and invasions of harmful locust. As a result of long-term researches in Uzbekistan more that 200 spices of locust were detected. The most dangerous pests on farming, pastures and sand-binding plants are *Dociostaurus maroccanus*, *Dociostaurus kraussi*, *Calliptamus turanicus*, *Caliptamus italicus*, *Dericorys albidula* and *Locusta migratoria*. *Dociostaurus maroccanus* is pest on pasture in Uzbekistan. In mass propagation period it damages for up to 80% of green mass and flies into pastures. During 1982-1983 it destroyed cotton crops of around 20 th.ha area. Over 1 mil.ha was treated against locust. In 2008 chemical treatment for *Dociostaurus maroccanus* control was effected on 520 th.ha. Reclamation of primary biotope soil for agriculture is rapid process, resulting to appearance of new ecosystem types on growth, with absolute priority of only single type of cultivated plant. Intensive culturing of cereals in desert and long-fallow areas developing zones in Uzbekistan brings locust habitation stages together with grain crops and increases

locust migration possibilities over the crops. Together with *Dociostaurus maroccanus* one can observe habitation of difference types of locust. Most of them are *Dociostaurus kraussi*, *Dociostaurus tartarus*, *Notostarus albicornis*, *Calliptamus turanicus*, *Sphingnotus satrapes*. Treatment of crops against *Dociostaurus maroccanus* all the locust complex and other insects is perished. Number of species composition changes took place due to dehydration process of Aral sea, which was recorded 50 years ago as one of the biggest lake in the world (fourth area place). Since 1960 Aral sea decreased it's dimension for over a half pf initial size – decreased for 75%. Interruption into an ecological balance in Aral sea area due to economical activity of human leaded to *Locusta migratoria* propagation station. The counter process occurred with *Calliptamus italicus*, environmental change favorably influence on development of this species, expends it's station. *Dericorys albidula* – I a habitant of desert Uzbekistan territories. The larva of *Dericorys albidula* evolves only on saxaul (*Haloxylon aphyllum, H. persicum* and *Salsola ricteri*). For over 20 years expansion of this species on desert is very rarely noted. The saxaul forest area in Uzbekistan is 700 th.ha. Reason of this locust type outbreak the fact that prior getting independence of Uzbekistan most of saxaul forests were destroyed being a good source of energy resource. Nowdays Uzbekistan is fully provided with hydrocarbons and saxaul sowing area increases year-by-year, mostly in Aral sea area. It is prescribed that this locust species develops only on saltwort growths (Solsola). Chemical methods of control are taken place only in plantations of saxaul. Before 1991 predominantly hexochloran was used against locust. Nowadays in view of current situation with locust propagation a new insecticide technology is applied, which enables to increase output and decrease application norms of insecticides. The new technology provides Ultra Low Volume spreading (ULV). The ULV method is more efficient, mostly in Uzbekistan with 71% desert area and problematic water delivery. By total transfer to ULV method we eliminate water delivery problems. For comparison, by ULV application spreading equipment norm considerably increased. By daily ULV application we can treat up to 500-700 ha a day, which is 25-30 times more that usual ordinary spreading equipment. Due to ecological disaster in Uzbekistan, our life makes us to transfer to safer locust control methods by application of ecological harmless preparations, eg. of benzoylurea group. In comparison with Nomolt and Dymeline, resting long-term residual effect, this method is of once treated sufficiency against locust, by preserving useful insects.

PP39

Impact of malathion and deltamethrin applied in ULV formulation on the honey bees *Apis mellifera*, under semi-field condition

Lajcen Idrissi Raji[1], Abdelghani Bouaichi[1], Abderrahim Hormatallah[2] and Mohamed Sarehane[2]

[1] *Centre National de Lutte Antiacridienne Ait Melloul, Maroc*

[2] *Institut Agronomique et Vétérinaire Hassan II, CHA Agadir*

The current study has been undertaken under semi-field conditions in order to evaluate the impact of Malathion and Deltamethrin in ULV formulation on the honey bees, *Apis mellifera* according to the CEB method n° 129. The lethal and repulsive effects induced by those insecticides commonly used in locust control has been assessed as direct application during the peak of foraging activity and as indirect treatment during the absence of foraging bees. Malathion, applied during the peak of foraging activity at the registered dose of 960 g a.i./ha

has exhibited a high risk against the honey bees. The lethal effects of Malathion applied in the presence of foraging bees has been characterised by a substantial mortality at day of treatment, 15 times higher than the average mortality due to captivity established three days before treatment. The repulsive rate calculated on the basis of the variation in average densities of foraging bees between treated and untreated zones, three days after compared to three days before treatments is about 87 %. Applied during the absence of foraging activity, the lethal effect of Malathion has decreased approximately to 55 % compared when applied during the presence of foraging bees. Deltamethrin applied at the recommended dose of 12.5 g a.i./ha, has however shown evidence of relatively minor risk against the honey bees compared to Malathion. The average mortality induced by Deltamethrin during the attendance of the foraging bees represented only 22 and 15 % of the mortality induced by the Malathion, a day and three days after treatment respectively. This ratio is set only to 5.6 % the day of treatment when Deltamethrin was applied during the absence of the foraging bees. This relatively risk-free effect of Deltamethrin is due to its short residual toxicity compared to Malathion.

PP40

Red locust in Southern Madagascar: suitable conditions for outbreaks and gregarious areas

Michel Lecoq[1], Emmanuel Gay Pierre[1] and My-Hanh Luong-Skovmand[1]
[1]*CIRAD Acridologie, France*

Recent outbreaks of the Red Locust *Nomadacris septemfasciata* Serville in Madagascar underlined the need for complementary research to improve understanding of population dynamics. Work was completed through field studies on a breeding site, investigations within rural populations and analyses of data from recent archives (2001-2007) collected at the National Locust Centre. This work leads to a finer comprehension of outbreak determinism and to a more precise delimitation of the zones most favourable for outbreaks and gregarisation. The key point for the success of breeding in the Red Locust (which has only one generation per year and an adult diapause during the dry season) is at the embryonic development level. December and January rains are of prime importance. A high breeding rate is related to good and regularly distributed rains throughout this period. A pluviometry of 250-300 mm /month seems the most favourable. Below 150 mm, embryonic mortality is high. Rains above 400 mm are also unfavourable. The use of this criterion can allow an early localisation of the sites presenting a higher risk of outbreak. In addition, the zones most favourable for gregarisation in the south of Madagascar were determined. These zones comprise several factors that are highly favourable for gregarisation: a massive arrival, at the beginning of the rainy season, of locust populations resulting from the dry season refugee zones and which are concentrated in restricted areas, a pluviometry allowing on average the best breeding rates observed in the south of the country, a recent deforestation that has increased the surface area of biotopes that are potentially favourable for breeding. As a result, an improvement of the strategy to control and prevent the Red Locust risk in Madagascar was proposed to the National Anti-Locust Centre.

PP41
Biotechnological approaches in pest management programmes

Seema Rathour[1], A.K. Karnatak[1] and D.C. Karnatak[1]
[1]*Biotech Park, Sectar G, Jankipuram, Lucknow*

Agriculture in India accounts for nearly 65% of the country's employment, 26% of the total GDP and nearly 20% of total export earning and supplier of raw material to major industries. The application of biotechnology techniques within the agriculture sector can potentially improve food security by raising crop tolerance to adverse weather and soil conditions, by enhancing adaptability of crops to different climates and by improving yields, pest resistance and nutrition, particularly of staple food crops. Biotechnology has contributed much to the field of insect pest management so far, through development of transgenic plants and other novel ecofriendly products to control insects. The steps involved in genetic engineering are selection of plant gene where introduction would be of positive value, identification of and isolation of such gene, transfer into plant cell and regeneration of complete plants from transfer cells/ tissue. Biotechnology has considerable potential to contribute to sustainable biological elements of IPM. Bt cotton is one of the major example. Rice, tomato, tobacco, sugarcane, potato and some other crops are resistant to *Chilo suppressalis Cnaphalocrocis medinalis scirpophaga incertulas Manduca sexta Lymantria dispar Heliothis virescens, H. zea, Pectinophora gossypiella, Spodoptera exigua, Trichoplusia ni, Diatraea saccharalis* and *Leptinotarsa decemlineata*. In IPM programme resistant plants are one of the most acceptable tools which are ecofriendly, non hazardous to non target organisms, no residue problems, no deleterious effect on natural enemies of insects, no pest resurgence and outbreak of secondary pests as has been seen with the use of insecticides. The future of biotechnology has much promise. Biotechnological innovations which improve the persistence or efficiency of these biological processes, for instance by improving survival or transmission rates of pathogens, or facilitating broadlybased quantitative crop resistance to pests, will be valuable to the sustainable IPM of the future. Beyond these areas, biotechnology has considerable potential application in improving mass production technologies for natural enemies of pests, and for improving diagnostic systems which allow scientists to recognize desirable plant genes and natural enemies, and which allow farmers to recognize potential pest problems before they cause damage. In its next generation, and with the benefit of the IPM experience, biotechnology stands to contribute greatly to sustainable pest management.

PP42
In vitro compatibility between metarhizium *Anisopliae var acridum* and neem seed oil

Wail Haroon[1], Jean Vassal[2], Abdalla Mohamed Abdalla[1], Michel Lecoq[2] and My Hanh Luong-Skovmand[2]
[1]*Department of Plant Protection, University of Kordofan, P O Box 160, El Obeid, Sudan*
[2]*CIRAD Acridologie, 34398 Montpellier, France*

The compatibility between *Metarhizium anisopliae* var. *acridum* (Deuteromycotina: Hyphomycetes) strain IMI 330189, and Neem seed oil *Azadirachta indica* A. Juss. was evaluated in the laboratory. The survival range of *M. anisopliae* in different concentrations of Neem oil is recognized. The fungus vegetative growth and conidia production were

considered as a yardstick for compatibility of the test materials. Water, diesel and groundnut oil dilutions of *M. anisopliae* were inoculated into Petri dishes containing semi-synthetic media + chloramphenicol (SSM+C) with different Neem oil concentrations and incubated for 10 days at temperatures of 20°C, 28°C and 34°C. The resulted fungus growth and the conidia produced were subjected to the classification model for in vitro products compatibility. At 28°C, all Neem concentrations below 2% were compatible with *M. anisopliae* and the concentrations 2% and 2.5% were moderately toxic, whereas at 20°C, 1% Neem was toxic to *M. anisopliae* when diluted in diesel and very toxic when diluted in water. On the other hand, at the higher temperature of 34°C all the tested concentrations were compatible with *M. anisopliae*. Generally, the fungus vegetative growth was more affected by Neem oil than the conidia production. The study concluded that Neem oil concentration in the mixture can be increased up to 1.5% with no deleterious effect on the fungus. Hence *M. anisopliae* and Neem could be mixed and used for locust control.

PP43

The fine structure of the Entomopathogenic fungus *Metarhizium anisopliae* infecting *Locusta migratoria* (Orthoptera: Acrididae)

Ying Yan[1], Fang Yu[1] and Long Zhang[1]
[1]*Key Lab for Biological Control of the Ministry of Agriculture, China Agricultural University*

The infection of *Locusta migratoria* by the entomopathogenic fungus *Metarhizium anisopliae* was studied using scanning and transmission electron microscopy. Conidia of *M. anisopliae* attached mostly to the socket of setae and intersegmental membranes. At the 28°C temperature at which the locusts were maintained, the fungal conidia germinated and produced appressoria within 24 h post-inoculation onto the cuticle. Three modes of infection of *M. anisopliae* condia were observed on the host cuticle: via a germ tube penetrating the cuticle, via an appresorium at the end of a germ tube or via an appresorium directly from the conidium However, penetration pegs were not observed until 2 days post-inoculation and they extended laterally between the sheets of procuticle and the spaces between the sheets changed because of the growth of penetrant structures. Penetrant hyphae started to invade the hemocoele by the third day. At 4 days, the fungus colonized the insect hemocoele and by 5 days had ruptured through the cuticle, and all the insects were dead.

PP44

Use of the biopesticide Green Guard® containing the entomopathogenic fungus *Metarhizium anisopliae* var. *acridum*, to control an outbreak of Migratory Locust, *Locusta migratoria*, in Timor Leste

Peter A Spurgin[1], H. McRae[1] and A. Monard[2]
[1]*APLC*
[2]*FAO*

The island of Timor lies to the north of Australia and is split into two separate countries; Timor Leste (formally known as East Timor), an independent state since 2000, and Nusa

Tenggara Timur (NTT), a province of Indonesia. The Timorese people are largely subsistence farmers with maize and rice the main food crops. Early in 2007 the UN Food and Agriculture Organisation (FAO) in Timor leste began receiving reports of increasing numbers of locusts damaging crops from several districts along the western border with NTT. The combined effects of an extended dry season and increasing locust activity led to an estimated 75% reduction in the maize crop in this important grain producing region. Ground and aerial surveys of the affected areas in March 2007 confirmed the species as Tropical Migratory Locust, *Locusta migratoria*, and determined that the outbreak straddled the politically sensitive border area of both countries and threatened developing rice crops. Given the difficult terrain and close proximity of the locust infestation to major watercourses and settlements throughout the area, aerial control using chemical pesticides presented real risks. Based on this, FAO and the TL Ministry of Agriculture (MAFP) approved the use of the biopesticide Green Guard® (formulated using the entomopathogenic fungus *Metarhizium anisopliae* var. *acridum*, strain FI-985), applied from a helicopter fitted with specialised ULV application equipment. This method of control had been used successfully in Australia by the Australian Plague Locust Commission (APLC) and offered the best option for a rapid and environmentally safe aerial control operation in Timor Leste. Funding for the project was provided by FAO (CERF) and the Australian Government (AusAID). The goals for the control operation were to protect existing rice crops and limit the potential for spread of the outbreak into other districts through the movement of swarms and further egg laying. From mid May to late June 2007 an aerial and ground spraying operation was undertaken against 56 high density adult swarm targets covering 2,318 ha treated using Green Guard® ULV. A follow-up ground spraying program by trained MAFP officers using both chemical and bio-pesticides treated a further 200 ha of small locust infestations close to crops and villages. The program was successful in reducing the total locust population within threatened areas in Western Timor Leste. This FAO control operation was significant because it demonstrated to the donor community that a biopesticide could be used successfully as part of a coordinated spraying program to control locusts in an area where aerial application of chemical pesticides had the potential to impact directly on rural communities as well as cause harm to sensitive aquatic environments throughout the region. It could be viewed as a model for tackling similar small scale locust control scenarios elsewhere in the world.

PP45
Locusts and grasshoppers as human being food

Aalya Mohamed Ibrahim Shomo[1]
[1]*Khartoum University, Faculty of Agricuture, Department of Crop Protection Khartoum, Sudan*

For further study tree locusts (sarieliel) samples *Anacridium melanorhodon melanorhodon* were collected from Mayo market in Khartoum while, the grasshoppers samples *Orientalis torbida* were collected from Alfashir city northen Darfur State in western Sudan. To find out the ratios of the moisture, ash, protein, oil content and total carbohydrates analysis were done for the complete tree locusts (without the wings and the legs), tree locusts (without the head and the abdomen contents), complete grasshoppers (without the head and the wings), grasshoppers (without the head and the abdomen contents) and the abdomen contents of the grasshoppers. However results indicated that the moisture content ratios were 6.7%, 4.7%,

4.6%, 4.2% and 7.4% respectively.the total ash ratios were 6.8%, 4.8%, 4.00%, 4.9% and 6.5% respectively. Protein contents were 54.7%, 59.5%, 45.1%, 27.7% and 37.2% respectively. Total oil content ratios were 19.4%, 21.75%, 38.4%, 23.4% and 19.5%.respectively. Total carbohydrates ratios were 12.4%, 9.25 %, 7.9%, 39.8% and 29.4% respectively. The results indicate that the locusts and grasshoppers are high in protein and fats.

SYSTEMATICS and PHYLOGENY

Oral Presentations

Chair: Charles BOMAR
Mediko SKS Hall (14:15 – 16:30 / June 24, 2009)

Evidence for a unique origin of the stridulatory file in Ensiferans

Olivier Béthoux [1]
[1]*Freiberg University of Mining and Technology, Department of Palaeontology, Germany*

Whether forewing structures involved in stridulation have been acquired convergently, or at once, among ensiferan lineages, is of prime interest for evolutionary biology, because of their striking similarity. Establishing proper homology hypotheses is essential in such case. New data on the forewing morphology of the earliest fossil material, and comparison with that of a selection of extant taxa, suggest that 'files' observed in ensiferans derived from a single structure, located on the vein *CuPb*.

Climatic fluctuations as motor for speciation processes in flightless Saltatoria (Insecta: Orthoptera)

Claudia Hemp[1]
[1]*University of Bayreuth, Animal Ecology II, Germany*

East Africa is known for its high degree of endemism, especially in the old basaltic rock mountains like the Eastern Arcs. Many genera of Saltatoria have radiated in montane areas, especially from the families with flightless members like Lentulidae, Eumastacidae, Acrididae and Tettigoniidae. In every isolated montane area different species are present. Their narrow ecological demands do not allow dispersion under the present climatic conditions. Their distribution pattern makes a reconstruction of the former climate (and thus the vegetation cover) possible when a spreading of common ancestors occurred and also corridors get apparent through which these ancestors originated. An overview of the projects dealing with different groups of flightless Saltatoria and first results are given.

Phylogeny and systematics of the *Isophya modesta* group (Phaneropteridae: Barbitistinae)

Dragan Chobanov[1] **and Beata Grzywacz**[2]
[1]*Institute of Zoology, Bulgarian Academy of Sciences, Sofia, Bulgaria*
[2]*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Krakow, Poland*

Phylogenetic relationships of the *Isophya modesta* group, distributed on the Balkans and in Central Europe with 15 taxa described, are studied by two different approaches. In the first approach an analysis based on data matrix including 14 taxa (outgroup *I. cania*) and 22 morphological and bioacoustic characters is accomplished using heuristic search in PAUP* 4.0 and results in 12 equally parsimoniuos trees. The *Isophya modesta* group is monophyletic with the strict consensus, the 50% majority rule consensus and the neighbour-joining analysis revealing 8, 10 and 12 monophyletic groups within the ingroup, respectively. The second

approach included maximum likelihood (ML) molecular analysis in PAUP* 4.0 and Bayesian inference (BI) in MrBayes 3.1.1 based on internal transcribed spacer 1 and 2 (ITS1, ITS2) sequences of rDNA and cytochrome oxidase subunit II (COII) and cytochrome B (cytB) of mtDNA of 12 taxa (outgroup *Barbitistes constrictus*). The ML-analysis shows weaker resolution, revealing 3 monophyletic groups and their paraphyly with the unresolved group *I. bureschi+B. constrictus*. The BI-analysis of rDNA shows similar results with 4 monophyletic groups, while IB of mtDNA differs considerably of all the other data and is subsequently rejected. On the basis of morphology and bioacoustics, a partial revision of the *Isophya modesta* group is accomplished with the following nomenclatural changes proposed: *I. pravdini pravdini*, syn.n. = *I. plevnensis*, *I. longicaudata* s.str., stat.rev., *I. longicaudata adamovici*, comb.n., *I. kisi*, syn.n. = *I. rhodopensis leonorae*, stat.n., *I. rhodopensis petkovi*, stat.n. The taxa are included in 4 species complexes with *I. bureschi* being basal taxon for the group.

Phylogeny of *Schistocerca* revisited: locust biogeography inferred from molecular fossils

Hojun Song[1], Matthew J. Moulton[1], Kevin Hiatt[1] and Michael F. Whiting[1]
[1]*Brigham Young University, USA*

Numts (nuclear mitochondrial pseudogenes) are non-functional segments of mitochondrial DNA (mtDNA) that have become translocated to the nuclear genome. Although numts can confound PCR-based molecular systematics using mtDNA, they can provide valuable information as molecular fossils about the evolutionary history of a group. Evolutionary history of the locust genus *Schistocerca* has been controversial, especially regarding the origin of the only African representative of the genus, *S. gregaria*. While a phylogeny based on morphology suggested a New World origin of the desert locust, a phylogeny based on mitochondrial DNA suggested an Old World origin of the species. Our preliminary study suggests that the members of *Schistocerca* have unusually high numbers of numts, which provides a unique opportunity to test biogeographic hypotheses using molecular fossils. We first generate numts of COI gene from the species of *Schistocerca* and reconstruct a phylogeny based on these data. We then reconstruct an independent phylogeny based on nuclear protein-coding genes to test whether mitochondrial data can adequately resolve the phylogeny of the genus. We deduce the diversification of *Schistocerca* and the evolution of numts based on these two datasets. We find that all species of *Schistocerca* have numts of COI that have been translocated multiple times throughout the diversification and after speciation event. Our data robustly suggest that *S. gregaria* is deeply nested within the New World *Schistocerca*, implying a single eastward transatlantic colonization after the genus diversified in the New World. We also find that the Galapagos endemic *Halmenus* is sister to two Galapagos representatives of *Schistocerca*, indicating a single colonization event to the island. Finally, we estimate divergence dates for the genus based on shared numts between different species.

Mitochondrial pseudogenes plague locust nuclear genomes

Karine Berthier[1], Marie-Pierre Chapuis[2], Seyed Mojtaba Moosavi[1], Donya Tohidi-Esfahani[1] and Gregory A. Sword[1]
[1]*The University of Sydney, School of Biological Sciences, The Molecular Ecology Lab, Sydney, Australia*
[2]*CIRAD, Locust Ecology and Control, Montpellier, France*

Mitochondrial DNA (mtDNA) sequences are commonly used in phylogenetic analyses and as DNA barcodes. However, recent studies have shown that the presence of nuclear copies of mtDNA sequences (numts) can mislead phylogenetic inferences and complicate species identification. Numts have been described in a variety of taxa including grasshoppers. We studied a region of the mitochondrial Cytochrome Oxidase 1 (COI) gene in two grasshopper species, *Locusta migratoria* (Lm) and *Chortoicetes terminifera* (Ct). We examined intra-individual variation in COI by analysing sequences from multiple clones of PCR products (114 and 110 clones in Lm and Ct, respectively). Neither the use of different DNA extraction protocols (Qiagen, Chelex and Alkaline lysis procedure) nor optimized PCR conditions successfully controlled for the presence of numts. In both locust species, we found (i) a prevalent haplotype matching with true mitocondrial COI sequences referenced in GenBank (36.8% and 28.2% of the clones in Lm and Ct, respectively), and (ii) numerous unique COI-like sequences (61.4% and 70% of the clones in Lm and Ct, respectively), hereafter referred as numts. Numts could be categorized as either proximal-numts (≤ 1% divergent) or distant-numts (≥ 10% divergent) based on their level of similarity to the true mitochondrial COI sequence. Intra-specific haplotype network analyses generally revealed that only proximal-numts connect to the primary mtCOI haplotype from the same individual (yielding a star-like network topology). Phylogenetic analysis of COI sequences from the Oedipodinae subfamily showed that numts were recently-derived and clustered within species' lineages. However, numts can be very similar across populations within species, and may pose a problem for phylogeographic analyses of populations and closely-related species.

Significance of male and female genitalia in the classification of Indian Acridoidea (Orthoptera)

Mohammad Kamil Usmani[1]
[1]*Department of Zoology, Aligarh Muslim University, India*

A comparative study on male and female genitalia was carried out in sixty seven Indian species of Acridoidea. An attempt has been made to describe and illustrate the different structures viz., epiphallus, aedeagus, supra-anal plate and cerci of male; spermatheca, ovipositor and sub genital plate of female in Acridoids with an aim to discover their significance in order to make the identification of genera and species, together with other generic characters more perfect and convenient. Shield or bridge-shaped condition of epiphallus; presence or absence of dorso-lateral appendices, oval sclerites and lophi on epiphallus; divided, undivided or flexured condition of aedeagus; presence or absence of gonopore process on aedeagus; condition of apical and pre-apical diverticula of spermatheca; presence or absence of glandular pouches of Comstock and Kellog on female subgenital plate;

rudimentary or well developed condition of egg-guide are taken as distinct family characters. Presence or absence of ancorae on epiphallus, long or short condition of aedeagal sclerites; elongate, slender or short and broad condition of ovipostor valves: presence or absence of Jannone's organs and setae on posterior margin of female subgenital plate; shape of diverticula of spermatheca are regarded as stable characters for separating the subfamilies. Shape of male supra-anal plate and cerci, broad or narrow condition of bridge, presence or absence of branch of bridge connecting lophi with bridge of epiphallus; mono, bi-or trilobate condition of lophi of epiphallus, length and upcurved or downcurved condition of apical valve of aedeagus, shape of posterior margin of female subgenital plate, presence of setae on the whole posterior margin or confined to lateral margins only; toothed, tuberculate or smooth condition of ovipositor valves, length of the lateral apodeme in relation to the dorsal valves are suggested as useful generic characters. shape of egg-guide of female subgenital plate, shape of ovipositor valves and apical tips, shape of male supra-anal plate and cerci, size of anterior and posterior lobes of lophi of epiphallus, size and shape of ancorae, shape of apical valves of aedeagus; size of apical and pre-apical diverticula and presence of protuberance on pre-apical diverticulum are taken as specific characters. These characters along with already recognized coventional characters have made the identification of families, subfamilies, genera and species more stable and practicable.

Bioacoustics, systematics and distribution of the *Phonochorion* genus (Orthoptera: Tettigoniidae: Phaneropterinae)

Hasan Sevgili[1], Selim S. Caglar[2] and İsmail K. Saglam[2]
[1]Harran University, Faculty of Arts and Sciences, Biology Department, Sanliurfa, Turkey
[2]Hacettepe University, Faculty of Science, Department of Biology, Ecological Sciences Research Laboratories, 06800, Beytepe, Ankara, Turkey

The *Phonochorion* genus (Orthoptera: Tettigoniidae: Phaneropterinae) is a little known group endemic to the Lesser Caucasus mountains. Only three species have been described within the genus: *Ph. satunini, Ph. artvinensis* and *Ph. uvarovi*. Apart from initial taxonomic descriptions and few geographic recordings no comprehensive systematic or biogeographic study has been conducted within this group. Our objective in this study is to conduct a through taxonomic and distributional revision of the *Phonochorion* genus in order to clear up the present confusion in the taxonomical status and distributional ranges of the species. Specimens were collected from 25 localities within the distributional ranges of all three species. Taxanomic revisions were based on morphology and bioacoustics data. The biogeographic pattern of morphologilcal variation was assessed using morphological indexes of known taxonomic importance; the pronotum/ovipositor ratio in females and length/width ratio of the subgenital plate in males. When the distribution of the genus is evaluated it was clearly seen that the Coruh Canyon is a major barrier for the dispersal of the species. When both bioacustic and morphological data are considered it is apparent that species level distinctiveness has not yet been reached for all characters in all of the extant taxa. Therefore it would seem that divergence within this group is quite recent and not yet complete. From a biogeographic context it is apparent that both the level of bioacoustic and morphological divergence is stronger between species in sympatry that those in allopatry. Our results

suggest that diversification between *Ph. uvarovi* and *Ph. artvinensis* could be the result of strong divergent sexual selection or ecological divergence whereas divergence of *Ph. satunini* seems most likely to be the product of allopatric isolation.

SYSTEMATICS and PHYLOGENY

Poster Presentations

PP46
Evolution of the copulatory apparatus in Ensifera (Orthoptera): introduction

Andrej V. Gorochov[1]
[1]*Zoological Institute, Russian Academy of Sciences, Russia*

For description of hypothesis on evolution of copulatory apparatus, it is necessary to select most suitable of recent phylogenetic schemes. Here these schemes are compared with each other by original variant of paleontological method which consists in comparison of minimized paleophylograms based on published phylograms by different authors. One of phylograms, supported by two independent investigations (morphological, by Gorochov; and molecular, by Flook with co-authors) and by this paleontological test, is put in base of above-mentioned evolutionary hypothesis. Evolution of copulatory apparatus in suborder Ensifera and its ancestors may be divided into 3 hypothetical stages reflected in some peculiarities of morphology: 1) highly hypothetic stage without copulation and without copulatory apparatus in most ancient (extinct) orthopteroid insects; 2) presence of independent organs for forming of spermatophore and for fixation of partners during copulation; 3) development of complicated organ with consolidation of these functions. Importance of usage of copulatory characters in generic and higher taxonomy (not only in species taxonomy) is discussed in light of most recent idea of "genital clock" which must replace old "key and lock" theory. This idea supposes that changes of copulative apparatus (if it is sufficiently complicated) follow after genetic drift with more uniform speed than external morphology and many peculiarities of biology and ecology, as this apparatus is less dependent upon situation in ecosystem.

PP47
Phylogeny of the European Saginae

Balázs Kolics[1], **Zoltan Acs**[2], **Dragan Petrov Chobanov**[3], **Shun Qiang Lo**[4], **Balázs Kovács**[5], **Deniz Şirin**[7], **János Taller**[1], **András Speciár**[6], **László Orbán**[4] **and Tamás Müller**[5]
[1]*Pannon University, Georgikon Faculty of Agriculture, Hungary*
[2]*Fitolab Ltd., Hungary*
[3]*Institute of Zoology, Bulgarian Academy of Sciences, Bulgaria*
[4]*Reproductive Genomics, Strategic Research Program, Temasek Life Sciences Laboratory, Singapore*
[5]*Szent István University, Faculty of Agricultural and Environmental Sciences, Hungary*
[6]*Balaton Limnological Research Institute of the Hungarian Academy of Sciences, Hungary*
[7]*Akdeniz University, Faculty of Arts and Sciences, Turkey*

The *Saga* genus (Charpentier, 1825) contains 13 species, among them the largest European orthopterans (Kaltenbach 1967). The only parthenogenetic and tetraploid species of the group is *Saga pedo* (Pallas 1771); protected throughout its territory which is several fold larger than that of its bisexual relatives. The *Saga* specimens, representing all 9 *Saga* species, were collected in Central Europe, the Balkan Peninsula and Asia Minor during summer 2006 and 2007. Mitochondrial and nuclear genes were sequenced to establish a phylogenic tree. The analysis of our data showed the following: European *Saga* species form a monophyletic

lineage. The most basal group appears to be the 'ephippigera-ornata' clade. The geographical transitional species *S. cappadocica* was positioned between European and Asian lineages. Our data support the idea that the European *Saga* lineage originated phylogeographically from the Asian clade. Our data also show significant differences of *S. c. gracilis* from *S. c. campbelli*, therefore we propose to place the former to a separate species level status, as *S. gracilis.*

PP48
Merits of nomenclatural procedures

Olivier Béthoux [1]
[1]*Freiberg University of Mining and Technology, Department of Palaeontology Germany*

The area of systematic biology is experiencing a scientific crisis, evidenced by the simultaneous use of distinct nomenclatural procedures. Merits of the various approaches are briefly exposed in this poster, with a special emphasis on the cladotypic procedure.

PP49
Grasshopper phylogeny: bringing exploration to science education

Charles R. Bomar[1] **and Stephen C. Nold**[1]
[1]*Department of Biology, University of Wisconsin-Stout, Menomonie WI, 54751, USA*

For many students introductory science courses are dull and uninteresting, even for those who will later enjoy a career in the sciences. Reasons for this lack of enthusiasm vary, including classroom activities that repeat advanced high school laboratories, course content that is too rich for students without previous science experience, or laboratories taught from a manual that promotes disconnected techniques without a particular theme or source of inquiry. To address these problems, we linked a first-year cell and molecular biology course with a specific faculty-driven research question. To address orthopteran speciation and morphological variations, the laboratory section of this course extracted, purified, amplified, and sequenced mitochondrial DNA from blue phase and wild type *Melanoplus femurrubrum* (DeGeer). Students discovered that wild type and blue phase variants were indistinguishable based on conserved cytochrome oxidase I gene sequences. During this experience, students developed a sense of the process of inquiry and original discovery. Most importantly, students saw the value in this approach since the data they generated ultimately ended up in a publication. This technique is powerful since students develop course-specific skills while growing as a scientist. Techniques such as these may also help to improve retention in the sciences and increase student's capacity for asking their own research questions at a later date.

PP50
Species file software and the Orthoptera species file

David C. Eades [1]
[1]*Illinois Natural History Survey, University of Illinois, USA*

The biggest change affecting the Orthoptera Species File (OSF) since the Orthopterists' Society meeting in Canada in 2005 has been the growth of Species File Software (SFS) as an entity separate from OSF. In the spring of 2009 the count of species outside of Orthoptera passed the count within Orthoptera. Termites are the only group within Polyneoptera not yet covered. Databases specialized for particular taxonomic groups play a critical role in the flow of data from research work to the large data aggregations that make the information more accessible to both specialists and to the general public. Electronic publication and the Internet provide major benefits in cost, accessibility and interactive presentation that can help users. SFS manages data for the taxonomic hierarchy, nomenclatural details, interactive Internet keys, and specimen data. There is extensive error checking at the time of data entry. Researchers located around the world can share in managing the data. SFS manages the flow of data to Species 2000 and other data aggregators. Important new developments are in progress or planned. Private species files are available to assist persons working on taxonomic revisions. When the work is published, the private copy can be merged back into OSF. Other developments include improved map generation, statistics about website usage, and web services to automate the exchange of data with other databases.

PP51
Taxonomy of *Chorthippus biguttulus* group (Orthoptera, Acrididae, Gomphocerinae) in Anatolia: morphometry support song based taxonomy

Deniz Sirin[1] **and Battal Çıplak**[1]
[1]*Department of Biology, Faculty of Arts and Sciences, Akdeniz University, Antalya, Turkey*

The *Chorthippus biguttulus* group, distributed in west Palaearctic, while intensively examined in Europe, is poorly known in Eastern Europe and West Asia, especially in the glacial refugia such as Anatolia. Currently, it is a general wisdom that species in this group are only recognizable by song characteristics. Morphologically cryptic and taxonomically controversial *Chorthippus biguttulus* group re-examined using morphometry. In this study, to test whether morphometry support song taxonomy, we measured 26 structures from 492 males belonging to 27 different populations of Anatolian members of *Chorthippus biguttulus* group (*C. bornhalmi, C. mollis, C.bozdaghi, C. ilkazi, C. biguttulus euhedickei*). We also studied 5 populations from Europe belonging to *C. bornhalmi, C. brunneus, C. mollis, C. biguttulus biguttulus* with the aim of comparison since they represent type locality. Data were analysed with factor analysis (FA) to find if there is structural associations among 27 morphometric characters. Canonical Discriminate Function (CDF) analysis was performed to ordinate the relationships between variables and cumulative values of variation produced by the factor scores. Results of male CDF suggested three distinct groups with nearly no overlapping. The axis of Function 2 clearly separates populations in subgroup-A from subgroup-B and subgroup-C. Second, axis of the Functions 1 separates subgroup-B and subgroup-C. Populations in subgroup-A corresponds to *C. brunneus* song type; those in

subgroup-B to *C. mollis* song type and that in subgroup-C to *C. biguttulus* song type. Although it is assumed that species in *Chorthippus biguttulus* group are cryptic in morphology, morphometry suggest congruent relationships with that of song.

PP52
The tribe Tetrataeniini (Acrididae, Leptyminae) a monophyletic group?

Marcos Gonçalves Lhano[1]
[1]*Federal University of Reconcavo of Bahia, Center of Agricultural, Environmental and Biological Sciences - Cruz das Almas/BA, Brazil*

The Neotropical subfamily Leptysminae (Orthoptera, Acrididae) was established by Amedegnato (1974), based mainly on the Neartic tribe Leptysmini proposed by Rehn & Eades (1961) and on two Neotropical tribes: Chloropseustini and Tetrataeniini. The author also divided this last one into two different generic groups: Oxybleptae and Tetrataeniae, according to their body shapes. The subfamily is formed by specimens that have the distal third of the hind tibia flattened, hook-shaped cercus and elongated or bacilliform body. According to some authors, this group derived from Ommatolampinae by ecological segregation and from Rhytidochrotinae by geographical isolation. In 1980, Roberts & Carbonell studied the group and divided it into two tribes: Leptysminae and Tetrataeniini (included here the tribe Chloropseustini). But many authors are still using the previous classification. This study aimed to test the monophyly of Tetrataeniini, the existence of generic groups inside the tribe and the relationship with Chloropseustini, using a cladistic approach based on external morphological characters (included male and female terminalia) and the internal male genitalia. Eighty four characters (53 from the external morphology and 31 from the phallic complex) from 54 species were used (all characters received the same weight and were treated as no-additive). *Microtylopteryx fusiformis* Rehn, 1905 (Ommatolampinae) and *Hylopedetes punctatus* Rowell & Bentos-Pereira, 2005 (Rhytidocrotinae) were used as outgroups. The matrix was analyzed using NONA 2.0 implemented inside WinClada ver. 1.00.08 (Nixon, 2002), 624 equally parsimonious trees (L= 393, Ci= 38, Ri= 77) were obtained. The strict consensus tree depicted the following generic relationship for the subfamily: ((*Chloropseustes*) (*Tetrataenia* (*Eumastusia* (*Mastusia* (*Oxybleptella* (*Guetaresia* (*Haroldgrantia* ((*Stenacris, Leptysma*) *Xenismacris*)))) (*Nadiacris* (*Cornops* (*Pseudostenopola* (*Stenopola*)))))))). Based on the results of the cladistic analysis the following conclusions were obtained (1) the tribe Chloropseustini constituted a monophyletic group with high support (Bremer support), defined by a large number of sinapomorphies; (2) Tetrataeniini did not resulted a monophyletic group because the tribe Leptysmini is included inside; (3) at the generic level, the actual classification is consistent with the cladistic results obtained herein; and (4) the generic groups Oxybleptae and Tetrataeniae did constitute natural groups.

PP53

Supraspecific systematics of groups currently belonging to *Platycleis* Fieber, 1852 and *Metrioptera* Wesmael, 1838 (Orthoptera: Tettigoniidae)

Bruno Massa [1]
[1]*Dipartimento SENFIMIZO, University of Palermo, Italy*

In the last decades, the use of subgenera has been the alternative to oligotypical genera. In his paper on *Platycleis* and *Metrioptera* Zeuner (1941) described 14 genera, ascribing to them ca. 80 species. Currently supraspecific taxa amount to 21, comprising 145 species. While the division into different genera was unanimously accepted for some groups of Tettigoniidae, in the case of Platycleidini (sensu Zeuner, 1941) it has prevailed the use of subgenera (Ragge, 1990). This research is based on the study of specimens preserved in different Museums. I obtained interesting results, of which I report here some conclusions. Pronotum disc: may be depressed, flat or rounded; median keel is generally present in metazona, mainly when pronotum is depressed or flat, but it is more or less obliterated when pronotum has rounded borders and disc. It resulted raised in *Platycleis*, to a lesser extent in *Tessellana, Metrioptera, Bicolorana, Roeseliana, Broughtonia, Vichetia, Zeuneriana, Parnassiana, Semenoviana, Yalvaciana* and *Montana*, all characterized by depressed or flat pronotum; conversely, it resulted obliterated or absent in *Alticolana, Eumetrioptera, Modestana, Sphagniana, Sporadiana, Squamiana, Sepiana, Incertana* and *Decorana*, all characterized by rounded pronotum borders and disc. Lateral hind margins of pronotum lobes: may be evidently excised, just excised or not excised at all. They may be perfectly triangular, as in *Sepiana*, or obliquely converging, such as in *Decorana, Incertana* and others. In *Platycleis* the excision of hind margins of pronotum lies ca. at 3/4 of its length, in *Tessellana* and *Montana* at 4/5, while in *Metrioptera, Bicolorana, Roeseliana, Broughtonia, Vichetia, Zeuneriana, Parnassiana* and *Semenoviana* pronotum is less evidently excised, just sinuous and extended in the last portion. Ratio "hind femora length/pronotum length": some taxa show high variability, as *Platycleis*, others are characterized by very long legs, as *Sepiana, Incertana, Tessellana, Montana, Modestana* and *Bicolorana*, some show very short femora, as *Eumetrioptera, Parnassiana, Sporadiana* and to a lesser extent *Zeuneriana*, remaining taxa have femora of intermediate length. Using the same criteria followed for other tribe of Tettigoniidae, results of this research consent to consider some subgenera raised to genus level.

PP54

The Rhaphidophoridae cave crickets of the Eastern Mediterranean area: a checklist of species from the Balkans, Greece and Turkey

Mauro Rampini[1], **Claudio Di Russo** [1], **Francesca Pavesi**[1] **and Marina Cobolli**[1]
[1]*Dipartimento di Biologia Animale e dell'Uomo, Università degli Studi di Roma "La Sapeinza"Viale dell'Università 32, 00185 Roma Italy*

Two genera of Rhaphidophoridae cave crickets are largely widespread in the subterranean habitats of the Mediterranean area, especially Southern Europe and Turkey. At the end of the last century 22 species belonging to the genus *Dolichopoda* Bolivar, 1880 and 12 species belonging to the genus *Troglophilus* Krauss, 1879 were reported in literature as inhabitants of

the caves of the Eastern Mediterranean area. Both genera are components of the parietal community, resulting important vectors of trophic energy within the caves. Morphologically these two genera differ in the number of spines on the hind tibiae and in the shape of genitalia. Furthermore on the basis of their ecology and of their morphological traits, i.e. the elongation of the appendages and body coloration, *Dolichopoda* species show a higher degree of cave adaptation than *Troglophilus*'. Most of the oriental *Dolichopoda* species are concentred in continental and insular Greece (17), and only few inhabit the Balkans (1) the Anatolia (2) and Trans-Caucasian area (2). On the contrary the *Troglophilus* genus has a very low number of species: 7 inhabit the Balkans, 3 Anatolia and 2 Aegean islands. Recent researches in these areas allowed us to identify and describe 11 new species of *Dolichopoda* (6 from the Ionic area, 2 from the Aegean islands and 3 from the Anatolia) and 3 of *Troglophilus* (1 from Santorini Island and 2 from Anatolia). The results of our work point out the richness of both genera in these regions: 48 out of 65 species and support the hypothesis of a common oriental origin for both genera, whose centre of dispersal, was in the former Aegean plate.

PP55

Paternal characteristics of song in *Anterastes* (Orthoptera, Tettigoniidae): Is there any evolutionary sign?

Mehmet Sait TAYLAN[1], Deniz SİRİN[1] and Battal CIPLAK[2]
[1]*Department of Biology, Graduate School of Applied and Natural Sciences, Akdeniz University, Antalya, Turkey*
[2]*Department of Biology, Faculty of Art and Science, Akdeniz University, Antalya, Turkey*

Anterastes (Orthoptera, Tettigoniinae) includes 10 species all of which described/diagnosed according to minor differences in morphology. A morphology based phylogenetic assumption suggests relationships of the species as (*A. uludaghensis* + ((*A. burri* + *A. serbicus* + *A. antitauricus*) + (*A. anatolicus* + *A. tolunayi* + (*A. niger* + (*A. turcicus* + *A. babadaghi* + *A. ucar*i)))). Paternal characteristics of male calling songs studied to test morphology based phylogeny. As in the phylogenetic tree, *A. uludaghensis* is the most aberrant species by the regularly repeating 4-element syllables (or diplosyllables) while others constitute a group by sharing 2-element syllables. Of the species with the 2-element syllables, the three species in *A. serbicus* –group and *A. tolunayi* produce a song containing regularly and continuously producing syllables which do not form separate multi echemes. However, *A. tolunayi* differs from other three by modified syllable type. In the four species of the *A. babadaghi* group which is the crown clade of the tree, there are syllables clusters or echemes separated by distinct gaps. The paternal characteristics of male calling song support the morphology based phylogenetic assumptions.

PP56
A website on European Orthoptera

Roy Kleukers[1], Baudewijn Odé [1], Luc Willemse [1] and Klaus-Gerhard Heller [2]
[1]*European Invertebrate Survey-Netherlands*
[2]*Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany*

In June 2009 the website Orthoptera of Europe (www.ortheur.org) will be launched. The first goal is to disclose photo's and sounds of as many species as possible. Everyone is invited to contribute. In a later stage the website will be extended with information on recognition, distribution, literature etc. We think this website will help amateurs and professionals alike and increase the interest for this group. Furthermore we hope that the website will provide a platform to exchange information between Orthoptera researchers. The project is organised by the European Invertebrate Survey the Netherlands.

PP57
Morphometry for taxonomy of *Anterastes*: partly congruent qualitative and quantitative morphologies

Asu AYTAÇ[1], Pınar KONU[1], Zehra BOZTEPE[1], Sarp KAYA[1] and Battal ÇIPLAK[1]
[1]*Department of Biology, Faculty of Art&Science, Akdeniz University Antalya-Turkey*

Anterastes is a Balkano-Anatolian genus and live in montane habitats. Ten species in the genus were diagnosed according to minor qualitative morphological differences. Fifteen morphological structures from male and 13 from female were measured and analyzed separately to see if metric morphology supports the species diagnoses by qualitative morphology. Different clustering analyses using Euclidian distance similarity were performed for different combinations of species; (i) nine species in the genus, (ii) three species in *A. serbicus* group and (iii) four species in the *A. babadaghi* group. The analysis for male suggested three clusters: the *A. niger* + *A. uludaghensis*, the *A. tolunayi* + *A. antitauricus* and the remaining 3 species. That for females suggested five clusters: *A. tolunayi*, *A. turcicus*, *A. niger*, *A.uludaghensis* and the other three species. Analyses of both male and female data from the *A. babadaghi* group suggested first *A. niger* as a distinct separate cluster. Remaining species clustered by male and female data differently. Female data suggest *A. turcicus* + (*A. babadaghi* + *A. ucari*), but male data suggest *A. babadaghi* + (*A. turcicus* + *A. ucari*). The clustering patterns produced from male and female data are also different for the *A. serbicus* lineage. Male data suggest *A. antitauricus* + (*A. serbicus*+ *A. burri*) and female data suggest *A. serbicus* + (*A. burri* + *A. antitauricus*). Morphometric data provide a considerable support to present status of the know species. However cluster patterns are not congruent with the known phylogeny. This incongruency may be due to evolving under similar ecological conditions. Since all species live in highland habitats and demand strict environmental conditions, possibly it leads to evolution of similar body size.

PP58

A phylogeographic study of *Ronderosia bergi* (Orthoptera: Acrididae) morphotypes

Josefina Silvia Alberghina[1], Maria Marta Cigliano[2], Elio Castillo[3], Dardo Marti[3], Carlos Lange[4] and Viviana Andrea Confalonieri[1]

[1]Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires. Ciudad de Buenos Aires. Argentina
[2]División Entomología, Museo de La Plata.La Plata, Argentina
[3]Laboratorio de Genética Evolutiva, Universidad Nacional de Misiones. Posadas. Argentina
[4]Centro de Estudios Parasitológicos y de Vectores, CIC-CCT La Plata CONICET-UNLP. La Plata. Argentina

Ronderosia bergi is one of the most widely distributed species of the tribe Dichroplini. It is found in Bolivia, Paraguay and Argentina, showing high variability in many phenotypic characters such as colour pattern, body size, and length of wings. The colour patterns had received different specific names (*Dichroplus distinguendus, D. brasiliensis, D. bicolor*). These were later considered as morphotypes of *Ronderosia bergi* by Cigliano (1997) because no differences in male genitalia and no morphological discontinuities were found among them to warrant separate specific status. However, the fact that viable hybrids were produced from laboratory crosses between individuals of different phenotypes and one mating type but not for the reciprocal cross raised questions about possible incipient reproductive isolation barriers. The aim of this study is to determine, through a phylogeographic study of a mitochondrial gene (cytochrome oxidase I), whether individuals of *R. bergii* belonging to the same morphotype are grouped within reciprocally monophyletic clades. Specimens with different morphotypes collected from several localities in Argentina, Bolivia and Paraguay were included in the analysis. *Atrachelacris grammineus, Ronderosia malloii* and *R. forcipatus* were used as outgroups. Phylogenetic analysis using Maximum Parsimony criteria showed *R. malloi* as the most basal group within the genus and *R. forcipatus* as the sister species of the *R. bergi* complex. Within this latter species, individuals were not grouped either by morphology or by geographical proximity, thus indicating that morphological discontinuities do not affect the biological species status.

PP59

A phylogenetic analysis of the "paranaense-pampeano" assembly of species (Orthoptera: Acrididae: Melanoplinae) based on morphological and molecular characters: testing the monophyly of this informal group

Pablo Adrián Dinghi[1], Viviana Andrea Confalonieri[1] and Maria Marta Cigliano[2]

[1]Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires. Ciudad de Buenos Aires. Argentina
[2]División Entomología, Museo de La Plata. La Plata. Argentina

The Melanoplinae is the largest subfamily of grasshoppers in the New World, inhabiting a broad range of habitats from Alaska to Patagonia. The tribe Dichroplini is the most diversified group among South American Melanoplinae. Within this tribe, the genera *Scotussa, Leiotettix, Ronderosia, Atrachelacris, Chlorus, Eurotettix* and have been grouped into the "Paranaense-Pampeano" generic group based exclusively on characters of the male

genitalia. The group is distributed in the biogeographic province giving rise to its name. Recent phylogenetic studies based on molecular data, albeit limited in sample size, showed very weak support values or no support for the group, depending on the methods used to evaluate the phylogenies. In this study we used molecular and morphological characters to test the monophyly of the "Paranaense-Pampeano" genus group. Morphological characters referred to the general morphology, male and female genitalia. Molecular studies involved the sequencing of part of a mitochondrial gene, the cytochrome oxidase I. Individual and combined phylogenetic analyses were performed under standard parsimony analysis and parsimony analysis under implied weights. Results showed that the Paranaense-Pampeano informal group within the Dichroplini tribe, previously recovered from morphological characters, can also be viewed as a natural group when molecular characters are considered. In general, the molecular data provided evidence for relationships that agreed more than they disagreed with the morphology-based-relationships. This analysis highlights the importance of combining all available evidence in order to produce the best-supported proposition of genealogical relationships.

PP60

Molecular composition of supernumerary (B) chromosomes from eastern populations of the grasshopper *Eyprepocnemis plorans*

Viktoria Dzyubenko[1], Alexander Bugrov[2], Tatiana Karamysheva[3] and Nikolay Rubtsov[3]

[1]*Novosibirsk State University, Pirogov str., 2, Novosibirsk 630090, Russia*

[2]*Institute of Systematics and Ecology of Animals, Russian Academy of Sciences, Siberian Branch, Frunze str. 11, Novosibirsk 630091 Russia.*

[3]*Institute of Cytology and Genetics, Russian Academy of Sciences, Siberian Branch, Pr. Lavrentjeva, Novosibirsk 630090, Russia*

We have analyzed the B chromosome polymorphism in populations of *E. plorans plorans* from Armenia and Turkey and *E. plorans meridionalis* from South Africa. Population of *E. plorans meridionalis* collected at South Africa lacked B chromosomes. In Armenian populations we found 6 new morphotypes of B chromosomes (Ba1, Ba2, Ba3, Ba3iso, Ba4 and Ba5). Turkish populations possess 2 types of supernumerary chromosomes (Bt1 and Btmini). The dominant Bt1 is similar to Ba3 found in Armenia. Grasshoppers from Armenian populations showed 18S rDNA in C-positive types of Bs and in pericentromeric regions of chromosomes S9 and S11. This suggests that "eastern" types of Bs originate from one of these autosomes (S9 or S11). FISH with microdissection B3- and B3c-probes made from hole Ba3 chromosome and interstitial part of its arm showed that B chromosomes consist of not only rDNA but and repeats of satDNA which reveal homology with pericentromeric regions of A chromosomes. C-negative Ba4 doesn't paint with any DNA-probes and only FISH with B3-probe paints its pericentromeric region. B4-probe made from hole Ba4 chromosome paints euchromatic areas of all chromosomes, S10 chromosome shows the brightest signal, that allows us to propose it as ancestors for Ba4. FISH B4-probe with C-positive B chromosomes shows signal at pericentromeric area only. This data suggests that pericentromeric satellite repeats of DNA of A and B chromosomes of *E. plorans* from different populations are homology. Pericentromeric area of chromosomes of *E. plorans meridionalis* from populations from South Africa doesn't paints with B3- and B4-probes.

Probably, the satellite repeats of DNA in these areas of chromosomes of *E. plorans plorans* and *E. plorans meridionalis* are different. Supported by grant of Russian Foundation for Basic Research No 09-04-00401a (for A. Bugrov)

PP61

Comparative analysis of rDNA and tDNA locations in the genus *Isophya* (Orthoptera, Phaneropterinae)

Elzbieta Warchalowska-Sliwa[1], Beata Grzywacz[1], Anna Maryanska-Nadachowska[1] and Dragan P. Chobanov[2]
[1]*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Poland*
[2]*Institute of Zoology, Bulgarian Academy of Sciences, Bulgaria*

The chromosomal location of the ribosomal 18S rDNA and telomeric repeates has been analyzed by means of fluorescence in situ hybridization in 20 species of the genus *Isophya* collected in Bulgaria, Poland, and Russia (Siberia). All species studied showed chromosome number consisting of 2n=31, X0 in males and 2n=32, XX in females. FISH probes were performed on spermatogonial mitoses and spermatocyte nuclei at different stages of meiosis in all species. In most of them rDNA was limited to two bivalents (M4 and S13 or M2 and M4) in contrast to four species that show 4–5-rDNA cluster. *I. rammei* was the only species showing additional rDNA in the X chromosome. The rDNA sites were restricted in the paracentromeric region, only in *I. rectipennis*, both rDNA clusters were observed in the telomeric position. In some species the size of the fluorescent region varies between homologues, this suggests the existence of a polymorphism for the number of copies of the ribosomal genes. Variation in the distribution of rDNA contributed novel phylogenetic marker in the genus *Isophya*. In most chromosomes of all species the FISH with the (TTAGG)n probe was detected at the distal ends of each autosome. Differences in the intensity of the hybridization signal were detected among most of the autosomes of each species, and in the X chromosome of some of them.

PP62

Using DNA sequences of two mitochondrial genes (*COI* and *COII*) for taxonomy and phylogeny of Tettigoniidae

Alexander G. Bugrov[1,3], O.S. Novikova[1, 2], A. V. Gorochov[4] and A.G. Blinov[2]
[1]*Institute of Systematics and Ecology of Animals, Russian Academy of Sciences, Siberian Branch, Frunze str. 11, Novosibirsk 630091 Russia.*
[2]*Institute of Cytology and Genetics, Russian Academy of Sciences, Siberian Branch, Pr. Lavrentjeva, Novosibirsk 630090, Russia*
[3] *Novosibirsk State University, Pirogov str., 2, Novosibirsk 630090, Russia.*
[4]*Zoological Institute of Russian Academy of Sciences, Universitetskaya naderezhnaya, 1, St. Petersburg 199034, Russia.*

Molecular phylogenetic analysis was used to examine a number of morphologically based hypotheses concerning the taxonomic status and relationships of the subfamilies in Tettigoniidae. Two mitochondrial gene (cytochrome oxidase subunit I and cytochrome oxidase subunit II) sequences were determined for six subfamilies: Bradyporinae, Tettigoniinae, Phaneropterinae, Conocephalinae, Mecopodinae and Hetrodinae. The results support a monophyletic Tettigoniidae and monophyly of all studied subfamilies. Bradyporinae were found to be more closely related to Tettigoniinae than Hetrodinae. *Hetrodes pupus* (Hetrodinae subfamily) has the highest rate of divergence of nucleotide sequences compared with the rest of katydids. Molecular analysis supports a hypothesis of closely relationship of Bradyporinae and Tettigoniinae and contradicts the suggestion that the external similarity of Bradyporinae and Hetrodinae katydids is a result of origin from a common ancestor. Supported by grant of Russian Foundation for Basic Research No 09-04-00401a (for A. Bugrov)

PP63

Assessing the effects of primer specificity on eliminating numt coamplification in DNA barcoding

Matthew J. Moulton[1], Hojun Song[1], and Michael F. Whiting[1]
[1]*Brigham Young University, Department of Biology, Provo, UT 84602, USA*

DNA barcoding is a method of species identification based on a short mitochondrial DNA fragment of Cytochrome Oxidase I. DNA barcoding has proven useful in a number of lineages, but has limitations when nuclear mitochondrial pseudogenes (numts) are present in a species, and this is especially problematic for Orthoptera. Numts can be coamplified with the orthologous mitochondrial DNA when using universal primers and this can lead to incorrect species identification and overestimation of the number of species. One frequently used method for avoiding numt coamplification is to design specific primers, but the efficacy of this method has not been thoroughly tested. Here, we test a hypothesis that increase in primer specificity would reduce numt coamplification by comparing sequence characteristics of four orthopteran species generated using the Folmer primers, Orthoptera-specific primers, and species-specific primers. We find that numts can be coamplified to some degree in all four lineages regardless of primer specificity. Moreover, we discover that primers of different specificity are capable of coamplifying similar types of numts. While many numts have stop codons or indels, a number of numts do not have these characteristics, making it difficult to distinguish from orthologous sequences. Our findings suggest that taxonomic impact of numt coamplification is quite severe and more care is necessary for DNA barcoding to work successfully.

PP64

Jurassic-Cretaceous fossil Hagloidea from China

Gu Junjie[1], Ren Dong[1] and Shih ChungKun[1]
[1]*Key Laboratory of Insect Evolution & Environmental Changes, Capital Normal University, Beijing 100048*

Widespread non-marine Mesozoic deposits in North China often contain plentiful fossil insects. Among them, fossil Orthopterans, a fairly abundant and diverse group of insects, have been collected in the Mesozoic fossil sites in Northeast China. Two key localities are the Middle Jurassic Jiulongshan Formation in the eastern Inner Mongolia, which includes the well-known Yanliao biota, and the Early Cretaceous Yixian Formation in western Liaoning and northern Hebei, including the famous Jehol biota. A group of new species of Hagloidea, as representatives for saltatorial Orthopterans, have been described from these localities. Since the first fossil Orthopteran was described by Lin Qibin in 1965, 82 species and 43 genera assigned to 2 families (Haglidae and Prophalangopsidae) of Hagloidea have been described from China. It includes a new subfamily Chifengiinae Hong, 1982 and 30 new genera. Most of the early works were carried out by Lin (1965, 1977, 1980, 1982) and Hong (1982, 1983, 1984, 1986, 1988), but validity of some of these species are being seriously questioned.
The collection of fossil insects in the Key Laboratory of Insect Evolution & Environmental Changes, Capital Normal University (CNU) has reached more than 150,000 pieces. Of which, we estimate that there are about 4000 pieces of Orthopteran fossils. Many of these materials have not been studied in details and the specimens remain unidentified. Many of these fossil specimens are well-preserved with bodies, antennae, wing venation or markings, ovipositor and even eggs. These specimens provide us opportunities to study taxonomy, morphology, defense mechanism, behavior, reproduction, and key data to understand evolutional changes and biogeographical dispersal.

Contact Information of all the Participants

Participant Name	Email
Abashidze, Eleonora	elena@gacor.org.ge
Abdalla, Abdalla Mohamed	khalil2004@hotmail.com
Abiodun, Odunayo Rıchard	aoyostate@consultant.com
Acheuk, Fatma	criquet72@yahoo.fr
Adebanjo, Ayoola Stephen	aoyostate@consultant.com
Akınbayode, Akınbıyı Alexander	aoyostate@consultant.com
Allegrucci, Giuliana	allegrucci@uniroma2.it
Amin, Ahmed	aahakaa@yahoo.com
Ammar, Mohamed	ben.hamouda@yahoo.fr
Atika, Guendouz Benrima	atiguen@yahoo.fr
Atitebi, Sherıff O	protocol_office2006@yahoo.com
Baei, Mazyar Sharıfzadeh	mazyar.sharifzadehqgmail.com
Balakrishnan, Rohini	rohini@ces.iisc.ernet.in
Bahia, Doumandjı Mıtıche	doumandjimitiche@yahoo.fr
Baldwyn, Torto	btorto17@yahoo.com
Balogun, Boanerge B.	protocol_office2006@yahoo.com
Başibüyük, Hasan H.	hbbuyuk@cumhuriyet.edu.tr
Bazelet, Corinna	corinna.bazelet@gmail.com
Benjamin	blukoki@yahoo.fr
Berger, Dirk	dirk.berger@senckenberg.de
Berthier, Karine	kberthier@usyd.edu.au
Béthoux, Olivier	obethoux@yahoo.fr
Blanchet, Elodie	elodie.blanchet@cirad.fr
Bomar, Charles R.	BomarC@uwstout.edu
Bouaichi, Abdelghani	Bouaichi@nextagadir.com
Bounfour, Malika	mbounfour@yahoo.com
Bozcuk Ali Nihat	bozcuk@hacettepe.edu.tr
Branson, David H.	dave.branson@ars.usda.gov
Braun, Holger	grillo@illinois.edu
Bruno, Massa	zoolappl@unipa.it
Bugrov, Alexander	victoriad@mail.ru
Bugrov, Alexander	bugrov@fen.nsu.ru
Bush, Sarah L.	bushsl@missouri.edu
Carron, Gilles	Gilles.Carron@unige.ch
Carbonell, Carlos S.	cecarbo@montevideo.com.uy
Chapius, Marie-Pierre	chapuimp@supagro.inra.fr
Chidi, Okhuelegbe Goodluck	protocol_office2006@yahoo.com
Chobanov, Dragan	dchobanov@gmail.com
Cigliano, Maria Marta	cigliano@fcnym.unlp.edu.ar
Ciplak, Battal	ciplak@akdeniz.edu.tr
Cohn, Theodore J.	tcohn@sunstroske.sdsu.edu
Confalonieri, Viviana Andrea	vconfalonieri@hotmail.com
Conteh, Rashid Abraham	sikysystemproduction07@yahoo.com
Daniel, Petit	daniel.petit@unilim.fr
Deen, Farid Shamsu	pharea88@yahoo.com

Contact Information of all the Participants

Participant Name	Email
Desutter-Grandcolas, Laure	desutter@mnhn.fr
Dewhurst, Charles	……..
Eades, David C.	dceades@illinois.edu
Ebbe, Mohamed A. Babah	maouldbabah@yahoo.fr
Egwuatu, Chukwudu Ejike	teresaphilip333@yahoo.com
Elsner, Norbert	nelsner@gwdg.de
Ely, Sidi Ould	sidiouldely@yahoo.com
Emmanuel, Guyandiga Guyzanga	emmanuelguyzanga@yahoo.fr
Emmanuel, Ezgugozie Emeza	protocol_office2006@yahoo.com
Foucart, Antoine	antoine.foucart@cirad.fr
Gangopadhyay, Arijit	jitari.ganguly@rediffmail.com
Ganguly, Arijit	ypkwsy@gilgsj.com
Gapparov, Furkat	furkat@globeinterstar.com
Gorochov, Andrej V.	orthopt@zin.ru
Gottsberger, Brigitte	brigitte.gottsberger@univie.ac.at
Grant, Paul B.C.	pbcgrant@sun.ac.za
Grzywacz, Beata	grzywacz@isez.pan.krakow.pl
Gu, Junjie	b7b7bb7@163.com
Guennouni, Badderdine	gnbadr@gmail.com
Gueye, Youssoupha	guyeyou@yahoo.fr
Gupta, Rakesh	rkguptaentoskuast@gmail.com
Haldar, Parimalendu	pa_haldar@yahoo.co.in
Halouane, Fatma	fatmahalouane@yahoo.fr
Hamouda, Amel Ben	ben.hamouda@yahoo.fr
Haroon, Wail	zckolr@qewqxx.com
Harrat, Abboud	abboud52@yahoo.fr
Hartbauer, Manfred	Manfred.Hartbauer@uni-graz.at
Heller, Klaus-Gerhard	heller.volleth@t-online.de
Hemp, Claudia	andreas.hemp@uni-bayreuth.de
Hochkirch, Axel	hochkirch@uni-trier.de
Holusa, Jaroslav	holusaj@seznam.cz
Hunter, David	davidmhunter@yahoo.com.au
Igboanugo, Nicholas	seenick4sure@yahoo.com
Ikhlayel, Mushir	mushir.1987@yahoo.com
Isah, Priscilla	protocol_office2006@yahoo.com
Ismael, Soumah	soumahismael78@yahoo.fr
Junjie, Gu	orthoptera@foxmail.com
Jurgen, Huybrechts	jurgen.huybrechts@bio.kuleuven.be
Kaňuch, Peter	Peter.Kanuch@ekol.slu.se
Kamara, Abu Bakarr	ympasl@gmail.com
Kamara, Mohamed	icaphr_int@yahoo.co.uk
Kaya, Sarp	kaya_sarp@hotmail.com
Kenyeres, Zoltán	kenyeresfirst@gmail.com
Kerth, Claudius	c.kerth@sheffield.ac.uk
Khadija, Abbassi	abbassi_khad@yahoo.fr

Contact Information of all the Participants

Participant Name	Email
Khalilov, Namiq Javanshir Oglu	dr.namik@rambler.ru
Kleukers, Roy	kleukers@naturalis.nl
Klimas, Dita	……
Klöpfel, Anja	Akloepf@gwdg.de
Knowles, Lacey	knowlesl@umich.edu
Kocarek, Petr	petr.kocarek@osu.cz
Kolics, Balázs	bkolics@gmail.com
Kokanowa, Ejebay	eoka04@rambler.ru
Korkmaz, Ertan Mahir	ekorkmaz@cumhuriyet.edu.tr
Kristin, Anton	kristin@savzv.sk
Laamari, Malik	laamarimalik@yahoo.fr
Latchininsky, Alexandre	latchini@uwyo.edu
Lecoq, Michel	lecoq@cirad.fr
Lehmann, Gerlind U.C.	gerlind.lehmann@t-online.de
Leila, Benfekih	acrido@yahoo.fr
Lhano, Marcos Gonçalves	marcos@ufrb.edu.br
Lucky, Mary	protocol_office2006@yahoo.com
Mansaray, Amara	ywofguinea@gmail.com
Mason, Andrew C.	amason@utsc.utoronto.ca
Massa, Bruno	zoolappl@unipa.it
Mazih, Ahmed	mazih@iavcha.ac.ma
Miller, Thomas	thomas.miller@ucr.edu
Mineau, Pierre	pierre.mineau@ec.gc.ca
Mohamed, Ammar	ammar.med@inat.agrinet.tn
Mohamed, Souare	soumahismael78@yahoo.fr
Mohamed, Sylla	aniekaiv@yahoo.fr
Mohamed, Ahmed Alasow	aaran193@yahoo.com
Monard, Annie	Annie.Monard@fao.org
Montealegre-Z, Fernando	bzfmz@bristol.ac.uk
Morris, Glenn K.	glenn.morris@utoronto.ca
Muidden, Adaebisi	protocol_office2006@yahoo.com
Mullie, Wim	wim.mullie@fao.org
Mustapha, Bounechada	Bounechadam@yahoo.fr
Mutun, Serap	smutun@ibu.edu.tr
Nacer, Tarai	tarai_nc@yahoo.com
Nadiradze, Kakha	knadirad@geo.net.ge
O.S., Novikova	novikova@bionet.nsc.ru
Obazuaye, Best	atilabng@yahoo.com
Obisesan, Christopher Omololu	christopheromololu@yahoo.com
Odé, Baudewijn	baudewijn.ode@hetnet.nl
Ofili, Tina Amaka	protocol_office2006@yahoo.com
Ofomata, Anthony C.	protocol_office2006@yahoo.com
Ojiaka, Goodluck Chidi	protocol_office2006@yahoo.com
Oladipo, Olabode Rahael	aoyostate@consultant.com
Olaniran, Oladele Abiodun	oaolaniran@lautech.edu.ng

Contact Information of all the Participants

Participant Name	Email
Oludare, Sampson Akinleye	universityofibadan40@gmail.com
Okhuelegbe, Emmanuel	protocol_office2006@yahoo.com
Okoli, Ugochuckwu D.	protocol_office2006@yahoo.com
Okuducu, Başak	basakokuducu@gmail.com
Oneal, Elen	eo22@duke.edu
Ott, Swidbert R.	sro21@cam.ac.uk
Petit, Daniel	daniel.petit@unilim.fr
Pitchers, Will	wrp201@ex.ac.uk
Popoola, Oluwashola Bayo	popoolaoluwashola1@yahoo.com
Raji, Lajcen Idrissi	raji_lahcen@yahoo.fr
Rampini, Mauro	mauro.rampini@uniroma1.it
Rathour, Seema	seemarathour@gmail.com
Ren, Dong	rendong@mail.onu.edu.com
Rentz, David	orthop1@tpg.com.au
Riede, Klaus	k.riede.zfmk@uni-bonn.de
Robert, Chidi Innocent	moblynk@yahoo.com
Rogers, Stephen M.	smr34@cam.ac.uk
Roland, Ogu Innocent	protocol_office2006@yahoo.com
Rostami, Mojtaba	dr_rostami.genetic@yahoo.com
Rowell, Hugh	hrowell@netplus.ch
Saglam, İsmail K.	hsevgili@gmail.com
Salman Selahattin	salman@gazi.edu.tr
Samways, Michael J.	samways@sun.ac.za
Schmitt, Laurence	laurence.schmitt@cirad.fr
Schul, Johannes	schulj@missouri.edu
Semiz, Gurkan	semiz@akdeniz.edu.tr
Sergeev, Michael G.	mgs@fen.nsu.ru
Sesay, Michael	ympasl@gmail.com
Shomo, Alia Mohammed	aliashomo@yahoo.com
Simonet, Gert	gert.simonet@bio.kuleuven.be
Singh, Awnindra Kumar	awnindrakumar@gmail.com
Sirin, Deniz	dsirin@daad-alumni.de
Sofrane, Zina	sofranezina1@yahoo.fr
Song, Hojun	hojun_song@byu.edu
Spurgin, Peter A.	peter.spurgin@daff.gov.au
Sradnick, Jan	jsradni@gwdg.de
Stritih, Nataša	natasa.stritih@nib.si
Sultana, Riffat	riffatumer@hotmail.com
Sword, Gregory	greg.sword@bio.usyd.edu
Tail, Ghania	ghaniatail@yahoo.fr
Tatsuta, Haruki	podisma@hotmail.com
Taylan, Mehmet Sait	msaittaylan@akdeniz.edu.tr
Temel, Burcu	burcutm185@hotmail.com
Tochie, Ajaegbu Emmanuel	protocol_office2006@yahoo.com
Umbers, Kate	kumbers@bio.mq.edu.au

Contact Information of all the Participants

Participant Name	Email
Usmani, Mohammad Kamil	usmanikamil94@gmail.com
Uthman, Mariam	aoyostate@consultant.com
Vahed, Karim	K.Vahed@Derby.ac.uk
Van Der Valk, Harold	harold.vandervalk@planet.nl
Vedenina, Varvara	vvedenina@googlemail.com
Verlinden, Heleen	Heleen.verlinden@bio.kuleuven.be
Vlk, Robert	vlk@ped.muni.cz
Warchalowska-Sliwa, Elzbieta	warchalowska@isez.pan.krakow.pl
Wilemse, Luc	willemse@nhn_leidenuniv.nl
Zamanian, Hossein	Avrhossein@gmail.com
Zhang, Long	locust@cau.edu.cn
Zohra, Bissaad Fatima	bissaad@yahoo.com
Zorovich, Maja	maja.zorovic@nib.si

SPONSORS

ICO-2009 Secretariat
Department of Biology
Akdeniz University
07058 Antalya, Turkey

ICO-2009 Congress Secretariat
SALTUR TURİZM VE SEYAHAT ACENTESİ
Atatürk Bulvarı No:175/8 06680
Kavaklıdere Ankara / TURKEY

C.I.R.A.D
Centre Coop.
Inter. Recherche
Agro pour Développement
Avenue Agropolis
34000 Montpellier, France

Palme Yayıncılık
Adnan Saygun Cad. No:10/A
Sıhhıye Ankara / TURKEY

Ulusal Sosyal ve
Uygulamalı Gerontoloji Derneği
Liman Mahallesi 27. Sokak
Tunalı Apartmanı
26/C Antalya / TURKEY

TURKISH AIRLINES
www.thy.com