

METALEPTEA

THE NEWSLETTER OF THE



ORTHOPTERISTS' SOCIETY

SPECIAL CONFERENCE ISSUE



*11th International
Congress of Orthopterology*

ORTHOPTERA IN SCIENTIFIC PROGRESS AND HUMAN CULTURE **Abstracts & Program**

Editor: Long Zhang
Liwei Zhang

Yinwei You
Qian Gao

Xuwei Yin
David Hunter

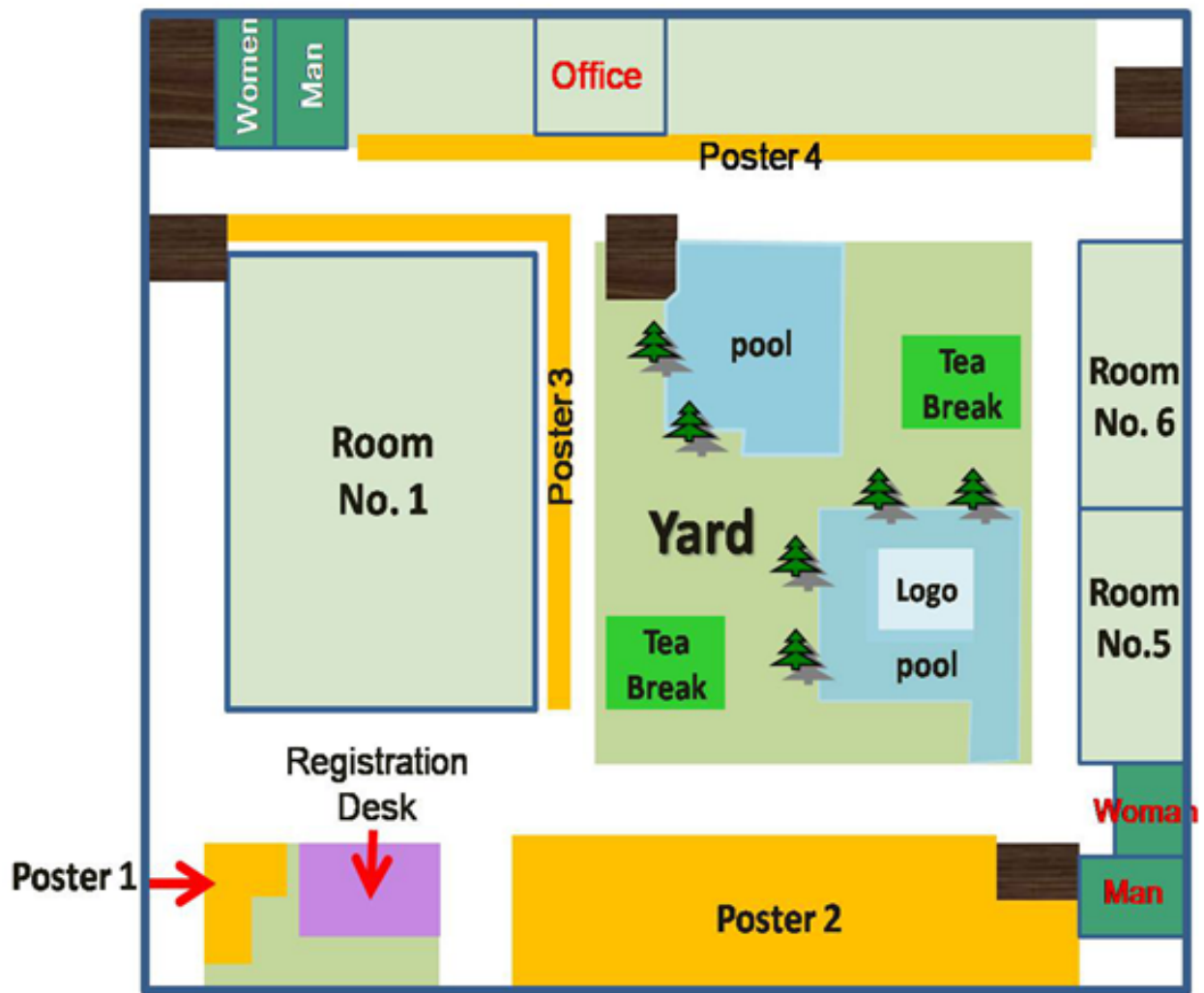
11th-15th, Aug, 2013
Kunming, China



Access Map for Location of the Hotel

1240m from Green Lake View Hotel to Yunda Hotel
从翠怡酒店到云大宾馆1240米





Conference Venue (First Floor)

Poster1: Reprints Exchange and Exhibition of Arts of Orthoptera

Poster2: Exhibition of Arts of Orthoptera

Symposium Orthoptera Conservation (Session Conservation and Ecology)

Symposium Orthoptera Sexual Behavior (Session Behavior)

Poster3: Symposium Orthopteran Functional Genomics (Session Molecular Biology)

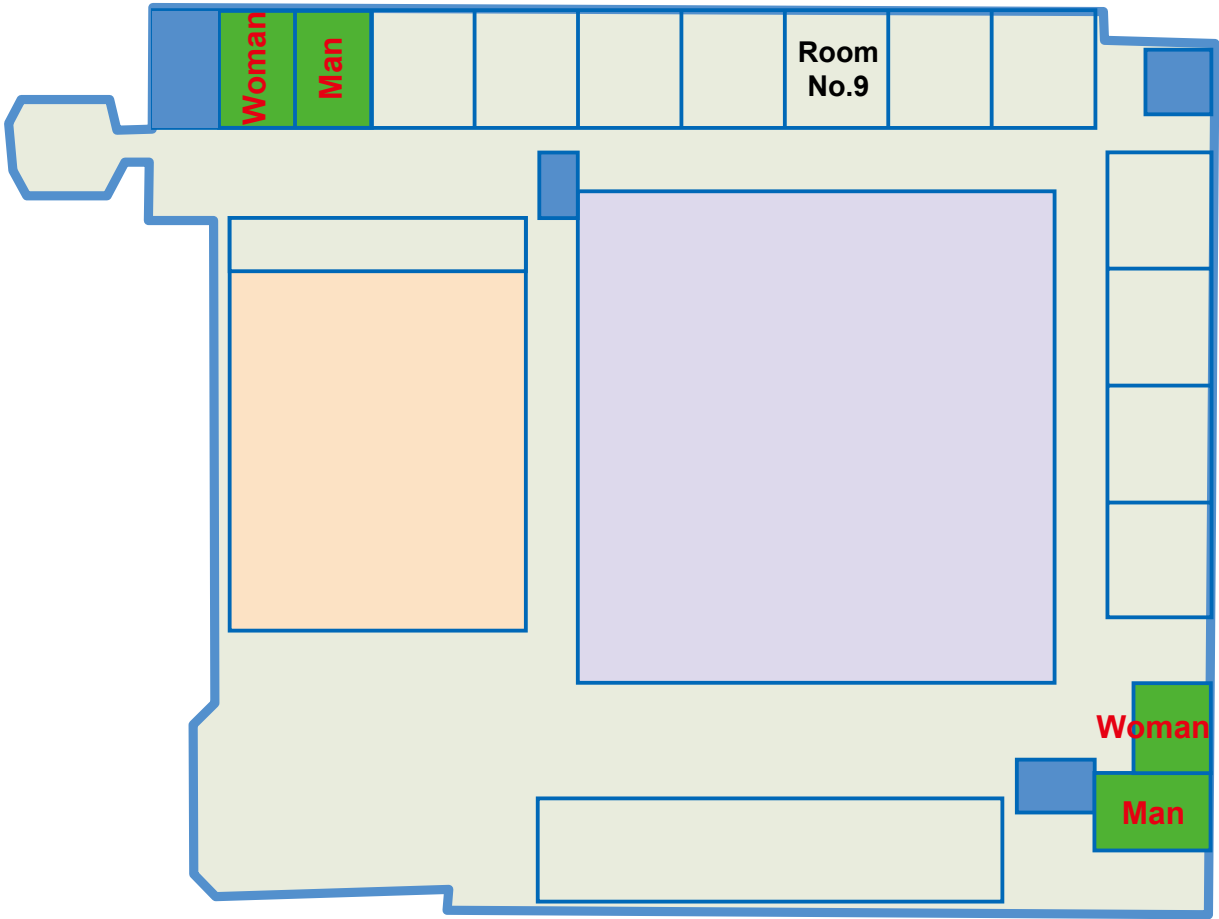
Symposium Orthoptera Systematics (Session Systematics)

Symposium Taxonomy of Orthoptera (Session Biogeography & Phylogeography)

Poster4: Symposium Grasshopper and Locust Control (Session Pest Control)

Symposium Orthoptera in Culture & Education

Symposium Orthoptera Communication (Session Physiology)



Conference Venue
(Second Floor)

Program at a glance

| | | | |
|-------------------------|-------------------------------------|-----------------------------|-----------------------------------|
| 11th-15th, Aug | | | |
| 8:00-22:00 | Registration | | |
| 12, Aug. (Day 1) | | | |
| | Room No. 1 | Room No. 5 | Room No. 6 |
| A.M. | Opening Ceremony Plenary Lecture | | |
| P.M. | | Sexual Behavior Behavior | Taxonomy Biogeography |
| | | | Conservation Ecology |
| 13, Aug. (Day 2) | | | |
| | Room No. 1 | Room No. 5 | Room No. 6 |
| A.M. | | Functional Genomics | Systematics |
| P.M. | | Molecular Biology | Systematics |
| | | | Grasshopper and Locust Control |
| | | | Pest Management |
| 14, Aug. (Day 3) | | | |
| | Room No. 1 | Room No. 5 | Room No. 6 |
| A.M. | | Workshop | Communication Physiology |
| P.M. | Plenary Lecture Closing Ceremony | | |
| | | | Culture & Education |
| 15, Aug. (Day 4) | | | |
| | Survey in Stone Forest | | |

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Program

11th-15th, Aug

8:00-22:00 Registration

11th, Aug

15:00-16:00 OS boarding member meeting

19:00-21:00 Organizing Committee Meeting

12, Aug. (Day 1)

9:00-10:00 Opening Ceremony Room No. 1

Chairman: Long Zhang

10:00-10:30 Tea Break and Photography

10:30-11:30 Plenary Lecture Room No. 1

Chairman: Charles Bomar

Axel Hochkirch (Trier University, Germany): *Orthoptera Conservation in the 21st Century - Where do we go from here?*

12:00-13:00 Lunch Yunda Restaurant

14:00-15:30 Orthoptera Conservation Room No. 9

Chairman: Michael Samways, University of Stellenbosch, South Africa

Co-Chairman: Shuguang Hao, CAS, China

14:00-14:30 Corey Bazelet (Stellenbosch University, South Africa): *Grasshopper bioindicators of effective large-scale ecological networks*

14:30-15:00 Klaus Riede (Zoological Research Museum Alexander Koenig, Germany): *Acceleration of Red List assessment and acoustic profiling for Orthoptera conservation*

15:00-15:30 Marcio Bolfarini (Universidade Estadual Paulista, Brazil): *Conservation of cave crickets in Brazil*

15:30-17:00 Session Conservation and Ecology Room No. 9

Chairman: Corey Bazelet, Stellenbosch University, South Africa

15:30-15:45 Carlos Sperber (Federal University of Viçosa, Brazil): *Environmental drivers of litter cricket diversity in Central Amazon forest*

15:45-16:00 Jessica Weyer (Trier University, Germany): *The combined effects of climate change and habitat fragmentation on the decline of a flightless wetland grasshopper*

16:00-16:15 Tea Break

- 16:15-16:30 Daniela Matenaar (Trier University, Germany): *Species richness of Orthoptera in the UNESCO World Heritage site "Cape Floral Region Protected Areas", South Africa*
- 16:30-16:45 Thomas Fartmann (University of Osnabrück, Germany): *Conservation of Orthoptera in Central European grasslands and heathlands*
- 16:45-17:00 Katja Rohde (Trier University, Germany): *Hybridization- an extinction risk*

19:00-21:00 Welcome Reception Yunda Restaurant**14:00-16:45 Orthoptera Sexual Behavior Room No. 5****Chairman:** Douglas Whitman, Illinois State University, USA**Co-Chairman:** Long Zhang, China Agricultural University, China

- 14:00-14:30 Douglas Whitman (Illinois State University, USA): *Sexual behavior and sexual selection in giant, poisonous lubber grasshoppers*
- 14:30-15:00 Kevin A. Judge (MacEwan University, Canada): *The evolution of weaponry and aggressive behavior in North American field crickets (Gryllidae, Gryllus)*
- 15:00-15:30 Gerlind Lehmann (Humboldt University Berlin, Germany): *Sexual selection and the evolution of mating systems within the species-rich bushcricket genus Poecilimon (Ensifera: Phaneropterinae)*
- 15:30-16:00 Liwei Zhang (China Agricultural University, China): *A locust pheromone sensed by an odorant-binding protein*

16:00-16:15 Tea Break

- 16:15-16:45 Koutaro Ould Maeno (The Mauritanian Desert Locust Centre, Mauritania): *Hill-topping and male-male sexual competition in lubber grasshoppers*

16:45-17:45 Session Behavior Room No. 5**Chairman:** Makio Takeda, Kobe University

- 16:45-17:00 Katie Gerstner (Illinois State University, USA): *Thirsty grasshoppers fight harder during contests over food*
- 17:00-17:15 Klaus-Gerhard Heller (Grillenstieg 18, 39120 Magdeburg, Germany): *Acoustic communication in Phaneropteridae – a global review with some new data*
- 17:15-17:30 Alexander Su (Illinois State University, USA): *Effects of body temperature on intraspecific competitive ability*
- 17:30-17:45 Varvara Vedenina (Russian Academy of Sciences, Russia): *Courtship songs in a new hybrid zone between Chorthippus albomarginatus and Ch. karelini (Acrididae: Gomphocerinae) in Russia*

19:00-21:00 Welcome Reception Yunda Restaurant

14:00-16:15 Taxonomy of Orthoptera Room No. 6

Chairman: Battal Ciplak, Akdeniz University, Turkey

Co-Chairman: Daochuan Zhang, Hebei University, China

14:00-14:30 Battal Ciplak (Akdeniz University, Turkey): *Species from an integrative perspective and quality of existing taxonomical data: game of the names versus natural entities*

14:30-15:00 Viviana Andrea Confalonieri (Universidad de Buenos Aires, Argentina): *High altitude grasshoppers of South America: defining biological units when genes, chromosomes and morphology tell different stories*

15:00-15:30 Claudia Hemp (University of Wuerzburg, Germany): *Ecological adaptations of grassland-inhabiting flightless Orthoptera: the subtribe Karniellina of Conocephalini (Conocephalinae, Tettigoniidae) as model group to understand modes and time of speciation patterns in East Africa*

15:30-16:00 Douglas Whitman (Illinois State University, USA): *Populations, not species, are the true unit of evolution*

16:00-16:15 Tea Break

16:15-17:45 Session Biogeography & Phylogeography Room No. 6

Chairman: Battal Ciplak, Akdeniz University, Turkey

16:15-16:30 Battal Ciplak (Akdeniz University, Turkey): *Speciation under climatic cycles of Pleistocene: a snapshot from Anatolio-Balkan genus Psorodonotus*

16:30-16:45 Karla Yotoko (Federal University of Viçosa, Brazil): *Molecular phylogeny, barcoding and taxonomy of predatory spiny katydids (Tettigoniidae: Listroscolidinae) from the Brazilian Atlantic Forest*

16:45-17:00 Sigfrid Alfred Ingrisich (Zoological Research Museum Alexander Koenig, Germany): *Are Agraeciini and Copiphorini natural subgroups of Conocephalinae? Considerations based on male cerci*

17:00-17:15 Marie-Pierre Chapuis (CIRAD, France): *Demographic processes shaping genetic variation of the solitary phase of the desert locust*

17:15-17:30 Mikhail Sergeev (Novosibirsk State University, Russia): *Digital mapping of orthopteran assemblages' distribution in South Siberia*

17:30-17:45 Derek Woller (University of Central Florida, USA): *An ancient ecosystem speaks volumes: analyzing speciation events in scrub islands of the southeastern U.S. via their endemics: Melanoplus grasshoppers belonging to the Puer Group*

19:00-21:00 Welcome Reception Yunda Restaurant

13, Aug. (Day 2)**8:30-11:45 Grasshopper and Locust Control Room No. 9**

Chairman: Alexandre Latchininsky, University of Wyoming, USA

Co-Chairman: Puyun Yang, Chinese National Agricultural Technology Extension Center, China

8:30-9:00 Alexandre Latchininsky (University of Wyoming, USA): *Locust and grasshopper control worldwide: an introduction. Grasshopper control: A North American Perspective*

9:00-9:30 Annie Monard (FAO UN, Italy): *Recent experience in large-scale locust campaigns and lessons learnt*

9:30-10:00 Gregory Sword (Texas A&M University, USA): *Integrating the ecology of phase change and collective movement into preventative locust management*

10:00-10:30 Chris Adriaansen (Australian Plague Locust Commission, Australia) : *Locust control: an Australian perspective*

10:30-10:45 Tea Break

10:45-11:15 Puyun Yang (Chinese National Agricultural Technology Extension Center, China) : *Sustainable management of locusts and grasshoppers in China*

11:15-11:45 David Hunter (Consultant in Locust and Grasshopper Control, Australia): *Are constant advances required to overcome increasing restrictions on the use of chemical pesticides?*

12:30-13:30 Lunch Meeting Yard**14:00-15:15 Session Pest Control Room No. 9**

Chairman: Alex Latchininsky, University of Wyoming, USA

Co-Chairman: David Hunter, Consultant in Locust and Grasshopper Control, Australia

14:00-14:15 Lin Li (China Agricultural University, China): *Design and implementation of GIS, RS, and GPS based information platform for locust control*

14:15-14:30 Batkhuyag Baldangombo (WWF Mongolia Programme Office, Mongolia): *Climate change and anthropogenic impacts on grasshopper distribution in Mongolia*

14:30-14:45 Carlos Lange (Universidad Nacional de La Plata, Argentina): *Microsporidia as grasshopper control agents in Argentina*

14:45-15:00 Christopher Adriaansen (Australian Plague Locust Commission, Australia): *A question of timing - An examination of Australian locust control strategies*

15:00-15:15 Peter Spurgin (Australian Plague Locust Commission, Australia): *Management of Red Locust populations in Tanzania – are current survey and control techniques working?*

15:15-18:00 Poster

19:00-21:00 Gala Dinner Aini Restaurant

8:30-11:45 Orthopteran Functional Genomics Room No. 5

Chairman: Gregory Sword, Texas A&M University, USA

Co-Chairman: Darron Cullen, University of Cambridge, UK

8:30-9:00 Kenji Tomioka (Okayama University, Japan): *Molecular dissection of the circadian clock in the cricket, Gryllus bimaculatus*

9:00-9:30 Heleen Verlinden (Catholic University of Leuven, Belgium): *RNA interference in the desert locust*

9:30-10:00 Xianhui Wang (Chinese Academy of Sciences, China): *The whole genome sequence of the migratory locust, Locusta migratoria*

10:00-10:15 Tea Break

10:15-10:45 Bart Boerjan (Catholic University of Leuven, Belgium): How epigenetic mechanisms might explain locust phenotypic plasticity

10:45-11:15 Darron Cullen (University of Cambridge, UK): Behavioural phase change in the Australian plague locust

11:15-11:45 Rut Vleugels (KULeuven, Belgium): Biogenic amine receptors in the desert locust and their role in behavioral gregarization

12:30-13:30 Lunch Meeting Yard

14:00-16:00 Session Molecular Biology Room No. 5

Chairman: Ioana C. Chintauan-Marquier, Muséum National d'Histoire Naturelle, France

14:00-14:15 Ioana C. Chintauan-Marquier (Muséum national d'histoire naturelle, France): *New Comparative Genomic Insights into Orthopteroïd Insects*

14:15-14:30 Bing Chen (Chinese Academy of Sciences, China): *Transgenerational Epigenetic Inheritance of Population Density-dependent Phase Change Plasticity in the Migratory Locust*

14:30-14:45 Zongyuan Ma (Beijing Institutes of Life Sciences, Chinese Academy of Sciences, China): *The gene expression profile during the development of solitary and gregarious phase of the migratory locust*

14:45-15:00 Beata Grzywacz-Gibala (Institute Systematics and Evolution of Animals Polish Academy of Sciences, Poland): *Barbitistini under the molecular eyeglass*

15:00-15:15 Enbo Ma (Shanxi University, China): *Molecular Cloning, Characterization and Functional Analysis of Glutathione S-Transferase genes from Locusta migratoria*

15:15-15:30 Jianzhen Zhang (Shanxi University, China): *Chitin Metabolism Enzymes of Locusta migratoria and their Application in Pest Control*

15:30-15:45 Nianjun Huang (Shaanxi Normal University, China): *Functional or Non-functional Structure,*

Which has more taxonomic Value: Geometric Morphometric analysis on Size and Shape Variation of the fore-wing and hind femur of Sinopodisma species (Orthoptera: Acridoidea)

15:45-16:00 Aleksandr Bugrov (Novosibirsk State University, Russia): *Using molecular markers in comparative cytogenetics of Pamphagidae grasshoppers with different types of the sex chromosome determination*

16:00-18:00 Poster

19:00-21:00 Gala Dinner Aini Restaurant

8:30-11:45 Orthoptera Systematics Room No. 6

Chairman: Hojun Song, University of Central Florida, USA

Co-Chairman: Yuan Huang, Shanxi Normal University, Xi'an, China

8:30-9:00 Hojun Song (University of Central Florida, USA): *Phylogenetic Systematics of Orthoptera*

9:00-9:30 Andrej V. Gorochov (Zoological Institute of the Russian Academy of Sciences, Russia):
Systematics of Basal Ensifera

9:30-10:00 Laure Desutter-Grancolas (Muséum national d'histoire naturelle, France): *Molecular phylogeny of Grylloidea (Orthoptera): laying the bases for a new, phylogenetic classification of crickets*

10:00-10:15 Tea Break

10:15-10:45 Ricardo Mariño-Pérez (University of Central Florida, USA): *Systematics of Pyrgomorphidae (Caelifera)*

10:45-11:15 Weian Deng (Hechi University, China): *Systematics of Tetrigidae*

11:15-11:45 Sam Heads (University of Illinois, USA): *Fossil Orthoptera*

12:30-13:30 Lunch Meeting Yard

14:00-15:00 Orthoptera Systematics Room No. 6

Chairman: Hojun Song, University of Central Florida, USA

Co-Chairman: Yuan Huang, Shanxi Normal University, China

14:00-14:30 Maria Marta Cigliano (Universidad Nacional de La Plata, Argentina): *Diversification patterns in Melanoplinae (Orthoptera: Acrididae) grasshoppers from the Andes highlands*

14:30-15:00 Jianhua Huang (Guangxi Normal University, China): *DNA barcoding and species boundary delimitation of selected species of Chinese Acridoidea (Orthoptera: Caelifera)*

15:00-17:15 Session Systematics Room No. 6

Chairman: Marcos Lhano, Universidade Federal do Recôncavo da Bahia, Brazil

15:00-15:15 Chunxiang Liu (Chinese Academy of Sciences, China): *Systematics and phylogeny of Atlanticus (Orthoptera: Tettigoniidae: Tettigoniinae) and its relatives, a Tertiary relict katydid genus*

15:15-15:30 Andrej V. Gorochov (Zoological Institute of the Russian Academy of Sciences, Russia): *Early evolution of the order Orthoptera and divergence of its highest taxa*

15:30-15:45 Pedro G. B. Souza Dias (University of Sao Paulo, Brazil): *Systematics and diversity of phalangopsid crickets (Ensifera, Grylloidea, Phalangopsidae) in Brazil*

15:45-16:00 Daochuan Zhang (Hebei University, China): *Systematics of Pamphagidae*

16:00-16:15 Tea Break

16:15-16:30 Olivier Béthoux (Muséum National d'Histoire Naturelle, France): *Cladotypic nomenclature applied to orthopterans*

16:30-16:45 Yongchao Zhi (Hebei University, China): *Molecular phylogenetic analysis of Chinese Acridoidea (Orthoptera)*

16:45-17:15 Makio Takeda (Kobe University, Japan): *Introgression of two Gryllus species from North America and a chromosome imprinting mechanism that expresses exclusively male trait for growth rate*

17:15-18:00 Poster

19:00-21:00 Gala Dinner Aini Restaurant

14, Aug. (Day 3)

8:30-11:15 Orthoptera in Culture & Education Room No. 9

Chairman: Charles Bomar, University of Wisconsin-Stout, USA

Co-Chairman: Qimiao Shao, BASF (China) Co. Ltd

8:30-9:00 Charles Bomar (University of Wisconsin-Stout, USA) : *From St. Urho to Heavy Metals: Delivery of Orthopteran content to non-entomological audiences*

9:00-9:30 Douglas Whitman (Illinois State University, USA) : *Use of the Lubber Grasshopper (Romalea sp) in science education*

9:30-10:00 Shao Qimiao (BASF (China) Co. Ltd): *History of Cricket Culture in China*

10:00-10:15 Tea Break

10:15-10:45 Ricardo Mariño-Pérez (University of Central Florida, USA): *Orthoptera in Mexican Culture*

10:45-11:00 Koutaro Ould Maeno (The Mauritanian Desert Locust Centre, Mauritania): *Perception of Orthoptera in religion and culture*

11:00-11:15 Ünal Mustafa (Abant İzzet Baysal University, Turkey): *Folk songs on Orthoptera in Turkish culture*

12:30-13:30 Lunch Yunda Restaurant

8:30-12:00 Workshop Room No. 5

Orthoptera Species File online (<http://orthoptera.speciesfile.org/>)

Chairman: Maria Marta Cigliano, Universidad Nacional de La Plata, Argentina

Co-Chairman: David Eades, University of Illinois, USA

12:30-13:30 Lunch Yunda Restaurant

8:30-10:45 Orthoptera Communication Room No. 6

Chairman: Klaus Riede, Zoological Research Museum Alexander Koenig, Germany

Co-Chairman: Wangpeng Shi, China Agricultural University, China

8:30-9:00 Tony Robillard (Muséum national d'histoire naturelle, France): *Integrative study of acoustic communication and evolution in crickets*

9:00-9:30 Fernando Montealegre Zapata (University of Lincoln, UK): *Biomechanics of hearing and singing in Ensifera: an evolutionary view*

9:30-10:00 Rohini Balakrishnan (Indian Institute of Science, India): *The acoustic world of a rain forest dusk chorus*

10:00-10:15 Tea Break

10:15-10:45 Heiner Römer (Karl-Franzens University, Austria): *Insect acoustic communication under noise: Lessons from the tropical rainforest*

10:45-12:00 Session Physiology Room No. 6

Chairman: Fernando Montealegre Zapata, University of Lincoln, UK

10:45-11:00 Matan Shelomi (University of California, USA): *Anatomy of the phasmid digestive tract and the function of the midgut appendices*

11:00-11:15 Babatunde Idowu (Federal University of Agriculture, Nigeria): *Impact of Antennectomy on the Growth Performance and Gut Enzymes Activities of variegated Grasshopper Zonocerus variegatus (L) (Orthoptera:Pyrgomophidae)*

11:15-11:30 Fatma Acheuk (Université M'hamed Bougara, Algeria): *Bioinsecticidal effects of a crud extract of Haplophyllum tuberculatum (Rutaceae) and teflubenzuron on Locusta migratoria (Orthoptera : Oedipodinae) reproduction*

11:30-11:45 James Woodman (Australian Plague Locust Commission, Australia): *Aspects of the ecological physiology of the Australian plague locust, Chortoicetes terminifera*

11:45-12:00 Koutaro Ould Maeno (The Mauritanian Desert Locust Centre, Mauritania): *Gregarious vs. solitary Desert Locusts: variation in progeny size, number, and starvation physiology and resistance*

12:30-13:30 Lunch Yunda Restaurant

14:00-15:30 Poster and Coffee Break

15:30-16:30 Plenary Lecture Room No. 1

Chairman: David Rentz

Le Kang (Chinese Academy of Science, China): *Molecular regulatory mechanism of phase change in locust*

16:30-18:00 Closing Ceremony Room No. 1

Chairman: María Marta Cigliano

19:30-21:00 Banquet Yunda Restaurant

15th, Aug. (Day4)

6:30-17:30 Survey of Orthopteran Insects in Stone Forest

Abstracts

Plenary lecture

Orthoptera conservation in the 21st Century - Where do we go from here?

Hochkirch, A

Trier University, Department of Biogeography, Trier, Germany

The preservation of biological diversity is one of the major challenges of modern mankind. We are facing a global crisis of decreasing species richness, caused by habitat degradation, pollution, overexploitation, spread of invasive species and climate change. While the decline of large vertebrates, such as rhinos, elephants and tigers receives a lot of public attention, a high number of insects vanish from our planet without anyone noticing. Halting the loss of biodiversity by 2020 is one of the “Aichi Biodiversity Targets”, which are part of the strategic plan developed during the Conference of the Parties of the Convention on Biological Diversity in Nagoya (Japan) in 2010. Reaching this target is virtually impossible considering the rapid growth of the human population and the economic growth in many parts of the world. It is even likely that we will not be able to evaluate the success of the strategic plan in 2020 due to the chronic lack of data on the distribution, population trends and threats of the majority of species. Even the most basic information – a complete inventory of global biodiversity – is far from completed. This is particularly true for insects, which probably represent the most species-rich taxon.

In comparison with other insect groups, our knowledge on Orthoptera diversity is relatively good. This is largely a result of the strong taxonomic efforts of some institutions, which mainly dealt with locust control. In fact, to the public, Orthoptera are mainly associated with locust plagues. Therefore, Orthoptera conservation is often considered a paradox. However, the majority of Orthoptera species have only rather small populations and a high number of flightless endemic species occur in the global hotspots of biodiversity, particularly in isolated mountain ranges, islands and coastal regions. Some of these species may occur in protected areas, which have been established for the conservation of birds, mammals or plants, but they are very rarely the focus of practical conservation projects. Nevertheless, a small number of practical Orthoptera conservation projects exist, dealing with the management of threatened or rare species, such as translocations of wetas in New Zealand or conservation management of the Crau Plain Grasshopper, *Prionotropis hystrix rhodanica*, in southern France. In some northern and central European countries, Orthoptera have become one of the most important indicator groups in landscape planning and conservation management. The publication of identification keys and field guides since the 1980s was one of the major drivers leading to this role, as it facilitated the utilization of Orthoptera for such purposes and simplified the compilation of inventories. For this reason, data on the distribution of Orthoptera has strongly increased in many European countries. This knowledge is crucial to the conservation of Orthoptera as without any information on the distribution, threats and population trends, prioritization is impossible. Red Lists exist in many European countries. They have triggered local Orthoptera conservation projects, such as translocation projects for field crickets in parts of Germany or habitat restoration for wetland grasshoppers. However, the number of conservation projects for Orthoptera is still rather limited and there is a need for stronger efforts in species-rich regions, particularly in the tropics.

The International Union for Conservation of Nature (IUCN) is the most influential environmental NGO with ca. 1200 member organizations (governmental organizations as well as NGOs) and ca. 11,000 voluntary experts from 160 countries grouped in six commissions. The first specialist group on orthopteroid insects was established in the 1980s and contributed a number of red list assessments to the present version of the IUCN Red List of Threatened Species in the 1990s. In 2010 the group was newly established under the name "IUCN SSC Grasshopper Specialist Group". Currently, there are 68 experts from 29 countries in the group. The aim of the Grasshopper Specialist Group is to raise awareness for the threats to Orthopteroid insects around the world, including Orthoptera s.s. (grasshoppers, crickets, bush-crickets, wetas), Phasmatodea (stick insects) and Mantodea (praying mantids). Red List assessments have been started for the European Orthoptera, East African endemic grasshoppers and South African bush-crickets. Threatened species of Orthoptera are regularly highlighted on the websites of the IUCN, including the "Amazing Species" initiative. The group has also a facebook page (as a closed group), where recent news and literature (pdfs) are posted. The website is hosted on the main website of the IUCN and a Newsletter (Newshopper) is posted twice a year. In addition to assessing the Red List status of Orthoptera species, the IUCN SSC Grasshopper Specialist Group also supports local conservation projects. In 2013, the conservation project for the Crau Plain Grasshopper, *Prionotropis hystrix rhodanica*, was started, including a mapping project, a population size estimate and an analysis of the habitat preferences. This project will become one of the first examples, where the IUCN handbook for Strategic Planning for Species Conservation has been used for invertebrates.

In order to increase the public attention for Orthoptera conservation, a stronger focus on outreach and education is needed. There are many arguments for the conservation of Orthoptera. Orthoptera are suitable bioindicators for small areas of endemism and also for sustainable land use. In openland ecosystems (particularly in grasslands) they often represent the most important primary consumers. Although they usually do not provide "ecosystem services" to humans, they are an important food source for many vertebrate species, particularly for birds (rollers, egrets, kestrels, harriers, bustards, bee-eaters, owls...), mammals and reptiles. Their songs contribute to a highly appreciated nature experience, which is illustrated by the popularity of "cricket cages" in China.

Conservation & Ecology

Acceleration of Red List assessment and acoustic profiling for Orthoptera conservation

Riede, K

Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany

Among the major challenges for insect Red List assessment and conservation is insufficient knowledge of species and the considerable cost for close monitoring of Orthoptera at intervals required for Red List assessments. About one third of (tropical) species still have to be described, and many Orthoptera are only known from singletons, i.e. only one sex is known. This is in stark contrast to the high data quality standards required for Red List assessments. Acoustic monitoring is particularly useful for assessments targeting selected singing species, rapid diversity assessments of entire communities, and species discovery. However, results from researchers undertaking acoustic surveys in Greece, Ecuador as well as from other authors, illustrate that considerable input from computational bioacoustics and sound databases are needed to develop the method's full potential. At present, acoustic profiling works well for certain species within well-defined geographical limits, such as endemic species ranges or protected areas. In addition, it has to be embedded within a strategic framework for efficient Orthoptera Red List assessment, including: 1) Data mining for endangered habitats and host plants associated with Orthoptera), and 2) Data mining of national Red Lists (<http://www.nationalredlist.org>), with a special focus on endemics. A first analysis of South American and European fauna showed that coverage by European national Red Lists is quite complete, while threat analysis in South America is still in its infancy, requiring identification of endangered habitats and food plants as a surrogate. As a first result, a list of endangered species with highly specific songs has been identified for targeted acoustic profiling. Finally, these insights have to be converted into a conservation strategy. Here I suggest integrating Orthoptera critical habitats into the Alliance for Zero Extinction critical site network (<http://www.zeroextinction.org/>), using acoustic profiling as a tool for monitoring selected species.

Environmental drivers of litter cricket diversity in Central Amazon forest

Sperber, CF¹; Szinwelski, N¹; Yotoko, KSC² and Mello, FAG³

¹Laboratory of Orthoptera, Federal University of Viçosa, Viçosa - MG, Brazil;

²Laboratory of Bioinformatics and Evolution, Federal University of Viçosa, Viçosa - MG, Brazil;

³Department of Zoology, São Paulo State University (UNESP), Botucatu - SP, Brazil

Species richness is determined by a dynamic equilibrium between local and regional processes. Within a single region, local species coexistence may be driven by ecological interactions, which may ultimately be molded by the environmental template. Here we address the question of which are the local environmental drivers of forest litter cricket diversity in the Central Amazon region. We aimed to test the hypotheses that resource availability, environmental conditions, habitat heterogeneity and predation risk, drive local cricket diversity. We sampled three forest areas, at least 15km apart, within the central Amazon region. In each area we set up 30 transects of five unbaited pitfall traps (n=90), at least 30m apart from each other, partially filled with ethanol fuel (ethanol with up to 3% gasoline), at least 30m apart from each other, and left them in the field for 48h. Before setting up the pitfall traps, we measured 11 potential bottom-up environmental drivers at each pitfall site: litter weight, shrub/tree density, shrub/tree trunk diameter and frequency of fruits on the forest floor (resource availability); fungi presence (both mycelia or fructification bodies, assumed to correlate to water availability), air humidity and temperature, soil moisture and light intensity (environmental conditions). We added litter depth as a further measure of environmental condition, related to habitat structure. Habitat spatial heterogeneity was evaluated by variance/mean ratio of air humidity, soil moisture, light intensity and air temperature, as well as spatial fungi presence heterogeneity; daily heterogeneity was evaluated by canopy cover, assumed to be correlated to buffering of daily temperature and humidity variation. Top-down drivers, measuring predation risk, were evaluated after trap removal from the field: we set sardine baits of 5g on the litter surface, 2m apart from each pitfall location, and measured the time to attack and proportion of attacked baits, after 3min. We used a frequentist statistical approach, adjusting generalized linear models with Poisson errors, corrected for over dispersion when necessary, with the number of species as the response variable. We evaluated the significance of explanatory terms by comparing nested models. We first adjusted separate models for each major potential driver group: resource availability, environmental conditions, habitat heterogeneity and predation risk. The significant effects within each of these models, was then adjusted in a unique, full model, so as to evaluate which drivers of cricket diversity predominated. We captured 3123 individuals, of which 1851 were assigned to 30 cricket species, all of them new to science. Among resource availability explanatory variables, diversity decreased with litter weight ($\chi^2=15.86$; $p<0.0001$) and increased with fruit availability ($\chi^2=10.16$; $p=0.0014$). Among environmental conditions explanatory variables, diversity increased with soil moisture ($\chi^2=9.63$; $p=0.0019$) and fungi presence ($\chi^2=6.89$; $p=0.0086$); among habitat heterogeneity variables, diversity decreased with fungi spatial heterogeneity ($\chi^2=20.90$; $p<0.0001$). Overall, when the full model was evaluated, only litter weight ($\chi^2=15.41$; $p<0.0001$) and fungi presence ($\chi^2=19.48$; $p<0.0001$) affected cricket diversity (Figure 1): diversity decreased with logarithm of litter weight and was positively affected by fungi presence. Our results showed that the

accumulation of litter on the forest floor decreases litter cricket diversity. At forest sites with low litter weight, on the other hand, average cricket diversity increases, but here is also an increase in diversity variance: there are low litter sites with high (up to 13) and low (2) species richness. Probably in forest sites with high litter weight, there is a predominance of decomposer organisms within the litter, which may make this habitat less hospitable for crickets, due to high risk of disease. Other possibilities are that high weighted litter is more compressed, and thus less permeable to cricket movement among the litter leaves or that high litter weight sites are less suitable for oviposition. Furthermore, our results indicated that given the same litter weight, sites where fungi are present have higher cricket diversity. We interpret this as due to a correlation between fungi presence and microhabitat humidity. Fungi presence tends to correlate positively with humidity. Evidence supporting this interpretation is the positive relation of soil moisture with cricket diversity that we detected in the separate model for environmental condition drivers. We conclude that litter weight and fungi presence are environmental drivers of litter cricket species richness in the Central Amazon forests, which outweigh the effects of fruit availability and soil moisture.

Acknowledgments Grants (CFS & NS) and financial support provided by CAPES, CNPq and FAPEMIG, Proc. 563360/2010-0 — EditalMCT/CNPq/MMA/MEC/CAPES/FNDCT – SISBIOTA

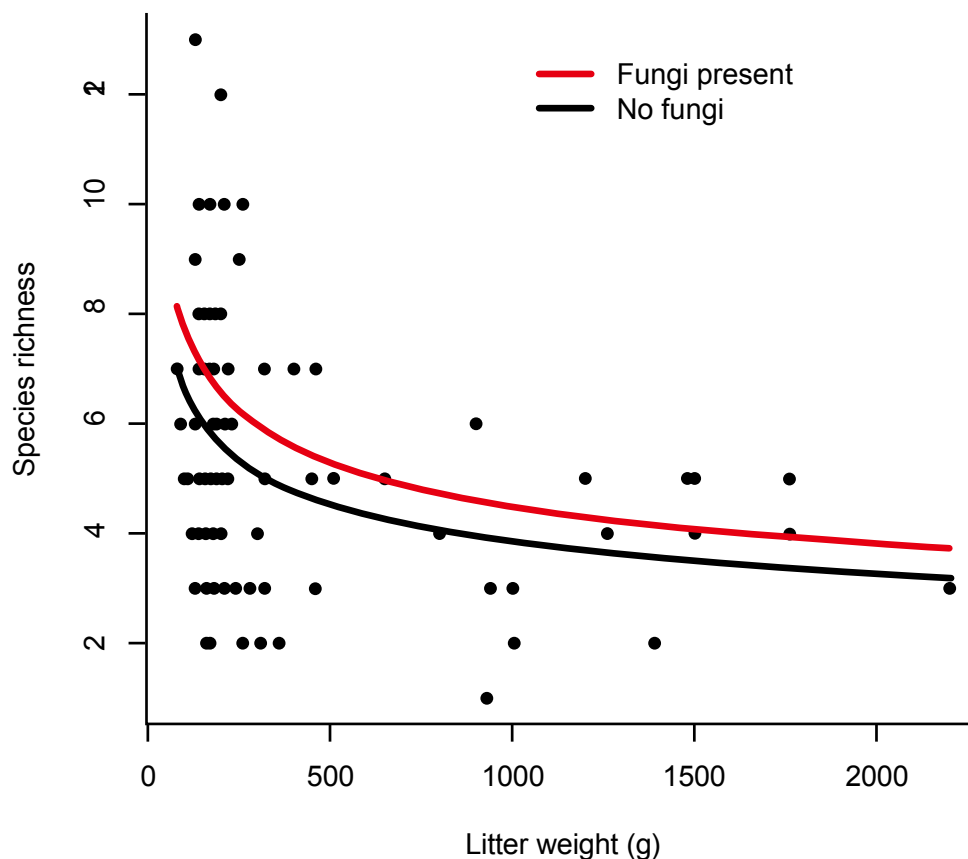


Figure 1, Litter cricket species richness in relation to litter weight (g) and fungi presence, in Central Amazon forest

Do environmental drivers explain cricket diversity differences among Amazon forests?

Sperber, CF¹; Szinwelski, N¹; Vargas, JMS²; Rodrigues, GCR¹; Souza, PRL¹ and Mello, FAG³

¹Laboratory of Orthoptera, Federal University of Viçosa, Viçosa – MG, Brazil;

²Laboratory of Bioinformatics and Evolution, Federal University of Viçosa, Viçosa – MG, Brazil;

³Department of Zoology, São Paulo State University (UNESP), Botucatu – SP, Brazil

Amazon forest litter cricket diversity decreases with litter weight and increases with fungi presence. Here we determined whether or not these local environmental drivers would explain differences in cricket diversity among distant forest areas. We sampled three areas that were ≥ 15 km apart: Adolpho Ducke Forest Reservoir (undisturbed 10,000ha upland forest on yellow latosol, adjacent to an urban area, (3°05'S 60°00'W), Campina Biological Reservoir (900ha campinarana forest, on hydromorphic carbic spodosol, 60km from any urban area, continuous with the adjacent forest, (2°35'S 60°2'W) and Tarumã-Mirim (upland forest on yellow latosol, within a region of high forest clearance due to real estate speculation (2°53'S 60°5'W). While upland forests (Ducke and Tarumã-Mirim) are characterized by trees of up to 25-35m height, the campinarana trees are lower (10-20m) and more scattered, with higher light intensity in the forest floor. In each area we set up 30 transects of five unbaited pitfall traps (n=90), at least 30m apart from each other, partially filled with ethanol fuel (ethanol with up to 3% gasoline), at least 30m apart from each other, and left them in the field for 48h. We measured 12 environmental variables, including resource availability, abiotic conditions, habitat heterogeneity and predation risk estimates, at each pitfall trap site, to evaluate if their effect on local species richness explained the differences between Amazon forest areas. We used a frequentist statistical approach, adjusting generalized linear models with Poisson errors, corrected for over dispersion when necessary, with the number of species per transect as the response variable. We evaluated the significance of explanatory terms by comparing nested models. We first adjusted separate models for each major environmental variable group: resource availability, abiotic conditions, habitat heterogeneity and predation risk. The environmental variables which presented significant effects on diversity in their group were then included in a full model, which also included the three sampled areas as the categorical explanatory variable, and all interaction terms of area and environmental variables (ANCOVA). We captured a total of 3123 individuals, of which 1851 were assigned to 30 cricket species, all of them new to science: 1746 individuals in 24 species at Ducke, 930 individuals in 11 species at Campina and 447 individuals in 18 species at Tarumã-Mirim. None of the environmental variables affected cricket diversity when sampled area effect was included in the model ($P > 0.09$). Local cricket species richness was higher at Ducke ($\chi^2 = 47.42$; $P < 0.0001$, Figure 1), and did not differ between campinarana and Tarumã-Mirim ($\chi^2 = 0.32$; $P = 0.56$). None of the measured environmental variables explained the differences between forest areas. This shows that, although there are local environmental drivers of cricket diversity, they do not explain differences between the sampled areas. Although the soil and forest characteristics of Ducke and Tarumã-Mirim are similar, cricket diversity at Tarumã-Mirim was low like that of campinarana. The low cricket diversity at the campinarana forest is consistent with it being a lower productivity forest, but this does not explain the low diversity at Tarumã-Mirim, which had similar soil and physiognomy characteristics to Ducke. We suggest that the low

diversity found at Tarumã-Mirim was promoted by the intense human activity in the region. Supporting this explanation was the strikingly low cricket abundance in Tarumã-Mirim: an average of 25 individuals per cricket species, while campinarana had 85 and Ducke 73. Human disturbance is probably causing a local extinction debt, *i.e.* a high probability of local extinction of the cricket species that are still living in that region. These extinctions are probably being delayed by immigration from nearby forested areas. This rescue effect is doomed to be progressively reduced, along the increase of deforestation and human disturbances. We conclude that to explain regional diversity differences, it is necessary to consider disturbance regimes as well as forest characteristics such as productivity and soil.

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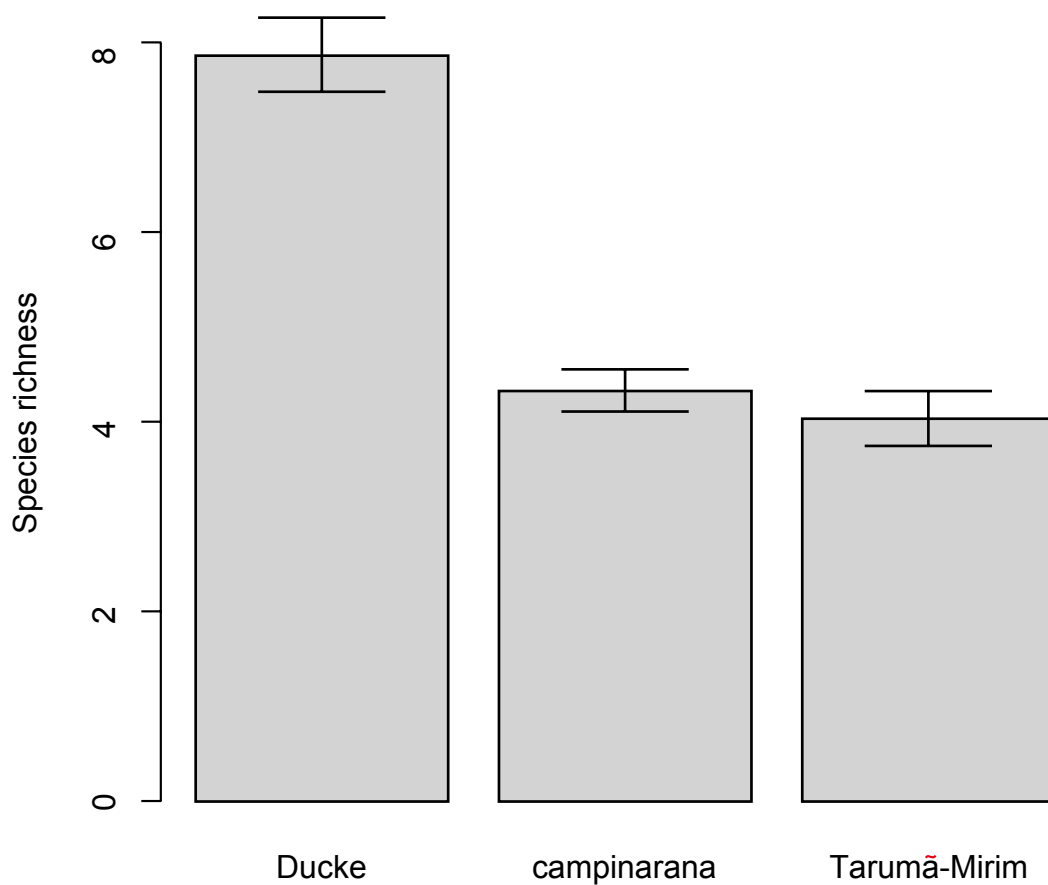


Figure 1, Litter cricket species richness in three areas of Central Amazon forest that were ≥ 15 km apart

Cricket diversity estimation through passive acoustic recording

Oliveira, GL¹; Jesus, FM¹; Zefa, E²; Mello, FAG³ and **Sperber, CF¹**

¹Laboratory of Orthoptera, Federal University of Viçosa, Viçosa - MG, Brazil;

²Department of Zoology and Genetics, Federal University of Pelotas, Pelotas – RS, Brazil;

³Department of Zoology, São Paulo State University (UNESP), Botucatu - SP, Brazil

E-mail: gabriellobregat@gmail.com

Estimating biodiversity is a challenge for field ecologists, mainly because of high costs and effort, and the short time available to conduct evaluations before natural habitats are further devastated by human rural and urban expansion. Thus, there is increasing pressure to evaluate diversity in vanishing environments, as well as to get to reliable answers in a short time. The calling song of crickets is species-specific due to its function, which is to attract conspecific mates. Therefore, acoustic inventorying of calling songs emitted by insects and other animals is a valuable tool for estimating diversity in natural habitats. Here we present initial data on acoustic diversity of crickets in three Atlantic forest remnants of potentially distinct areas of endemism: Parque Nacional e Histórico do Monte Pascoal, Itamaraju, BA (16°51' S; 39°16' W), Reserva Biológica de Duas Bocas, Cariacica, ES (20°14' S; 40°28' W) and Reserva Natural Vale (19°08' S; 40°04' W). The areas were selected based on endemism information on other taxa, mainly birds. We compared the diversity of acoustic ethospecies found in our recordings with that of morphospecies captured in pitfall traps. For each forest remnant, acoustic sampling was conducted ≥ 500 m inside the forest using a Song Meter SM2 passive sound recording device, fixed at 2m above ground level, and programmed to record between 17:00 to 23:30. For pitfall sampling, in each area we set up 30 transects (n=30 per area) of five unbaited pitfall traps each, partially filled with ethanol fuel (ethanol with up to 3% gasoline), at least 30m apart from each other, and left them in the field for 48h. We analyzed the recordings using software SongScope to get sonograms of 22050 Hz, which includes all frequency bands known for cricket acoustic signals. Each acoustic signal identified in the recordings was then individually analyzed with software Avisoft SAS-Lab Lite to get the frequency and temporal parameters (pulse rate, chirp duration) necessary to identify different ethospecies (Figure 1). We identified 22 cricket ethospecies in Cariacica, 16 in Linhares and 14 in Itamaraju. In the same areas, pitfall traps captured 19, 14 and 12 morphospecies, respectively. The number of ethospecies identified in the sonograms was higher than morphospecies captured at pitfall traps in all three remnants analyzed, even though acoustic recording sample was smaller considering time spent at sampling (6h30min of acoustic recording against 48h of pitfall traps). One explanation for the higher species detection efficiency of the calling records is that acoustic recording is capable of sampling species that occur in all vegetation strata, from the ground to the canopy, while pitfall traps capture only those crickets active at ground level. A considerable number of cricket species have lost their ability to emit acoustic signals. These species can only be detected in non-acoustic sampling, such as pitfall traps. Besides, pitfall trap captures provide the specimens essential for species identification and description. Therefore, we suggest the use of both passive acoustic sampling and pitfall sampling as complementary methods to evaluate cricket diversity. To identify the recorded ethospecies it is mandatory to capture adult individuals, which is not always

possible. However even without identification, the diversity information obtained through passive acoustic recording is invaluable, since it provides complementary information to other sampling methods, and provides information on the non-sampled species present in the environment.

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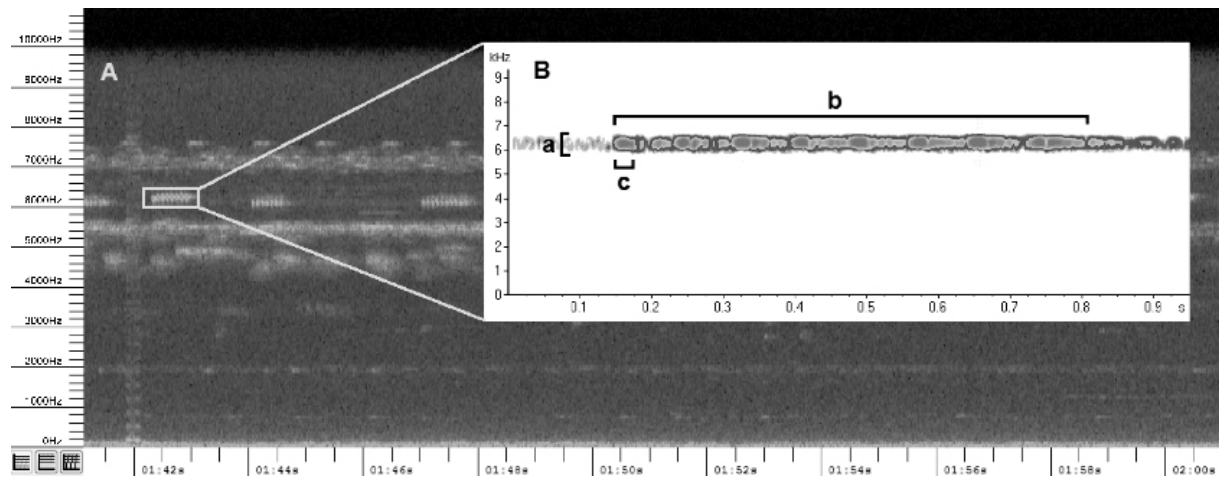


Figure 1, Schematic diagram of sound analysis. A) Sonogram of a five minutes acoustic recording analyzed in SongScope software. B) Sonogram of an individualized acoustic signal analyzed in Avisoft SAS-Lab Lite software. Some of the acoustic parameters utilized to determine distinct ethospecies: a) Frequency band; b) *chirp* duration; c) a pulse (a single closure of cricket's tegmen)

Local environmental drivers of litter cricket diversity in Atlantic forest regeneration patches

Jesus, FM; Oliveira, GL and Sperber, CF

Laboratory of Orthoptera, Federal University of Viçosa, Viçosa - MG, Brazil

E-mail: fabieneuab@gmail.com

The Atlantic forests of southeastern Brazil have suffered intensive deforestation, being reduced to less than 10% of its pristine area, with the remaining forest being mostly restricted to small habitat fragments. Large areas of this region now have their forests restricted to hilltops, partially because of specific environmental laws which protect vegetation cover on hilltops, but also because soils are poor there. Several of the areas examined were abandoned coffee plantations, where the forest has been regenerating for the last 80 years. Here we evaluated if there are local environmental drivers of forest litter cricket diversity in these forest patches. Our hypotheses were that primary productivity, forest regeneration status, habitat structural complexity or spatial heterogeneity affected cricket diversity. We sampled 18 secondary forest fragments that varied in size from 3.15 to 299ha, scattered within a 400km² area around the city of Viçosa, MG, Brazil. With larger fragments, each was divided in equal 5ha quadrants, drawn on aerial photographs, so as to choose randomly the quadrants to be sampled. Sampling effort (n=36) was proportional to fragment size, with one sampling unit in small fragments (up to 8.6ha), four in medium fragments (30 to 61ha), and six in those that were large (> 93ha). Each sampling unit had 12 pitfall traps, in four groups of three traps, with at least 30m between groups, which were left for 48h in the field. We tested if the following local environmental variables affected litter cricket diversity: trunk diameter at breast level, tree height and standing tree biomass (=trunk diameter x tree height) (assumed to be positively correlated to regeneration stage); distance among trees, presence of lianas or of pioneer tree species (assumed to be inversely correlated to regeneration stage); density of understory (as an estimate of habitat structure complexity); and variance/mean ratio of tree trunk diameter, distance among trees, tree height and density of understory (as estimates of spatial habitat heterogeneity). We adjusted generalized linear models, with Poisson errors, using number of cricket species as response variable. Explanatory variables were all numerical, so that all analyses corresponded to multiple regressions. We evaluated significance of effects comparing nested models with (χ^2 test), so as to attain the minimum adequate model. Fitted models were subjected to residual analysis and evaluation of over dispersion. Our results detected only one local environmental driver of cricket species richness: cricket species richness increased with tree height ($\chi^2 = 7.05$, $P = 0.007$, Figure 1). All remaining local environmental variables did not affect cricket species richness ($P > 0.17$). Therefore we discarded primary productivity and habitat structure as local environmental drivers of cricket diversity. Our results showed, however, that even when inserted in a fragmented landscape, with differing landscape drivers, such as forest habitat area and isolation, there is at least one local environmental variable that affects litter cricket diversity. We interpret this driver - tree height - as correlated to regeneration stage. Forest patches with higher trees are those that have been regenerating for longer. This may have led to an accumulation of higher cricket diversity through succession and recolonization of these forest patches. Tree height may correlate with both resource availability and vertical stratification. Higher trees have more foliage resource for herbivorous

insects, hence more prey for insect predators, as well as more fruit for frugivores. Higher trees may also provide more perching microhabitats for calling male crickets. Forest sites with higher trees may also present higher air humidity and lower desiccation risk. Finally, higher trees may provide higher litter production, providing more shelter or higher availability of resources for litter dwelling cricket. Our results show that forest litter cricket diversity has local environmental drivers, related to tree height in that within forest patches of the fragmented Atlantic forest, forest sites with higher trees have higher litter cricket diversity.

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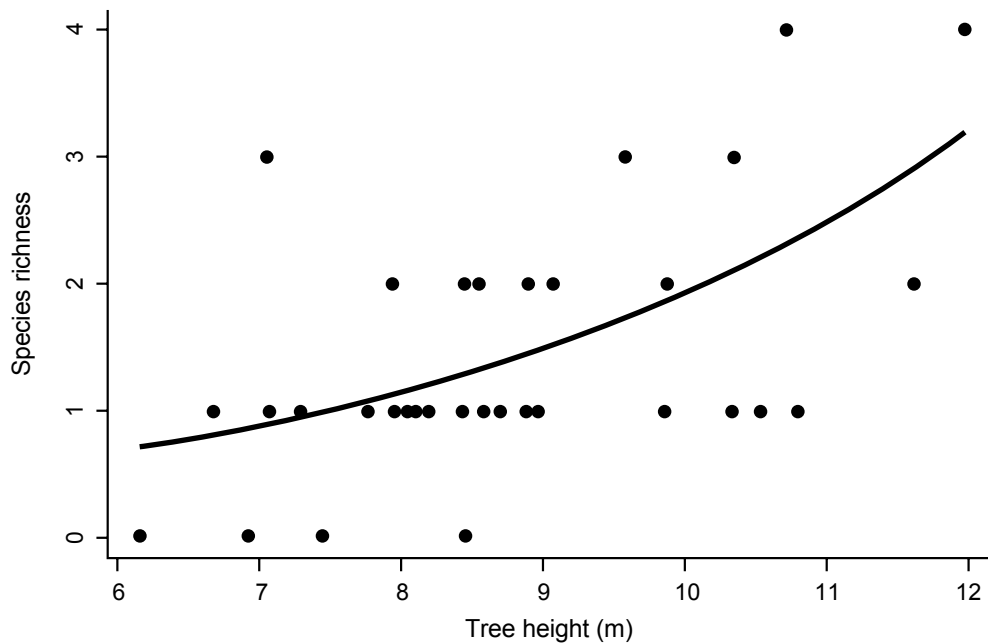


Figure 1, Litter cricket species richness in relation to tree height (m) in Atlantic forest regenerations

Consumption, digestion and assimilation efficiencies of some preferred food plants to an Indian crop pest grasshopper, *Oxya fuscovittata* (Marschall) (Orthoptera: Acrididae)

Das, A

Department of Zoology, Dinabandhu Mahavidyalaya, Bongaon, 24 Pgs (N), 743235, WB, India

E-mail: dasamlan@yahoo.co.in

Food plant preference, chemical properties of diet, consumption, digestion and assimilation efficiencies of food in an Indian pest grasshopper, *Oxya fuscovittata* (Marschall)(Orthoptera: Acrididae), were investigated. Because of the polyphagous nature of the feeding habits of this pest, twelve selected food plants from two families viz., Poaceae and Cyperaceae, were used for a 'choice test'. For the six plants most favored in the choice tests, chemical and physical properties including protein, carbohydrate, lipid, ash, fiber and water content were examined. Following these tests, nutritional ecology was used to determine the three most favored host plants, and these were further analysed for their consumption Index (CI), approximate digestibility (AD), efficiency of conversion of digested food (ECD) and efficiency of conversion of ingested food (ECI). These factors were analysed for correlations between food plant preference, chemical properties of the food and how efficient the insect was in converting that food into body mass. The results showed that lower fiber and higher water content of the leaves are more important to the insect in selection of food plants than protein, carbohydrate or fat content. Among the three most preferred food plants, CI and AD values differed marginally but ECD and ECI values were not significantly different from each other with either sex of the pest.

The Orthoptera in a stand of *Artemisia herba alba* in the central steppe (Mergueb, M'sila) in Algeria

Chebouti-meziou, N^{1*}; Merabet, A¹; Chebouti, Y³; Býssaad, FZ¹; Behidj, N¹ and Doumandji, S²

¹*Department of Biology, University of Boumerdes (UMBB), Algeria;*

²*National School Superior Agronomy, Algiers (ENSA), Algeria;*

³*National Institute of Forest Research, Algiers, Algeria;*

Laboratory of soft technology valorization physical-chemical characterization and biodiversity

*Corresponding author: chNADJIBA@yahoo.fr

This work focuses on the bio-ecological study of the orthoptera found in the Mergueb (M'sila) nature reserve. The orthoptera associated with a stand of *Artemisia herba alba* consist of 18 species of grasshopper, half of which belong to the subfamily Oedipodinae. There are four species in subfamily Gomphocerinae and two species of Calliptaminae. By contrast, the subfamilies Acridinae, the Truxalinae, the Pyrgomorphinae and Dericorythinae are each represented by only one species. The most frequently found species was *Calliptamus barbarus* (25.3% of specimens caught) followed *Sphingonotus tricinctus* (23.1%) and *Sphingonotus rubescens* (16.7%).

There are additional species but these are found in low numbers and include *Acrotylus patruelis*, *Calliptamus barbarus*, *Sphingonotus tricinctus* and *Ramburiella hispanica*, which seem to have only one generation per year. Moreover, there is only one species of Ensifera (Decticinae) present : *Platycleis intermedia*.

Grasshopper (Orthoptera: Acridoidea) assemblages on *Eichhornia azurea* and *Eichhornia crassipes* floating meadows in Northeast Argentina.

Franceschini, MC¹⁻² and de Wysiecki, ML³⁻⁴

¹Centro de Ecología Aplicada del Litoral- CECOAL (CCT Nordeste - CONICET-UNNE), Corrientes, Argentina;

²Cátedra de Limnología- FACENA, Univ. Nacional del Nordeste (UNNE), Argentina;

³Centro de Estudios Parasitológicos y de Vectores- CEPAVE (CCT La Plata - CONICET-UNLP). La Plata, Argentina;

⁴Facultad de Ciencias Naturales y Museo-Universidad Nacional de La Plata (UNLP), Argentina

Eichhornia azurea and *Eichhornia crassipes* (Pontederiaceae) form cohesive and dense floating meadows that may cover great part of the water surface in many lakes and wetlands of South America. The Acridoidea associated with aquatic environments represent a small percentage of Orthoptera but, within this group some species are important components of food webs because they consume some floating plants, while others live on the margins of flooding zones and shores of running waters. In South America the relationship between the Orthoptera assemblages and macrophytes in floodplain environments is scarcely known. The aim of this study was 1) to determine the species composition and to evaluate the seasonal variations in the abundance of Acridoidea that live in *E. crassipes* and *E. azurea* floating meadows in two lakes, one connected to the Paraná River and the other isolated, 2) to determine the relationship between grasshopper abundance and vegetation biomass of each lake. The study area includes two lakes, one of which, El Puente (27°26' S, 58° 51' W), has a connection with the Paraná River during flooding and the other, Pampín (27°30'S, 58°45'O) which is isolated. In El Puente, *E. crassipes* is the prevailing plant whereas in Pampín there is a plurispecific plant cover, with *E. azurea* prevailing and associated with the "floating mats" of *Oxycaryum. cubense* f. *paraguayense* (Cyperaceae). Grasshoppers were sampled seasonally (fall 2006 to summer 2007). Individuals were captured from a boat using a sweep net. Abundance was expressed as the number of individuals captured per minute. Plant biomass was sampled seasonally using an aluminum ring with a 0.30 m² area. All green leaves and roots within the boundaries of the ring were cut, separated and dried. The leaves were separated as to whether they were emerged or submerged. The emerged leaves were considered as refuge and food for the Acridoidea. Grasshopper species richness (S), diversity index (H') and total abundance in each lake at each sampling time was calculated. The similarity of the grasshopper communities present in both lakes was evaluated using the Jaccard Index. Grasshopper species were classified according to their frequency of occurrence as constant (>50%), accessory (25-50%), or accidental (<25%) species.

A total of 10 species of grasshoppers were collected in both lakes, belonging to two families, Acrididae and Romaleidae. In *E. crassipes* floating meadows, nine species were recorded (*Cornops aquaticum*, *Allotruxalis gracilis*, *Paulinia acuminata*, *Dichroplus exilis*, *Dichromorpha australis*, *Coryacris angustipennis*, Morphospecie 2, Morphospecie 3 and Morphospecie 4). Acridoidea abundance varied between seasons (Kruskal Wallis test, $p= 0.03$), reaching the maximum value in summer (63.33 individuals/ minute). *Cornops aquaticum* was the dominant species and its abundance

varied between seasons ($p= 0.03$), reaching the maximum value in summer. The remaining species did not show significant seasonal differences. In *E. azurea* floating meadows, five species were recorded (*C. aquaticum*, *Tucayaca gracilis*, *P. acuminata*, *C. angustipennis* and Morphospecie 1). Acridoidea abundance varied between seasons as well ($p= 0.03$), reaching a maximum in spring (12.25 individuals captured/minute). *Cornops aquaticum* and *P. acuminata* abundances were significantly higher in spring ($p= 0.047$) and summer ($p= 0.036$), respectively. The remaining species did not show significant seasonal differences ($p> 0.05$). Comparing both floating meadows, there were significant differences in grasshopper total abundance ($p< 0.0001$) and *C. aquaticum* abundance ($p= 0.0001$), being higher in *E. crassipes*. The remaining species did not show significant differences ($p>0.05$). *C. aquaticum* was the dominant species, representing 94.5% and 62.5% of total individuals collected in *E. crassipes* and *E. azurea*, respectively. This insect showed a significant correlation with the grasshopper total abundance in *E. crassipes* ($r_s= 1.00$; $p= 0.0009$) and in *E. azurea* ($r_s= 0.84$; $p= 0.0006$). *Eichhornia crassipes* and *E. azurea* showed the highest biomass values in summer. *E. azurea* showed a significant difference in leaf biomass between seasons (Kruskal Wallis test, $p= 0.03$). The emerged leaves represented 52-62% and 16.5-36.6% of the total plant biomass in *E. crassipes* and *E. azurea*, respectively. In *E. crassipes* there was a significant correlation between the total grasshopper abundance and the total plant biomass ($r_s= 0.70$; $p= 0.020$) and leaves of *E. crassipes* ($r_s= 0.77$; $p= 0.011$). *Cornops aquaticum* showed a significant correlation with total plant biomass ($r_s= 0.70$; $p= 0.020$) and leaves ($r_s= 0.77$; $p= 0.011$) of the same plant. In *E. azurea* there was a significant correlation between grasshopper abundance and the total biomass ($r_s= 0.58$; $p= 0.048$) and leaves ($r_s= 0.64$; $p= 0.026$) of a given plant. No significant correlation was recorded between grasshopper abundance and *O. cubense* leaves ($r_s= 0.41$; $p= 0.180$). The diversity index H' was different between sites ($p<0.05$), and it was higher in *E. azurea* (0.88) than in *E. crassipes* (0.45). Both floating meadows shared 40% of the grasshopper species ($I_j= 0.4$). Most species were accidental species and *C. aquaticum* was the only species found in both aquatic habitats.

The results of this study allowed analyzing and comparing Orthoptera assemblages in a floodplain lake permanently connected to the Paraná River and the isolated lake. The connectivity with the river and the macrophyte composition are the most important forces that should be considered while explaining the abundance and richness of Orthoptera assemblages. *E. crassipes* floating meadows, which was connected permanently, had higher vegetation biomass and higher grasshopper richness and total grasshopper abundance proving to be a more diverse assemblage. Acridoidea abundance varied between seasons reaching the maximum value in spring. *C. aquaticum* was the dominant species in both floating meadows and the only constant species. This insect lays its egg-pods inside the petioles of *Eichhornia* spp., and nymphs and adults feed on its leaf laminas suggesting a high specificity to these host plants. Among the species recorded there were semi-aquatic and terrestrial grasshoppers, which may use the macrophytes as food and shelter. *C. aquaticum* and *P. acuminata* are semi-aquatic species of special interest because they are being studied for their possible liberation in nonnative areas as biological control agent of *E. crassipes* and *Salvinia molesta*, two of the most noxious aquatic weeds in the world.

Grasshopper bioindicators of effective large-scale ecological networks

Bazelet, CS¹ and Samways, MJ¹

¹Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, 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, and are managed and designed to conserve regional biodiversity. However, little research has demonstrated whether ENs fulfill their intended purpose and which qualities contribute most to their efficacy. Working in South Africa's extensive ENs of remnant grassland in a transformed timber plantation matrix, we assess the relative contribution of environmental variables at the local vs. the regional spatial scale using grasshoppers, a sensitive and reliable bioindicator taxon, to make informed recommendations regarding the allocation of funds for optimization of existing and planning of future ENs. Results indicate that management of the landscape (e.g. prescribed fires or grazing) had a larger impact on the grasshopper assemblage than design of the landscape (e.g. including wide corridors to connect isolated patches of semi-natural habitat). This effect was consistent across years but varied among grasshopper taxa. Grasshoppers and butterflies evinced similar responses to EN design and management, and three grasshopper species could be employed as bioindicators of high quality habitat in South Africa's ENs. The conservation significance of these results is that EN effort should focus on maintaining a heterogeneous landscape, and that grasshoppers can now be effectively applied as bioindicators for monitoring of EN landscapes.

Notes on southern Africa Jerusalem crickets (Orthoptera: Stenopelmatidae: *Sia*)

Bazelet, CS^{1,2} and Weissman, DB³

¹*Steinhardt Museum, Department of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel;*

²*Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa;*

³*Department of Entomology, California Academy of Sciences, San Francisco, CA, USA*

The Old World Jerusalem cricket (JC) subfamily Siinae contains the one genus (*Sia*), with two subgenera: *Sia* (*Sia*) that has two fully winged species from southeast Asia, and *Sia* (*Maxentius*) with four wingless species from southern Africa. Because there is a dearth of published data about the behavior and biology of these insects, we present new field and laboratory research on southern African *Sia* (*Maxentius*), gather museum and literature information, and present guidelines for collecting and rearing specimens. While we make no taxonomic decisions, this review should be useful for future studies, including a needed taxonomic revision. We also compare results from these southern African JCs with recent investigations on related New World taxa, where fascinating biological traits and extensive cryptic biodiversity have been uncovered. DNA analysis reveals that these Old and New World JCs are polyphyletic.

Species richness of Orthoptera in the UNESCO World Heritage site “Cape Floral Region Protected Areas”, South Africa

Matenaar, D; Broeder, L; Fingerle, M; Wirtz, S; Seidt, F and Hochkirch, A
Trier University, Department of Biogeography, D-54286 Trier, Germany

The loss of biodiversity is one of the major challenges of modern mankind. The preservation of biodiversity in protected areas is generally believed to be the most effective tool for sustainable conservation of biodiversity. Protected areas are particularly necessary in regions with a high biodiversity, i.e. biodiversity hotspots. One biodiversity hotspot covering a whole floristic kingdom is the Capensis in South Africa. Due to its enormous plant diversity and high rate of endemism, eight reserves situated in this Fynbos-biome were proclaimed UNESCO world heritage (Cape Floral Region Protected Areas) in 2004. However, data on species richness, biogeography, ecological processes, bionomics and evolution of most endemic taxa is still scarce, particularly for insects. Such data is essential for developing effective conservation strategies and management plans in order to prevent the loss of biodiversity. The distribution and species composition of Orthoptera in the Cape Floral Region Protected Areas was studied during three field trips in 2012 and 2013. In each reserve, five plots representing different vegetation types were surveyed for one hour each. First results indicate that diversity strongly depends on vegetation structure and coverage. Nevertheless some species, especially species belonging to Lentulidae and Pyrgomorphidae, seem to depend on the occurrence of specific plant genera. Furthermore a strongly differing Orthoptera assemblage in the Eastern Cape (Baviaanskloof Nature Reserve) compared to the Western Cape was detected. Baviaanskloof Nature Reserve, which is famous for covering five biomes on a comparatively small area, had the highest diversity of Orthoptera. A molecular phylogeny of the lentulid genus *Betiscoides* suggests that flightless taxa may comprise a high number of cryptic, hitherto undescribed species.

The combined effects of climate change and habitat fragmentation on the decline of a flightless wetland grasshopper

Weyer, J; Rohde, K; Weinberger, J; Mayer, M; Hau, Y; Kranz, N; Ruf, K; v. Wenzlalowicz, M; Schneider, B; Chipperfield, J; Elle, O; Veith, M and Hochkirch, A.

Trier University, Department of Biogeography, D-54296 Trier, Germany

Deterioration and fragmentation of wetlands is of major concern for nature conservation. Many biota are strongly dependent on wetlands, including a large number of invertebrates. We studied population trends, mobility, population genetics and landscape genetics of an endangered grasshopper, *Chorthippus montanus*. Our results suggest that this species is strongly threatened by climate change as it has lost all populations < 400 m in Rhineland-Palatinate during the last 30 years. Furthermore, we found a very low mobility of this species on five study sites. However, mobility correlated positively with habitat size and negatively with vegetation density. We also performed mark-release experiments, which showed that mobility increased dramatically in unsuitable habitat (forest). In hybridization and mate choice experiments, we found that *Ch. montanus* may hybridize with *Ch. parallelus*, particularly when heterospecific abundance is much higher than conspecific abundance. This might explain the records of intermediate morphotypes at localities where *Ch. montanus* went extinct.

To analyse the population genetics of *Ch. montanus* we sampled hind legs at 14 study sites (ca. 40 individuals per population). We genotyped 570 specimens at 10 polymorphic microsatellite loci (six of them were originally developed for *Ch. parallelus*, the remaining four were developed during our study for *Ch. montanus*). For evaluating the impact of land use change, particularly the increasing cultivation of biofuel plants like maize, on the population connectivity of *Ch. montanus*, we performed a landscape genetic analysis. For this analysis we produced a land use grid-map with a resolution of 30 x 30 meters using ArcGIS® Release 10. The final grid map contained ten land use categories: wet grassland (= potential habitat for the species), nutrient-poor grassland, other wetland habitats (e.g.: reeds, marshes, etc.), dry grassland, pasture and hay meadows, farmland, constructed areas (e.g.: settlements, roads, etc.), broadleaf deciduous forest, conifer forest and lentic waters. Three land use conversion scenarios (10%, 30% and 50% transformation from grassland to farmland for biofuel production) were chosen to test for the potential effects of the planned increase in biofuel production. To make these models as realistic as possible, we blocked all grid cells in protected areas (including nature reserves and Natura 2000 sites) as well as grid cells with a slope > 10%, which are unlikely to be used as farmland. A Structure and Geneland analysis revealed that the 14 genotyped populations were strongly isolated. Using a novel landscape genetics approach, we tested three models of population divergence (panmixia, isolation by distance and isolation by resistance). While the panmixia model turned out to be the worst model, we did not detect any significant difference between the isolation by distance and the isolation by resistance model. Nevertheless, the isolation by resistance model fitted slightly better than isolation by distance. Constructed areas (like human settlements, roads etc.) had the highest resistance value followed by forests. All other land use categories revealed no significant separable resistance value for our study species. One reason for these results might be the strong isolation of the sampled *Ch. montanus* populations, which is caused by its low mobility with little geneflow among

populations.

Altogether, our results suggest that *Ch. montanus* is strongly threatened by climate change. Due to the strong fragmentation of the populations and its low dispersal abilities, it is not able to rapidly colonize suitable habitat. After periods of drought, it might be displaced by hybridization with *Ch. parallelus*.

Conservation of Orthoptera in Central European grasslands and heathlands

Fartmann, T

Ecology, Department of Biology/Chemistry, University of Osnabrück, Barbarastr, 11, 49069 Osnabrück, Germany

Grasslands and heathlands are among the most important habitats for Orthoptera in Central Europe. However, the formerly widespread habitats are nowadays restricted to small and isolated remnants. Without land use they undergo succession, a process that is additionally accelerated by the increasing amount of atmospheric nitrogen deposition.

The aim of this talk is to show how fragmentation and succession affect Orthoptera of central European grasslands and heathlands. Based on several field studies using box-quadrat sampling throughout Central Europe and an oviposition experiment, I will give recommendations for the management of species-rich Orthoptera habitats.

Grassland and heathland Orthoptera showed a clear response to succession. Each successional stage harboured a unique assemblage. Additionally, many Orthoptera species were dependent on mosaics of different stages, since they fulfill microhabitat shifts during their nymphal development, or adults regularly shift between different stages. Species richness of habitat specialists was highest in the earliest seral stages. In contrast, density of all species peaked at the intermediate successional stage. Early successional stages are most likely to be preferred by specialized Orthoptera because they provide suitable oviposition sites (bare ground) and warm microclimatic conditions. The density peak in the mid-successional stage probably reflects a trade-off between favourable ambient temperatures for optimal development, sufficient food and shelter against predators.

Although all successional stages are relevant for conservation, early and mid-successional stages are the most important. Consequently, conservation management should aim at the reintroduction of traditional, low-intensive land use (grazing, sod-cutting) in abandoned grasslands and heathlands that create mosaics of different stages.

***Temnomastax hamus* Rehn & Rehn, 1942 (Orthoptera: Eumastacidae) at the Pantanal of Mato Grosso, Brazil: expanding its South American range**

Silva, DSM^{1a}; Olivier, RS²; Souza, AV¹; Oliveira, DJ¹; **Lhano, MG^{1b}** and Marques, MI³

¹*Universidade Federal do Recôncavo da Bahia (UFRB), Centro de Ciências Agrárias, Ambientais e Biológicas (CCAAB), Laboratório de Ecologia e Taxonomia de Insetos (LETI). Programa de Pós-Graduação em Ciências Agrárias. Rua Rui Barbosa, 710 – 44380-000, Cruz das Almas/BA, Brazil; E-mail: a - danielasantos.biology@gmail.com; b - marcos@ufrb.edu.br*

²*Universidade Federal de Mato Grosso do Sul (UFMS), Centro de Ciências Biológicas e da Saúde (CCBS), Laboratório de Zoologia. Cidade Universitária, 79070-900, Campo Grande/MS, Brazil;*

³*Universidade Federal de Mato Grosso (UFMT), Programa de Pós Graduação em Ecologia e Conservação da Biodiversidade. Av. Fernando Corrêa da Costa, nº 2367 – Bairro Boa Esperança, 78060-900, Cuiabá/MT, Brazil*

This study reports the presence of the species *Temnomastax hamus* Rehn & Rehn, 1942 near the city of Poconé, Mato Grosso State, expanding the distribution of this species to the Brazilian Pantanal. Its grasshoppers are small arboreal popularly known as 'monkey grasshoppers' or 'grasshopper clown', found predominantly in tropical regions near forests. The subfamily Temnomastacinae occurs exclusively in South America, with records for the driest parts of Brazil, Paraguay and Bolivia, and comprises two genera: *Eutemnomastax* (with four species restricted to northeastern Brazil) and *Temnomastax* (with seven species spread at Bolivia, Paraguay and Brazil, over almost the entire Cerrado domain). For *Temnomastax hamus* this information is still scarce, little is known about their life cycle, habitat and distribution. The information regarding this species in gathered are only three texts: Rehn & Rehn (1942, Proc. Acad. Nat. Sci. Philad. 94:18) and Descamps (1973, Ann. Soc. Ent. Fr. NS 9(4): 943-974; 1982, Bull. Soc. Ent. Fr. 87(5/6):161-298). *T. hamus* is characterized by an average size, slender body, braquipterous wings and cercus with very sharp curve, having the appearance as its name suggests a hook (the lat. *hamus*, 'hook'.) The species has records for Brazil in the Southeast (Minas Gerais and São Paulo) and Midwest (Mato Grosso and Goiás) and for the central area of Paraguay (San Pedro, Caaguazu and Paraguari). The specimen was collected in October 2012 (dry season) at the Pantanal, Porto Cercado county. The area is located on the stretch between the Bento Gomes River (16°18'55"S and 56°32'33"W) and the Base of Advanced Studies of the Federal University of Mato Grosso (16°30'03"S and 56°24'47"W), at the SESC Pantanal Farm. An entomological net was used to capture specimens at the day light and it was found in the forest formations bounded (ridges). After collecting, the grasshopper was transported to the Laboratory of Ecology and Taxonomy of Insects (UFRB). The determination of the species was taken using the Rehn & Rehn (*l.c.*) and Descamps (*l.c.*). This record is based on a single male collected but this appointment is an important contribution to knowledge about the geographic distribution of this specie. Considering the importance of this group and the conservation of Pantanal grasshoppers, this new record indicates that this species is not confined to the points before registred (dry areas) and possibly can be find at the whole central and western portions of western Bolivia and Paraguay. Descamps (*l.c.*) indicated that is difficult to find more than two species of Temnomastacinae occurring sympatrically, but the data

provided so far for *T. hamus* indicate that it is sympatric with *T. latens* in the state of Minas Gerais. The absence of data on biological and ecological relationships of Temnomastacinae' species (especially *T. hamus*) hinders to formulate hypotheses which could explain the presence of this species at the Pantanal region, but it becomes even more important to the conservation of their local habitats, since data on species distribution are essential to developing conservation strategies.

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Population variance of *Cornops frenatum frenatum* (Marschall, 1836) (Leptysmiinae) in *Heliconia* spp. L

Oliveira, DJ^{1a}; Lhano, MG^{1b}; Silva, DSM¹; Vieira, AS¹ and Oliveira, JMS².

¹Universidade Federal do Recôncavo da Bahia (UFRB), Centro de Ciências Agrárias, Ambientais e Biológicas (CCAAB), Laboratório de Ecologia e Taxonomia de Insetos (LETI); Programa de Pós-Graduação em Ciências Agrárias. Rua Rui Barbosa, 710 – 44380-000, Cruz das Almas/BA, Brazil. E-mail: a - daibio21@gmail.com; b - marcos@ufrb.edu.br

²Instituto Politécnico de Bragança (IPB), Escola Superior Agrária (ESA), Mestrado em Agroecologia, Campus de Santa Apolónia, Apt. 1172, 5301-855. Bragança, Portugal

Cornops frenatum frenatum (Marschall, 1836) (Orthoptera: Acrididae) are widely distributed in the tropical area of South America and was recently found at Conceição do Jacuípe county, state of Bahia, Brazil. This species lives specifically on plants of *Heliconia* spp. performing its cycle and acting as defoliating, causing damage and decreasing the productivity of these plants. Many grasshoppers are essential members of the fauna in ecosystems, making the study of their populations very important due to its use as a potential controller of pests and weeds, as its control by the injuries that they can cause in agricultural systems. Climatic conditions such as temperature, humidity and solar radiation are factors modulating population and may modify the intensity, duration and periodicity of reproduction and lifecycle of *C. f. frenatum*. The aim of this work was to evaluate the variation of the population of *C. f. frenatum* in *Heliconia* spp L. and the influence of climate on it. The experiment was conducted on a farm producer of tropical flowers located at Conceição do Jacuípe (12°21'14"S 38°48'16"O), Bahia, Brazil. Individuals were collected monthly, from the February/2012 to January/2013 through active manual collection using entomological nets. Trails were established along the planting and grasshoppers were captured during a 60 minutes period. In order to potentiate the sampling, the search was made by four people, distant from each other about 10 meters. Captured individuals were placed in plastic bags with leaves of *Heliconia* sp. with moist cotton, and thermoplastic packed in boxes in order to avoid the stress of the specimen collected. The insects collected were transported to the Laboratory of Ecology and Taxonomy of Insects, Federal University of Recôncavo of Bahia (UFRB) for subsequent separation according to sex and stage of development. Data relating to temperature (°C), solar radiation (kJm⁻²) and humidity (%) were obtained by automatic station of the National Institute of Meteorology - INMET (A413), located next to the collection place. To verify that the data were normally distributed, was used the Kolmogorov-Smirnov test. Also was analyzed the association of environmental variables to the total number of individuals collected through a correlation matrix, through the Pearson coefficients, adopting a significance level of 5%. It was observed that the population of *C. f. frenatum* presents nymphs and adults throughout the year, as both were found in all sampling months. We collected 401 individuals, and of this total 236 were adults and 165 nymphs, obtaining 57% of adult females and 43% males; 55% of nymphs were classified as "A" (up to 12 mm long, early stages development) and 46 % in the category "B" (above 12.5 mm long-last stages of development). In the period from december to march, there was the highest values of temperature (26.3±0.5°C), as well the largest solar radiation values (1744.32±85.65kJm⁻²) and lower humidity

values ($68.22 \pm 2.75\%$). For the period from december to march the total value of individuals collected was 19% the total collected in a year. However, between the months May to August was verified the lowest values of temperature ($22.7 \pm 0.9^\circ\text{C}$) and solar radiation ($1294.46 \pm 108.63 \text{ kJm}^{-2}$) with higher humidity values ($80 \pm 2.7\%$). For the period from May to August the total value of individuals collected was 44% the total collected in a year. It was found that the correlations between the total number of individuals and the monthly values of temperature and solar radiation were negative (-0.74 and -0.78) and significant ($p < 0,05$). There was a hard correlation between the monthly values of humidity and the number of individuals ($r = 0.80$), and the hypothesis testing of correlation between these variables was significant at the 5% level. Thus it appears that the variation in populations of *C. f. frenatum* in *Heliconia* spp. presents association with environmental parameters such as humidity, temperature and solar radiation. This study was funding by CAPES (Brazilian Ministry of Education) and Federal University of the Reconcavo of Bahia (UFRB).

A report on the occurrence of *Neocurtilla hexadactyla* (Perty, 1832) and *Scapteriscus didactylus* (Latreille, 1804) (Orthoptera, Gryllotalpidae) at the Pantanal of Poconé, Mato Grosso, Brazil

Santos, ENS^{1a}; Oliveira, DJ¹; Lima, RM¹; Silva, DSM¹; Morselli, JP¹; Marques, MI² and **Lhano, MG^{1b}**

¹*Universidade Federal do Recôncavo da Bahia (UFRB), Centro de Ciências Agrárias, Ambientais e Biológicas (CCAAB), Laboratório de Ecologia e Taxonomia de Insetos (LETI). Rua Rui Barbosa, 710 – 44380-000, Cruz das Almas/BA, Brazil.*

E-mail: a: dudu_nss@hotmail.com; b: marcos@ufrb.edu.br

²*Universidade Federal de Mato Grosso (UFMT), Programa de Pós Graduação em Ecologia e Conservação da Biodiversidade. Av. Fernando Corrêa da Costa, nº 2367 – Bairro Boa Esperança, 78060-900, Cuiabá/MT, Brazil*

This study reports the presence of the species *Neocurtilla hexadactyla* (Perty, 1832) and *Scapteriscus didactylus* (Latreille, 1804) in Poconé, Mato Grosso state, expanding the distribution of this species to the Brazilian Pantanal. Mole crickets (Gryllotalpidae) are a group of insects related to the crickets (Gryllidae) and highly adapted for burrowing underground, where they spend most of their lives. Gryllotalpidae comprise two recent subfamilies: Gryllotalpinae and Scapteriscinae. These crickets exhibit autapomorphic characters within the suborder Ensifera, as the first pair of legs modified being fossorial whose function is to dig elaborate tunnels where its use to spend most of their lives (except *Gryllotalpella*). The subfamily Gryllotalpinae presents five genera and eighty valid species, distributed over all continents, especially in the Americas and except at the poles. Within these genera, two occur in Brazil: *Neocurtilla* (Kirby, 1906) and *Gryllotalpella* (Rehn, 1917). The subfamily Scapteriscinae has two genus and about twenty-five described species, but only *Scapteriscus* is recorded for Brazil. The specimens were collected during the month of July of 2011 (dry season) by active sampling using an entomological net in an area located at the Base of Advanced Studies of the Federal University of Mato Grosso (16°30'03"S and 56°24'47"W). The specimens were determined using identification keys and the characters of the external morphology was compared with the original descriptions of the taxa. Were analyzed 25 adult specimens belonging the subfamilies Gryllotalpinae and Scapteriscinae. Among the captured species were recorded for the first time in the state of Mato Grosso the presence of the species *N. hexadactyla* and *S. didactylus*. *N. hexadactyla* presents as diagnosis characters, the trochanter anterior lenticular and small, width of pronotum less than 7 mm and tegminas less than half the length of the abdomen. They are omnivores and prefer very moist and loamy soils. *S. didactylus* present the length of eyespot 0.60 to 0.65 mm, interocular distance greater than 1.0 mm, usually interocular distance greater than 2.2 mm and ocellar-ocular distance generally greater than 0.32 mm. Exhibit a greater affinity for sandy soils and, according to availability of resources in their habitat, its diet can vary from leaves to other arthropods. Considering that the collected species *S. didactylus* and *N. hexadactylus* had no previously records in this biome until now, the results confirms the importance of the Brazilian Pantanal and the necessity of more fieldwork providing a better understanding of local diversity of mole crickets and the distribution of Gryllotalpidae in wetlands.

Phylogenetic relationships for *Strinatia* species Chopard, 1970" (Orthoptera, Phalangopsidae, Luzarinae)"**Bolfarini, MP** and de Mello F, AG¹*Laboratory of Insecta Taxonomy, State University of São Paulo, Botucatu – SP, Brazil*

The analyzes of relatedness between groups of Orthoptera and proposed phylogenetic relationship to taxonomic categories of the highest hierarchical level (suborder levels and superfamily) have emerged recently. The nature of the character fonts to be relatively varied. Phylogenetic groups located on lower levels (e. g families and genera) are much rarer, especially for Ensifera. Phalangopsidae, also known "spider crickets", has controversies in their classification. Several authors is seen as a subfamily in Gryllidae: Phalangopsinae, however, others have raised to family status. Desutter (1988) divided the "spider crickets" in three families: Paragryllidae, Neoacilidae and Phalangopsidae, although these families and several other subfamilies are regularly organized as subfamilies or tribes of Gryllidae, or synonymized with other subgroups of gryllids. Although Phalangopsidae be the most diversified family of Grylloidea in *Neotropica* (Desutter-Grandcolas 1992b), a large amount of work is the list of citations fauna, and only a few focus on aspects of evolutionary biology. Phalangopsidae has the following subfamilies: Cachoplistinae, Paragryllinae, Phalangopsinae, Phaloriinae, Rumeinae and Luzarinae, this last is the genre *Strinatia*. The object this study is establish relatedness relations of *Strinatia* species through cladistic method of phylogenetic reconstruction, using characters of body composition of male and female adults. We employ the phallic-complex terminology of Desutter (1987, 1988, 1990), with the corrections made by that author in a subsequent contribution (Desutter-Grandcolas, 2003). Character selection and analyses were based on detailed examinations of male genitalia and external morphology, performed on available Luzarinae genera and outgroup species. For analytic purposes, observations included 30 terminal taxa and 38 morphological characters (all binary), of which 25 were from the external morphology, 11 were from internal male genitalia and 2 were from external female genitalia; these characters were organized into a data matrix for further analyses. All characters were considered as unordered and equally weighted. Incomparable data were represented through a hyphen and unobserved characters were represented through a question mark in the matrix. The "group + notation (Amorim, 1982) was adopted in the results and discussion section. The Winclada software version 1.00.08 (Nixon, 2002) was used in order to build the matrix and the analysis was executed in the TNT (Goloboff, Farris & Nixon, 2003) and NONA (Goloboff, 1999) software programs, supported by Winclada. Parsimony analyses were performed through both exhaustive (implicit enumeration) and heuristic search algorithms, respectively. For the heuristic search were used the following options: "maximum trees to keep = 100 "number of replications (mult*N) = 1, "starting trees per rep (hold/) = 1, "random seed = 0, "unconstrained search, and search strategy Multiple TBR + TBR (mult*max*) ("default of program). Character polarity was based on the outgroup comparison method (Nixon & Carpenter, 1993). Eight genera were used in the analysis comprised the outgroup: *Eidmanacris* Chopard, 1956; *Bambuina* de Mello, Horta & Bolfarini, 2013; *Endophallusia* de Mello, 1990; *Mesaia* n. gen. Bolfarini & Mello (in prep); *Tupinamba* n. gen. Bolfarini & Mello (in prep); *Adenopygus* de Mello & Bolfarini, 2012; *Aracamby* de Mello, 1993; *Vanzoliniella* de Mello & Cezar

dos Reis, 1994; *Ottedana* de Mello & de Andrade, 2004. Phylogenetic reconstructions at the level of species with frequency presents problems such as low number of synapomorphies, high number of autapomorphies, many parallels and reversals. This probably is due to factors of various kinds such as: 1 - presence of many recent adjustments, 2 - nature of the characters - ordinary crafted by natural selection or sexual selection - the latter taken as rapidly evolving and divergent, 3 - recent cladogenetic events. A phylogenetic hypothesis for species of *Strinatia* presented in his cladograma grouping into two major groups - southern Minas Gerais and northeastern São Paulo and another in northern Paran and southern São Paulo, resulting in the relation: ((*cancelloae* (*gnaspini* (*ibitipoca* (*atibaiensis* + *valinhensis*)))) (*boraceana* + *caissara*) (*ribeiraopirensis*) (*brevipennis* (*ricardo* + *elinae*)), (*apiaiensis* (*tamandarensis* + *campolargoensis*)) (*cerroazulensis* (*guapiarana* (*arataka* (*leo* (*adrianopolensis* + *atratus*)))))).

Taxonomic study of genus *Strinatia* Chopard, 1970" (Orthoptera, Phalangopsidae, Luzarinae)**Bolfarini MP**; Dias PGBS and de Mello FAG¹*Laboratory of Insecta Taxonomy, State University of São Paulo, Botucatu – SP, Brazil*

Morphologically, phalangopsid crickets comprises species with long legs, in relation to the body size, small and vertical head, with antennal scapes well developed. Its fore tibiae not carry more than two apical spurs and its posterior tibiae are serrated and armed with apical and dorsal spurs. At the level of the tarsus, it's noted that the first posterior tarsomeres carry one or two rows of dorsal spines and their median tarsomeres are not regressed. The combination of characters of the tibia and the tarsus, which is separately in other families of Grylloidea, is typical of all Phalangopsidae. In the Neotropical Region, phalangopsid crickets can be distinguished from other taxa by the number of dorsal spines of posterior tibia, equal to 4 (rarely 5) internal and 4 external (except Neoacolini and Strogulomorphini). However, the male genitalia are the main criteria for recognizing Phalangopsidae. Chopard (1970) described the genus *Strinatia* based on *S. brevipennis*, whose specimens were collected in the limestone cave called "Cave of the Sands" in Iporanga, Ribeira Valley, State of São Paulo. Mesa et. al. (1999), added *S. teresopolis* to genus, based on a small lot of specimens found in the Organ Mountains on the outskirts of Teresopolis, Rio de Janeiro. Bolfarini (2011) added two new species, *S. gnaspinii* and *S. cancelloae* (*in prep.*), both from the Mantiqueira Escarpment (São Francisco Xavier district, São José dos Campos, São Paulo). The genus *Strinatia* is closely related to other phalangopsids as *Endophallusia*, *Eidmanacris* and *Adenopygus* mainly by marbled slender body, short wings rounded at the posterior margin and supranal plate with anterior margin straight. However other characters are reported in this study, differing *Strinatia* from other related genera like the morphology of metanotal structures and subgenital plate elongate. Describing new species of the genus *Strinatia*, redescribe the known species, adding new information to provide a complete diagnosis and develop an identification key for the species, is the objective of the present study. The specimens were collected manually at night on forest trails and caves on their habitats. Drawings, comparisons and descriptions were made under a stereomicroscope; a graduated eyepiece was employed for measurements. The male genitalia, after dissection, were treated with a 10% potassium hydroxide solution for 24 hours to remove muscular tissues, and then analyzed. Photographs were taken with a stereomicroscope (Zeiss SteREO Discovery V.20), and the images were analyzed using image-editing software. We employ the phallic-complex terminology of Desutter (1987, 1988, 1990), with the corrections made by that author in a later contribution (Desutter-Grandcolas, 2003). The results of the study, was raised to the presence of 20 species of the genus *Strinatia* distributed mainly in the Ribeira Iguape Valley, Mantiqueira Escarpment; and the known species *S. teresopolis* was redescribed and transferred to the new genus *Mesaia* gen. n. (*in prep.*).

Hybridization - an extinction risk

Rohde, K; Weyer, J; Hau, Y; Lemke I and Hochkirch, A

Trier University, Department of Biogeography, D-54286 Trier, Germany

Climate change and fragmentation modify the natural habitat of many wetland biota and lead to new compositions of biodiversity in these ecosystems. While the direct effects of climatic factors on Orthoptera are well known, indirect effects due to biotic interactions remain poorly understood. The Water-Meadow Grasshopper, *Chorthippus montanus* (Charpentier, 1825) and the Meadow Grasshopper, *Chorthippus parallelus* (Zetterstedt, 1821) occur sympatrically in large parts of the Palaearctic. While *C. parallelus* is a very widespread generalist species, *C. montanus* has a scattered distribution and occurs only in permanently moist habitats, such as water meadows, bogs and marshes. Due to their close relationship and their similar songs, hybridization is likely to occur in syntopic populations. As both species are flightless and the populations of *C. montanus* are highly fragmented, decreasing habitat suitability due to climate change may increase the risk of hybridization in this species and ultimately lead to genetic displacement of this threatened species.

To investigate the risk of hybridization between these two species, we studied mate choice in conspecific, mixed and heterospecific situations and with increasing density of heterospecifics. The results showed that *C. montanus* females are very choosy, while *C. parallelus* readily accept *C. montanus* males as mates. However, when increasing the density of *C. parallelus* the frequency of interspecific mating increased also for *C. montanus* females. We also crossed the species artificially in the lab to study their hybridization potential. The offspring was viable and reached adulthood, but the wings were deformed (although possibly caused by the keeping conditions). The hybrid song was intermediate between both taxa. To study the frequency of hybridization in the field, we analyzed the population genetic structure of 15 populations of *C. montanus* and *C. parallelus* in the Hunsrueck Mountains, Rhineland-Palatinate. We sampled hind legs of about 40 individuals per population and species and also of specimens with intermediate morphotypes. In total, we genotyped 1073 individuals at 10 polymorphic microsatellite loci and performed a Structure analysis. Hybrids were found in most of the sampled populations, supporting the hypothesis that there is a risk of genetic displacement of *C. montanus*. The hybridization rate varied between 0% and 13%, depending on habitat and population size. Nevertheless, there are still many open questions. For example, it is unknown if hybrids are fecund and if backcrosses are more likely with *C. parallelus* or *C. montanus*. This might strongly influence hybridization dynamics in this species.

Does the Pantanal seasonality influence the temporal ratio of adult and immature in a grasshoppers community?

Souza, AV^{1a}; Macedo, EF¹; **Lhano, MG^{1b}**; Marques, MI²; Silva, DSM¹; Santos, ENS¹; Oliveira, DJ¹ and Silva, FRJ²

¹*Universidade Federal do Recôncavo da Bahia (UFRB), Centro de Ciências Agrárias, Ambientais e Biológicas (CCAAB), Laboratório de Ecologia e Taxonomia de Insetos (LETI). Programa de Pós-Graduação em Ciências Agrárias. Rua Rui Barbosa, 710 – 44380-000, Cruz das Almas/BA, Brazil; E-mail: a: drica_67@hotmail.com; b: marcos@ufrb.edu.br*

²*Universidade Federal de Mato Grosso (UFMT), Programa de Pós Graduação em Ecologia e Conservação da Biodiversidade. Av. Fernando Corrêa da Costa, nº 2367 – Bairro Boa Esperança, 78060-900, Cuiabá/MT, Brazil*

The Brazilian North Pantanal at the Mato Grosso state presents a monomodal seasonal gradient comprehending periods of low water, dry, flooding and high water seasons, which acts as a large reservoir of water, carbon deposit and rescue providing a significant effect on controlling the emission of gases that contribute to global warming. Although it is recognized by the expressiveness of plants and animals, data on the abundance and composition of insects in this biome are still scarce. Grasshoppers (Orthoptera: Caelifera) are fundamental within ecosystems as defoliators as well as consumers of organic matter decaying plant and moss, contributing to nutrients recycling. The aim of this study was to evaluate the ratio between the adult and immature stages of grasshoppers along the gradient seasonality of the Pantanal of Mato Grosso, Brazil. Samples were collected between the period of Drought' 2011 to Drought' 2012, in a region located in the northern Pantanal, Porto Cercado county, on the stretch between the Bento Gomes River and the Advanced Studies Base of the Federal University of Mato Grosso, in three distinct areas. The study areas meet an altitudinal and flood gradient: A1 - presents a higher land and low amplitude flooding, predominantly savannah park and 'murundu' fields with distinctive landscape units ridges and woods covered with cerrado vegetation and predominantly sandy soil; A2 - middle land with terrain height and intermediate range inundation, preponderantly showing dry forests and / or transitional areas of woodland forests, where the soil is sandy silty type; A3 - the lower lands that occurs near the Cuiabá River and receives direct influence from it, with high flood and richer in sediment, which reflects the productivity of the region, whose characteristic vegetation consists of floodplain forests with predominance of macrophytes that occur in lagoons and bays forming banks of aquatic vegetation. Each gathering was performed in one day fieldwork in each area, during 120 minutes divided into two periods of 60 minutes in the morning. The specimens were sampled using entomological nets and after, they were eviscerated, mounted on entomological pins properly labeled and the individuals separated in adults and immature. The obtained results suggest that the ratio between the adult and immature stages of grasshoppers was influenced by seasonality gradient in the Pantanal, since there has been an alternation between the predominance of certain stages of grasshopper across the study areas and in each period, where in periods in which the variation in water level was more stable and defined (drought and flooding) was found a predominance of adult stage grasshopper and on the other hand, in subsequent seasons

considered more unstable and transitional (high water and low water) occurred the predominance of immature stage grasshoppers. The collection and analysis of this pattern is fundamental to understand the dynamics of the grasshopper community in terms of the seasonal fluctuations of Pantanal biome, as well as to contribute to the preservation and maintenance of these insects in wetland biotopes, considering, within a holistic environment point of view, the importance to carry out conservation policies and environmental resources management plans, aiming to form the basis of a sustainable use of those resources. This study is the part of the project "*Analysis of the effect of flooding on the structure and composition of communities of terrestrial arthropods: a comparative study between the wetlands and not flooded in the Pantanal of Mato Grosso*" funded by FAPEMAT (PRONEX 09/2009, Proc. 838265/2009) and Federal University of the Reconcavo of Bahia (UFRB).

Aspects of the ecological physiology of the Australian plague locust, *Chortoicetes terminifera***Woodman, JD***Australian Plague Locust Commission, Australian Government Department of Agriculture, Fisheries and Forestry, Canberra, Australia*

The Australian plague locust, *Chortoicetes terminifera*, occupies the grasslands, deserts and agricultural areas of the mainland interior and is therefore exposed to extremes in temperature, rainfall and humidity. An ongoing eco-physiological research program is seeking to quantify environmental tolerances that are critical to survival and development. Cold tolerance research on first-instar nymphs has shown supercooling points ranging from -9.3 to -14.6°C , with pre-freezing mortality dependent on feeding and rate of cooling. Heat tolerance research on first-instar nymphs has shown a critical upper limit of $53.3 \pm 1.0^{\circ}\text{C}$ with death preceded by changes in behaviour, gas exchange, water loss and excretion. Heat mortality at temperatures below the critical limit was dependent on food availability. Research on the effects of flooding has shown that egg viability after inundation is strongly dependent on temperature, flood duration and embryonic development stage at the time of flooding. The water immersion tolerance of hatchling nymphs was strongly dependent on immersion temperature, whereby survival ranged from time to 50% mortality (LT_{50}) = 8.12 ± 0.26 h at 15°C to 4.93 ± 0.30 h at 25°C after nymphs entered a coma-like state within two minutes. Collectively, this research is improving our understanding of the population dynamics of the species, which is essential to successful population monitoring, forecasting and management.

Studies on the temperature adaptability of migratory locust, *Locusta migratoria manilensis* (Meyen) (Orthoptera: Acridoidea)

Tu, XB and Zhang, ZH

State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, 100193, P.R. China

Outbreak of Migratory locust *Locusta migratoria manilensis* (Meyen) was together with drought and flood, considered one of the three most severe natural disasters causing damage to crop production in ancient China. It is an important agricultural pest distributes broadly in eastern monsoon zone of China. The occurrence and distribution of locust are related closely to meteorological factors especially with temperature changes. However, how would global climate change affect locust dynamic? In this paper, we studied the relationship between locust plague and temperature. Results showed that at the optimum temperature range for locust development, locust population would increase with temperature arising. Beyond the optimum temperature range, locust population would decrease. Compared the temperature varies between years of locust plague and not causing plague. Results showed temperature varied non-regularly, and there was an overlapping temperature interval which defined as the most suitable temperature range for locust development. Overlapping temperature was not decisive to locust plague in these areas, because it would enhance locust population densities. Overall, it is not suitable for saying "temperature increasing or decreasing will promote locust plague", except "occurrence areas will increase with temperature growing". As temperature growing could accelerate the development rate and diffusion. Was it certainly that locust population density would enhance with temperature increasing? In the tolerated temperature range, temperature rising should be advantageous to the locust population in the same year, but to the next year, locust population would convert as a result of different geographical distribution area. At 1 and 2 generation areas, temperature rising was detrimental for locust population growth, because diapausing rate of eggs was negatively related to EAT in winter. At 3 and 4 generation areas, temperature rising would be beneficial for locust population. We have predicted the population density of migratory locust in a long time, it will be helpful for locust management.

Study on the Adaptability of Grasshopper in Inner Mongolia Steppe

Wu, HH and Zhang, ZH

Scientific Observation and Experimental Station of Pests in Xilingol Rangeland, Ministry of Agriculture, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193

The objective of this study is to investigate the ecological relationship between plant community structure and grasshopper community structure in the typical grasslands of Inner Mongolia. In this experiment, Canonical analysis, double screening for stepwise regression and redundancy analysis (RDA) were used to analyze the relationship between plant community structure and grasshopper community structure. Then, cage and orthogonal test was used to test the relationship between *Oedaleus asiaticus*, *Dasyhippus barbipes* and *Angaracris barabensis* in Inner Mongolian Steppe. These results indicated that the biomass loss of *Leymus chinensis* was negatively correlated with the grasshopper species richness index and positively correlated with the relative abundance of *Dasyhippus barbipes* in the *L. chinensis* steppe. The relative abundance of *Oedaleus decorus asiaticus* was positively correlated with the biomass loss of *Stipa krylovii* in the *S. krylovii* steppe and the steppe dominated by *S. krylovii* with the forb diverse. Canonical correlation analysis showed that there was a positive correlation ($r = 0.955$, $P < 0.05$) between the comprehensive factor of grasshopper and the comprehensive factor of host plant. And the intraspecific competition between *O. asiaticus* and *D. barbipes* increased with their density increases, but increased with the plant food decrease. The intraspecific competition of *A. barabensis* did not relate with its density because of the unsuitable habitat. Results of orthogonal test indicated that *O. asiaticus* had strong interspecific competition ability, and the habitat has more important effect on *D. barbipes*'s competitive ability. In the relationship between plants and grasshoppers, probably the habitat condition consists of structure of plant community can cause more effects on community composition of some grasshoppers than the food plants. The existence of the dominant grasshoppers decided by the dominant plants causes high infestation rate of the dominant plants. Habitat and population density can affect the community dynamic of grasshoppers. *O. asiaticus* has stronger interspecific competition ability than *D. barbipes* and *A. barabensis* when the habitat is suitable.

Study on the relation between grasshopper outbreak and vegetation community on typical grassland in Yanchi County

H, Wenguang¹; M, Xiaoming¹;ZH, Rong²;Zh, Mengmeng² and W, Shuhua²

¹*The Grassland Workstation of Ningxia, Yinchuan 750002, China;*

²*Institute of Plant Protection, Ningxia Academy of Agriculture and Forestry Sciences, Yinchuan 750002, China*

The relation between ecological distribution characteristics of grasshopper and environmental factors is a theoretical basis to reveal geographic occurrence features of grasshopper. The relation between grasshopper composition and vegetation community was studied by using the methods of field investigation and quantitative analysis in typical steppe of Ningxia. The results showed: There were 24 different species of grasshoppers in typical steppe of Mahuang mount, the main species were *Calliptamus barbarus*, *Oedaleus asiaticus*, *Angaracris rhodopa*, *Bryodema nigroptera*, *Bryodemella tuberculatum*, *Calliptamus abbreviates*, *Compsorhipis davidiana*, *Chort hippus dubius*, *C. albonemus*. The numbers of individuals, species richness and diversity had positive correlation with the diversity, biomass and coverage of vegetation, and had negative correlation with the evenness and height of vegetation. The numbers of individuals, species richness and diversity had negative correlation with the dominance of the families of Gramineae and Compositae, and had positive correlation with the dominance of the families of Leguminosae and others. *O. asiaticus*, *A. rhodopa* and *C. albonemus* showed the best performance in terms of selectivity for grass forages, *E. coerulipes* and *F. beicki* for Compositae forages based on the correlation between dominant species and vegetation community. *C. albonemus*, *F. beicki* and *E. coerulipes* were preferred to the poor vegetation conditions, while *A. rhodopa* were preferred to the good vegetation conditions.

Studies on the Community Structure of Grasshoppers on Different Types of Grassland In Ningxia

W, Shuhua¹; G, Liyuan¹; ZH, Rong^{1*}; H, Wenguang² and Y, Zhao²

¹*Institute of Plant Protection, Ningxia Academy of Agriculture and Forestry Sciences, Yinchuan 750002, China;*

²*The Grassland Workstation of Ningxia, Yinchuan 750002, China*

Analyzed on community compositions and dominant species of 4 types of natural grassland. The results showed that there are 70 species of Orthoptera:Acridoidea and Tetrigoidea in Ningxia Grassland, different types of grassland result in the Characteristics of Community Structure of Insect. Among them 22 species of desert region grasshopper, the main species are *Epacromius barbarous*, *Filchnerella beicki*, *Eotmethis holanensis*, *Zichya alashanica* and so on, 24 species grasshoppers of typical steppe where are one of Locusts most serious regional , the main species are *Chorthippus alonemus*, *Oedaleus asiaticus*, *Calliptamus abbreviatus*, *Angaracris rhodopa*, *Gampsocleis inflata* and so on, 19 species of meadow range- land area , the main species are *Tetrix tartara*, *Omocestus haerrhoidalis*, *Gampsocleis inflata* and so on.

Responses of grasshoppers to vegetation and interactions with natural enemies in Mahuang Mountain, Ningxia

Zh, Mengmeng^{1,2}; Zh, Zehua¹ and Zh, Rong²*

¹*Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China;*

²*Institute of Plant Protection, Ningxia Academy of Agricultural and Forestry Sciences, Yinchuan 750002*

Grasshopper was an important component in grassland ecosystem, which plays a key role in ecological balance and stability of food chain. The relationship between grasshopper and vegetation was one of the hottest topics in ecology. Three sites in Ningxia were selected for system monitoring points from 2010 to 2012, which aimed to study spatial and temporal dynamics of grasshopper and vegetation. *Filchnerella beicki* and *Chorthippus alonemus* was dominant grasshopper, which were typical arid species and moist species respectively. Carabid beetles may be important natural enemies of grasshoppers, in which *Pesudotaphoxenus brevipennis* and *Pseudotaphoxenus mongolicus* were the dominant species. Grasshopper was not only related to vegetation, but also was correlated to environmental humidity. These results supplied important basis and data for integrated pest control of grasshopper, biodiversity conservation, and grassland restoration.

Systematics

Review of the Fossil Tridactyloidea (Orthoptera: Caelifera)**Heads, SW**

Curator of Orthoptera, Illinois Natural History Survey, University of Illinois, USA

E-mail: swheads@illinois.edu

The pygmy mole crickets (Tridactylidae), mud crickets (Ripterygidae) and sandgropers (Cylindrachetidae) together comprise a highly autapomorphic group of basal Caelifera, united in the superfamily Tridactyloidea. Monophyly of the Tridactyloidea is supported by a suite of robust morphological and molecular characters and while its position at the base of the caeliferan radiation is generally accepted, details of their origins and relationships with other caeliferan groups remain enigmatic. The highly derived morphologies of extant tridactyloids obscure their major group relationships and also complicate study of their ingroup phylogeny. However, exceptionally preserved fossil representatives (both rock compressions and amber inclusions) promise to shed much-needed light on the evolution of this fascinating group of orthopterans. Here, I provide a review of the tridactyloid fossil record and an overview of their phylogenetic significance.

Molecular phylogeny of Grylloidea (Orthoptera): laying the bases for a new, phylogenetic classification of crickets**Desutter-Grandcolas, L***Muséum national d'Histoire naturelle, Département Systématique et Évolution, UMR 7205 CNRS, case postale 50, 57 rue Cuvier, F-75231 Paris cedex 05, France*

Phylogenies are the most crucial references to test hypotheses of evolution and establish classification systems. Based on hypotheses of primary homologies, phylogeny can be used to infer hypotheses of character ancestral states and transformation series, in the same way as it proposes hypotheses of taxa relationships built on the congruence of all the characters used for reconstruction. The use of a data matrix, as well as explicit and powerful reconstruction algorithms also guarantee the repeatability of the analyses. Cricket phylogeny has been little analyzed this way, even though this clade is one of the richest model for studies in bioacoustics and behavioral ecology, owing to the diversity of its communication modes, stridulatory structures, signal properties, habitats, or nuptial behaviors. In the same way, cricket classification clearly needs the stability that only a robust phylogeny can bring to classificatory systems.

We gather an in group of more than 200 terminals representing more than 94% of all supra generic groups listed in the Orthoptera Species File or proposed in previous taxonomic literature for crickets, and document each terminal with a set of 8 mitochondrial and nuclear markers (about 4000 bp). We run parsimony, Maximum Likelihood and Bayesian analyses, and assess the robustness of the different nodes. Our results test the monophyly of the crickets, and will allow proposing the first phylogeny-based classification for this clade. Ultimately, we will discuss the implication of our phylogenetic hypothesis on cricket evolution.

Diversification patterns in Melanoplineae (Orthoptera: Acrididae) grasshoppers from the Andes highlands

Cigliano, MM^{1,2}; Pocco, ME^{1,2} and Lange, CE²

¹*Division Entomología, Museo de La Plata, La Plata, Argentina*

²*Centro de Estudios Parasitológicos y de Vectores (CEPAVE), CCT La Plata, CONICET, La Plata, Argentina*

Members of the Melanoplineae subfamily usually dominate both in species and in number of individuals in most temperate grasshopper communities of the Americas and are one of the main components of Acrididae fauna in the high Andes of South America. The Andes are characterized by a long list of outstanding features including numerous endemic organisms with interesting life histories. Despite their young age, the tropical Andes are highly diverse due to recent geological uplift. Different scenarios including habitat diversity resulting from differences in orogeny, topography, soils, climate and elevation have been proposed to explain the diversification of high Andean taxa.

Species have spread North and South along this mountain chain, and also up and down in elevation during colder times through repeated glaciations. The Andes provide altitudinal zoned habitats from rainforest to Paramo to glaciated peaks, an East–West differentiation into wetter and drier slopes through rain shadow effects. So far, there is no comprehensive study of melanopline fauna of the Andes, and there are only few records of highland species of the Peruvian and Bolivian Andes. Recent surveys that resulted in the discovery of several new melanopline taxa illustrate discrepancies between perceived and actual species diversity. Cladistics-biogeographic analyses on Melanoplineae taxa were conducted to test the different scenarios proposed to explain diversification patterns of distinct possible geographic modes of speciation in montane habitats of Bolivia and Peru.

Phylogenetic systematics of Orthoptera

Song, H

Department of Biology, University of Central Florida, Orlando, FL, U.S.A

With more than 23,000 valid species, Orthoptera is the most diverse member of the group of polyneopteran insect orders. Despite the familiarity, the phylogenetic relationships within Orthoptera are poorly understood because of a long history of conflicting taxonomic classification schemes based on different character sets. In this presentation, I present the most comprehensive higher-level phylogeny of Orthoptera to date based on complete mitochondrial genomes and nuclear genes. Using the extensive fossil evidence known from the Carboniferous to the Tertiary, I estimate divergence time for the major groups within the order. The analysis suggests that the current diversity of Orthoptera is a result of both gradual and rapid radiation followed by a number of extinctions. The current distribution is a result of both deep vicariance and recent dispersal. I also re-examine the current classification scheme in light of the phylogeny and present a phylogeny-based natural classification scheme for Orthoptera.

Are Agraeciini and Copiphorini natural subgroups of Conocephalinae? Considerations based on male cerci

Ingrisch, S

Zoological Research Museum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany

The subdivision of Conocephalinae goes back to Redtenbacher (1891) who recognised three tribes: Agraeciini (today 98 valid genera), Copiphorini (50 genera) and Conocephalini (20 genera). Although a few additional tribes have been described since then (Armadillagraeciini Rentz, Su & Ueshima, 2012, 3 genera; Coniungopterini Rentz & Gurney, 1985, 3 genera; Euconchophorini Gorochov, 1988, 5 genera), the classical 3 tribes still cover the majority of genera and species.

The Conocephalini are a rather uniform group of small meadow katydids that are at the current state of knowledge well delimited. Regarding the other two tribes, it is easy to distinguish Agraeciini from Copiphorini in the Old World, but in the Americas, the right assignment of a genus to one of both tribes may be difficult (e.g. Walker, T.J. & Gurney, A.B. (1972). *Ann. Entomol. Soc. Amer.* 65: 460-474). This study aims to analyse the validity of Agraeciini and Copiphorini as separate natural subgroups of Conocephalinae.

My previous taxonomical and morphological studies of Conocephalinae mainly from SE Asia found that the male cercus is a valuable character for the separation of species and helpful for the classification of genera. As the male cerci are an important tool for attaching to the female abdomen during mating one can suppose that the correct shape of the cerci works as an isolating mechanism between species. However, in one subgroup of Conocephalinae the situation is quite different: in the Old World genera currently arranged under Copiphorini. In seven African and five Asian genera with together 137 species there are only two different shapes of male cerci with hardly any variation between the species that use one of these shapes. The cerci have either two acute apical internal teeth with the more proximal tooth larger and little sinuate (type A), or one short acute apical-internal tooth and a long upcurved internal tooth at very base (type B). The apical tooth in type B is distinctly smaller than in type A. As published studies show, there are also some American genera that have one or the other of these cercus types, but in general the male cerci of American Copiphorini are not well studied.

The following conclusions may be drawn from the anomaly that species from different genera have identical cercus shapes:

1. The male cerci in this group do not function as an isolating mechanism between species: instead there is a pre-mating mechanism, the species-specific stridulation (e.g. Bailey, W.J. (1976). *J. Nat. Hist.* 10: 511–528).
2. The male cerci are a conservative character that did not change during radiation. They can thus be regarded as synapomorphies of the genera concerned.
3. As there are two different shapes of cerci, there are two evolutionary lines, leaving it open as to whether there is a single common ancestor or parallel evolution. But as also the general characters are similar, with several species assigned to the wrong genus if judged by the shape of the male cercus, one may suppose that they form a natural group.

4. In contrast to the Asian Agraeciini that live in forested areas, they occur in wet, open grassland. Thus one may suppose that they are phylogenetically rather young and evolved together with the spread of open grasslands.

The question that arises is whether this group of genera is related to *Copiphora* (the type genus of Copiphorini) or is it closer to another group. As far as can be judged from descriptions and images in Naskrecki (2000: Katydids of Costa Rica. Volume 1, Philadelphia), the male cerci in the genus *Copiphora* differ from those of the Old World Copiphorini and they also differ between species. Thus it is unlikely that the latter are close to *Copiphora*. In contrast, studying the cerci of the genera *Lesina* and *Ellatodon* (subtribe Eumegalotondina = syn. Lesini) proved that they are somewhat intermediate between both of the cercus shapes discussed before although their shape is more similar to type B. From the latter they only differ by a larger apical tooth and the proximal tooth not arising at the very cercus base but somewhat behind it.

Formally it would thus be reasonable to rise Lesini to the rank of a full tribe [the family group name Lesini de Jong, 1942 is given preference over Eumegalodonidae Brongniart, 1892 since the type genus *Eumegalodon* Brongniart, 1892 is a generic homonym of the mollusc genus *Eumegalodon* Guembel, 1862] and include the Old World Copiphorini and the corresponding American genera to the Lesini. This hypothesis should however be tested by additional evidence including gene sequencing. The relationships between the Lesini in the new sense to other groups of Conocephalinae as well as that between the remaining American Copiphorini to the Agraeciini should be evaluated in future studies. The type genera of both tribes are from South America. For practical reasons it may be discussed if we should give up the current subdivision of Conocephalinae until we have more evidence on the phylogenetic relations between the genera and/or use smaller groups of genera for which there is evidence for monophyly as a basis for a tribal division.

Carboniferous Archaeorthoptera from The Xiaheyan entomofauna (Ningxia, China): recent discoveries and perspectives

Gu, JJ¹; Béthoux, O²; Yue, Y³ and Ren, D⁴

¹College of Biological Science and Engineering, North University of Nationalities, 204 Wenchangbeijie, Xixia District, Yinchuan 750021;

²CR2P UMR 7207, MNHN, UPMC, CNRS, 8 rue Buffon, CP38, 75005 Paris, France;

³College of Life Sciences, Ningxia University, 539 West Helanshan Road, Xixia District, Yinchuan 750021, China;

⁴College of Life Sciences, Capital Normal University, 105 Xisanhuanbeilu, Haidian District, Beijing 100048, China.

E-mail: orthoptera_gu@aliyun.com, 61741036@qq.com

During the last decade, nearly three thousand winged insect specimens have been collected from the Late Carboniferous locality of Xiaheyan Village (Zhongwei City, Ningxia Hui Autonomous Region, China). Most specimens are archaeorthopterans (i.e., stem-Orthoptera), with isolated well-preserved wings, and a few preserve body structures and a complete set of wing pairs. This entomofauna exhibits a high abundance and diversity of archaeorthopterans, accounting for more than 80% of the total numbers found. Some new species have been described, including a rare panorthopteran *Heterologus duyiwuer* Béthoux, Gu et Ren 2011 that allowed a new primary homology for the branches of CuA + CuPac to be conjectured. Several abundant species like *Longzhua loculata* Gu, Béthoux et Ren 2011, and *Miamia maimai* Béthoux et al. 2012, were documented based on a large sample, from which data on wing venation intra-specific variability could be derived. The range of variation proved to be more significant than previously appreciated. The relevance of many 'genus-level' contemporaneous and related taxa, erected based on characters observed in a single (or few) individuals, may have to be reconsidered. In addition to wing venation, some specimens preserved body structures that improved our knowledge on the morphology and ecology of early archaeorthopterans. The abundant species *L. loculata* had strong mandibles and elongated prothorax indicating a carnivorous and predatory habits. According the head morphology, *M. maimai* may not possess the impressive mandibles documented in other predatory types. Many other species recorded by an abundant sample will be described in the future. This exceptional sample gives us an unprecedented opportunity to investigate morphology, intra-specific variability, and diversity of Late Carboniferous archaeorthopterans.

The Orthoptera in a stand of *Artemisia herba alba* in the central steppe (Mergueb, M'sila) in Algeria

Chebouti-mezyou, N^{1*}; Merabet, A¹; Chebouti, Y³; Bissaad, FZ¹; Behidj, N¹ and Doumandji, S²

¹Department of Biology, University of Boumerdes (UMBB), Algeria;

²National School Superior Agronomy, Algiers (ENSA), Algeria;

³National Institute of Forest Research, Algiers, Algeria;

Laboratory of soft technology valorization physical-chemical characterization and biodiversity

*Corresponding author: chNADJIBA@yahoo.fr

This work focuses on the bio-ecological study of the orthoptera found in the Mergueb (M'sila) nature reserve. The orthoptera associated with a stand of *Artemisia herba alba* consist of 18 species of grasshopper, half of which belong to the subfamily Oedipodinae. There are four species in subfamily Gomphocerinae and two species of Calliptaminae. By contrast, the subfamilies Acridinae, the Truxalinae, the Pyrgomorphinae and Dericorythinae are each represented by only one species. The most frequently found species was *Calliptamus barbarus* (25.3% of specimens caught) followed *Sphingonotus tricinctus* (23.1%) and *Sphingonotus rubescens* (16.7%).

There are additional species but these are found in low numbers and include *Acrotylus patruelis*, *Calliptamus barbarus*, *Sphingonotus tricinctus* and *Ramburiella hispanica*, which seem to have only one generation per year. Moreover, there is only one species of Ensifera (Decticinae) present : *Platycleis intermedia*.

Systematics of *Phlugioloopsis* (Orthoptera: Tettigoniidae: Meconematinae) in China

Bian, X and Shi, FM¹

College of Life Sciences, Hebei University, Baoding, 071002, P. R. China

¹Corresponding author: shif_m@126.com

Phlugioloopsis is a brachypterous genus, which belongs to the tribe Meconematini, Meconematinae, Tettigoniidae. So far, the subfamily contains 19 genera and more than 80 species which are recorded in the tribe all over the world; they are mainly distributed in the Orient. Twelve genera and 62 species are recorded in China and most are Chinese endemic genera and species. In this paper, the tettigoniid genus *Phlugioloopsis* was reviewed in the following 3 aspects:

(1) The generic characters of *Phlugioloopsis* were revised; 15 new species of the genus have been described by us since 2012; a new key to all species of the genus was provided; and the structures of mandibles and male stridulatory files in some species were described.

Results showed that the genus of *Phlugioloopsis* is different from other genera in the morphology of male stridulatory files and the teeth denth, so the characteristic of male stridulatory files may be used as one of the distinguishing characteristics of *Phlugioloopsis*.

(2) Fragments of the mitochondrial COI gene (643bp) of 193 individuals and the mitochondrial Cytb gene (617bp) of 182 individuals were sequenced using universal primers from 16 *Phlugioloopsis* species for ingroup and 3 brachypterous species for outgroup, i. e. *Cecidophagula liangshana* sp. nov., *Pseudocosmetura anjiensis* (Shi & Zheng, 1998) and *Neocyrtopsis platycata* (Shi & Zheng, 1994). The base composition, base substitution frequency and substitution pattern, substitution saturation analysis, interspecies and intraspecies genetic distance and substitution saturation analysis of DNA sequences were analyzed by some biosofts such as Clustal X 1.83, BEMG 1.1 and MEGA 5.05. Based on the data set of COI gene, Cytb gene and their combined datasets, we reconstructed the phylogenetic framework through MP and BI in the PAUP and Mrbayes software. Meanwhile, the haplotypes of COI gene and molecular identified for COI gene and Cytb gene with three Distance-based methods in TaxonDNA were analyzed for *Phlugioloopsis* species.

The analysis indicated that the MP and BI trees of *Phlugioloopsis* using single or combined datasets did not show the phylogenetic relationships of 16 species, but the monology of 8 new species, i. e. *P. complanispinis* Bian, Shi & Chang, 2013, *P. damingshanis* Bian, Shi & Chang, 2012, *P. digitusis* Bian, Shi & Chang, 2012, *P. emarginata* Bian, Shi & Chang, 2013, *P. huangi* Bian, Shi & Chang, 2012, *P. tribranchis* Bian, Shi & Chang, 2012, *P. xinanensis* Bian, Shi & Chang, 2013 and *P. pectinis* Bian, Shi & Chang, 2012, were supported by the phylogenetic tree. From the morphological view, *P. xinanensis* Bian, Shi & Chang, 2013 was similar to *P. brevis* Xia & Liu, 1993, while in the 6 phylogenetic trees the sister group relationship of *P. xinanensis* Bian, Shi & Chang, 2013 and *P. ventralis* Wang, Li & Liu, 2012 was highly supported. Most individuals of each known species were clustered in one clade, and the individuals sampled from the same place formed a secondary clade with a high bootstrap value, such as *P. tuberculata* Xia & Li, 1993, *P. grahami* (Tinkham, 1944), *P. ventralis* Wang, Li & Liu, 2012, and *P. brevis* Xia & Liu, 1993. Further studies are needed to account for the relationships of *P. adentis* Bian, Shi & Chang, 2012, *P. trullis* Bian, Shi & Chang, 2012 and *P. yunnanensis* Shi & Ou, 2005. The

synonymisation of *Acyrtaspis* Bei-Bienko, 1955 with *Phlugiolopsis* Zeuner, 1940 and *P. fallax* Xia & Liu, 1993 with *P. minuta* (Tinkham, 1943) were characterized by morphological characters what were supported by molecular data using single and combined datasets. According to the BM and BCM criteria, 128 queries are identified (66.32%), 40 are ambiguous (20.72%), and 25 are misidentified (12.93%) for COI gene. For Cytb sequence, 128 queries are identified (70.32%), 46 are ambiguous (19.78%), and 18 are misidentified (9.89%) by the BM and BCM criteria.

(3) Ecological niche models, maximum entropy (MaxEnt), based on the known distribution of *Phlugiolopsis* and 19 environmental variables in WorldClim were used to predict the potential geographical distribution of the genus in this paper. The precipitation of warmest quarter was the most important environmental variable affecting its distribution. *Phlugiolopsis* is mainly found in the western mountains, hilly subarea of Southwestern and the western mountains, and high plateaus subarea of Central China. While we did not find its potential distribution area in the north Yangtze River area, we speculated that Yunnan-Guizhou Plateau is the original center of the genus.

Early evolution of the order Orthoptera and divergence of its highest taxa

Gorochov, AV

Zoological Institute, Russian Academy of Sciences, 1 Universitetskaya Emb., Saint Petersburg 199034, Russia; orthopt@zin.ru

Phylogenetic taxonomy, usually recognizing only holophyletic groups as true taxa, is of little use for ancient groups that contain numerous fossil species and may include ancestors of some younger groups. Evolutionary taxonomy recognizes both variants of monophyletic taxa: paraphyletic and holophyletic. The latter views allow one to form higher taxa having more or less similar both morphological structure and mode of life; these taxa give possibility for their morphological diagnostics and may be considered as certain organizational steps in the evolutionary ladder. It is necessary to understand that classification of organisms is a product of scientific work, but not a certain reality of what exists in Nature. However, phylogeny is a historic reality and consequently our phylogenetic schemes may be put at the base of a most suitable classification, if we could add to these schemes, some data about rate of evolutionary changes in the groups studied. One of many problems of this study is the absence of dependable phylogenetic methodology. In this connection, study of fossil remnants, documenting the real history of organisms, for restoration of sequence of their morphological changes may be especially useful.

There are a few hypotheses about origin of Orthoptera. All of them are insufficiently grounded, but the hypothesis about independent branching of Orthoptera and Phasmatoptera from unknown Carboniferous representatives of the fossil order Titanoptera (usual in the Carboniferous and Triassic) is additionally supported by the new finds of Titanopterans in the Permian deposits. The first division of Orthoptera into two high taxa, Oedischiidea (paraphyletic infraorder) and Elcanidea (holophyletic infraorder), had a place in the Carboniferous: both taxa belong to the paraphyletic suborder Ensifera. The origin of the Recent paraphyletic infraorder Tettigoniidea from Sylvoedischiinae (one of the groups of Oedischiidea) and the branching of the Recent holophyletic infraorder Gryllidea from Hagloedischiidae (a most primitive group of Tettigoniidea) are well supported by the Permian and Triassic fossils. Another very high taxon, known from the same time as Tettigoniidea and Gryllidea, is the holophyletic suborder Caelifera. Its ancestors are less clear. However, the fossil remnants suppose that these ancestors might belong to the family Proparagrillacrididae from the infraorder Oedischiidea. At present, this family is known from the Late Permian to the Late Triassic, and, thus, it may be older than Caelifera. Both infraorders of Caelifera, Acrididea and Tridactylidea, are known from the Triassic. Their common monophyly (but not a sequence of branching) is evident.

Evolution of the copulatory apparatus in Ensifera (Orthoptera): Grylloidea.**Gorochov, AV***Zoological Institute, Russian Academy of Sciences, 1 Universitetskaya Emb., Saint Petersburg
199034, Russia;*

Email: orthopt@zin.ru

This communication is a continuation of the previous poster "Evolution of the copulatory apparatus in Ensifera (Orthoptera): introduction" which was presented at the 10th International Congress of Orthopterology in Antalya (Turkey, 2009). Main trends in the evolution of cricket copulatory apparatus were probably connected with the transformation of simple membranous (hagloid) male genitalia, characteristic of ancient groups of Ensifera, into a complicated organ with highly specialized sclerites for fixation of the female during copulation. Possibly, this evolutionary process was accompanied by the reduction and disappearance of hooks or other abdominal processes which might be used by these ancient groups for female fixation (preservation of trend to formation of the latter copulatory structures may be observed in many other groups of Orthoptera). Sclerites in the male genitalia independently appeared in Grylloidea not less than four times: in Gryllotalpidae, Myrmecophilidae (including Bothriophylacinae), Gryllidae and Mogoplistidae. This hypothesis, proposed by me in 1984, was one of the reasons for division of the Recent Grylloidea into four families. Each of the three first families acquired sclerites in the male genitalia once, but Mogoplistidae possibly acquired them more than once: male genitalia of the tribe Mogoplistini are of the hagloid type, membranous, while in the majority of genera of Arachnocephalini (Mogoplistinae), in *Pseudomogoplistes* (Mogoplistinae) and in Malgasiinae, male genitalia have three types of sclerites which might have also appeared independently. Moreover, many sclerites of male genitalia in the Grylloidea (including additional ones inside some of its families) are formed independently and have significant convergent similarity; this is a reason that nomenclature of the male genital structures partly based on their function and position, but not only on their homology, is more simple and much more suitable for descriptions and morphological investigations.

The Stenopelmatoidea is a holophyletic taxon originated from the Late Mesozoic Hagloidea, or does it consist of remnants of the ancient ensiferans originally lacking stridulatory apparatus in tegmina?

Gorochov, AV

*Zoological Institute, Russian Academy of Sciences, 1 Universitetskaya Emb., Saint Petersburg
199034, Russia;*

E-mail: orthopt@zinru

The superfamily Stenopelmatoidea is considered as a good taxon with a few families by some former and recent orthopterologists. These families are Anostomatidae, Rhabdophoridae and Stenopelmatidae; often the subfamilies Gryllacridinae and Schizodactylinae, included here in Stenopelmatidae, are also considered as separate families. These taxa are with a few distinct synapomorphies but have also some features that are very primitive such as the absence of tegminal stridulatory apparatus. Some researchers, basing their conclusions on morphological and paleontological data, believe that this absence is a result of reduction and loss, but others think that it is an inheritance from ancient ensiferans that originally lacked such apparatus. The recent molecular investigations give non-identical results; sometimes these investigations suggest different phylogenetic relations for different families and some subfamilies of Stenopelmatoidea.

This complicated situation is in need of some additional data, and especially of paleontological sequences allowing one to organize fossil remnants (true traces of the real phylogenetic process) in a chain connecting the recent groups with each other and with their common ancestors. It is reasonable to analyse these remnants comparing them with the recently published data on paleontological sequences and including all the other relevant data on the taxa studied. Such analysis allow one to find more numerous and logical evidences for origin of one of the stenopelmatoid families (Anostomatidae) from the Late Mesozoic Hagloidea, to connect this family with all the other stenopelmatoids by additional morphological characters, and to explain (hypothetically) some contradictions in the molecular phylogenetic schemes.

Systematics of Tetrigidae (Orthoptera) in China

Deng, W¹ and Zheng, ZM²

¹ *Department of Chemistry and Life Science, Hechi University, Yizhou 546300, Guangxi, China*

² *Institute of Zoology, Shaanxi Normal University, Xi'an 710062, China*

The Tetrigidae contains 7 subfamilies 50 genera 600 species that occur in China. This is a monophyletic group defined traditionally by an elongated pronotum covering the entire abdomen and a tarsal formula of 2-2-3. The Tetrigidae from China are being systematically revised by clarification of the taxonomic status of groups within it through determining the utility of the characters used for diagnosis, biology and geographical distribution, taxonomy and phylogeny. Empirical results show that Tetrigidae is distributed mainly in Southern China, but there exist problems and disputes with the current taxonomy of this group. A lot of new species have been described in China, mainly based on traditional morphology. But by using zoogeography, molecular biology and cladistic systematics, it is hoped to revise the Tetrigidae, reconstructing the phylogeny and clarifying the geographic distribution of individual species.

Systematics and diversity of phalangopsid (Ensifera, Grylloidea, Phalangopsidae) crickets in Brazil

Dias, PGBS¹ and Bolfarini, MP¹

¹*Department of Zoology, Biosciences Institute, University of Sao Paulo, Rua do Matao, trav 14, n 101, CEP 05508-900, Cidade Universitária, São Paulo, Brazil*

E-mail: pedrogdias@gmail.com

Phalangopsidae is the most common taxon of Grylloidea that inhabit the understories of tropical forests of Neotropical Region, where at least 70% of the 195 described genera of this group occurs. Phalangopsid crickets are known as long-legged or spider-like crickets due its large development of posterior legs in relation to the body length. Other morphological characters used to define this taxon are the shape of head, relatively small in relation to pronotum, a proeminal antennal scape and the presence of several brown or brownish maculae along the body. Most of the 905 recognized species are brachipterous, mainly the males (few species are completely apterous) and it can inhabit the leaf litter, trees, trunks, barks and any kind of natural cavities, including caves, leaving out to forage at night on litter, rocks and trunks. Its species are easily found in the field, mainly in nocturnal collectings.

According to Desutter-Grandcolas's classification, three subfamilies occurs in Brazilian territory: Phalangopsinae, Paragryllinae and Luzarinae. Luzarinae comprises the most diverse taxon with 57 described species in 25 genera. This subfamily is characterized by some morphological characters as the reduction in fore wings in adult males (females frequently apterous), with reduced or absent venation, the loss or reduction of hind wings and the truncation of the 5th joint of maxillary palp obliquous. Although these features can be seen in others taxa of Phalangopsidae, it's the male genitalia the main character to define this taxon: the male genitalia of Luzarinae have the tendency to the large development of the endophallus and endophallic apodeme and the elongation of the pseudepiphallus and pseudepiphallic arms. According to Desutter-Grandcolas, Luzarinae is subdivided in three groups, based on characters of male phallic complex, mainly characters of endophallic structures. The groups were named A, B and C, but were not formally published and thus don't have status of tribe or any other taxonomic ranks. This classification is not adopted by other authors and is used by Brazilian taxonomists.

Most of all Luzarinae species (38) were described from the Brazilian Atlantic Forest. This biome is a tropical forest occurring along the Atlantic Coast and considered now as a biodiversity hotspot due the great number of endemic species and large deforestation; only 7% of this forest is preserved. Possibly a large species irradiation of Luzarinae occurred throughout this biome, perhaps due to speciation events and the recent history of this vegetation. This phenomena is observed on the "group C" which presents 33 species in 14 genera, the almost totality of Luzarinae species from Atlantic Forest.

Since 2007, 9 field trips were made through this biome, reaching 6 states and several localities, aiming to sample new areas and find undescribed taxa. These collectings led to discovery of at least 25 undescribed species, almost half of the known diversity of Luzarinae in Brazilian territory. These results show the lack of studies on taxonomic and systematics of crickets, leading to the current taxonomic impediment. It will be presented some new species found, maps of distribution and the extant diversity of Luzarinae in Atlantic Forest.

Systematics of Pyrgomorphidae

Mariño-Pérez,R

Department of Biology, University of Central Florida, Orlando, USA

The family Pyrgomorphidae (Orthoptera: Caelifera: Acridomorpha), commonly known as gaudy grasshoppers, is defined by the presence of a groove in the fastigium and internal genitalia structures. It consists of 477 species in 149 genera. They are primarily distributed in the Old World with only 29 species found in Australia and 29 in the New World. Currently the family is divided in two subfamilies, Pyrgomorphinae and Orthacridinae, with a total of 31 tribes and 5 genera *incertae sedis*. Despite many interesting features of the family, such as aposematic coloration, wing reduction, plague potential and its use as human food, there is no phylogenetic hypothesis available for Pyrgomorphidae. Although the most recent phylogenetic analysis based of mitochondrial genome data places as a sister group of the superfamily Acridoidea, the relationships within Pyrgomorphidae are vague and poorly understood, and even there are not synapomorphies that define the two subfamilies. In order to understand the evolution of this family, we reconstruct a phylogeny based on morphological characters, both from external and internal morphology (genitalia). We used 42 ingroup genera representing all the 18 current pyrgomorphine tribes and 10 of the 13 orthacridine tribes. We tested the monophyly of the family and other previously suggested internal groups (subfamilies and tribes) and comment on interesting evolutionary trends such the evolution of chemical defense and its correlation with warning coloration and the evolution of wing reduction. Finally, taking into account the geologically recent appearance of the group (70-20 mya); we discussed the peculiar biogeography of the group.

Systematics and diversity of phalangopsid crickets (Ensifera, Grylloidea, Phalangopsidae) in Brazil

Souza Dias, PGB

University of Sao Paulo, Sao Paulo, Brazil

E-mail: pedrogdias@gmail.com

Phalangopsidae is the most common taxon of Grylloidea that inhabit the tropical forests' understories of Neotropical Region, where at least 70% of the 195 described genera of this group occurs. Phalangopsid crickets are known as long-legged or spider-like crickets due its large development of posterior legs in relation to the body length. Other morphological characters used to define this taxon are the shape of head, relatively small in relation to pronotum, a prominent antennal scape and the presence of several brown or brownish maculae along the body. Most of the 905 recognized species are brachipterous, mainly the males (few species are completely apterous) and it can inhabit the leaf litter, trees, trunks, barks and any kind of natural cavities, including caves, leaving out to forage at night on litter, rocks and trunks. Its species are easily found in the field, mainly in nocturnal collectings.

In Brazil occurs at least 80 species, distributed in three subfamilies (the number of species in parentheses): Luzarinae (57), Phalangopsinae (7) and Paragryllinae (16). The taxonomy of Phalangopsidae is poorly understood and this taxon can be considered as a family of Grylloidea or a subfamily of Gryllidae. This current debate can be seen in recent papers where a group can be referred as a tribe, subtribe or subfamily according to the classification system employed (*sensu* Desutter-Grandcolas, *sensu* Gorokhov or *sensu* Orthoptera Species File) There is also no consensus on the sclerites nomenclature and interpretation of the male phallic complex, the main character used on crickets' taxonomy. Brazilian taxonomists, for practical reasons, use the classification system proposed by Desutter-Grandcolas.

Brazil is the largest and most sampled country in South America. Although phalangopsid species are distributed throughout Brazilian biomes, mainly on tropical forests, its diversity is poorly known. Thus, the discovery of undescribed genera and species is relatively common. The Atlantic Forest is the most well-known Brazilian biome and the best sampled, with 47 species described while Cerrado (Brazilian Savannah) and Amazonia, two large biomes which together represent almost the entire Brazilian territory, have only 10 species described each. Other large and important Brazilian biomes are Pantanal and Caatinga who does not have any species described. This demonstrates the lack of studies with this group in the country resulting in the absence of data that support taxonomic works and a unified taxonomic classification system. There is also no systematic studies using phylogenetic method, so that the evolutionary relations between the Phalangopsidae groups are unknown.

Here it will be presented results of scientific expeditions made over the last six years, in several localities, including the discovery and records of dozens of new species. Besides, it will be discussed the state of the art and perspectives on the study of Phalangopsidae in Brazil in the following years.

Systematics and phylogeny of *Atlanticus* (Orthoptera: Tettigoniidae: Tettigoniinae) and its relatives, a Tertiary relict katydid genus

Liu, CX¹; Wang, YY¹ and Heller, K-G²

¹*Institute of Zoology, Chinese Academy of Sciences, Beijing, China*

²*Magdeburg, Germany*

The genus *Atlanticus* Scudder belongs to the contentious tribe Drymadusini (Orthoptera: Tettigoniidae: Tettigoniinae). *Atlanticus* presents a disjunctive distribution and is considered to be a Tertiary relict katydid genus, previously comprising 1 subgenus (*Atlanticus*) and 10 valid species from eastern North America and 2 subgenera (*Atlanticus*, *Sinpacificus*) and 14 valid species from eastern Asia. The research on the genus might reveal how past climate events have effected change of fauna. Several authors inferred the origin of the genus, and also predicted that China would be rich in new species of the genus *Atlanticus*. Firstly, based on investigation of male stridulatory apparatus, as well as of previously used characters, including male and female abdominal apex and measurements of various structures, we corrected the previous improper characters to differentiate the subgenera, noted incorrect synonyms, and provided descriptions of numerous new species of *Atlanticus* from China. Secondly, based on sequences of two mitochondrial and two nuclear genes, we reconstructed phylogeny of *Atlanticus* and its relatives distributed in eastern Asia or Europe. The results show that according to these data the tribe Drymadusini is monophyletic (based on sequences of *Drymadusa*, *Anadrymadusa*, *Mongolodectes*, *Paratlanticus* and *Atlanticus*) with *Glyphonotus* as its sister group. The eastern Asian genus *Kansua* Uvarov, previously with ill-defined systematic position, should also be put into the tribe Drymadusini, and the previous included two subgenera of the genus *Atlanticus* should be raised to genus level. Significantly, the obtained clades based on molecular data strongly support the species based on the morphology, also showing rich species diversity. Our research will provide new clues of the origin of the originally designated genus *Atlanticus* and the effects of the past climate change on the fauna.

Cladotypic nomenclature applied to orthopterans

Béthoux, O

CR2P UMR 7207, MNHN, UPMC, CNRS, 8 rue Buffon, CP38, 75005 Paris, France

E-mail: obethoux@mnhn.fr

The nomenclatural procedure most commonly used is the ICZN-governed one, and is primarily characterized by binominal species names, and the application of ranks, some with standardized endings. Actual examples, selected from among fossil and extant orthopterans *s.l.*, will be used to demonstrate the inadequacy of this procedure. In order to address the corresponding issues, an alternative procedure, namely the cladotypic one, has been recently developed. Under this procedure, taxon names are associated with a definition involving a hypothesis of character (state) homology. To achieve this, the definition includes a formulation of a character (state; ideally together with its antonym), and the designation of two type species (in the facts, two type specimens). Lanham's species names, composed of the species epithet and full authorship data, are favoured. To date, this approach has mainly been applied to fossil and extant orthopterans. Cases selected among these applications will be presented (namely the *Miamia*, *Tcholmanvissiella*, and *Grylloptera* cases), demonstrating the higher optimality of the procedure in its current state. Future applications will allow further testing of the procedure.

Molecular phylogenetic analysis of Chinese Acridoidea (Orthoptera)

Zhi, YC; Yin, XC and Zhang, DC*

College of Life Sciences, Hebei University, Baoding, Hebei 071002, P.R. China

**Corresponding author: daochuanzhang@yahoo.com.cn*

The commonly used system of classification of Chinese Acridoidea was made by Yin Xiangchu and later revised by Xia Kailing. It has been widely accepted, and was supported by morphological data. In their system, Acridoidea was divided into 8 families: Pamphagidae, Chrotogonidae, Acrididae, Pyrgomorphidae, Catantopidae, Oedipodidae, Arcypteridae and Gomphoceridae. However, this taxonomic system is not completely supported in some phylogenetic analyses based on mtDNA sequences. One possible reason for such contrasting results may be insufficient molecular data, with only a single gene or some partial gene sequences. Thus, using all PCGs of the mitogenome will contribute to understanding of phylogenetic relationships in the Chinese Acridoidea.

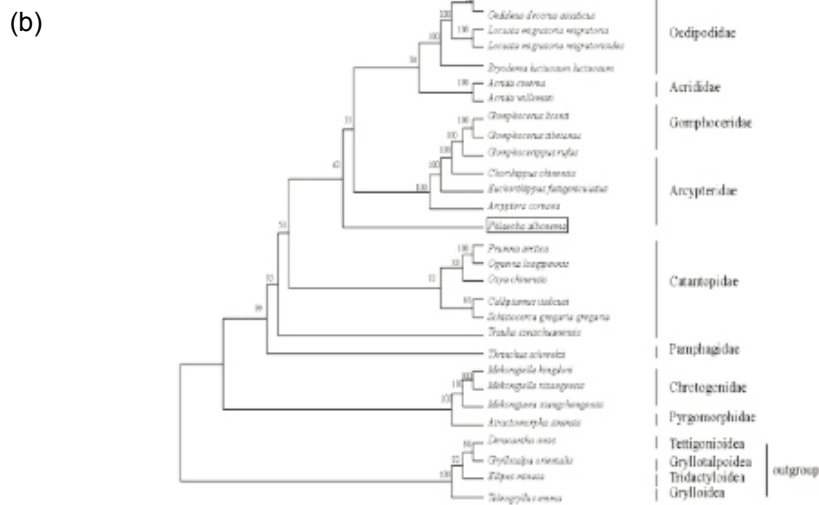
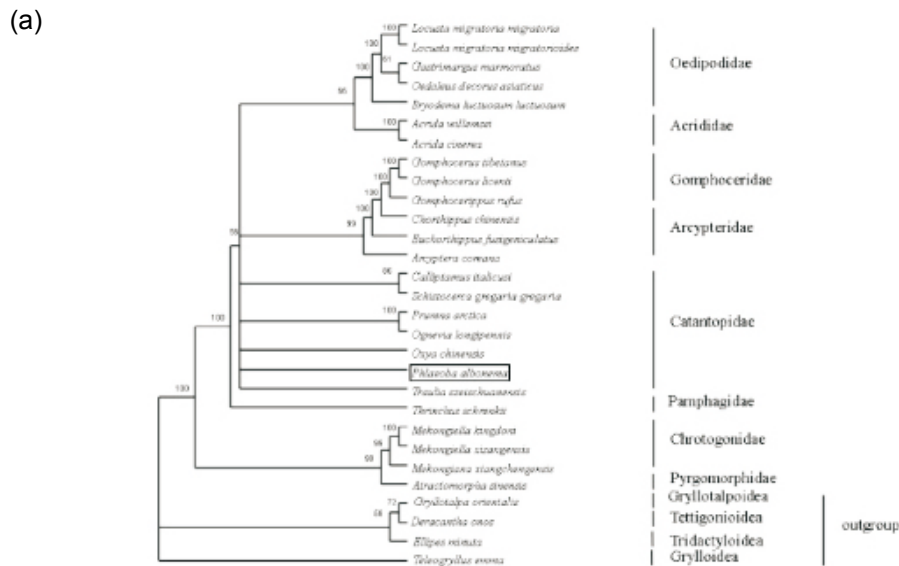
A total of 25 Acridoidea mitogenomes were available in the GenBank and were included in our analyses. We selected *Ellipes minuta* (Tridactyloidea), *Deracantha onos* (Tettigonioidea), *Gryllotalpa orientalis* (Gryllotalpoidea) and *Teleogryllus emma* (Grylloidea) as outgroups. Because the inclusion of third codon positions of the PCGs may negatively affect the phylogenetic reconstruction of the polyneoptera, we performed phylogenetic analyses with the first and second codons of PCGs. MP, ML and BI approaches were used for phylogenetic analysis. MP analyses were conducted using PAUP* 4.0b10, and bootstrap support was calculated from 1,000 bootstrap replicates. ML analysis was also carried out in PAUP with GTR+I+G model and parameter values estimated by ModelTest. BI analysis was performed using MrBayes ver.3.1.2. Initial runs were conducted on 1,000,000 generations starting with a random tree and employing four simultaneous monte carlo markov chains. Each set was sampled every 100 generations with a burn in of 25%. Stationarity was considered to be reached when the average standard deviation of split frequencies was less than 0.01. Bayesian posterior probabilities were estimated on a 50% majority rule consensus tree of the remaining trees.

MP, ML and BI analyses performed on PCGs generated similar tree topologies (Figure 1). All the trees were basically consistent, only differing on the support values of nodes. They showed the monophyly of Acridoidea had been well supported. In the three tree topologies we reconstructed, Acridoidea was divided into two major clades. In the first clade, Chrotogonidae and Pyrgomorphidae formed a sister group with a very high support value. According to Yin's system, they were primitive groups. In Otte's studies, both of the families were put into Pyrgomorphidae(Pyrgomorpoidea). In another clade, the Pamphagidae was invariably separated from other clades and resolved as a monophyletic group with uniformly high bootstrap values. Acrididae (except *Phlaeoba albonema*) and Oedipodidae had a sister-group relationship, which was on the top of the trees. All of our topologies supported Oedipodidae as monophyletic. *Phlaeoba albonema* was a separate clade and occupied the specific position in the BI and ML trees. However, it was inserted into Catantopidae. Arcypteridae clustered with Gomphoceridae with very strong bootstrap proportion values. But they were not a monophyletic lineage. This was in accordance with the Otte's analyses. In his analyses, both of Arcypteridae and Gomphoceridae belonged to Gomphocerinae (Acrididae). Catantopidae was divided

into two or more parts. It did not be supported as one monophyletic group. The six Catantopidae grasshoppers belonged to five subfamilies in Otte's studies. Although they did not cluster a clade, they located in the adjacent position.

In this study, we analyzed phylogenetic relationships of 25 Acridoidea species using ML, MP and BI based on the first and second codons of PCGs from mitogenomes. Our results revealed that Acridoidea was supported as a monophyletic group. It was basically consistent with the Yin's taxonomic system of Chinese Acridoidea. The Oedipodidae, Pamphagidae, Chrotogonidae and Pyrgomorphidae were supported as monophyletic. According to the three trees and Yin's studies, we speculate the phylogenetic relationship of Chinese Acridoidea is:

((Pyrgomorphidae + Chrotogonidae) + (Pamphagidae + (Catantopidae + ((Arcypteridae + Gomphoceridae) + (Acrididae + Oedipodidae))))). Our research does not completely support the previously morphological studies of Chinese Acridoidea and only provides a molecular evidence for family taxonomy. Clearly, additional molecular markers and more taxa may be more helpful in clarifying evolutionary relationships.



(c)

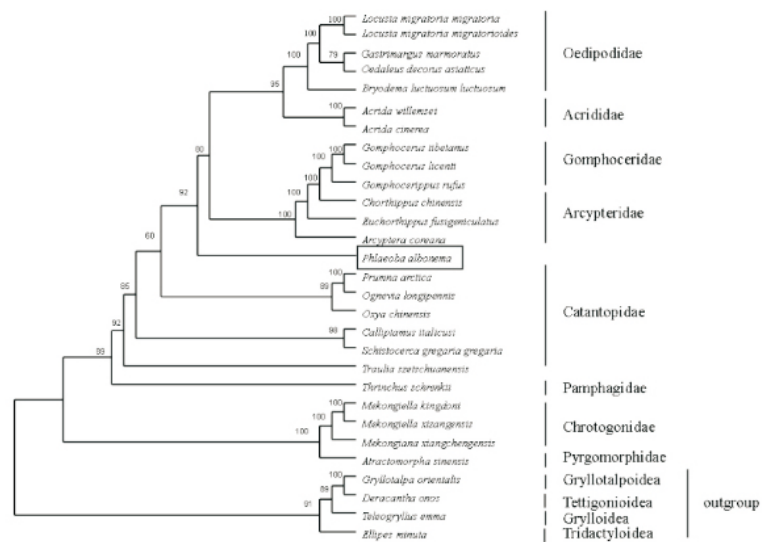


Figure 1, Phylogenetic trees built from the combined PCGs dataset: (a) MP, (b) ML, and (c) BI analyses

Molecular phylogeny of Pamphagidae (Orthoptera: Acridoidea) from China based on mitochondrial cytochrome oxidase I sequences

LANG, L; SONG, WW; ZHAO, XY; WEN, CJ and **ZHANG, DC** *

College of Life Sciences, Hebei University, Baoding 071002

Grasshoppers of Pamphagidae (Orthoptera: Acridoidea) distributed mainly in the arid regions of Eurasia and Africa with 96 described genera (Eades and Otte, 2013). Among them, 14 genera distribute in North and Northwest of China (Zheng, 1993; Xia et al., 1994; Cao and Yin, 2008). The shared characters of this family are: body often very rough, head not conical, vertex inclined forward, usually forming a right or obtuse angle with frons, fastigial furrow present, fastigial foveolae absent, most species with Krauss's organ, lower basal lobe of hind femur longer than the upper one, the medial area of external side of hind femur with granular or club-like sculpture, epiphallus shield-like, appendices absent.

The family Pamphagidae is classified differently by various authors. Kirby (1910) put pamphagids into Thrinchinae or Pamphaginae which belong to Acrididae (Acrididae Macleay, 1821). Uvarov (1943) divided Pamphaginae, which belong to Acrididae, into 9 tribes. Bey-Bienko & Mistshenko (1951) divided Pamphaginae, which belong to Acrididae, into 2 tribes (Thrinchini, pamphagini). Dirsh (1961, 1965, 1975) divided Pamphagidae, which belong to Acridoidea, into 4 subfamilies (Echinotropinae, Porthetinae, Akicerinae, Pamphaginae). Zhang *et al.* (2003) proposed a taxonomic system of the family based on a morphological study of pamphagids from Eurasia, and provided a new taxonomic system for the Eurasian Pamphagidae, in which the 47 known genera were classified into 6 subfamilies Prionotropisinae Zhang et al. 2003, Thrinchinae Kirby 1910, Pamphaginae Burmeister 1840, Tropidaucheninae Zhang et al. 2003, Nocarodesinae Bolivar 1916, Orchaminae Zhang et al. 2003, Pamphagids from China belong to the former three subfamilies (Zhang et al., 2003).

The mitochondrial DNA (mtDNA) sequences have been extensively used to investigate the relationships of populations within species and the relationships of closely related species for their rapid evolution rate. More recently, the use of mtDNA sequences to study the phylogenetic relationships and evolutionary history of certain groups has been advocated (DeSalle, 1992; Kambhampati, 1995; Kambhampati et al., 1996; Vogler and Pearson, 1996; Flook and Rowell, 1997; Chapco et al., 1999; Flook et al., 1999, 2000; Davison et al., 2001; Renet et al., 2002; Yin et al., 2003; Bu and Zheng, 2005; Li et al., 2005; Zhang et al., 2005, 2008). The purpose of this study is to discuss the phylogeny of some genera of Pamphagidae from China and to examine the taxonomic system of Eurasian Pamphagidae using cytochrome oxidase subunit I (*cox1*) gene sequences.

11 species of Pamphagidae from 7 genera were sequenced to obtain mtDNA data, along with 2 species from the GenBank nucleotide database. The results of sequence comparisons showed the *cox1* gene is 1534 bp in length, including 326 variable sites and 211 parsimonious information sites. The percentage of A+T is 67.1% in the nucleotide sequences, showing a strong AT bias. Genetic distances among subfamilies are 0.08. Using *Locusta migratoria* as outgroup, the phylogenetic trees were reconstructed with NJ, MP, ML and Bayesian inferences, and the results showed that the clustering results were approximately identical to that of classical morphological classification,

the genus *Asiotmethis* of Prionotropisinae did not get together with other species of Prionotropisinae, classification position of *Asiotmethis* should be further discussed by both genetic markers and morphological features. The current genus *Filchnerella* of Prionotropisinae was not a monophyletic group.

Table 1. Species and their localities in the study and GenBank Accession number for the *cox1* sequences of each sample.

| Subfamily* | Species | Sampling locality | Accession no | Reference |
|------------------|-----------------------------------|-------------------|--------------|--------------------------|
| Pamphaginae | <i>Haplotropis brunneriana</i> | Heilongjiang | JF412672 | Present study |
| Pamphaginae | <i>Sulcotropis cyanipes</i> | Shanxi | KC894753 | Present study |
| Thrinchinae | <i>Thrinchus schrenkii</i> | Xinjiang | NC014610 | Present study |
| Prionotropisinae | <i>Asiotmethiszacharjin</i> | Xinjiang | JF412673 | Present study |
| Prionotropisinae | <i>A. jubatus</i> | Xinjiang | KF017587 | Present study |
| Prionotropisinae | <i>Beybienkia songorica</i> | Gansu | JF412671 | Present study |
| Prionotropisinae | <i>Rhinotmethishummeli</i> | Neimenggu | JF412675 | Present study |
| Prionotropisinae | <i>Filchnerella kukunoirs</i> | Gansu | JF412674 | Present study |
| Prionotropisinae | <i>F. yongdengensis</i> | Gansu | JF412676 | Present study |
| Prionotropisinae | <i>F. pamphagides</i> | Gansu | KF017586 | Present study |
| Prionotropisinae | <i>F. beicki</i> | Ningxia | KC831767 | Present study |
| Prionotropisinae | <i>F. helanshanensis</i> | Neimenggu | JX468877 | Zhang <i>et al.</i> 2013 |
| Prionotropisinae | <i>Pseudotmethis rubimarginis</i> | Neimenggu | JX468878 | Zhang <i>et al.</i> 2013 |

* the division of subfamily according to Zhang *et al.*(2003).

Table 2, Kimura-2 parameter distance (lower triangle) and standard errors (up triangle) of *cox1* gene of 13 species of Pamphagidae

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|----|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 1 | | 0.005 | 0.009 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.007 | 0.009 | 0.008 | 0.008 | 0.011 |
| 2 | 0.036 | | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.009 | 0.008 | 0.008 | 0.011 |
| 3 | 0.102 | 0.092 | | 0.003 | 0.008 | 0.009 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.007 | 0.008 | 0.011 |
| 4 | 0.097 | 0.085 | 0.016 | | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.008 | 0.007 | 0.008 | 0.011 |
| 5 | 0.090 | 0.086 | 0.097 | 0.090 | | 0.003 | 0.004 | 0.006 | 0.005 | 0.005 | 0.006 | 0.006 | 0.008 | 0.012 |
| 6 | 0.088 | 0.088 | 0.096 | 0.090 | 0.011 | | 0.004 | 0.006 | 0.005 | 0.006 | 0.006 | 0.007 | 0.008 | 0.012 |
| 7 | 0.094 | 0.089 | 0.093 | 0.093 | 0.024 | 0.024 | | 0.005 | 0.005 | 0.006 | 0.006 | 0.007 | 0.008 | 0.012 |
| 8 | 0.098 | 0.090 | 0.088 | 0.084 | 0.045 | 0.048 | 0.045 | | 0.002 | 0.004 | 0.007 | 0.007 | 0.008 | 0.012 |
| 9 | 0.097 | 0.090 | 0.090 | 0.085 | 0.044 | 0.044 | 0.043 | 0.008 | | 0.004 | 0.006 | 0.007 | 0.008 | 0.012 |
| 10 | 0.091 | 0.086 | 0.096 | 0.090 | 0.043 | 0.046 | 0.046 | 0.029 | 0.028 | | 0.007 | 0.007 | 0.008 | 0.011 |
| 11 | 0.108 | 0.103 | 0.094 | 0.093 | 0.050 | 0.051 | 0.051 | 0.062 | 0.057 | 0.061 | | 0.007 | 0.008 | 0.012 |
| 12 | 0.099 | 0.097 | 0.093 | 0.091 | 0.062 | 0.060 | 0.063 | 0.063 | 0.060 | 0.061 | 0.066 | | 0.009 | 0.011 |
| 13 | 0.107 | 0.103 | 0.099 | 0.096 | 0.089 | 0.091 | 0.094 | 0.093 | 0.094 | 0.097 | 0.093 | 0.105 | | 0.012 |
| 14 | 0.185 | 0.177 | 0.182 | 0.174 | 0.184 | 0.185 | 0.179 | 0.178 | 0.179 | 0.180 | 0.186 | 0.183 | 0.184 | |

1 *H. Brunneriana*, 2 *S. Cyanipes*, 3 *A. Zacharjin*, 4 *A. Jubatus*, 5 *F. Helanshanensis*, 6 *P. Rubimarginis*, 7 *F. Beicki*, 8 *F. Yongdengensis*, 9 *F. Pamphagides*, 10 *R. Hummeli*, 11 *F. Kukunoirs*, 12 *B. Songorica*, 13 *T. Schrenkii*, 14 *Locusta migratoria*.

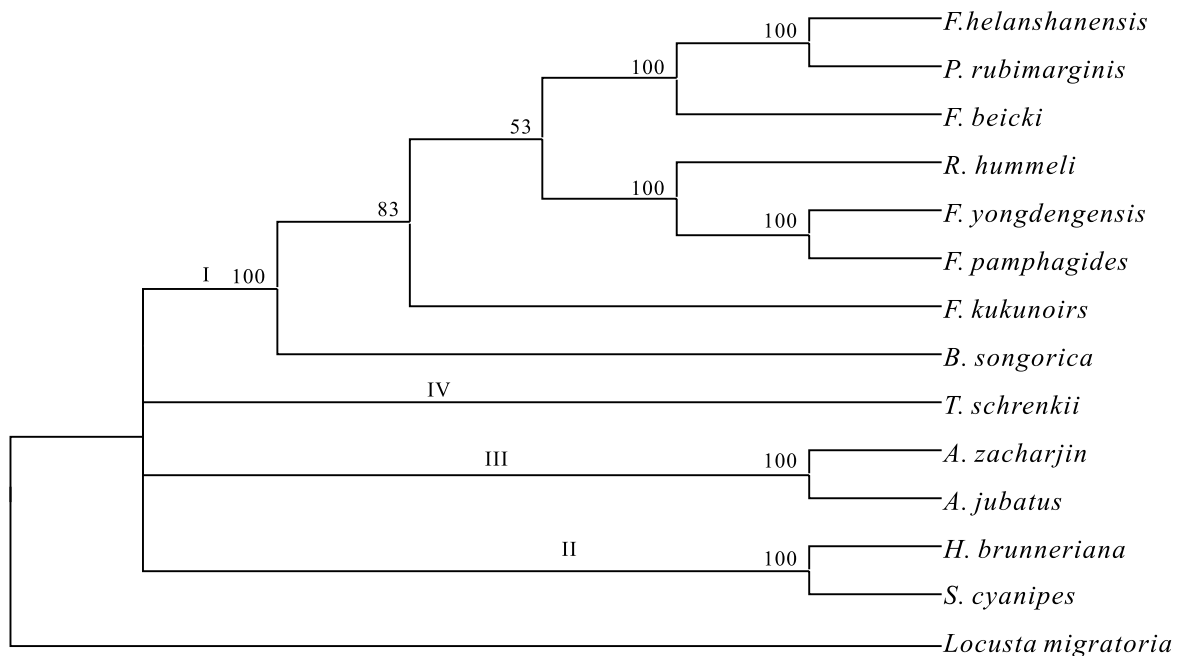


Figure 1, Phylogenetic tree based on neighbour joining method

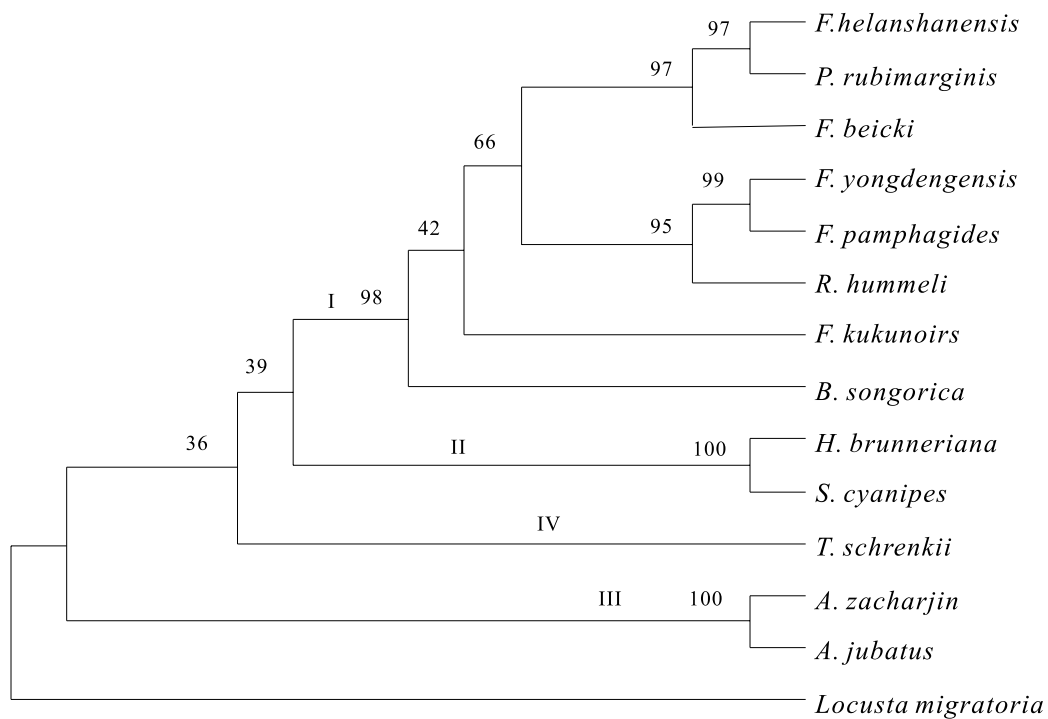


Figure 2, Phylogenetic tree based on maximum parsimony method

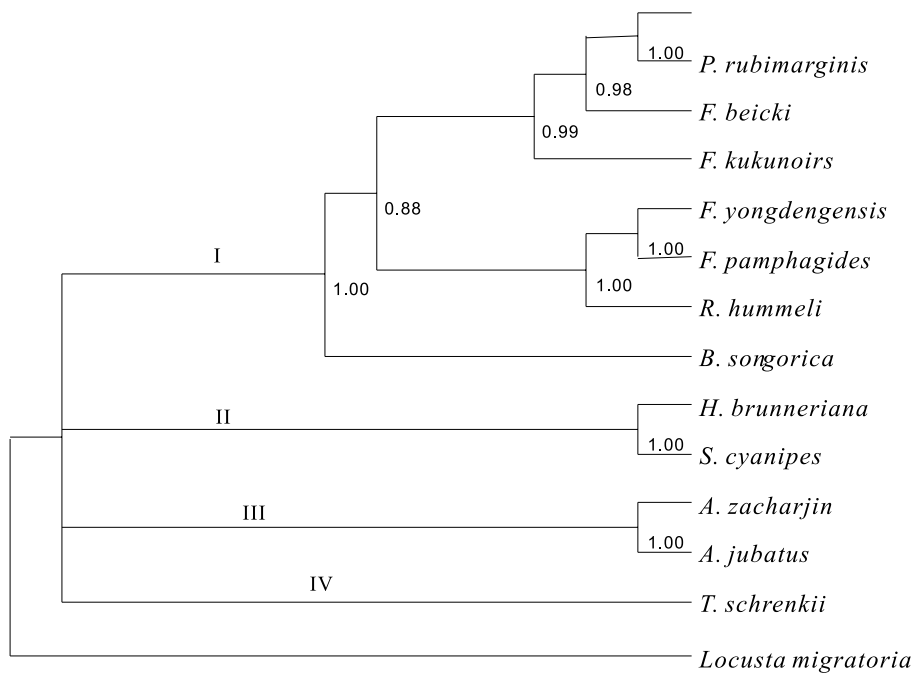


Figure 3, Phylogenetic tree based on Bayesian method

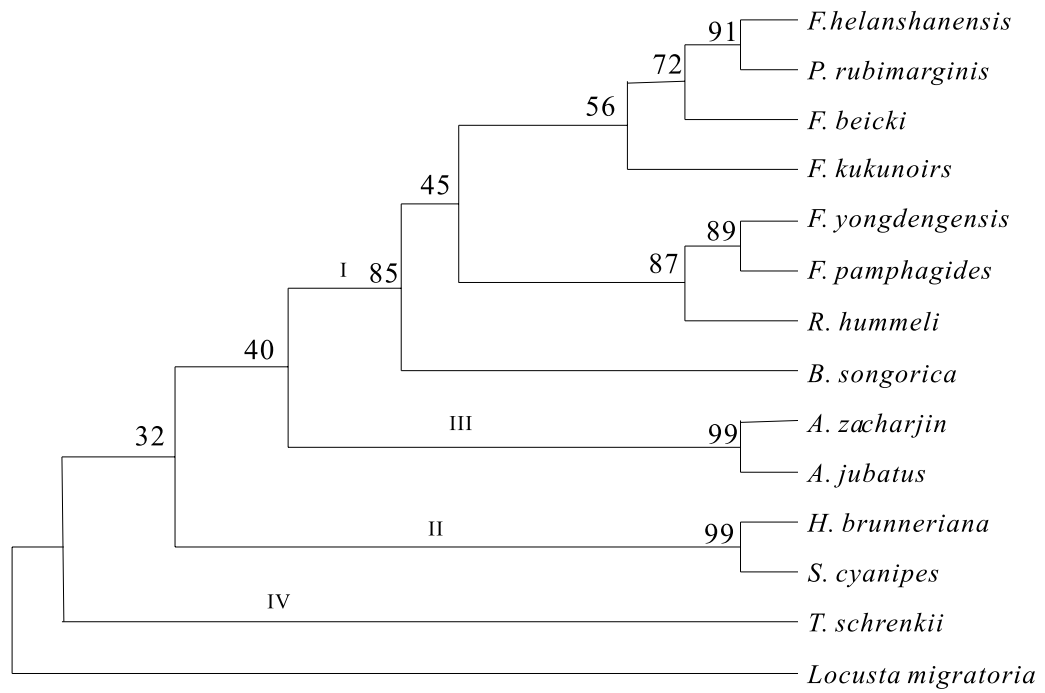


Figure 4, Phylogenetic tree based on maximum likelihood method

Species diversity and list of Acridoidea(Insecta, Orthoptera) from China

Xinjiang, L^{1,2}; Zhenqun, Z¹ and DaoChuan, Z^{1*}

¹College of Life Sciences, Hebei University, Baoding, Hebei 071002, P.R. China;

²Northwest Plateau Institute of Biology, Chinese Academy of Sciences, Xining, Qinghai 810001, P.R. China

*Correspondence: Tel/Fax: 86 312 5079707

E-mail: daochuanzhang@aliyun.com

Acridoidea belongs to Insecta, Orthoptera, Acridodea, which is the largest group in the Orthoptera. 4 volumes of Fauna Sinica (Insecta, Orthoptera, Acridodea) have been published in China, which were the most systematic monograph on grasshopper from China and reported 238 genera 957 species grasshoppers which belongs to 8 families, 42 subfamilies (Xia et al, 1994; Zheng et al, 1998; Yin et al, 2003; Li et al, 2006). In this years, with the Investigation of species diversity going on, many new species have been found in China and that didn't included in Fauna Sinica. Based on the Fauna Sinica and huge amounts of papers about recent reports on new taxa of Chinese grasshopper, and referred to *A Synonymic Catalogue of Grasshoppers and Their Allies of the World* (Yin et al, 1996) and *Orthoptera Species File Online* (Eades et al, 2013), the research summarized the quantity of Acridoidea species we have known and give the list. The result dedicates that there are 8 families, 42 subfamilies, 272 genera, 1309 species in Acridoidea insects as far as we known. Which contained Pamphagidae: 3 subfamilies, 14 genera, 52 species; Chrotogonidae: 5 subfamilies, 9 genera, 23 species; Pyrgomorphidae: 2 genera, 16 species; Catantopidae: 17 subfamilies, 109 genera, 475 species; Oedipodidae: 4 subfamilies, 44 genera, 177 species; Arcypteridae: 4 subfamilies, 53 genera, 379 species; Gomphoceridae: 3 subfamilies, 11 genera, 47 species; Acrididae: 6 subfamilies, 32 genera, 140 species, respectively. In all known species, there are 34 genera 352 species didn't included in Fauna Sinica, which is 1 genera 14 species, 1 genera 6 species, 5 species, 14 genera 120 species, 5 genera 53 species, 9 genera 97 species, 7 species and 4 genera 50 species in the 8 families respectively (Table 1).

Tab. 1 Composition table of Acridoidea from China

| family | Known species | Species didn't in Fauna Sinica |
|----------------|--|--------------------------------|
| Pamphagidae | 3 subfamily 14 genera 52 species | 1 genera 14 species |
| Chrotogonidae | 5 subfamily 9 genera 23 species | 1 genera 6 species |
| Pyrgomorphidae | 2 genera 16 species | 5 species |
| Catantopidae | 17 subfamily 109 genera 475 species | 14 genera 120 species |
| Oedipodidae | 4 subfamily 42 genera 177 species | 5 genera 53 species |
| Arcypteridae | 4 subfamily 53 genera 379 species | 9 genera 97 species |
| Gomphoceridae | 3 subfamily 11 genera 47 species | 7 species |
| Acrididae | 6 subfamily 32 genera 140 species | 4 genera 50 species |
| | 42 subfamilies, 272 genera, 1309 species | 34 genera 352 species |

The Phylogenetic Relationships of Orthoptera Deduced from Complete Mitochondrial Genomes

Wang, X and Huang, Y

School of Life Sciences, Shaanxi Normal University

The phylogenetic of Orthoptera had long been debated. In this study, we presented phylogenetic analyses covered 12 of 14 superfamilies in Orthoptera using complete mitochondrial genome sequences, so as to obtain the phylogenetic relationships of higher categories of Orthoptera. Protein coding genes and ribosomal RNAs were assembled into six data sets. Phylogenetic relationships were inferred by Maximum likelihood and Bayesian inference method for each data set. The monophyly of Caelifera, Ensifera and all superfamilies could be supported by most data sets. The relationships of superfamilies within Ensifera were (Grylloidea, (Rhaphidophoroidea, (Hagloidea, Tettigonioidea))), while that among Caelifera were (Tridactyloidea, (Tetrigoidea, (Eumastacoidea, (Tanaoceroidea, (Pneumoroidea, Trigonopterygoidea), (Pyrgomorphoidea, Acridoidea)))). The phylogenetic relationships among Acrididea were complex, three main groups were formed, but the relationships among and within these groups remain unsolved. These results suggest that the mitochondrial genome data could be useful utilities in phylogenetic analyses of Orthoptera and could provide a long term scenario of Orthopteran evolution.

GRASSHOPPERS (ACRIDOIDEA) OF MONGOLIAN PLATEAU

Altanchimeg, D¹ and Nonnaizab²

¹*Institute of Biology, Mongolian Academy of Sciences, Mongolia*

²*Normal University of Inner Mongolia, China*

The Mongolian Plateau is the part of the Central Asian Plateau which is situated between 87°40' -122°15'N and 37°46'-53°08'E. Territory area is approximately 2.6 million square kilometers. It is boundary by the Greater Hyangan mountains to the east, the Yin mountains to the south, the Altai mountains to the west and the Sayan and Khentii mountains to the north. Natural zone is divided into forest steppe, steppe, desert steppe and desert.

Zubovsky (1899), Bolivar (1901), Krauss (1901), Miram (1906-1907, 1926), Adelung (1909), Ikonnikov (1911), Uvarov (1914), Pilnov E. (1916), Sjostedt (1932), Mori (1935), Furukawa (1936), Shiraki (1936 a,b), Ramme (1951), Kazanskii K.A. (1930), Bei Bienko (1932-1934, 1948, 1950), Bei Bienko and Mistchenko (1951), Mistchenko (1936-1990), Zheng Zhe Min (1963-present), Steinmann (1964, 1967, 1968, 1971), Bazyluk (1963, 1969-1971), Chogsomjav L. (1963 -1999), Pravdin F.N. (1964), Namkhaidorj B. (1967), Orischenko A.D. (1960), Gunther (1970, 1971), Yin Xiang Chu (1974-present), Li Hong Chang (1977-present), Storojenko (1983-present), Li Bao Ping, Yin Xiang Chu (1987), Kang Le, Mao Wen Hua (1990), Nonnaizab (1999-present), and other researchers have been contributed to systematic and distribution studies of grasshoppers of Mongolian Plateau.

We have proposed to establish species composition of grasshoppers in Mongolian plateau under cooperation between Institute of Biology, Mongolian Academy of Science, Mongolia and Normal University of Inner Mongolia, China since 2002. There are 260 species represent 71 genera belong to 23 tribes, 3 subfamilies and 2 families grasshoppers registered in Mongolian plateau based on publication and our research results so far (Table 1). Seventy sex species (28.5%) of that are endemic and almost of them are distributed desert steppe and desert zones. Our results are shown that we recorded *Aeropedellus chogsomjavi* sp.n. new to science, *Chorthippus* (*G.*) *mollis* (Charp.), *Chorthippus vagans* (Ev.), *Aiolopus thalassinus* (Fabr.), *Bryodema heptapotanicum* B.-Bien., *Bryodema miramae* B.-Bien. and *Bryodema semenovi* Ikon. are new for Mongolia.

Table 1, Composition of grasshoppers in Mongolian Plateau

| Family | Subfamily | Tribe | Number of genus | Number of species | Number of endemic species |
|-------------|--------------|------------------|-----------------|-------------------|---------------------------|
| Pamphagidae | Trichiinae | Trinchiini | 8 | 23 | 18 |
| | Pamphaginae | Haplotropini | 1 | 2 | 1 |
| Acrididae | Catantopinae | Dericorythini | 1 | 1 | - |
| | | Egnatiini | 1 | 1 | - |
| | | Oxyini | 1 | 5 | - |
| | | Melanoplinae | 6 | 10 | 2 |
| | | Caloptenini | 1 | 5 | - |
| | | Acridini | 1 | 3 | - |
| | | Truxalini | 1 | 1 | - |
| | | Ochrilidini | 1 | 1 | - |
| | | Chrysochroantini | 7 | 23 | 10 |
| | | Hypernephiini | 1 | 8 | 8 |
| | | Arcypterini | 2 | 3 | - |
| | | Aulacobothrini | 2 | 7 | - |
| | | Dociostaurini | 3 | 3 | - |
| | | Gomphocerini | 16 | 105 | 22 |
| | | Parapleurini | 2 | 3 | 1 |
| | | Epacromiini | 2 | 4 | - |
| | | Locustini | 3 | 5 | 1 |
| | | Oedipodini | 1 | 1 | - |
| | | Bryodemini | 4 | 25 | 9 |
| | | Trilophidiini | 1 | 1 | - |
| | | Sphingonotini | 5 | 20 | 4 |
| 2 | 3 | 23 | 71 | 260 | 76 |

Note: Species composition of grasshoppers in Mongolian plateau will be changed. Because however we have compiled above scientists publication and our study results but we have not compiled all publication on grasshoppers of two countries. The territory of Mongolian plateau is so huge; therefore our survey has not reached all country for today.

Phylogeny analysis on partial sequence of 12S rRNA genes of two species in *Oedaleus* Fieber

Tai, LH; Nonnaizab; Bao, YH; Zhu, WW and Zhang, SN
Inner Mongolia Normal University, Huhhot 010022, China

Oedaleus decorus asiaticus Bei-Bienko and *Oedaleus infernalis* Saussure which belonged to genera *Oedaleus* Fieber, family Oedipodidae are distributed in Inner Mongolia, Ning Xia, Gan Su, Qing Hai and He Bei. And these kinds of grasshoppers are the main members which result in the grasshoppers' calamity in the grassland and crops in Northern China.

Mitochondria DNA is the vector of extranuclear genetic information in the animal body and being applied more and more widely in phylogenetic studies on insects and other animal species. In a general way, 12S rDNA of mitochondria is a more conservative sequence among individuals within a species in animals. It can be used in phylogenetic relationship analysis among genera, different species groups and differentiation interspecies effectively.

In this paper, partial sequence of mitochondria 12S rRNA gene which used as molecular marker of *O. decorus asiaticus* and *O. infernalis* in Inner Mongolia were obtained. Seven higher homologous sequences were found out by BLAST method from GenBank, and analyzed homology with CLUSTAL 2.1 software. Phylogenetic tree were established with MEGA 5.10 software and analyzed phylogenetic relationship preliminarily. The research will provided molecular biology data for molecular evolution of Oedipodidae insects and determining their relationships.

The results indicated that the lengths of partial sequence of 12S rRNA genes from *O. decorus asiaticus* and *O. infernalis* were 382bp and 383bp respectively (Figure. 1). Both the sequences had high homology with corresponding fragment from GenBank, which include same species of different sources (*O. decorus asiaticus* EU513374.1 & *O. infernalis* AY560521.1), the same genus (*O. manjius* AY560522.1) and the different subfamily (*Locusta migratoria* JN858212.1 & JN858210.1 and *Gastrimargus marmoratus* EU527334.1 & EU513373.1), ranged from 93% to 100%. Phylogenetic relationship analysis (Figure. 2) showed that the same species from different sources were close together. Nine samples of five species were basically divided into three clusters, of which *O. decorus asiaticus* and *Locusta migratoria* gathered into one cluster, *O. infernalis* and *O. manjius* the other, while *Gastrimargus marmoratus* belonged to the category of its own. However, the result of the first cluster was inconsistent with morphological classification of grasshoppers, which needs further research. The reason of this unsatisfactory result might be ascribed to the fact that only 12S rDNA molecular marker was selected and the partial sequence of gene we got was still short, leading to limited information.

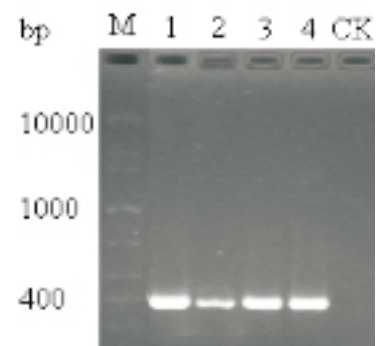


Figure 1, Electrophoresis of PCR products of 12S rRNA genes from two species of *Oedaleus*: M: DNA Marker 1-2: *O. decorus asiaticus* 3-4: *O. infernalis* CK: negative control

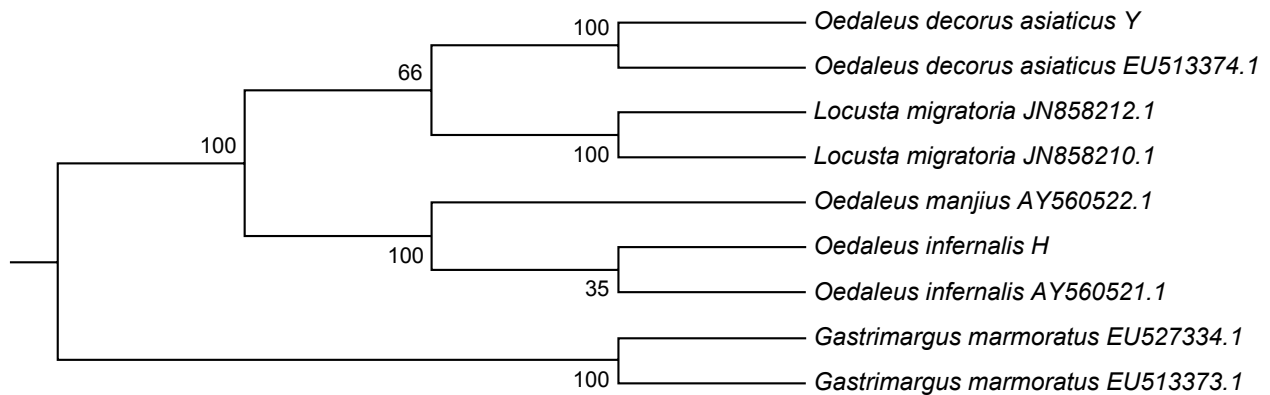


Figure 2, Phylogenetic relationship analysis

In summation, mitochondria 12S rRNA is a relatively conservative sequence. And very little changes occurred at differentiation process of intergenera and interspecies in Oedipodidae. It is insufficient to analyze phylogenetic relationship of genera and species categories by using part of 12S rDNA sequences. Thus with only one gene as molecular marker or the analyzed gene sequence is too short will both affect the accuracy of the analysis result. Therefore, multiple gene sequences should be used to get more data information for in order to gain more exact conclusion in future molecular phylogeny researches.

Introgression of two *Gryllus* species from North America and a chromosome imprinting mechanism that expresses exclusively male trait for growth rate

Makio T.

Graduate School of Agricultural Science, Kobe University

Email: mtakeda@kobe-u.ac.jp

Gryllus firmus and *G. ovisopsis* both lay diapause eggs for overwintering. These species interbreed unidirectionally, i.e. *G. ovisopsis* female and *G. firmus* male and offspring nymphs grow normally without showing abnormalities conventionally termed Haldane's rule: heterozygotic sex would not grow normally. However, the growth rate of hybrid generation between the two species was not intermediate between the parental species but the male trait dominated, i.e., *Gryllus firmus* trait. This is a similar situation found in body size determination in mouse where IGF gene of male is expressed over female allele in terms of chromosome imprinting. This mechanism seems to universally occur among cricket for growth control, since the same trend was observed in the cross between the fast-growing geographic stock and the slow-growing geographic stock of *Modycogryllus siamensis* from China.

Taxonomy & Biogeography

Ecological adaptations of grassland-inhabiting flightless Orthoptera: the subtribe Karniellina of Conocephalini (Conocephalinae, Tettigoniidae) as model group to understand modes and time of speciation patterns in East Africa

Hemp, C

Coordinator KiLi research unit, University of Wuerzburg, Germany

E-mail: Claudia.hemp@uni-wuerzburg.de

The genera of Karniellina probably evolved at a time when grasslands spread in East Africa due to an increasing aridification of the climate. The earliest lineage, the genus *Karniella*, is adapted to more forested habitats while the majority of the genera of Karniellina prefer open grasslands. Major splits within Karniellina probably occurred with the emergence of savannah grasslands due to the ongoing fragmentation of forest habitats several millions years ago, but most species within the genera are geologically young, their radiation being boosted by climatic fluctuations of the past 1–2 Ma.

A biogeographic study of South American Melanoplineae: pattern of diversification along the Andes Mountain Chain

Dinghi, PA¹; Confalonieri VA¹ and Cigliano, MM²

¹*Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina;*

²*División Entomología, Museo de La Plata, La Plata, Argentina*

Melanoplineae is one of the largest subfamilies and, one of the main components of the Acrididae fauna in the American Continent (except in the rain forest biomes). The systematics of this group is controversial, with different authors recognizing different numbers of tribes, and an evolutionary history that remains unclear. Three scenarios have been proposed to explain the early biogeographic history of the Melanoplineae. The first posed a Eurasian origin of the group followed by migrations to North America, and then South America (Amédégnato, 1977). The second proposed an ancient Laurentian origin with the Nearctic region as centre, from which migrations began towards the Palaearctic and the Neotropic regions (Vickery, 1987). The third one, which is based on molecular studies (Amédégnato et al., 2003), suggests a South American origin followed by a substantial number of northward, eastward and/or westward migrations.

The Andes, the world's longest mountain chain, seems to be the main basis for speciation and diversification events for this group, harboring a great taxonomic and ecological diversity. Despite their young age, it is highly diverse due to recent geological uplift. Doan (2003) proposed a South-to-North Speciation Hypothesis (SNSH) for speciation of high Andean taxa, following a South-to-North pattern generally coinciding with the progression of final uplift of the Andes. According to this scenario, a phylogenetic hypothesis of relationships of a taxonomic group occurring in the high Andes would show a branching pattern in which the southernmost species diverged first, followed by the more northern species, and so on in a northerly pattern. Early studies based on the morphological diversification of *Ponderacris* (Melanoplineae), posited a North-to-South progression of speciation (Ronderos & Carbonell, 1971) but recently, Pocco *et al.* (2012) postulated just the opposite direction for this same genus: i.e. a South-to-North speciation pattern, in accordance with the progressive Andean uplift.

Considering these issues, a molecular phylogenetic approach was carried out in order to test the different scenarios proposed for the Melanoplineae diversification in South America, especially for those distributed along the Andes Mountain chain, and also to solve some taxonomic controversies within the group. To these purposes, COI and NADH2 mitochondrial genes from several Melanoplineae species collected from Argentina to Venezuela along the Andes, were sequenced and analyzed. The following genera were included (sorted by tribe and bio-region): *Jivarus* Giglio-Tos, *Urubamba* Brunerand *Nahuelia* Liebermann (Jivarini), which are distributed in the Venezuela and Ecuador 'Páramos', and in Argentinean Patagonic Andes; *Maeacris* Ronderos (Jivarini) from the Peruvian 'Puna'; *Coyacris* Ronderos, *Chlorus* Giglio-Tos, *Ponderacris* Ronderos & Cigliano, *Boliviacris* Ronderos & Cigliano, *Baeacris* Rowell & Carbonell (Dichroplini), all from the 'Yungas' of Argentina, Perú and Bolivia; *Orotettix* Ronderos & Carbonell (Dichroplini), distributed in the Peruvian 'Puna'; *Chibchacris* Hebard, *Timotes* Roberts (Dichroplini) from the Venezuelan 'Páramos'; and finally, the *insertae sedis* genera

Pediella Roberts, *Huaylasacris* Cigliano, Pocco & Lange, *Tiyuantiyana* (Cigliano, unpublished), all from Peruvian 'Puna'; and *Meridacris* Roberts, from the Venezuelan 'Páramos'. *Locusta migratoria* (L.) and several *Melanoplus* Stål (Melanoplini) species from North America were used as outgroup. The latter corresponding sequences were downloaded from the GeneBank.

Bayesian and Maximum Parsimony (MP) searches were performed. The evolutionary model selected for the Bayesian search was GTR. Both searching criteria yielded similar topologies. Six distinct monophyletic clades were recovered. *Maeacris* (Jivarini) and the *insertae sedis* genus *Tiyuantiyana* resolves as the most basal sister group. Then, a cluster formed by the two *insertae sedis* genera *Pediella* and *Huaylasacris* emerge basally to the rest groups. These basal clades belong both to the Peruvian 'Puna', supporting a South American origin for the Melanoplini, and to this region as the primary centre. The rest tribes resolve as follows: (Dichroplini, (Jivarini, Melanoplini)). Again, a South to North pattern of diversification was observed within both 'Jivarini' and Dichroplini groups. Within the former, the most basal species is distributed in Patagonia (Argentina), and the most derivate in the Venezuelan 'Páramos'. Within Dichroplini, the most basal species belongs to the Yungas of Argentina, Bolivia and Perú, and the most derivate to the Venezuelan 'Páramos'. Finally, the position of North American Melanoplini also supports the South American origin and posterior dispersion to the north. On the other hand, the taxonomic status of the Jivarini tribe is again questioned. This preliminary study suggests the need of a reformulation and/or creation of new taxonomic entities in order to maintain the natural groups within this subfamily. Summarizing, the biogeographical history of each main evolutionary group show similar direction of diversification, congruently supporting the SNSH. However, further analyses will be necessary in order to determine if this process was in concert with the Andes geological uplift.

Unraveling the diversification history of “*Trimerotropis pallidipennis*” (Oedipodinae: Acrididae) species group in South America: a delimitation analysis reveals new genetic lineages

Guzmán, NV¹; Cigliano, MM²; Pietrokovsky, S and Confalonieri VA¹

¹*Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina;*

²*División Entomología, Museo de La Plata, La Plata, Argentina*

The “*Trimerotropis pallidipennis* species complex” represents a group of band-winged grasshoppers distributed over North and South America. Since diagnostic characters are vague and intraspecific variability is high, the taxonomic status of the South American representatives of this group has a high degree of uncertainty, hindering taxonomic decisions on the basis of morphological traits only. Originally, six species had been described: *T. pallidipennis*, with the subspecies *T. pallidipennis pallidipennis* (Burmeister, 1838) and *T. pallidipennis andeana* Rehn, 1939; *Trimerotropis ochraceipennis* (Blanchard, 1851), *Trimerotropis atacamensis* (Philippi, 1860), *Trimerotropis chloris* (Philippi, 1863), *Trimerotropis flavipennis* (Philippi, 1863) and *Trimerotropis irrorata* (Philippi, 1863). Yet, the latter four names are now considered synonyms of *T. ochraceipennis* (Amedeo gnato & Carbonell, 2001), while *T. pallidipennis andeana* has been raised to the status of species (Otte, 1995). More recently, species delimitation analyses based on molecular markers revealed that the complex would be composed by at least three distinct genetic lineages: *Trimerotropis pallidipennis* from North America, *Trimerotropis ochraceipennis* from Chile and an undescribed *Trimerotropis* species from Argentina (Husemann et al., 2013). Peruvian specimens taxonomically assigned to *T. andeana* resolved as paraphyletic, i.e. they joined either to *T. pallidipennis* from Argentina or *T. ochraceipennis*. Moreover, these genetic lineages can also be distinguished on cytological grounds: in *Trimerotropis* sp. from Argentina the four medium chromosomes are polymorphic for inversions, a karyotypic feature that differentiates this species from North American *T. pallidipennis*, in which the same chromosomes are always monomorphic. In contrast, in *T. ochraceipennis* two of the medium-sized chromosomes are fixed for the submetacentric state. Finally, the karyotype of Peruvian specimens remains unknown. Biogeographic analysis indicated a North American origin of the species complex and suggested that colonization of South America would have occurred during the Pleistocene after the closure of the Isthmus de Panama. Subsequent diversification in South America was the result of range expansion and vicariance, possibly in response to later Pleistocene glaciations.

In this study, we performed phylogenetic and coalescent analyses in order to establish the specific status of Peruvian specimens (i.e. *T. andeana*), by sequencing two mitochondrial and one nuclear genes. To this purpose we included new specimens from Peru, Chile and Argentina. Our results indicated that Peruvian specimens are clustered in at least two different genetic lineages: one integrated by those individuals collected at the central coast of Peru, at sea level. The other one includes those individuals collected at higher altitudes along the Andes Mountains, along with those individuals from Chile, taxonomically identified as *T. ochraceipennis*. This latter group is closer to the *Trimerotropis* clade from Argentina. Interestingly, the new genetic lineage from Peru identified in this study has the same karyotype as *T. pallidipennis* form from North America.

Biogeographic analyses along with molecular clock approaches indicate that after the second dispersal event leading to range expansion from Peru and Ecuador to southern latitudes, at least two vicariant events occurred. The first one led to the split between the more northern Peruvian form and the ancestor of the two remaining lineages. A second vicariant event led to the split between the Chilean plus Southern Peruvian specimens from the Argentinian clade. The time estimated for both split events corresponds to the periods when the Andes were substantially covered with ice sheets, undoubtedly constituting a physical barrier leading to allopatric diversification. It can be speculated that during this process, chromosomal rearrangements could have played an important role.

High-altitude South American grasshoppers: defining biological units when genes, chromosomes and morphology tell different stories.

Confalonieri, VA¹; Guzman, NV¹; Minutolo, C¹; Pocco, M² and Cigliano, MM²

¹*Departamento de Ecología, Genética y Evolución, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Instituto IEGEBA (CONICET-UBA), Buenos Aires, Argentina;*

²*División Entomología, Museo de la Plata, La Plata, Argentina*

The diversification of high-altitude grasshoppers in South America is a complex process, most probably related to tectonic and orogenic activities, and also to climatic factors. Many new biological units emerged during the late Pliocene and Pleistocene in the Andes Mountain range, and, in some cases, divergence may have occurred too recently to be detected by taxonomic or traditional molecular phylogenetic methods. *Orotettix* (Melanoplinae) and *Trimerotropis* (Oedipodinae) are two genera of Acrididae inhabiting high-altitude areas under arid and semiarid conditions in South America. *Orotettix* is represented by five morphologically differentiated species in Peru, while *Trimerotropis* is probably composed of at least two South American chromosomally differentiated genetic lineages, which are inconsistent with the existing taxonomic classification. Traditional molecular phylogenetic analyses and multilocus coalescent approaches, combined with the study of morphological and chromosomal characters have revealed a complex scenario of species differentiation for these two genera. Molecular clock inferences suggest that the second Andean uplift and climatic fluctuations during glacial and interglacial periods mainly accounted for the diversification of *Orotettix* and *Trimerotropis*, respectively. In the latter, chromosomal rearrangement has undoubtedly played a major role in triggering both speciation processes and adaptation to altitudinal clines along the hillsides. In these studies, the use of multiple sources of variation (genes, chromosomes, morphology) in several individuals and populations has helped to elucidate the complex biogeographic scenario of diversification of both Andean genera.

Velarifictorus micado*, a ring species of cricket*He, Z** and Takeda M*Graduate School of Agricultural Science, Kobe University, 1-1 Rokko-dai, Nada, Kobe, Hyogo 657-8501, Japan*

The cricket *Velarifictorus micado* has a wide distribution in East Asia and it is also an introduced species into the USA. In Japan, they have two types life-cycle, both are univoltine, but some overwinter in the egg stage while others overwinter as nymphs. We sequenced and analyzed the COI gene of 33 individuals from China, Japan, Korea, Taiwan, Vietnam, Cambodia and the USA. The results showed that the USA individuals came from different countries. The two different life-cycles in Japan are due to two colonizations, one from North China and one from Taiwan, and the significant differences in the ovipositor indicate that they have reproductive isolation.

Ethanol fuel improves pitfall traps through rapid sinking and death of captured orthopterans

Szinwelski, N¹; Yotoko, KSC²; Solar, RS³; Seleme, LR¹ and Sperber, CF¹

¹Laboratory of Orthoptera, Federal University of Viçosa, Viçosa – MG, Brazil;

²Laboratory of Bioinformatics and Evolution, Federal University of Viçosa, Viçosa – MG, Brazil;

³Laboratory of Community Ecology, Federal University of Viçosa, Viçosa – MG, Brazil

In a previous work, we proposed replacing traditional killing solutions for pitfall traps with ethanol fuel (Szinwelski et al. 2012 - Zookeys, 196: 11-22), which results in significantly higher Orthoptera species richness and abundance than traditional killing solutions. We found that ethanol fuel (which is ethanol containing up to 3% gasoline) collects the whole species spectrum sampled by other solutions, showing that it minimizes sampling bias. We also showed that ethanol fuel adequately preserves DNA and morphology of the captured individuals. For ecological studies, however, the use of ethanol fuel as the pitfall killing solution could be problematic if it attracts individuals by its odor. In this work, we aimed to evaluate why ethanol fuel samples present higher species richness and accumulated abundance than other killing solutions. We tested the hypotheses that (i) ethanol fuel is attractive and that (ii) ethanol fuel reduces escape, through faster sinking or death than other killing solutions. To test our first hypothesis, we run a manipulative experiment in the field, in a remnant of semi-deciduous Atlantic forest in Viçosa municipality, Minas Gerais State, Brazil. In this experiment, we tested the attractiveness of four different solutions: water (negative control), commercial alcohol (92.8°GL), 100% ethanol fuel, and sugarcane juice (positive control). We used commercial ethanol to distinguish whether the attraction is caused by ethanol *per se* or by traces of gasoline contained in ethanol fuel. We used polyethylene vials of 20 cm in diameter and 22 cm deep as pitfall traps, filled with 500 ml of a killing solution comprised of water + 2.5% neutral detergent. In each pitfall trap, we attached two PET tubes (2 cm in diameter, 15 ml each), glued to the inside of the trap with gluing tape, 180° from each other, containing one of the four solutions. We established a transect of 1700 m, starting at 200 m from the forest edge. At the beginning of the transect, a set of four pitfall traps, each containing one of the four solutions chosen at random, was placed perpendicular to the transect, 30 m apart from one another. After the next 50 m on the transect, we placed another set of pitfall traps, repeating this procedure a total of 30 times. The traps were left in the field for 48 h and then removed to identify and store the specimens in ethanol fuel. To test if ethanol fuel is attractive, we compared the number of species (richness) and individuals (abundance) captured *per* pitfall trap (our response variables) among the four attractive solutions (explanatory variables) using one-way analysis of variance (ANOVA), adjusting generalized linear models (GLMs) with Poisson error distribution and corrected for over- or under-dispersion using quasi-Poisson when necessary. To test our second hypothesis, we marked the time (in seconds) that individuals of *Gryllus* sp. (reared in the Laboratory of Orthoptera – UFV) took to sink (= touch the bottom of the pitfall) and die (= complete immobilization) in 500ml on each of the three killing solutions used in our previous work (100% ethanol fuel; 80% commercial alcohol (80°GL) + 10% glycerin + 10% formaldehyde, and 90% commercial alcohol (80°GL) + 10% glycerin). After death, we removed the cricket from the vial, labeled it and stored it. We repeated this procedure 30 times for each killing solution. We performed one-way analysis of variance (ANOVA),

adjusting generalized linear models (GLMs) with normal error distribution. We considered time of cricket sinking and dying as response variables in separate statistical models, and the type of killing solution as explanatory factor, with three levels. We used contrast analyses to evaluate the differences among the explanatory factor levels, simplifying the complete model by amalgamating non-significantly levels. We used Chi-square (X^2) test for Poisson error distributions, and F test when corrected for over- or under-dispersion and for normal error models. All models were subjected to residual analyses, and all analyses were done using R 2.12.1. In our field manipulative experiment, we collected 393 individuals of eight species from three Orthoptera families Gryllidae, Phalangopsidae and Trigonidiidae (Table 1). Species richness ($F_{1,119} = 13.81$; $P < 0.001$; Fig. 1A) and abundance ($F_{1,119} = 5.89$; $P < 0.001$; Fig. 1B) *per* trap were higher in traps filled with sugarcane than in those containing the other solutions. There was no difference in attraction *per* trap among the other solutions (richness: $F_{1,118} = 0.86$; $P = 0.35$; abundance: $F_{1,118} = 3.06$; $P < 0.08$). Our laboratory experiment showed that ethanol fuel reduces escape, since the sinking time in this solution was significantly shorter ($F_{1,88} = 27.15$; $P < 0.0001$) than in the other two ($F_{2,87} = 2.22$; $P < 0.13$). Time of death was lower in ethanol fuel, followed by solutions 2 and 3 ($F_{2,87} = 81.30$; $P < 0.0001$). We conclude that ethanol fuel is not attractive for orthopterans, and that the higher species richness and abundance in pitfall traps with this killing solution is due to quicker sinking and quicker dying of the individuals that fall into the killing solution. Ethanol fuel captures a larger species spectrum than other killing solutions, including species that are generally under-sampled. Therefore, we strongly recommend the use of ethanol fuel as a killing solution for sampling and storing collected individuals for both scientific and ethical reasons.

Table 1, Number of individuals of each taxa sampled in a field experiment to test attractiveness of four different solutions

| Taxa | Tested solutions | | | |
|---|------------------|--------------------|--------------|-----------|
| | Sugarcane | Commercial alcohol | Ethanol fuel | Water |
| <i>Ectecous</i> sp.1 Saussure, 1878 | 32 | 24 | 38 | 11 |
| <i>Eidmanacris bidentata</i> Sperber, 1998 | 4 | 3 | 1 | 4 |
| <i>Endecous</i> sp.1 Saussure, 1878 | 2 | - | - | - |
| <i>Gryllus</i> sp.1 L., 1758 | 4 | 3 | - | - |
| <i>Mellopsis doucasae</i> Mews et al., 2010 | 3 | - | - | - |
| <i>Phoremia rolfsi</i> Pereira et al., 2011 | 28 | 18 | 7 | 19 |
| <i>Phoremia zefai</i> Pereira et al., 2011 | 39 | 35 | 36 | 30 |
| <i>Zucchiella matiottiae</i> Pereira et al., 2011 | 21 | 16 | 6 | 9 |
| Total | 133 | 99 | 88 | 73 |

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An ancient ecosystem speaks volumes: analyzing speciation events in scrub islands of the southeastern U.S. via their endemics: *Melanoplus* grasshoppers belonging to the Puer Group

Woller, DA and Song, H

University of Central Florida

One of the most ancient ecosystems in the southeastern U.S. is scrub, often associated with ridge systems, mainly in Florida, which are thought to have been used as refugia during the sea level rises of the Pleistocene era. Following recession of the waters these habitats effectively remained islands due partly to unique soil composition as well as a relative lack of plant diversity. Thus, scrub is now home to a myriad of floral and faunal endemics. Specifically, this ecosystem is a wellspring of endemism in arthropods, like those in the grasshopper genus, *Melanoplus* (Orthoptera: Acrididae: Melanoplinae). The majority of the southeastern members of this genus possess short wings, so they are unable to fly. Due to this fact and their propensity to be endemic to specific habitats and southeastern regions, these *Melanoplus* species are ideal candidates for examining speciation hypotheses. To test such hypotheses, the Puer Group, comprised of 24 species with related morphology, was chosen as it spans four neighboring states (Florida, Georgia, South Carolina, and North Carolina), contains many scrub endemics, and its males are possessed of great variation in their genitalia. Using a number of anonymous SCNPS and known mitochondrial genes, a phylogeny was reconstructed to illuminate the relationships between Puer Group members, the gateway to testing possible modes of speciation, such as cryptic female choice, allopatry, and habitat requirements. Additionally, a novel approach to investigating functional morphology of genitalia will be addressed through the discussion of the applications of micro-CT scans and SEM imaging.

On the historical biogeography of the Desert locust, *Schistocerca gregaria*

Chapuis, M-P¹; Plantamp, C¹; Blondin, L¹; Foucart, A¹ and Bazelet, C²

¹*UPR Bioagresseurs analyse et maîtrise du risque, CIRAD, Montpellier, France;*

²*University of Stellenbosch, Department of Conservation Ecology and Entomology, 7602 Matieland, South Africa*

The desert locust, *Schistocerca gregaria*, is found in disjunct Southern and Northern areas of Africa. While the subspecies *S. g. gregaria* is a feared agricultural pest since early civilization, with plagues documented from West Africa to Southwest Asia, the anecdotic *S. g. flaviventris* inhabit 2500 km Southern in the Namib and Kalahari deserts. Questions have been raised regarding the taxonomic distinctness of *S. g. flaviventris* and *S. g. gregaria* subspecies, which are morphologically very similar. However, fixed and diagnosable differences in traits under genetic control are a criterion for subspecies designation. In this study, we used DNA barcoding to delimit taxonomical entities by amplifying a standard 658-bp fragment of Cytochrome C Oxidase Subunit I gene (COI) and 28 versatile microsatellite markers to assess the evolutionary relationships of closely related populations or subspecies. COI sequences clustered into two monophyletic lineages concordant with geography. In addition, characteristic point mutations allowed a clear diagnose between the two subspecies. Microsatellite genotyping of 13 populations showed that the two taxonomic units were not united by gene flow. The levels of genetic divergence were 5 to 30 times greater between *S. g. flaviventris* and *S. g. gregaria* than within subspecies. Our research also suggested that mid-Holocene climatic changes triggered the present geographical distribution and diversification of the desert locust subspecies. Indeed, Approximate Bayesian Computation estimated a divergence time between subspecies of around 7000 years ago, which corresponds to the mid-Holocene, a time of greater humidity, where the vegetation cover in Africa was dominated by forest and closed vegetation landscapes. It is likely that between the drier last glacial maximum and the divergence time of the subspecies (a period of 18,000 years), a continuous arid range stretched from southwestern Africa to northern Africa. At mid-Holocene, deserts and grasslands retreated and the extant tropical rainforest belt isolated northern and southern populations of the desert locust.

Digital mapping of orthopteran assemblages' distribution in South Siberia

Sergeev, MG^{1,2} and Molodtsov, VV¹

¹*Novosibirsk State University;*

²*Institute of Systematics and Ecology of Animals, Siberian Branch, Russian Academy of Sciences*

Digital mapping of orthopteran populations has been discussed in many publications during recent decades. These discussions are mainly associated with pest species, especially locusts and, in some cases with mapping of the distribution of endangered species. However, each species is a member of different assemblages (or taxocoenoses) in which it plays certain roles. An assemblage is composed of the settlements of all species inhabiting more or less similar habitat. The abundance, biomass, and other features of the assemblages define the role of Orthoptera in every ecosystem and relationships between different species of these insects. The main aim of this abstract is to discuss one of the first attempts of orthopteran assemblage digital mapping.

Qualitative data were collected in the southern part of West Siberia from 1972 until 2011. Samples collected during a fixed time period were made in every habitat studied. The classification of 666 samples was made by the Euclidian distances and Ward's method of clustering. This classification was compared with the digital map of vegetation of the West-Siberian Plain. The boundaries of the vegetation map were mainly used for extra- and interpolation of orthopteran assemblage distribution over the southern part of West Siberia.

Classification of orthopteran assemblages is developed for the south-eastern part of West-Siberian Plain, the northern part of the Altay Mountains and for the adjacent outskirts of the Kazakh Uplands for the first time: 5 types, 3 subtypes, and 12 classes are revealed. These classes do not completely coincide with the classes of vegetation on published maps. Several groups of the assemblages are associated with locust/grasshopper outbreaks. More or less uniform orthopteran assemblages inhabit some contours with quite different vegetation, while by contrast, there are some areas with uniform vegetation that should be divided on the basis of Orthopteran distribution. As a result, the first variant of the digital map of orthopteran assemblages' distribution is created. Evaluation of the distribution patterns of orthopteran assemblages revealed that the main factor determining these patterns is geographical zonality. The regional trend is also significant both for the forest-steppes and steppes. Opportunities of regionalization on the basis of orthopteran assemblages are discussed for the studied area and some similar and distinct features of faunistic and geozoological regionalization schemes determined. Possible changes of these assemblages due to invasions of some species are described.

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Altitudinal distribution patterns of Orthoptera and Plecoptera in the North Altay Mts.**Sergeev, MG**^{1,2}; Baturina, NS¹ and Hudiakova, NE³¹*Novosibirsk State University;*²*Institute of Systematics and Ecology of Animals, Siberian Branch, Russian Academy of Sciences;*³*Gorno-Altaysk State University*

Some patterns of altitudinal distribution were described both on the quantitative and qualitative levels for different taxa of the Orthopteroid insects and for different mountain systems. The main part of these publications is associated with species/subspecies distribution along the altitudinal gradient of some mountain ridges and with evaluation of biological diversity levels and endangered species disposition. The distribution patterns of biogeographical boundaries are revealed in several publications. In 1988-1992 Sergeev analyzed Orthoptera distribution through 30 mountain—plain transects and described three main types of boundaries between the mountain and plain faunas: (1) The geomorphological junctions between plains and mountain faunas is pronounced (the outer zone of the mountains of Central Asia and the Mediterranean). (2) A clearly marked barrier is absent (the northern slopes of Dzungarian Alatau, Kirgiz, Talas and Peter the Great Ranges; the southern slopes of the Allay Range). (3) A barrier separating mountain tops is highly significant (the south Siberia). Altitudinal distribution of local populations and assemblages is also described for several regions (Altay Mts., Alps, etc.). However, general patterns of orthopteran altitudinal distribution remain unclear. That is why many types of mountain systems should be studied from this point of view. The main aims of this publication are to analyze and to compare the altitudinal distribution patterns of two quite different orders of the Orthopteroid insects: terrestrial Orthoptera and amphibiotic Plecoptera in the North Altay Mts.

Qualitative and quantitative data were collected in the North Altay Mts. (Iolgo, Cherginskij, Anujskij, Bastshelakskij, and Seminskij Ranges, from 1977 until 2012 — Orthoptera; the Sema, Cherga, Sarasa, Peschanaja, and Anuy Rivers, in 2009–2012 — Plecoptera). We try to study all habitats applicable for local Orthoptera and Plecoptera. Altitudes were determined by GPS/altimeter or by contour lines on local maps. Besides our own data, some published and unpublished data were used. On this stage of studies, all known locations for each species were distributed over 200-meters altitudinal intervals.

Altitudinal distribution is analyzed for 55 species of Orthoptera and 18 species of Plecoptera:

| Altitudes, m | Orthoptera/species | Plecoptera/species |
|-----------------|--------------------|--------------------|
| 1,800–2,000 | 1 | no rivers |
| 1,600–1,800 | 4 | 2 |
| 1,400–1,600 | 2 | 1 |
| 1,200–1,400 | 3 | 4 |
| 1,000–1,200 | 14 | 6 |
| 800–1,000 | 29 | 5 |
| 600–800 | 27 | 8 |
| 400–600 | 48 | 7 |
| 200–400 | 37 | 8 |
| Piedmont plains | 23 | 0 |

Almost all species of both orders are associated with relatively low altitudes. More or less thermophilous orthopteran insects prefer the local steppes and dry meadows of the low altitudinal belts (lower than 1,000 m). Stoneflies prefer running water with relatively low temperatures. No orthopteran species inhabit the specific altitudinal belt. However, the Italian locust (*Calliptamus italicus*), *Oedaleus decorus*, and *Oedipoda caerulescens* are found only on the piedmont plains. The only endemic of the Altay Mts., namely the odonturine katydid *Isophya altaica*, is distributed through almost all altitudes up to the timber-line. The similar distribution pattern is revealed for stoneflies. However, these insects were not found in the streams on the piedmont plains.

The low altitudinal belts of the North Altay Mts. are seriously transformed and used for agricultural and logging activities. Besides that, some recreational areas are actively developed during last decades. These transformations may result in population decreasing/elimination of some species inhabiting the limited set of preferable habitats (e.g., *Chorthippus hammarstroemi*, *Celes skalozubovi*, *Mecostethus alliaceus*) and in invasion of several abundant thermophilous pests (*Calliptamus italicus*, *Oedaleus decorus*).

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Local wandering of *Stauroderus scalaris* (Fischer de Waldheim) and *Calliptamus italicus* (Linnaeus) in the spatially structured steppe-meadow landscapes

Sergeev, MG^{1,2}; Kazakova, IG² and Vanjkova, IA¹

¹*Novosibirsk State University;*

²*Institute of Systematics and Ecology of Animals, Siberian Branch, Russian Academy of Sciences*

Wandering is important process supporting population structures and changing population dynamics. This process was studied for different grasshopper and locust species and for different landscapes. However, the main part of these researches are associated with more or less natural ecosystems, sometimes with uniform gradients of environmental conditions, but without evident heterogeneity and developed spatial structures such as barriers, corridors etc. The main aim of this publication is to discuss some aspects of acridid wandering in spatially structured landscapes of the southern part of Siberia.

We studied wandering of two acridid species: the Italian locust (*Calliptamus italicus*) and *Stauroderus scalaris*. The Italian locust was investigated during its outbreaks (2000) in the northern steppes of West Siberia. The model polygon included several different plots: the grazed meadow steppes, different agricultural fields, forest belts, forested patches. The position of the hopper bands was determined by GPS and compared with the local landscape structure. Wandering of *Stauroderus scalaris* was studied in the central part of the Altay Mts. in 1988–1989. The model polygon included plots: different types of meadow steppes and meadows on slopes, the road and some agricultural fields. The series of adult females and males were captured, marked and released in the central point of the polygon. After that, positions of marked and unmarked specimens were determined relative to this central point.

In the spatially structured landscapes of the northern steppes, the local migrations of the Italian locust bands were limited and relatively slow. Their pattern is mainly determined by distribution of preferable plant patches. Some local barriers are manifested in evident concentrations of hoppers. Small and dense bands of the Italian locust did not migrate practically until mass generation of the 3d hoppers. This is related to the well-know low migration capabilities of younger hoppers and their inclination to site with the dominance of forbs. The barrier role of the forest belt stretching along the eastern part of the model plot is clear: the hopper bands ignored the forest belt and migrated over either steppe habitats or broad belts with very sparse vegetation. In the central part of the Altay Mts., wandering of adults of *Stauroderus scalaris* is evidently determined by distribution of patches of preferable vegetations.

In both areas, anthropogenic transformation of the native steppe landscapes leads to the appearance of additional barriers such as forest belts and agricultural fields. The spatial structures of these types limit opportunities of local migration.

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Taxonomy of *Psorodonotus*: qualitative versus quantitative morphology

Kaya, S and Ciplak, B

*Department of Biology, Faculty of Science, Akdeniz University, 07058 Campus, Antalya, Turkey**Tel: +90 242 310 23 56, Fax: +90 242 227 89 11**E-mail: ciplak@akdeniz.edu.tr*

Psorodonotus Brunner von Wattenwyl (Orthoptera, Tettigoniidae) includes 13 taxa ranged in Caucasus, Anatolia and Balkans. Its present internal taxonomy solely based on qualitative morphology is problematic. As in other tettigoniids male cercus is the main structure to produce taxonomical characters. We have studied geometric morphometry of male cercus to test its productivity as a source of taxonomical characters. Besides it will be possible to estimate evolution of cercus using a phylogenetic tree of the species. In total 755 photos representing 37 different populations of the genus were taken. Similarities in male cerci are assessed by 19 landmarks. Digitized photos were standardized, aligned and transferred to numeric data using suitable computer programmes. A canonical variate analysis applied to data suggested four clusters: (1) *P. davisii*, (2) *P. soganli*, (3) *P. specularis* and (4) remaining eight species. A second canonical variate analysis applied to fourth group suggested three clusters; the first includes *P. anatolicus*, *P. caucasicus*, *P. ebneri*, *P. fieberi*, *P. salmani*, the second *P. rugulosus* and two populations from *P. venosus* group and the third other populations of *P. venosus*. *P. illyricus* ranges between *P. caucasicus* and *P. venosus* clusters. Regarding phylogenetic relationships and clustering patterns of the canonical analyses following conclusions were made: (1) male cercus offers useful diagnostic characters to be used in taxonomy of the genus, (2) similarities/dissimilarities between different populations are not always homologies, (3) clustering of two populations of *P. venosus* from southern edge of its range with members of *P. rugulosus* indicate convergence.

Speciation under climatic cycles of Pleistocene: a snapshot from Anatolio-Balkan genus *Psorodonotus*

Kaya, S and **Ciplak, B**

Department of Biology, Faculty of Science, Akdeniz University, 07058 Campus, Antalya, Turkey

Tel: +90 242 310 23 56, Fax: +90 242 227 89 11

E-mail: ciplak@akdeniz.edu.tr

Psorodonotus Brunner von Wattenwyl(Orthoptera, Tettigoniidae) is found in the Caucasus, in Anatolia and in the Balkans and according to presently valid taxonomy, this genus includes 13 known taxa. These insects occur in euxinic vegetation or highland meadows and always above 1600 m. From the distribution pattern and habitat preference, we estimate that radiation of the genus is mediated by glacial ages of the Pleistocene. To test this phylogeographic assumption, we studied mitochondrial COI from representative populations. We defined 141 different haplotypes from 467 samples which were obtained from 31 populations representing 10 species. Different analyses suggested similar phylogenetic relationships except the basal branching events. All phylogenetic procedures suggest that there are two species groups. One is the *P. caucasicus* group including *P. caucasicus*, *P. ebneri*, *P. illyricus*, *P. fieberi* and *P. specularis*. The second is the *P. venosus* group that includes *P. venosus* and *P. rugulosus*. The remaining species *P. davisi* and *P. soganli* can be considered either independent clades or basal to the *P. caucasicus* group. Regarding phylogenetic relationships and branching pattern of the tree, the following conclusions were made: (1) the genus has a Caucasian origin, (2) two different faunal exchanges have occurred between the Caucasus and the Balkans, the first being from the Caucasus to the Balkans possibly through the Black Sea Region of Turkey and the second is from the Balkans to the Caucasus through Taurus Way. (3) *P. venosus* originated possibly from being originally present in Caucasian part of Turkey and then extended its range to the Zagros Mountains in the south. Some of the most southern populations of this group exhibit features of new species morphologically, however, they are within the clade genetically.

Molecular phylogeny, barcoding and taxonomy of spiny predatory katydids (Tettigoniidae: Listroscelidinae) from the Brazilian Atlantic Forest

Fialho, VS¹; Chamorro-Rengifo, J²; Lopes-Andrade, C² and Yotoko, KSC¹

¹Laboratory of Bioinformatics and Evolution;

²Laboratory of Systematics and Biology of Coleoptera, Federal University of Viçosa, Viçosa – MG, Brazil

Ecological and historical processes of fauna diversification have been widely studied under the light of phylogeography and phylogeny, which deal with the spatial arrangements of genetic lineages, especially within and among closely related species. These approaches were extensively used in studies on the fauna of tropical forests, but studies on the fauna of forests of the Southern Hemisphere are still rare, especially concerning the Brazilian Atlantic Forest (AF). The AF is one of the priority areas for Brazilian biodiversity conservation, as it has high endemism and species richness, and also because it shelters extinction-threatened species. In the present work, we focused on the systematics of Listroscelidinae (Orthoptera: Tettigoniidae), a subfamily of katydids highly diversified in Brazil. Unfortunately, there has been no taxonomic study on Listroscelidinae since the work of Piza (1982) and nothing is known on the natural history and geographic distribution of its species. We used mitochondrial and nuclear sequences in order to propose hypotheses on phylogenetic relationships of these katydids and establish a small mitochondrial sequence (about 500 base pairs) to be used as a DNA barcode for rapid identification and diagnosis of species. In parallel, we revisited the classification of the subfamily by means of external morphological characters. The katydids were sought in 15 Conservation Units (CU) of AF, from northern Rio de Janeiro to south of Bahia, from November 2011 to January 2012. As most katydids, Listroscelidinae are active at night, our collection period was between 1900hr and 0100 hr with the aid of flashlights. Each CU was sampled at least for three consecutive nights. We captured specimens with transparent plastic pots of 500 mL with lid and photographed them alive. We preserved one mid or hind leg of each individual in absolute ethyl alcohol and maintained the samples at -20°C for molecular procedures. Individuals were dried, pinned, labeled and deposited in scientific collections. We examined, compared and photographed pinned specimens under a Zeiss Stemi 2000-C stereomicroscope equipped with a Canon EOS 1000D, or under a Zeiss Discovery V8 stereomicroscope with a Zeiss MRc Axiocam. For each final image, we combined 15-25 photomicrographs of different focus depths using the image stacking softwares CombineZP and Zeiss AxioVision 4.8. Color images are available at the Orthoptera Species File. In addition to the specimens collected in field expeditions, we have also examined specimens deposited in scientific collections, suitable for descriptions of new species and the taxonomic revision of *Listroscelis*. We isolated the total DNA of each individual using the protocol described in Szwinski et al. (2012). A 1,600-bp fragment of the COI gene and a 1,300-bp fragment of the rRNA 18S were amplified by touchdown PCR, using annealing temperatures from 55 to 45°C . Sequencing of the PCR products was performed using the services of Macrogen. We evaluated and edited the resulting chromatograms with the program Consed (Gordon, et al., 1998), and aligned both sequences in Mega 5.0 (Tamura et al., 2011). Since COI is a coding sequence, we translated these sequences to their putative amino acid sequences, aligned them and reversed to the nucleotide sequence. We eliminated all the putative

amino acid sequences that showed unexpected stop codons or gaps of one or two positions. We also discarded sequences that showed double peaks in the chromatogram. It is possible that these sequences are fragments of mitochondrial DNA that migrated to the nucleus (Cristiano et al., 2012), a very common phenomenon in Orthoptera (Berthier et al., 2011), which we will study in more depth elsewhere. We estimated the phylogenetic relationships of both genes through Bayesian inference using the Markov Chain Monte Carlo (MCMC) method as implemented in MrBayes 3.1 (Huelsenbeck & Ronquist, 2001), using the model inferred with MrModeltest version 2.0 (Nylander, 2004). Two simultaneous and independent runs, each containing one cold and three heated chains, were processed for 10^7 generations, each starting from a random tree. These trees were sampled every 1000 generations, resulting in 10^4 samples, from which 25% were burned-out. The remaining topologies were used to build a majority-rule consensus trees, rooted with sequences of *Oxia chinensis* (Thunberg) (Orthoptera: Acrididae, GenBank accession number: NC010219). Sequences suitable for DNA Barcode shall be short, with little intraspecific and high interspecific divergence. Therefore, we seek in our alignment COI for a region that fulfill these assumptions and built a distance tree using the Neighbor-joining method (Saitou & Nei 1987) with Kimura 2-parameters model (Kimura 1980). We compared this tree with the phylogenetic tree from the Bayesian analysis based on complete sequences of COI. We collected a total of 99 specimens of Listroscelidinae in ten conservation units. Our morphological analyzes allowed us to recognize 14 species of four genera (eight new described species, two of them classified within a new genus allocated within a new tribe). Other two species are possibly new but we did not describe them because males are unknown. Unfortunately, because of the presence of numts, we were unable to generate COI sequences for all species and only 12 of them were included in our phylogenetic analyses (figure 1A and 1B). The complete alignment of 48 COI gene sequences resulted in 1290 aligned sites, of which 540 are variable. In Figure 1A, after separating the outgroup species (*O. chinensis*), the remaining species split into two separate groups. The first group (PP = 0.66) clusters all species of *Cerberodon* Perty, *Monocerophora* Walker and *Listroscelis* Serville, all tightly defined (PP = 1.00). Specimens of *Cerberodon* split into two well-defined subgroups, the first (PP = 1.0) comprising four specimens of *C. viridis* and the second (PP = 1.0) grouping two individuals of *Cerberodon* sp.1. *Monocerophora* was also divided into two tightly defined groups, corresponding to two species: *M. spinosa* (three sequences, PP = 1.0) and *M. minax* (four sequences, PP = 1.00). Within *Listroscelis*, we found genetic differentiation compatible with the subdivision into five species, all tightly defined. The second group contains members of the new genus found in this work. This group also split into two well-defined subgroups (each with PP = 1.00), corresponding to two morphological species. The complete alignment of 48 18S gene sequences resulted in 1615 aligned sites, of which only 11 are variable. In Figure 1B, as in Figure 1A, Listroscelidinae specimens split into two tightly defined groups: the first including the genera *Cerberodon*, *Monocerophora* and *Listroscelis*, but without any distinction between *Monocerophora* and *Listroscelis*; the second group comprising the specimens of the new genus, subdivided in two different species. Based on our molecular results and on morphological features, we propose the clade containing the new genus as a new tribe, and include *Cerberodon* and *Monocerophora* in Listroscelidini. A visual analysis revealed that the 5' portion of COI had greater variation between species than within them. We then delimit a fragment of 500bp between sites 2394

and 2890 of the complete mitochondrial genome of *O. chinensis*. The dendrogram obtained was similar to the phylogenetic hypotheses based on complete COI (Figure 1A) and addresses the need to distinguish between species. Our morphological and molecular results are congruent, as species and genera defined morphologically also appeared as well-supported monophyletic groups in the COI tree (Figure 2). The 18S tree, in turn, addressed more basal relationships and provided evidence that *Monocerophora* and *Listroscelis* share a recent common ancestor, with *Cerberodon* as sister group, which could not be detected by COI. This tree also supports the new genus as a separate clade, defined here as a new tribe. The topology differences between genes used here were expected and result from inherent differences in mitochondrial and nuclear genomes. While mitochondrial DNA have higher rates of nucleotide substitution, which makes it an excellent tool to distinguish closely related species, nuclear DNA evolves more slowly, making it useful in trying to resolve deeper phylogenetic branches. In fact, all sequences of *Monocerophora* and *Listroscelis* were identical in the 18S tree (Figure 1B).

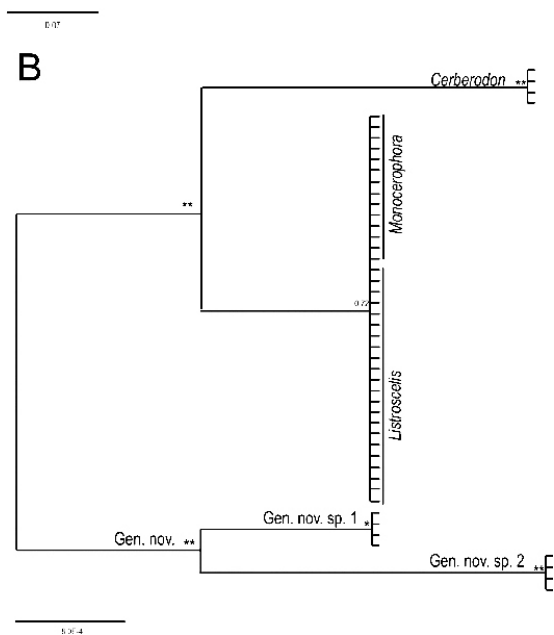
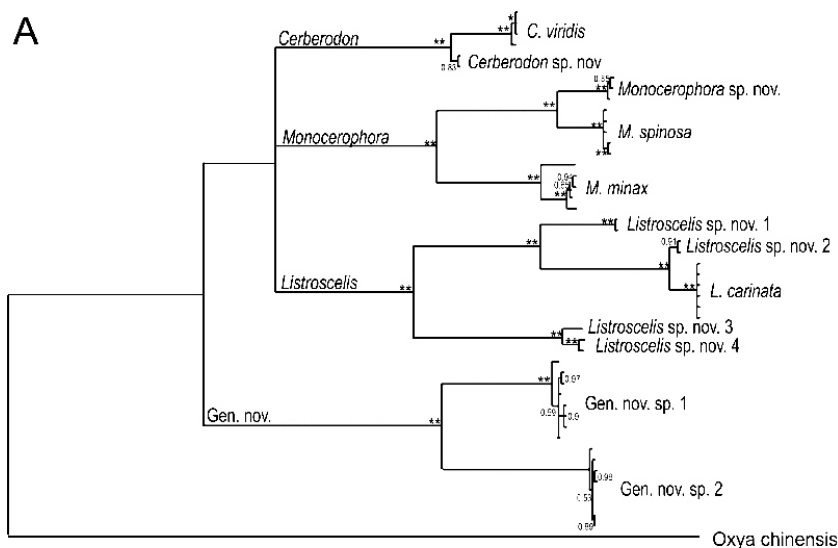


Figure 1: A – Phylogenetic hypothesis based on 48 COI mitochondrial sequences. B – Phylogenetic hypothesis based on 48 18S nuclear sequences. *PP > 0.95; **PP > 0.99.

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Are Agraeciini and Copiphorini natural subgroups of Conocephalinae? Considerations based on male cerci

Ingrisch, S

Zoological Research Museum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany

The subdivision of Conocephalinae goes back to Redtenbacher (1891) who recognised three tribes: Agraeciini (today 98 valid genera), Copiphorini (50 genera) and Conocephalini (20 genera). Although a few additional tribes have been described since then (Armadillagraeciini Rentz, Su & Ueshima, 2012, 3 genera; Coniungopterini Rentz & Gurney, 1985, 3 genera; Euconchophorini Gorochov, 1988, 5 genera), the classical 3 tribes still cover the majority of genera and species.

The Conocephalini are a rather uniform group of small meadow katydids that are at the current state of knowledge well delimited. Regarding the other two tribes, it is easy to distinguish Agraeciini from Copiphorini in the Old World, but in the Americas, the right assignment of a genus to one of both tribes may be difficult (e.g. Walker, T.J. & Gurney, A.B. (1972). *Ann. Entomol. Soc. Amer.* 65: 460-474). This study aims to analyse the validity of Agraeciini and Copiphorini as separate natural subgroups of Conocephalinae.

My previous taxonomical and morphological studies of Conocephalinae mainly from SE Asia found that the male cercus is a valuable character for the separation of species and helpful for the classification of genera. As the male cerci are an important tool for attaching to the female abdomen during mating one can suppose that the correct shape of the cerci works as an isolating mechanism between species.

However, in one subgroup of Conocephalinae the situation is quite different: in the Old World genera currently arranged under Copiphorini. In seven African and five Asian genera with together 137 species there are only two different shapes of male cerci with hardly any variation between the species that use one of these shapes. The cerci have either two acute apical internal teeth with the more proximal tooth larger and little sinuate (type A), or one short acute apical-internal tooth and a long upcurved internal tooth at very base (type B). The apical tooth in type B is distinctly smaller than in type A. As published studies show, there are also some American genera that have one or the other of these cercus types, but in general the male cerci of American Copiphorini are not well studied.

The following conclusions may be drawn from the anomaly that species from different genera have identical cercus shapes:

1. The male cerci in this group do not function as an isolating mechanism between species: instead there is a pre-mating mechanism, the species-specific stridulation (e.g. Bailey, W.J. (1976). *J. Nat. Hist.* 10: 511–528).
2. The male cerci are a conservative character that did not change during radiation. They can thus be regarded as synapomorphies of the genera concerned.
3. As there are two different shapes of cerci, there are two evolutionary lines, leaving it open as to whether there is a single common ancestor or parallel evolution. But as also the general characters are similar, with several species assigned to the wrong genus if judged by the shape of the male cercus, one may suppose that they form a natural group.
4. In contrast to the Asian Agraeciini that live in forested areas, they occur in wet, open grassland.

Thus one may suppose that they are phylogenetically rather young and evolved together with the spread of open grasslands.

The question that arises is whether this group of genera is related to *Copiphora* (the type genus of Copiphorini) or is it closer to another group. As far as can be judged from descriptions and images in Naskrecki (2000: Katydidids of Costa Rica. Volume 1, Philadelphia), the male cerci in the genus *Copiphora* differ from those of the Old World Copiphorini and they also differ between species. Thus it is unlikely that the latter are close to *Copiphora*. In contrast, studying the cerci of the genera *Lesina* and *Ellatodon* (subtribe Eumegalotondina = syn. Lesini) proved that they are somewhat intermediate between both of the cercus shapes discussed before although their shape is more similar to type B. From the latter they only differ by a larger apical tooth and the proximal tooth not arising at the very cercus base but somewhat behind it.

Formally it would thus be reasonable to rise Lesini to the rank of a full tribe [the family group name Lesini de Jong, 1942 is given preference over Eumegalodonidae Brongniart, 1892 since the type genus *Eumegalodon* Brongniart, 1892 is a generic homonym of the mollusc genus *Eumegalodon* Guembel, 1862] and include the Old World Copiphorini and the corresponding American genera to the Lesini. This hypothesis should however be tested by additional evidence including gene sequencing.

The relationships between the Lesini in the new sense to other groups of Conocephalinae as well as that between the remaining American Copiphorini to the Agraeciini should be evaluated in future studies. The type genera of both tribes are from South America. For practical reasons it may be discussed if we should give up the current subdivision of Conocephalinae until we have more evidence on the phylogenetic relations between the genera and/or use smaller groups of genera for which there is evidence for monophyly as a basis for a tribal division.

***Xyronotus aztecus* Saussure, 1884 (Orthoptera: Trigonopterygoidea: Xyronotidae) a relict species from cloud forest in Central Mexico**

Eduardo Rivera-García y Arturo Bonet

Instituto de Ecología A. C. (INECOL), Red de Interacciones Multitróficas, Antigua carretera a Coatepec No. 351. El Haya, 91070, Xalapa, Veracruz, México

E-mail: eduardo.rivera@inecol.edu.mx; arturo.bonet@inecol.edu.mx

Xyronotidae family consists of four species endemic to Mexico: *Xyronotus aztecus* Saussure 1884, *Axyronotus cantralli* Dirsh & Mason 1979; *X. cohni* Dirsh & Mason 1979 and *X. hubelli* Dirsh & Mason 1979 which belong to the superfamily Trigonopterygoidea in Caelifera. There are 10 records from the nineteenth century to the present, some old records with more than 100 years, so the current geographical distribution of the family is fractional. Along with the family Trigonopterygidae, from Southeast Asia and Oceania with 16 species, they are evolutionarily close to Acridoidea. Leavitt *et al.* (2013) did not use Xyronotidae for representing Acridoidea phylogeny, however it is assumed that the family is ancient and is related to the basal lineages of Acridoidea. Both families with distant geographic distributions may have a common ancestor. The four species that have been collected in cloud forests located in central and southern Mexico: *X. aztecus* in the center part (Plan de Hayas, Huatusco and Cordoba, Veracruz) of the Sierra Madre Oriental of Mexico, *X. cohni* and *X. hubelli*, in the Sierra de Juarez, Oaxaca and *A. cantralli* in the mountains of Chiapas. *X. aztecus* was collected and studied for the first time by Bolivar and Urrutia in 1884 with an old record from Cordoba, Veracruz, he gave a description though Saussure in 1884 was the author of the original description. Recently, Orthoptera collections in the cloud forest from Xalapa contained samples of *X. aztecus*, expanding its distribution at this locality. The objective of this paper is to present new records of *X. aztecus* in the region of Xalapa and some observations on its biology, and discuss its importance as a relict species (*sensu* living fossil Dirsh 1975) of Acridoidea for preservation in cloud forests. In summer (August to November) of 2011, Orthoptera collections were performed on three green areas of Xalapa, Veracruz where we collected 213 specimens of 24 species, mostly from altered environments. In a cloud forest well preserved "Santuario del Bosque de Niebla (SBN) *X. aztecus* individuals were collected, expanding its distribution to Xalapa. We recorded the collection site within the forest and obtained their maximum density was estimated at $1/27 \text{ m}^2$ ($N = 9$; calculated by the nearest neighbor distance (Southwood 1978).

In the last half of 2012, we kept together, in the laboratory, seven individuals, preserved between 45 days to six months alive (until February), of which were recorded the first data of its longevity, different instars, sex and possible plants for food. The specimens were collected from August to November in different developmental stages (nymphs and adults), collected nymphs changed to the adult stage. Nymph sex could not be determined with the naked eye because the characteristic genital cerci of male appear in the last instar (about five). It is found in soil and on plants of shrub layer at heights up to 80 cm.

The nymphs and adults were fed with new leaf "May flower", *Palicourea padifolia* (Roem and

Shult.), C. M. Taylor and Lorence (Rubiaceae), a plant found in the cloud forest. They ate well from August to November decreasing eating and activity from November to February. The adults feed on the edge of the leaf leaving a gap in the shape of elongated circle. When they are not eating they are resting on stems and leaves. Three male and female pairs were observed for copula, though mating was unconfirmed, one of them for more than 24 hours, no visible ootheca was seen. These are the first observations on the biology of *X. aztecus*. Its longevity, from egg to adult death lasts six to seven months. We need to know the ootheca and early instars nymphs. We do not know if their populations are extensive in their range or are in adjacent vegetation types. We need to analyze *X. aztecus* mitochondrial genome, as well as, from the three closely related species so that Xyronotidae can be represented in the Acridoidea phylogeny made by Leavitt *et al.* (2013).

Xyronotidae family is well represented in the cloud forest of central and southern Mexico. The populations have adapted to the climatic conditions from the Pleistocene to the present. The four species have been well maintained since its origins. The relationship with other basal lineages Acridoidea still is an open issue hoping we can answered soon. The location of this species in Xalapa' s cloud forest protected area (SBN) strengthens the conservation of this area as a site of relict species protection.

Ecological zoogeography studies on Central-European Orthopterans

Kenyeres, Z¹; Bauer, N² and Rácz, IA³

¹*Acrida Conservational Research L.P., Tapolca, Hungary;*

²*Hungarian Natural History Museum, Department of Botany, Budapest, Hungary;*

³*University of Debrecen, Department of Zoology and Evolution, Debrecen, Hungary*

Based on that the recent fine-scale distribution patterns of species are determined rather by ecological than historical factors we examined the methods of ecological zoogeography on distribution patterns of grasshopper species and species-groups in a Central-European low mountain range (Bakony Region of the Transdanubian Mts (W-Hungary)).

In the study area (~3700 km²) the cover of the natural habitats based on GIS maps is ~60 percent. Out of this the potential grasshopper habitats (natural grasslands, pastures and shrubby ecotones) is 17.5 percent. Further that studied region shows large heterogeneity in climatic features.

Analyses were carried out on digital presence-absence maps of 84 species at the scale of 2.5×2.5 UTM-grid. The following abiotic background variables and variables of the grasshopper fauna were connected to the UTM-quadrates: altitude; annual mean temperature; annual rainfall; insolation in April and July; species number; relative frequency of the species; relative frequency of arboricol, arbusticol, silvicol, pratinicol, graminicol, geophilous and pseudo-psammophilous life-forms; relative frequency of thermophilous, moderate-thermophilous, mesophilous, moderate-hygrophilous and hygrophilous species; diversity (*DQ*) of life-forms and eco-types.

Based on the results the zoogeographical differences of microregions in the Orthoptera fauna are not manifested in the distribution of species groups of different faunal-types, but in the distribution of species groups of different eco-types. We revealed that distribution patterns of the Orthopteran species-groups and species are mainly determined by annual rainfall, insolation in April and landscape structure.

We can conclude that using methods of ecological zoogeography in zoogeographical analyses is recommended and distribution patterns of Orthopteran species groups with different ecological requirement are very usable for the determination of zoogeographical borders at microregional scale.

Re-emergence of *Dichroplus maculipennis* (Blanchard) (Orthoptera: Acrididae: Melanoplinae) as a pest in the Pampas region of Argentina.

Mariottini, Y¹, De Wysiecki ML^{1,2}

¹Centro de Estudios Parasitológicos y de Vectores (CEPAVE), CCT La Plata-CONICET-UNLP, La Plata, Argentina.

²Facultad de Ciencias Naturales y Museo- Universidad Nacional de La Plata (UNLP).Argentina.

Dichroplus maculipennis is one of the most widely distributed species of the genus, occurring in much of Argentina and Chile, southernmost Brazil (Rio Grande do Sul), and Uruguay. In Argentina, *D. maculipennis* is distributed in a triangle that stretches from Buenos Aires and Entre Rios provinces in the East to southern Catamarca province in the North, and southern Santa Cruz province in Patagonia. The species is one of the most damaging of the country, mainly in areas of the Pampas and Patagonia regions. It has been categorized as a major pest of several crops, and natural and improved pastures. *Dichroplus maculipennis* is a univoltine, polyphagous, species. In the early 80's, *D. maculipennis* was reported to account for approximately 70% of the grasshopper communities of the Pampas, being numerically the most important species in several counties of southern Buenos Aires province. Since then, however, different studies conducted in the Pampas recorded a conspicuous decrease in its abundance, a trend not observed in Patagonia. Several factors were suggested in order to explain the apparent decline of *D. maculipennis* in the Pampas such as climate change, insecticide campaigns against pests, switches in patterns of land use, and intrinsic characteristics in the biology of the species.

The main objective of this study was to determine the status of *D. maculipennis* in representative plant communities of the southern Pampas region (Laprida county) for eight consecutive seasons (2005-06 to 2012-13). The collecting sites were classified into four categories: native grasslands" (extensive coverage of native grasses), halophilous grasslands (extensive coverage of *Distichlis spicata*), implanted pastures (mostly *Agropyron*), and disturbed grasslands (grazed native grasses with significant coverage of introduced weeds like *Cardus pycnocephalus* and *Centaurea calcitrapa*). Three replicates of each category were established, which were constant throughout the study.

Dichroplus maculipennis' density varied significantly in all plant communities ($p < 0.0001$). The lowest densities [0.10 ± 0.04 ind/m² (0-1.7 ind/m²)] were recorded in the first season. Afterwards, there was a progressive and significant increase until the 2009-10 season ($p < 0.0001$) when the highest density values were recorded [27.8 ± 3.1 ind/m² (2.8 -56.3 ind/m²) on average]. Subsequently, in the next three sampling periods, a decrease in density was registered. While in season 2010-11 the density was still high [15.6 ± 0.9 ind/m² (0-26.11 ind/m²) on average], it was significantly lower than in the previous season ($p < 0.0001$). In the last two seasons average densities were lower (8.23 ± 0.53 ind/m² in 2011-12; 3.56 ± 0.25 ind/m² in 2012-13), but significantly higher than in the first one. There were no significant differences between densities of the four plant communities in each season ($p > 0.05$).

In this way, we determined that a *D. maculipennis* outbreak of historic magnitude began in late 2008 and early 2009. It included not only high densities of up to 75 ind/m² but also the characteristic in-masse, swarm-like dispersal flights known for the species, causing significant economic losses to farmers and ranchers. This phenomenon involved at least 12 counties in Buenos Aires province, covering an approximate area of 2.5 million hectares.

It is well known that the weather is one of the most influential factors in the population dynamics of the different species of grasshoppers. Drier conditions and high temperatures tend to favor the development, survival, and reproduction of many grasshoppers species. Considering this, is important to highlight, that the 2008-09 season, when began the *D. maculipennis* outbreak, was the driest in 47 yr, while the temperature was also well above historical records.

During the first three seasons, abundance of *D. maculipennis* in grasshopper communities of the study area was less than 10%, being found mostly in halophilous grasslands. However, starting in 2009 *D. maculipennis* became the dominant species in all plant communities in the area, with

abundances higher than or equal to 50%. Data provided by this study shows that, after almost 30 years of low abundance in grasshopper communities of the Pampas, *D. maculipennis* has re-emerged as one of the most important pest species of Argentina.

Species from an integrative perspective and quality of existing taxonomical data: game of the names versus natural entities**Ciplak B**

Department of Biology, Faculty of Science, Akdeniz University 07058 Antalya, Turkey

New approaches and methods brought taxonomy to a new era in late 20th century and early 21st. The most prominent advancements were lived in alfa taxonomy. Especially taxonomical rearrangements based on molecular markers, which are the most effective tools to determine reproductive units, has changed existing species more than by half. Presentation concentrates to delimitation of the species using integrated data from *Anterastes*, two species groups in *Poecilimon* (*Tettigoniidae*) and a species group from *Chorthippus* (*Acrididae*), under the references criteria of different species concepts. Following conclusions were made. (1) The combined data suggest a considerable rectification of the existing taxonomy for each lineage. (2) The existing classification is largely established by traditional approaches and methodologies, but it is far of reflecting real natural entities, (3) there are several cryptic species waiting to be discovered, (4) Homopolasies may be common among morphological phenotypes, thus misleading in delimitation of the species, (5) divergence in sexual phenotypes such as song characteristics may be different in allopatric and sympatric speciation and (6) different species concepts largely agree on the same taxonomical arrangements.

Sexual Selection & Behavior

Sexual behavior and sexual selection in giant, poisonous lubber grasshoppers

Whitman, DW¹; Coombs, CB² and Hunter, T³

¹*School of Biological Sciences, Illinois State University, Normal, IL, 61790-4120, USA;*

²*University of Illinois, Urbana, IL, USA;*

³*Massachusetts Institute of Technology, Cambridge, MA, USA*

E-mail: dwwhitm@ilstu.edu

Male Eastern Lubber grasshoppers, *Romalea microptera*, (Fam. Romaleidae) from the southeastern USA become sexually active about 15 d after the adult molt, and females begin producing a sexual pheromone at about the same time. Males actively seek and mount females, who fight vigorously to dislodge them. Males use acoustic, visual, chemical, and tactile cues to orient to, and copulate with females. Copulation involves a complex genitalic locking mechanism that firmly secures the female to the males. Males pass multiple, sequential spermatophores to the female, filling her spermatheca with sperm, probably as a form of intra-male sperm competition. Fierce anti-male behavior by females against amorous males may be a form of inter-sexual selection by females, because only strong, healthy males can overcome the vigorous defenses of the larger females. After copulation, males remain on the backs of females, mate-guarding them until the female oviposits. Mate-guarding prevents copulations by rival males, thus assuring paternity for the mated male. The mating urge is strong, and mating and mate-guarding males refuse to release females, even when a male's antennae or leg is cut off with scissors.

Hill-topping and male-male sexual competition in lubber grasshoppers**Maeno, KO¹** and Whitman, DW²¹*Centre National de Lutte Antiacridienne (CNLA), Nouakchott, Bp: 665, Mauritania.**E-mail: otokomaeno@yahoo.co.jp;*²*School of Biological Sciences, Illinois State University, Normal, IL 61790-4120, USA**E-mail: dwwhitm@ilstu.edu*

Many animals hill-top (aggregate at elevated sites) as a means of finding mates, but this behavior has never been observed among the ~ 28,000 species of Orthoptera and Phasmida. However, marsh-inhabiting Eastern Lubber grasshoppers, *Romalea microptera*, from Florida, USA, hill-top. Nymphs and young adults disperse throughout the marsh, living and feeding above water on emergent plants. This is adaptive, because dry land contains more predators and parasites than the marsh habitat. However, females must return to elevated, dry land to oviposit. Males aggregate at these "mating and oviposition grounds" and mate with incoming females. Sexual competition at these sites is intense, with males fighting fiercely for possession of scarce females (male-to-female ratios are as high as 85:1). After mating, males mate-guard females from rival males until the female oviposits, thus assuring his paternity. Virtually all females entering the oviposition sites are gravid and ready to lay eggs. After the female lays, the male dismounts and seeks a new partner, and the female quickly returns to the marsh. The Everglades topography is extremely flat. Slight differences in elevation, as little as 5 cm, can determine dry vs. flooded soil. These small elevation differences represent "hills", and lubbers can detect and orient to these small "hills" in the otherwise flat and flooded marsh habitat.

The evolution of weaponry and aggressive behaviour in North American field crickets (Gryllidae, *Gryllus*)

Judge, KA¹; Smith, BE²; Ohlmann, S¹ and Cade, WH²

¹MacEwan University, Canada

²Department of Biological Sciences, University of Lethbridge, Canada

Sexual selection research has traditionally focussed on female choice over male-male competition because the former mechanism was initially controversial and its theoretical foundations were not immediately recognized. This has resulted in the underdevelopment of research into the evolution of male-male competition and the traits that they use during aggressive physical combat over females - weaponry - despite the fact that the natural world abounds with examples of male weapons. My collaborators and I are currently studying the relationship between male weaponry and aggressive behaviour in nine species of field crickets, a group that has become a model system both for the study of male-male competition, as well as for the sport of cricket fighting in China. Over the past two years we have videoed aggressive contests between pairs of male crickets and then preserved the bodies of the participants for measurement of body size and weaponry size, with the aim of understanding what traits cause males to win fights over females. Previous work has shown that in *Gryllus pennsylvanicus*, males with relatively larger heads and mouthparts win more fights than males with relatively smaller heads and mouthparts. Our current study will test this finding across nine species found in North America with the predictions that: 1) species with the greatest degree of weaponry (i.e. head and mouthparts) elaboration will fight more often, and 2) more closely related species will be more similar in weaponry elaboration than more distantly related species. I will present preliminary results of this research for three of the nine species (*G. firmus*+*G. pennsylvanicus*+*G. ovisopis*) and discuss these results in the light of ancient practical knowledge of cricket aggressive behaviour from the time of Chia Szu-Tao (賈似道).

Sexual selection and the evolution of mating systems within the species rich bushcricket genus *Poecilimon* (Ensifera: Phaneropterinae)

Lehmann, GUC

Department of Biology, Behavioural Physiology, Humboldt University, Berlin, Germany

Sexual selection is traditionally characterized by the dualism of male-male competition and female choice. However, mating decisions and the underlying mating strategies are highly flexible and influence each other. Several forces shape mating strategies, including the reproductive interests of the individuals involved, the costs of different strategies and the subsequent investment patterns of individuals. Bushcricket (Tettigoniidae) males signal their willingness to mate through their mating songs, which give females the opportunity to choose between different males without direct contact. Female choice has also driven males to present a huge spermatophore during copulation. Males try to optimize their investment in the spermatophore, so that they also have energy reserves for song production.

While male calling patterns are well studied, the evolution of receiver (hearing) adaptations is a rather neglected topic in Orthoptera as well as other groups. Within the subfamily Phaneropterinae mating communication is generally bidirectional, females answer the male's call with a short response song. However, in the large genus *Poecilimon* females of several species have lost their ability to answer and have returned to a unidirectional acoustic system, with corresponding physical and neurological changes to their auditory system. I present how plastic and dynamic mating strategies in bushcrickets are with regard to investment patterns, the mating behaviour and the receiver (hearing) system.

Courtship songs in a new hybrid zone between *Chorthippus albomarginatus* and *Ch. karelini* (Acrididae: Gomphocerinae) in Russia

Vedenina, V and Shestakov, L

Institute for Information Transmission Problems, Russian Academy of Sciences, Moscow, Russia

E-mail: vvedenina@googlemail.com

Sibling species of the *Chorthippus albomarginatus* group are very similar in morphology and in calling songs, but they have different courtship songs. They are outstanding among all European grasshopper species since they have an extremely complex and elaborate courtship behaviour. The two species, *Ch. albomarginatus* and *Ch. oschei*, were previously shown to hybridize in a wide mosaic zone in the Ukraine and Moldova (Vedenina, Helversen, 2003; Vedenina, 2011). Recently, we found a new hybrid zone between *Ch. albomarginatus* and the third species of this group, *Ch. karelini*, in the territory of European Russia. On the basis of analysis of the courtship songs and stridulatory movements of the hind legs, we found individuals whose songs were intermediate between the *albomarginatus* and *karelini* type. Figure 1 shows a transition between A1 and C elements of the *albomarginatus* song and *karelini* song through intermediate variants. Similarly to the hybrid songs between *albomarginatus* and *oschei*, the songs recorded in the two new localities showed novel element combinations and increased among- and within variability. A distance between the two localities, where hybrid songs were recorded, were approximately 70 km. This indicates that the hybrid zone between *albomarginatus* and *karelini* could be relatively wide, similar to the zone between *albomarginatus* and *oschei*.

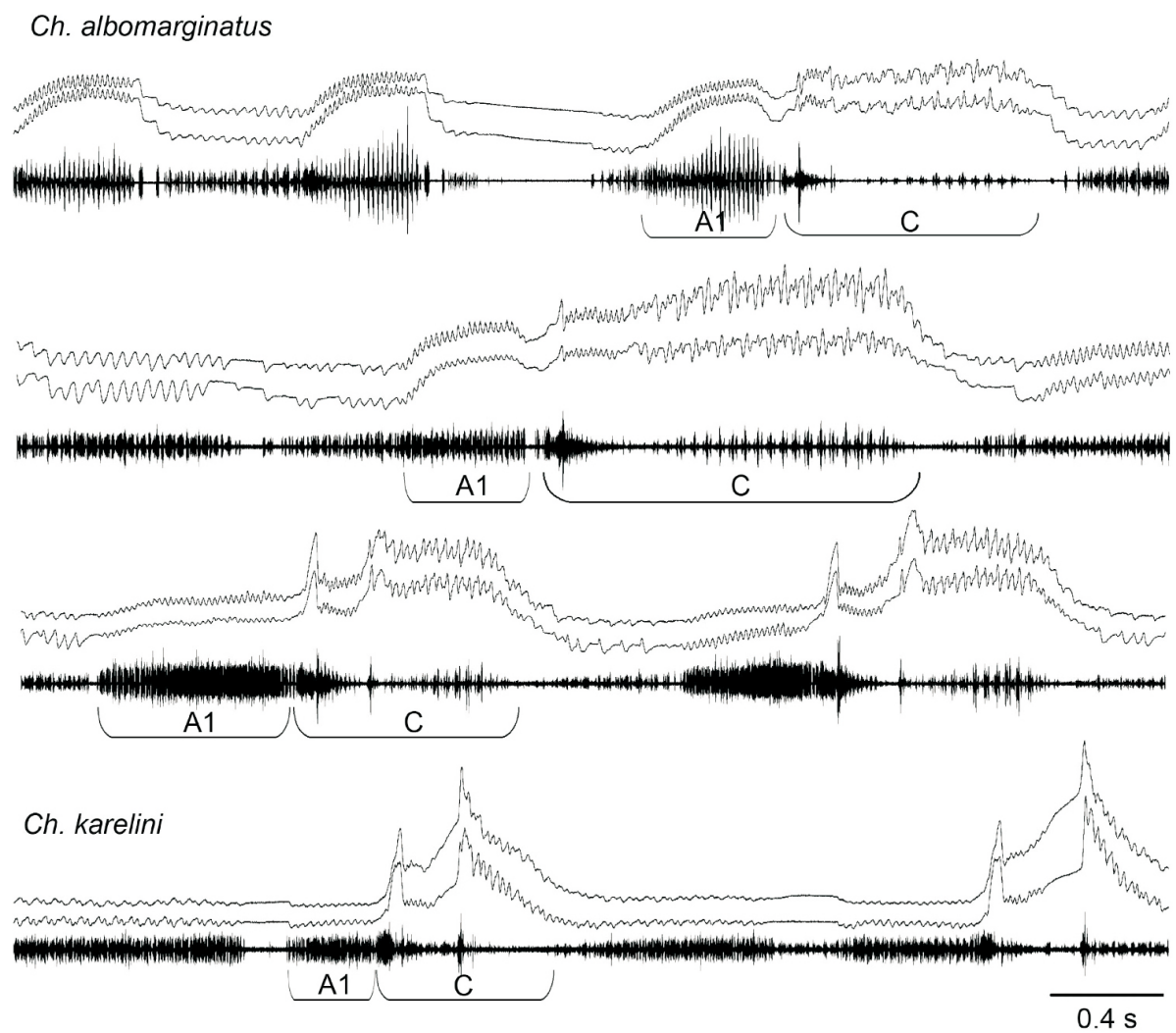


Figure 1, The songs of *Ch. albomarginatus* and *Ch. karelini* and of intermediates from the hybridization zone showing transitions in the A1 and C elements

Acoustic communication in Phaneropteridae – a global review with some new data

Heller, K-G¹; Hemp, C² and Ingrisch, S³

¹*Grillenstieg 18, 39120 Magdeburg, Germany;*

²*University of Würzburg, Germany;*

³*Zoological Research Museum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany*

Phaneropteridae is the largest (sub)family within the bush-crickets/katydids (Tettigonioidea), with a world-wide distribution. In its acoustic communication, it differs from all other tettigonioid groups: the females respond to the male song typically and primarily with their own acoustic signals. This type of responding was lost only in a few species with wingless females. In the present study we have examine if and how responding by sound may have influenced other aspects of the acoustic communication system.

According to our literature review, information about the song patterns of about 330 species of Phaneropteridae have been published world-wide. Included in this number are ca. 170 species of Barbitistini, a flight-less west palaeartic tribe, which are treated separately, but do not differ from the general pattern. Among other characters, the songs have been analysed concerning number of syllables and number of syllable and interval types. Much less data, however, are available concerning other aspects of sound communication like song intensity, mechanisms of sound production, acoustic behaviour of males and females and hearing. Stridulatory organs are described from a relatively large number of species, but often in combination with taxonomic studies without any connection to acoustics.

Compared to other tettigonioids, the songs of many phaneropterid species do not differ essentially in their sound pattern. However, on all continents there are some species with very (long and) complex songs, exceeding in these characters nearly all other Ensifera species – acoustical birds of paradise among Orthoptera. Their songs contain several different types of syllables and intervals of various duration. As examples we will present species of the genera *Horatosphaga* and *Monticolaria* from Africa, *Amblycorypha* from America, *Ducetia* and *Ectadia* from Asia and Australia, and *Acrometopa* and *Polysarcus* from Europe. For the production of these songs complicated neuro-muscular patterns are used, sometimes accompanied and supported by complex stridulatory files. So in a quantitative comparison, the range of phaneropterid songs, reaching from very simple to extremely complex, is by far more variable that in other tettigoniid families. Similarly, only few other tettigonioid species are outside the numbers of teeth on the stridulatory file given by phaneropterids: 10-14 in *Elimaea* to 350-380 in *Hemielimaea* species.

However, since there are so few data on the behaviour of most species and especially for females, we are still very limited in our understanding of the reasons behind the huge song variability. Of course, sexual selection by females responding preferentially to special song types could be an important evolutionary force, but probably only in combination with some unknown ecological and behavioural factors.

Effects of body temperature on intraspecific competitive ability

Su, A; Demkovich, Z; Majd, N; Hunter, P; Schratz, S; Mahnke, B; Grant, J and Whitman, DW
Illinois State University, Normal, IL, USA

Competition is integral to organismal behavior, ecology and evolution. Very little work has investigated body temperature as a dominant factor in deciding the outcome of competitive contests. We test the hypothesis that a warm body temperature improves intraspecific competitive ability in insects. In the laboratory, we pair warm (36°C) and cool (26°C) lubber grasshoppers, *Romalea microptera*, in contests for food and mates. Our results show a significant difference in favor of the warm grasshoppers, and that body temperature can be a strong factor in determining intraspecific competitive ability. We discuss the ramifications of this for ecology, behavior, evolution and competition research and theory.

Motivation Influences Intraspecific Competitive Ability in Grasshoppers

Gerstner, KF; Osterman, MJ; Mardoian, B; Hirt, KK; Wright, J; Gyetvan, M; Varecha, R; Lutgen, S; Privitt, J; Smith, N; Swartout, N and Whitman, DW

Illinois State University, USA.

E-mail: kfgerst@ilstu.edu

Virtually all organisms are influenced by competition, and researchers have identified numerous factors that allow individuals to win contests (e.g., size, age, health, strength, experience, etc.). Interestingly, few scientists have examined the role of motivation in competition. We tested the hypothesis that motivation influences competitive ability by pairing *Romalea microptera* grasshoppers that differed in motivation, in contests over food. We altered the motivation level in our animals by starving or desiccating them for different periods. We then allowed two individuals to compete over a small piece of food; the individual that ate the most food won the contest. Our results show that competitive ability is directly related to motivation level (i.e., hungry or thirsty individuals won more contests). During fights, contestants displayed numerous aggressive/defensive behaviors, including body rock, body jerk, leg rise, leg jerk, sparing, abdomen curl, wing flick, wing rise, and vertical posturing. For individuals, as the motivation levels increased, so did the number and intensity of aggressive behaviors. However, the number and intensity of aggressive behaviors was also influenced by the difference in motivation of the two contestants. Aggressive behaviors increased when both contestants were equally highly motivated, but decreased when contestants differed greatly in motivation, because the less-motivated individual typically retreated early. Hence, contest intensity increased when grasshoppers were evenly matched in motivation. Our results suggest that researchers studying animal competition should consider motivation.

A dual-role pheromone between sexes mediated by an odorant binding protein in locust

Guo, M^{1*}; Zhang LW^{1*}; Zhuo, FY¹; Xu, HZ¹; Zheng, N¹; Li, J¹ and Zhang, L^{1†}

¹Department of Entomology, China Agricultural University, Beijing 100193, China

*These authors contributed equally to this work.

†corresponding author: locust@cau.edu.cn

Locusts, which can aggregate into huge swarms and invade and destroy crops destructively, are an important agricultural pest¹. Their population explosions may be attributed to efficient reproduction behaviours, which are mediated and enhanced by potential sex pheromones. However, the molecular mechanisms underlying chemosensation to chemical cues for courtship in the oriental migratory locust, *Locusta migratoria manilensis*, remain unknown. Here we show a putative male-specific and dual-functional sex pheromone in young adult *L. migratoria* and elucidate an important component involved in primary signal transduction outside olfactory receptor neurons. 2-heptanone, which is only secreted by male locust, showed highly efficient binding capacity toward the locust odorant binding protein *LmigOBP4*. Electroantennogram (EAG) responses to this odorant revealed sexually significant differences between wild-type locusts and locusts injected with ds-RNA for *Lmigobp4*. Behaviourally, 2-heptanone induced different responses between sexes at certain levels, attracting females and repelling males. However, tendencies in the selection of this putative pheromone by both sexes were altered in locusts treated with an RNAi against *Lmigobp4*. We conclude that 2-heptanone has dual roles in young adult males and females. Additionally, *LmigOBP4* plays essential roles of regulating sensitivity in signal transduction downstream of this putative locust sex pheromone.

Gregarious vs. solitary Desert Locusts: variation in progeny size, number, and starvation physiology and resistance

Maeno, KO^{1,2*}; Piou, C¹; Babah, MAO² and Nakamura S³

¹*CIRAD, UPR Bioagresseurs analyse et maîtrise du risque, F-34398 Montpellier, France;*

²*The Mauritanian Desert Locust Centre: Centre National de Lutte Antiacridienne (CNLA), Nouakchott, Bp: 665, Mauritania;*

³*Japan International Research Center for Agricultural Sciences (JIRCAS), Ohwashi 1-1, Tsukuba, Ibaraki, 305-8686, Japan*

Female desert locusts, *Schistocerca gregaria*, epigenetically modify their progeny quality and quantity in response to crowding. Gregarious (crowd-reared) adult females produce larger but fewer progeny than do solitarious (isolated-reared) females. Hatchlings from gregarious females also show better survival. The reasons for these differences are unclear. This study investigated 1) the effects of rearing density on the variation in egg size within single egg pods; 2) the starvation tolerance of hatchlings from mothers with different phases and 3) physiological differences in hatchling energy reserves. Our results confirmed that isolated-reared females produce smaller but more eggs than crowd-reared females, and that the variation in egg size within single egg pods was greater for crowd-reared females than for isolated females. A trade-off (negative relationship) between egg size and number of eggs per individual egg pod was observed for both crowded and isolated groups. When starved, gregarious hatchlings (from crowd-reared females) survived significantly longer than solitarious ones (from isolated-reared females). For solitarious hatchlings, survival time was longer as hatchling body size increased, but for gregarious hatchlings, relatively small individuals survived as long as larger hatchlings. The percentage of water content per fresh body weight was almost equal between the two phases, both before and after starvation. In contrast, the percentage of lipid content per dry body weight was significantly higher in gregarious hatchlings than in solitarious ones before starvation, but became almost equal after starvation. These results demonstrated that crowded female adults not only trade-off to modify their progeny size and quantity, and also increase variability in progeny size and variability in energy reserves of these progeny. We hypothesize that gregarious females enhance their fitness by producing progeny differently adapted to high environmental variability and particularly to starvation conditions.

How do crickets detect opponents?

Hiraguchi, T¹; Kurabayashi, D² and Yamaguchi, T¹

¹*Kawasaki College of Allied Health Professions*

²*Department of Mechanical and Control Engineering, Tokyo Institute of Technology*

Crickets usually probe forward when they walk or flight. However, antecedent to the initial stage of aggressive encounter, they probe the opponent standing in front of them with an antenna quickly and then unsheathe. What is the special cue to switch the antennal motor patterns in the antecedent part to their adaptive behavioral choice?

In this study, we would like to find the special cues switch the searching behavioral patterns. We focused on antennal moving and legs as the vibration detectors, and investigated the occurrence of searching behaviors.

We used field crickets *Gryllus bimaculatus* that often shows cricket fight (**PinYin**) in this study. To analyze the antennal movement, we recorded their behavior with high-speed video camera (View Plus, Tokyo) and fed data into PC system. The frame rate was 100 fps. This rate was sufficiently to observe rapid antennal movements. We extracted antennal position data of each frame from sequences. We also used some kinds of metal plate and plastic plate as the floor in the recording chamber to investigate the floor vibration effects. We measured the solidity of each material by the durometer.

Almost of crickets used their antennae alternately in searching. Before starting antennal fencing or caress, they once changed searching pattern to "one antenna searching" rapidly. Changing of floor material in experimental chamber affects timing of behavioral choice. On the soft material, cricket could not detect opponent sufficiently. Because Animals always stand in lying position, mechanosensory systems on the ventral side include their legs always detect the vibration from the ground. This means some changes in surround could be transmitted from floor material to the body by legs in the case of cricket.

Almost individuals could not notice the opponent easily without ground vibration. Thus vibration must be the indispensable important cues to control their motor patterns in territorial behavior. In the expression of territorial claims action involving the struggle, especially, it was considered that the initial stage was quite important to decide following behavior. And the other mechanosensory information to change their behavior should be also considered for the following reasons.

To toggle antennal movement patterns, information from the sensory organs in limb or on the surface of ventral side detected ground vibration, when animals encountered at close range. For territory maintenance behavior, cricket could detect others by floor that directly contacted on their body. From very short latency, Vibration of the floor would be powerful information to change antennal movement with the highest priority.

Thus, is thought to induce the movement of body parts, varying animal excitement level mechanical sensory information. Vibration caused by movement of the animal body, that phenomenon happens, regardless of biological, non-biological environment. Cricket mechanosensory systems suitably developed to accept and distinguish the biological vibration from other. Therefore, this cricket behavior would be considered as one of the suitable biological model that turn on and off or switch the simple equipment in machinery and process an inexpensive task switching system.

Communication & Physiology

Biomechanics of hearing and singing in Ensifera: an evolutionary view**Montealegre-Z, F¹**; Gu, JJ²; Robert, D³ and Ren, D⁴¹*University of Lincoln, School of Life Sciences, LN2 2LG, United Kingdom;*²*College of Biological Science and Engineering, North University of Nationalities, 204 Wenchangbeijie, Xixia District, Yinchuan 750021;*³ *School of Biological Sciences, University of Bristol, BS8 1UG;*⁴*College of Life Sciences, Capital Normal University, 105 Xisanhuanbeilu, Haidian District, Beijing 100048, China*

Acoustic communication in animals involves the evolution singing and hearing organs. In insects, two fundamental forms of hearing organs exist: tympanal and flagellar ears. Tympanal ears of insects in general are superficially similar to those of vertebrates. In insects, as they evolved at least 17 times independently, tympanal ears display a vast diversity of forms and functions. This diversity provides valuable material to investigate alternative mechanisms, using microscale architectures and biophysical solutions to common problems of acoustic detection. Tympanal ears are used for the long-range detection of the pressure component of the propagating sound field. Katydid (Insecta: Orthoptera: Tettigoniidae) are considered to be amongst the first animals to have evolved acoustic communication. Today, the sounds they use extend well beyond the human audio range, but their ancestors communicated in the audio range. Singing organs have usually evolved in males and consist of a stridulatory apparatus located in their forewings. One wing bears a file that is rubbed against a scraper in the opposite wing. Across living species, the range of sound frequencies is wide, spanning 1 kHz to ca. 150 kHz³. Both males and females have evolved ears that are used in the contexts of both social communication and predator detection. Their hearing organs are very small and consist of tympanal membranes that typically span one millimeter or less, and are located in the fore legs. Yet, despite small physical dimensions, these ears carry out the elementary tasks of acoustic detection usually attributed to vertebrate ears. In here we will present recent results of our research group on sound production organs and ear biomechanics in extinct and extant katydid species. Modern katydids exhibit an asymmetric stridulatory apparatus and two forms of sound production, resonant (pure tone) and non-resonant (broadband). Our data suggests that modern katydids evolved from ancestors that used a symmetric sound generator and pure tones at low frequencies (ca 6 kHz). In the hearing mechanism in katydids the biophysical solutions are functionally similar to those of the sophisticated mammalian ears (sound detection, impedance conversion and auditory frequency analysis), yet involve very different morphological specializations, constituting a remarkable case of convergent evolution. Enticingly, these results suggest the possibility that sound communication and sensory perception in these insects are more refined than previously surmised. We propose some hypotheses to explain how such sophisticated microscale hearing organs evolved using extant and extinct species.

The acoustic world of a rain forest dusk chorus

Jain, M; Diwakar, S; Bahuleyan, J; Deb, R and **Balakrishnan, R**

Indian Institute of Science, Bangalore, India

A rain forest dusk chorus typically consists of a large number of individuals of acoustically signaling species calling at the same time. The resultant perception to human ears is a loud cacophony of sound. The signaling individuals however are obviously successful in overcoming the problems of acoustic masking interference posed by this soundscape. Using a combination of analysis of signal structure, intensity and transmission on the one hand, and of signaling behaviour, including call timing and calling site location on the other, we have attempted to reconstruct the auditory landscape of the nocturnal rain forest in a spatially explicit three-dimensional simulation model. We then use this model to probe the role of signal intensity and receiver tuning as strategies to minimize masking interference by different species in the chorus. We also use this model to obtain estimates of acoustic masking taking into account the axes of time, space, signal intensity and receiver tuning.

Insect acoustic communication under noise: Lessons from the tropical rainforest.

Römer, H

Karl-Franzens University, Zoology, A-8010 Graz, Austria

Insects often communicate by sound in mixed species choruses; like humans and many vertebrates in crowded social environments they thus have to solve cocktail-party-like problems in order to ensure successful communication with conspecifics. This is even more a problem in species-rich environments like tropical rainforests, where background noise levels of up to 60 dB SPL have been measured. In this environment, the calling activity of crickets constitutes the main audio frequency band between about 2 to 9 kHz. Calling song carrier frequencies of sympatric species sometimes do not differ by more than 200 Hz. Current models of peripheral and central nervous processing in crickets cannot explain how signal detection, discrimination and localization is achieved under these masking noise conditions. Here I present data how adaptations in frequency tuning and mechanisms of spatial release from masking may facilitate communication under these conditions.

Using neurophysiological methods we investigated the effect of natural background noise (masker) on signal detection thresholds in two tropical cricket species *Paroecanthus podagrosus* and *Diatrypa* sp., both in the laboratory and outdoors. We identified three 'bottom-up' mechanisms which contribute to an excellent neuronal representation of conspecific signals despite the masking background. First, the sharply tuned frequency selectivity of the receiver reduces the amount of masking energy around the species-specific calling song frequency. We studied the frequency tuning of an auditory neuron mediating phonotaxis in the rainforest cricket *Paroecanthus podagrosus* suffering from strong competition, in comparison with the same, homologous neuron in European field crickets where such competition does not exist. As predicted, the rainforest species exhibits a more selective tuning compared to the European counterparts. The filter reduced background nocturnal noise levels by 26 dB, compared to only 16 and 10 dB in the two European species. We also quantified the performance of the sensory filter under the different filter regimes, by examining the representation of the species-specific amplitude modulation of the male calling song, when embedded in background noise. Again, the filter of the rainforest cricket performed significantly better in representing this important signal parameter. The neuronal representation of the calling song pattern within receivers is maintained for a wide range of signal-to-noise ratios, due to the more sharply tuned sensory system and selective attention mechanisms.

Laboratory experiments yielded a masked threshold at an average signal-to-noise ratio (SNR) of -8 dB, when masker and signal were broadcast from the same side. Displacing the masker by 180° from the signal improved SNRs by further 6 to 9 dB, a phenomenon known as spatial release from masking. Surprisingly, experiments carried out directly in the nocturnal rainforest yielded SNRs of about -23 dB compared with those in the laboratory with the same masker, where SNRs reached only -14.5 and -16 dB in both species. Finally, a neuronal gain control mechanism enhances the contrast between the responses to signals and the masker, by inhibition of neuronal activity in inter-stimulus intervals.

Thus, conventional speaker playbacks in the lab apparently do not properly reconstruct the masking

noise situation in a spatially realistic manner, since under real world conditions multiple sound sources are spatially distributed in space. Our results also indicate that without knowledge of the receiver properties and the spatial release mechanisms the detrimental effect of noise may be strongly overestimated.

Anatomy of the phasmid digestive tract and the function of the midgut appendices

Shelomi, M

University of California, Davis, USA

The digestive tracts of the Phasmatodea are unique among the insects. The most striking differences are in the midgut, which contains a heavily pleated anterior section and a posterior section with several rows of long, hollow tubules originating from pyriform projections. The roles of these tubes and ampules, referred to as the appendices of the midgut, are unknown. They were hypothesized to be modified Malpighian tubules and to thus function in excretion, but this function has never been demonstrated in the lab, and it would be redundant given that phasmids have normal Malpighian tubules as well as these appendices. The extent of these appendices' presence in the Phasmatodea is also unknown. This paper represents efforts to understand all aspects of the Phasmid digestive tract, with a goal towards determining what the appendices actually do.

Specimens were obtained from live cultures of several species from various phasmid clades (Diapheromeridae: Necroschiinae; Heteropterygidae: Obriminae; Phasmatidae: Cladomorphinae, Clitumninae, Eurycanthinae, Extatosomatinae; Phylliidae: Phylliinae; Pseudophasmatidae: Pseudophasmatinae). For stereomicroscopy, phasmids were vitally stained with over fifty different histological stains for periods of time ranging from thirty minutes to two weeks. Anatomical drawings of the phasmid digestive tract were produced and compared to the known phasmid phylogeny. For light microscopy, excised phasmid guts were fixed in Bouin's solution, dehydrated, embedded in paraffin, sectioned, and stained in several solutions. Tissue was also preserved in Karnovsky's solution and sent for scanning electron microscopy.

Phasmids all have similar digestive tracts following a basic plan unique to that order, but they show remarkable differences in the number of midgut appendices across their phylogeny: basal phasmids have as few as two appendices total. The ampules of the appendices open into the midgut, but are blocked by the peritrophic membrane. Microscopy suggests the appendices are not regenerative crypts. The tubules are hollow and end blindly near the hindgut. The appendices do not function like Malpighian tubules, and pick up very few dyes other than a few cationic dyes, which are retained by the ampule wall for long lengths of time. They thus are unlikely to have an excretory role. Dye absorption is based on active transport, and the ampules and tubules are highly tracheated.

The purpose of the ampules is likely sequestration and storage, with modifications on this theme across the diversity of the phasmids. Items being stored include toxins and/or microbes, the latter of which may also serve a role in nutritional storage. This paper demonstrates just how little we know about even highly studied systems. The laboratory stick insect, *Carausius morosus*, has long been a model organism and will soon have its full genome sequenced. To better make use of such data, a complete understanding of its basic biology is needed. This research helps solve one of the biggest mysteries in phasmid physiology, but more work is needed determining exactly how these appendices function and how they evolved.

Impact of Antennectomy on the Growth Performance and Gut Enzymes Activities of variegated Grasshopper *Zonocerus variegatus* (L) (Orthoptera: Pyrgomophidae)

Ademolu, KO and **Idowu, AB**

Biological Sciences Department, Federal University of Agriculture, Abeokuta, Nigeria

E-mail: kennyademolu@yahoo.com

The attraction of most insects to food is by olfaction through the aid of antennae. The effect of antennectomy on the growth performance and gut enzymes activities of *Zonocerus variegatus* was examined in this study. Antennectomy significantly affected the food intake and the weight gained by the insects as those without antennae consumed less food and recorded less weight gain compared to those with intact antennae. Amylase, glucosidase, lipase and cellulase activities were detected in the insects though in varying levels. Insects with intact antennae recorded significantly higher gut enzyme activity than antennectomised insects. Amylase activity was significantly higher than activity of other enzymes suggesting its importance in diets.

Bioinsecticidal effects of a crude extract of *Haplophyllum tuberculatum* (Rutaceae) and teflubenzuron on *Locusta migratoria* (Orthoptera: Oedipodinae) reproduction

Acheuk, F¹; Cusson, M²; Abdellaoui, K³; Bendifellah, L¹ and Doumandji-Mitiche, B⁴

¹*Département de Biologie, Faculté des Sciences, Université M'hamed Bougara, Avenue de l'indépendance, 35000 Boumerdes, Algeria;*

²*Centre de Foresterie des Laurentides, Service canadien des forêts, Ressources naturelles Canada, 1055 rue du PEPS, Québec, Québec G1V 4C7, Canada;*

³*Département des Sciences Biologiques et de la Protection des Végétaux, Institut Supérieur Agronomique de Chott-Mariem, 4042, Université de Sousse, Tunisia;*

⁴*Département de Zoologie Agricole et Forestière, Ecole Nationale Supérieure d'Agronomie, 16200 El-Harrach, Alger, Algeria*

The bioinsecticidal effects of a methanolic extract of the plant *Haplophyllum tuberculatum* (ME-Ht) and of teflubenzuron (TFB) were compared on several reproductive variables in females of *Locusta migratoria*. The test products were administered orally to newly emerged females at doses of 1500 (ME-Ht) and 10 µg/female (TFB). The methanolic extract and TFB had comparable effects on several of the variables examined. Both significantly delayed the first oviposition and reduced fecundity and fertility. ME-Ht and TFB also displayed similar effects on ovarian growth, vitellogenesis and ecdysteroid titers. Both treatments induced a drop in hemolymph protein levels as well as a reduction in vitellogenin uptake by the oocytes. This delay in oogenesis was accompanied by a resorption of terminal oocytes. However, whereas TFB completely blocked egg hatch, ME-Ht only had a modest inhibitory effect on this variable. Hemolymph and ovarian ecdysteroid titers, as measured by radioimmunoassay, were similar and low in both control and treated females, except for a peak observed only in control females at the end of vitellogenesis. We discuss the functional significance of the observed effects in the context of the putative modes of action of the methanolic plant extract and TFB.

Supercooling capacity and cold hardiness of the eggs of the band-winged grasshopper, *Oedaleus asiaticus* (Orthoptera: Acrididae)

Pang, BP; Li, N and Zhou, XR

College of Agriculture, Inner Mongolia Agricultural University, Hohhot 010019, China

The band-winged grasshopper, *Oedaleus asiaticus* Bei-Bienko, is one of the most dominant and economically important grasshopper species in the steppe grasslands and farming-pastoral ecotone in northern China and often requires chemical control during outbreaks. This species prefers overgrazed steppes and xerophytous habitats, and therefore, it has been suggested as an indicator species for steppe deterioration in the typical steppe zone in Inner Mongolia. Many strategies have been developed by insects to survive adverse environmental conditions. Cold hardiness is a common strategy of insects to survive cold winters and it is affected by many environmental factors like food, temperature and humidity. Cold hardiness is defined as the capacity of a species to survive long or short-term exposure to low temperature. This species is univoltine and overwinters as eggs in soil. Therefore, the cold hardiness of its eggs was examined in the laboratory.

Water content in soil significantly affected the super cooling point (SCP), water content and fat content of pre-diapause eggs (Table 1). With the increase of water content in soil, the SCP and water content of pre-diapause eggs rose whereas the fat content declined. The SCP in soil at a water content of 4% was significantly lower than when water content was 10% or 13%. The water content of eggs in soil at 4% was significantly lower in soil with 4% water but the fat content was higher. Correlation analysis showed that there was a significant relationship between the SCP and water content ($R^2=0.9821$, $P=0.0090$, $F=109.49$) or fat content of pre-diapause eggs ($R^2=0.9786$, $P=0.0108$, $F=91.31$).

Most eggs had low SCPs throughout their development, but in the first 30 days (when eggs were still in the pre-diapause stage) a few eggs had much higher SCPs (Table 2). By 60 days after oviposition, when eggs had reached the diapause stage, eggs had lower SCPs (Table 2). There was only one low SCP group in eggs after 60 days of oviposition. The developmental stages affected significantly the SCP, water content and fat content of eggs (SCP: $F_{(5,173)}=9.43$, $P=0.0001$; water content: $F_{(5,173)}=48.55$, $P<0.0001$; fat content: $F_{(5,12)}=67.51$, $P<0.0001$). As embryonic development progressed, the SCP and water content of eggs declined as the fat content increased (Table 3). Correlation analysis showed that there was a significant relationship between the SCP and fat content of eggs ($R^2=0.8728$, $P=0.0063$, $F=27.44$). Although there was a tendency for the SCP to decline with decreasing water content in eggs, there was no significant relationship between them at $P=0.05$ ($R^2=0.6216$, $P=0.0624$, $F=6.57$). The survival rates of diapause eggs were significantly different among different temperature treatments ($F_{(5,24)}=549.08$, $P<0.0001$). The survival rate of eggs kept at $>-20^\circ\text{C}$ was $>88\%$ but survival declined significantly to 56.77% at -25°C , and dropped to zero at -30°C . The sigmoid increase in survival rate with increasing exposure temperature was well described by the Weibull function: $P=1-\exp(-((t+33.00)/8.93)^{2.51})$ (t : temperature; $F=132.25$, $P=0.0012$, $R^2=0.9888$). For diapause eggs exposed to low temperature for 12 h, the lethal temperatures for 10%, 50% and 90% mortality were estimated to be -29.4°C , -25.3°C and -20.6°C , respectively, and the lowest temperature for survival of any diapause

eggs was about -30°C .

For diapause eggs kept at -20°C , survival rates decreased slowly with increasing duration of exposure. The survival rates of diapause eggs were significantly different among different time treatments ($F_{(6,21)}=13.19$, $P<0.0001$). There was no significant difference between exposure for 0 d and 0.5 d, but the survival rates declined after 1 d exposure. The Probit function was used to describe the relationship between survival rates and duration of exposure to low temperature. The function was $\ln(p/(1-p))= 2.2491-0.0685t$ (t: time; $F=38.754$, $P<0.0001$, $R^2=0.5985$). The LT_{10} , LT_{50} , and LT_{90} values for diapause eggs kept at -20°C were estimated to be 0.8 d, 32.8 d and 64.9 d respectively. As the mean SCPs of diapause eggs were similar to the temperature that led to 50% mortality after 12 h exposure, the SCP of eggs can be considered as a good indicator of cold hardiness for *O. asiaticus* and this grasshopper is a freeze-intolerant insect.

Table 1, super cooling point, water content and fat content of pre-diapause eggs in soil with different water content

| Water content of soil (%) | SCP ($^{\circ}\text{C}$) | Water content of egg (%) | Fat content of egg (%) |
|---------------------------|----------------------------|--------------------------|-------------------------|
| 4 | $-22.50\pm 0.31\text{b}$ | $55.22\pm 0.72\text{b}$ | $10.87\pm 0.44\text{a}$ |
| 7 | $-20.13\pm 0.93\text{ab}$ | $66.46\pm 1.16\text{a}$ | $9.55\pm 0.37\text{b}$ |
| 10 | $-19.58\pm 0.96\text{a}$ | $67.83\pm 0.60\text{a}$ | $9.08\pm 0.19\text{b}$ |
| 13 | $-19.61\pm 0.73\text{a}$ | $69.81\pm 1.94\text{a}$ | $8.91\pm 0.14\text{b}$ |

Means in the column followed by the same letters are not significantly different ($P> 0.05$, LSD).

Table 2, super cooling point of eggs in different developmental stages

| Days after oviposition | N | High SCP group | | | Low SCP group | | |
|------------------------|----|-----------------------------|------------------------------|----------------|-----------------------------|------------------------------|----------------|
| | | Mean ($^{\circ}\text{C}$) | Range ($^{\circ}\text{C}$) | Percentage (%) | Mean ($^{\circ}\text{C}$) | Range ($^{\circ}\text{C}$) | Percentage (%) |
| 1 | 42 | $-11.0\pm 1.35\text{a}$ | -8.3~-13.9 | 9.52 | $-21.9\pm 0.40\text{a}$ | -19.7~-23.6 | 90.48 |
| 15 | 23 | $-11.1\pm 3.50\text{a}$ | -7.6~-14.6 | 8.70 | $-21.9\pm 0.22\text{a}$ | -17.2~-24.2 | 91.30 |
| 30 | 45 | $-11.9\pm 1.40\text{a}$ | -9.2~-13.9 | 6.67 | $-21.8\pm 0.20\text{a}$ | -19.7~-23.6 | 93.33 |
| 60 | 23 | - | - | - | $-23.2\pm 0.46\text{ab}$ | -19.6~-27.2 | 100 |
| 90 | 23 | - | - | - | $-23.5\pm 0.47\text{bc}$ | -19.2~-27.1 | 100 |
| 120 | 23 | - | - | - | $-24.9\pm 0.50\text{c}$ | -19.2~-28.4 | 100 |

Means in the column followed by the same letters are not significantly different ($P> 0.05$, LSD).

Table 3, super cooling point, water content and fat content of eggs in different developmental stages

| Days after oviposition | SCP (°C) | Water content (%) | Fat content (%) |
|------------------------|--------------|-------------------|-----------------|
| 1 | -20.75±0.53a | 68.02±0.76a | 9.79±0.41d |
| 15 | -20.99±0.78a | 60.11±1.23b | 10.09±0.15cd |
| 30 | -21.11±0.40a | 51.42±1.47c | 10.69±0.11c |
| 60 | -23.23±0.50b | 50.19±1.46cd | 12.19±0.18b |
| 90 | -23.47±0.47b | 48.16±0.88d | 13.97±0.08a |
| 120 | -24.86±0.51b | 47.24±1.02d | 13.60±0.11a |

Means in the column followed by the same letters are not significantly different ($P > 0.05$, LSD).

Aspects of the ecological physiology of the Australian plague locust, *Chortoicetes terminifera***Woodman, JD***Australian Plague Locust Commission, Australian Government Department of Agriculture, Fisheries and Forestry, Canberra, Australia*

The Australian plague locust, *Chortoicetes terminifera*, occupies the grasslands, deserts and agricultural areas of the mainland interior of Australia and is therefore exposed to extremes in temperature, rainfall and humidity. An ongoing eco-physiological research program is seeking to quantify environmental tolerances that are critical to survival and development. Cold tolerance research on first-instar nymphs has shown supercooling points ranging from -9.3 to -14.6°C , with pre-freezing mortality dependent on feeding and rate of cooling. Heat tolerance research on first-instar nymphs has shown a critical upper limit of $53.3 \pm 1.0^{\circ}\text{C}$ with death preceded by changes in behaviour, gas exchange, water loss and excretion. Heat mortality at temperatures below the critical limit was dependent on food availability. Research on the effects of flooding has shown that egg viability after inundation is strongly dependent on temperature, flood duration and embryonic development stage at the time of flooding. When immersed in water, nymphs entered a coma-like state within two minutes, but survived for a substantial period thereafter: the time to 50% mortality (LT_{50}) ranged from 8.12 ± 0.26 h at 15°C to 4.93 ± 0.30 h at 25°C . Collectively, this research is improving our understanding of the population dynamics of the species, which is essential to successful population monitoring, forecasting and management.

Acceleration of Red List assessment and acoustic profiling for Orthoptera conservation

Riede, K

Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany

Among the major challenges for insect Red List assessment and conservation is insufficient knowledge of species and the considerable cost for close monitoring of Orthoptera at intervals required for Red List assessments. About one third of (tropical) species still have to be described, and many Orthoptera are only known from singletons, i.e. not even the other sex is known. This is in stark contrast to the high data quality standards required for Red List assessments. Acoustic monitoring is particularly useful for assessments targeting selected singing species, rapid diversity assessments of entire communities, and species discovery. However, results from researchers undertaking acoustic surveys in Greece, Ecuador as well as from other authors, illustrate that considerable input from computational bioacoustics and sound databases are needed to develop the method's full potential. At present, acoustic profiling works well for certain species within well-defined geographical limits, such as endemic species ranges or protected areas. In addition, it has to be embedded within a strategic framework for efficient Orthoptera Red List assessment, including: 1) Data mining for endangered habitats and host plants associated with Orthoptera), and 2) Data mining of national Red Lists (<http://www.nationalredlist.org>), with a special focus on endemics. A first analysis of South American and European fauna showed that coverage by European national Red Lists is quite complete, while threat analysis in South America is still in its infancy, requiring identification of endangered habitats and food plants as a surrogate. As a first result, a list of endangered species with highly specific songs has been identified for targeted acoustic profiling. Finally, these insights have to be converted into a conservation strategy. Here I suggest integrating Orthoptera critical habitats into the Alliance for Zero Extinction critical site network (<http://www.zeroextinction.org/>), using acoustic profiling as a tool for monitoring selected species.

Acoustic communication in Phaneropteridae – a global review with some new data

Heller, K-G¹; Hemp, C² and Ingrisch, S³

¹*Grillenstieg 18, 39120 Magdeburg, Germany;*

²*University of Würzburg, Germany;*

³*Zoological Research Museum A, Koenig, Adenauerallee 160, 53113 Bonn, Germany*

Phaneropteridae is the largest (sub)family within the bush-crickets/katydids (Tettigoniodea), with a world-wide distribution. In its acoustic communication, it differs from all other tettigonioid groups: the females respond to the male song typically and primarily with own acoustic signals. This type of responding was lost only in a few species with wingless females. In the present study we have examine if and how responding by sound may have influenced other aspects of the acoustic communication system.

According to our literature review, information about the song patterns of about 330 species of Phaneropteridae have been published world-wide. Included in this number are ca. 170 species of Barbitistini, a flight-less west palaeartic tribe, which are treated separately, but do not differ from the general pattern. Among other characters, the songs have been analysed concerning number of syllables and number of syllable and interval types. Much less data, however, are available concerning other aspects of sound communication like song intensity, mechanisms of sound production, acoustic behaviour of males and females and hearing. Stridulatory organs are described from a relatively large number of species, but often in combination with taxonomic studies without any connection to acoustics.

Compared to other tettigonioids, the songs of many phaneropterid species do not differ essentially in sound pattern. However, on all continents some species with very (long and) complex songs are found, exceeding in these characters nearly all other Ensifera species – acoustical birds of paradise among Orthoptera. Their songs contain several different types of syllables and intervals of various duration. As examples we will present species of the genera *Horatosphaga* and *Monticolaria* from Africa, *Amblycorypha* from America, *Ducetia* and *Ectadia* from Asia and Australia, and *Acrometopa* and *Polysarcus* from Europe. For the production of these songs complicated neuro-muscular patterns are used, sometimes accompanied and supported by complex stridulatory files. So in a quantitative comparison, the range of phaneropterid songs, reaching from very simple to extremely complex, is by far more variable that in other tettigoniid families. Similarly, only few other tettigonioid species are outside the numbers of teeth on the stridulatory file given by phaneropterids: 10-14 in *Elimaea* to 350-380 in *Hemielimaea* species.

However, since there are so few data of the behaviour of most species and especially for females, we are still very limited in our understanding of the reasons behind the huge song variability. Of course, sexual selection by females responding preferentially to special song types could be an important evolutionary force, but probably only in combination with some unknown ecological and behavioural factors.

Tympanotriba vittata*, a katydid with strange stridulatory adaptations*Braun, H¹**; Morris, GK² and Wirkner, CS³¹*División Entomología, Museo de La Plata, Argentina;*²*Department of Ecology & Evolutionary Biology, University of Toronto at Mississauga, Canada;*³*Institut für Biowissenschaften, Universität Rostock, Germany*

A flightless tiny conocephaloid katydid, *Tympanotriba vittata*, stridulates with unique air compartments enclosed by extraordinarily developed wings of the males. Females are apterous. First described in 1971 from southeastern Brazil, the species has gone unrecorded in the literature ever since. Recently we found it to be common in Iguazú National Park, Argentina, where it sings from herbaceous vegetation at high densities, males calling day and night, often in chorus. They use nonresonant tegmino-tegmina stridulation to produce an exceptionally broad-band continuous frequency spectrum from 20 to 60 kHz. Each call lasts about 150 ms and consists of four time-domain elements, the third and fourth differing in spectrum. More limited sound energy is also produced in the audio range, making its song readily apparent to the human ear. Calls are repeated continuously. The air mass loading the sound-radiating speculum is bounded laterally by a series of semitransparent tall costal wing cells, possibly serving as secondary sound radiators, but certainly enhancing the subalar volume; a markedly flattened dorsum of the abdomen contributes to this subalar space. The metathoracic wings are substantial and fleshy and extend almost the length of the overlying mesothoracic tegmina; they lie apposed in the midline making a wall between the space beneath the engaged file and scraper and enclosing the large compartment below with a strangely shaped posterior opening. For a dozen specimens at 10-cm distances the sound field was explored: dorsal, left and right lateral, frontal and rear sound levels were obtained; experiments in loading of wing regions with wax were conducted. No costal enhancement of lateral sound levels was apparent. Its broad-band spectrum may be an adaptation for the distance-ranging within the cluttered understory vegetation of patchily distributed forest clearings.

Grasshopper & Locust Control

Locust biological control: why it has been used in certain areas but not in others**Babah Ebbe, MAO¹** and Hunter, DM²¹*Centre National de lutte antiacridienne, BP:655, Tinnessoueilem, Nouakchott, Mauritania;**E-mail: maoudbabah@yahoo.fr*²*Locust and Grasshopper Control, 125 William Webb Drive, McKellar, ACT 2617, Australia*

Metarhizium acridum (Driver & Milner) J.F. Bisch., Rehner & Humber (Hypocreales: Clavicipitaceae), is a pathogen which, has been developed over the last years for the control of locusts and grasshoppers. It is regarded as being of low risk to humans and livestock, while having few effects on non-target organisms; despite that, its use against the Desert locust in Africa is still almost insignificant while it has been largely and regularly used in Australia for more than 10 years as part of locust management by the Australian Plague Locust Commission. During seasons with locusts, applications of *Metarhizium* range from 10,000-25,000 ha per year in Australia, which is 5-15% of the total area sprayed. It has also been used against the Red locust in Tanzania, the grasshopper in Senegal and its use was also recently extended to China. Therefore, the legitimate question here is why it is not used against the Desert locust? Some tentative ideas on the reasons include several technical difficulties such as the high temperatures common in Desert locust areas, which make storage and transport difficult and can reduce the effectiveness of the fungus after application. In addition it has a higher price compared to synthetic chemical insecticides, and its slower action means it is difficult to use for ground applications against individual bands because treated bands can march and mix with those that are untreated. Often it has only been used against hopper bands, which is another limitation. However, all of these technical problems have been overcome elsewhere: for instance *Metarhizium* has been used during summer in Australian deserts where temperatures are commonly above 40° C and it has been successfully used against Red locust adults in Tanzania. Therefore it would seem that, despite some significant efforts made by FAO and its regional commissions (CLCPRO...etc.), IFAD and other international donors, there are other non-biological reasons that are behind this slow use against the desert locust in Africa (e.g. conservative mind set, political reasons, logistics and inadequate finances ...etc.) and these aspects will be discussed. This presentation will present in detail the various comparative aspects of the problem and discuss a range of potential solutions.

A question of timing - An examination of Australian locust control strategies**Adriaansen,C***Australian Plague Locust Commission, Canberra, Australia*

The Australian Plague Locust Commission (APLC) has operated as a national organisation focussed on the monitoring and management of pest locust species in Australia for almost 40 years, with financial support from the governments of the four affected State jurisdictions and the Australian Government.

The approach taken by APLC to locust monitoring and management is examined to assess its fit with preventive locust control concepts, and how the drivers of and limitations to control response affect APLC's ability to consistently adopt a preventive strategy. Levels of infestation and treatment during the years of APLC's existence show varying degrees of congruence and are reviewed to demonstrate the level of success in applying a preventive strategy in Australia.

The practices and techniques utilised by APLC, along with the background against which APLC operates, are discussed to determine their applicability to other large, multi-jurisdictional locust management programs.

Locust and grasshopper control worldwide: an introduction. Grasshopper control: a North American perspective.**Latchininsky, AV***University of Wyoming, Laramie, WY, USA*

Locusts and grasshoppers (Orthoptera: Caelifera, Acridoidea) are an essential component of temperate and tropical grassland ecosystems worldwide. They stimulate plant growth, participate in nutrient cycling, and play important role in food chains (Latchininsky et al., 2011). On the other hand, under certain conditions, they can produce devastating plagues and become a major threat to crop and forage production and global food security. Locust and grasshopper outbreaks have occurred on all continents except Antarctica affecting the livelihoods of ten percent of world's population. During outbreaks a tremendous effort is applied to control these pests. Current management strategies are essentially curative, consisting of large-scale applications of broad-spectrum insecticides to pest infestations (Symmons, 2009). In 2003–2005, eight million people suffered from 80 to 100% crop losses inflicted by the Desert locust *Schistocerca gregaria* (Forskål) swarms. To combat the locusts, 13 million hectares in 26 countries on three continents were treated with broad-spectrum neurotoxins (Brader et al., 2006). Such transcontinental operations, including the food aid for affected population, cost over half a billion US dollars to the world community (Belayneh, 2005). In the recent years, the importance of locust and grasshopper pests appears to have grown due to climate change, which expands their distribution ranges and accelerates their population dynamics.

Since many locusts and grasshoppers inhabit desert and semi-desert areas in developing countries, management of these pests is largely dependent on socio-economic factors such as donors' geopolitical interests, availability of funds, and stakeholder inputs (Peveling, 2005). Locusts and grasshoppers produce outbreaks (and thus require control) at irregular intervals, which makes the sustainability of management infrastructure (e.g., survey programs, pesticide application and logistical expertise) even more challenging. Simultaneous consideration of environmental, social and economic systems is fundamental for shifting towards a preventive and sustainable locust management system (Lecoq, 2005).

In the past couple of decades several important technological advances were introduced into practice of locust and grasshopper monitoring and management worldwide. In the domain of survey, the use of the Global Positioning System (GPS) devices allowed to dramatically increase the accuracy of georeferencing and mapping the infestations (Latchininsky & Sivanpillai, 2010). Georeferenced information also allows for building-up historical databases of locust and grasshopper infestations, which helps to improve forecasting. Another relatively recent innovation consists in the use of information from meteorological and Earth observing satellites for locust habitat monitoring. Satellite data incorporated in a Geographic Information System (GIS) are routinely used by the Desert Locust Information System (DLIS) of the Food and Agriculture Organization of the United Nations (FAO UN) and by Australian Plague Locust Commission (APLC) for monitoring and forecasting Desert locust and Australian Plague locust *Chortoicetes terminifera* (Walker) (Cressman, 2013; Deveson, 2013).

Although satellite and GIS information contributed to improving the forecasting capabilities of locust control agencies, its operational use is currently limited to just two above-mentioned locust species. Additionally, post-outbreak damage assessments using satellite data are practiced for Oriental Migratory locust *Locusta migratoria manilensis* (Meyen) in China (Ma et al., 2005). For other locusts and grasshoppers applications of the satellite technology are either non-existent or still in the research phase (see a comprehensive review by Latchininsky, 2013).

Regarding control strategies and technologies, the Ultra-Low Volume spraying of oil-based pesticide formulations remains the leading application technology in many locust-affected countries although in Central Asia, its use is still limited compared to conventional full-volume and water-based spraying (Latchininsky & Gapparov, 2007). Older chemistry, such is the organophosphates, still predominate in large-scale control programs in certain regions of Africa and Asia despite growing ecological and human health concerns. For example, the bulk of the 13 million ha treated against the Desert locust in 2003-2005 was treated with organophosphates (Belayneh, 2005). Synthetic pyrethroids, neonicotinoids and phenyl-pyrazoles are also widely used. Some countries are applying benzoyl-urea insect growth regulators (IGR) to nymphal infestations, which is more compatible with a preventive control strategy. Biological control agents, namely commercial formulations of the fungus *Metarhizium acridum* are slowly making its way into locust control practice in Africa, Asia and Australia, but its progress is impeded by limited availability, relatively short shelf life and higher costs compared to conventional pesticides. Currently the fungal bioinsecticides are mostly considered as a “niche product” for applications in ecologically sensitive or organic production areas, although their use may grow with increasing restrictions imposed on conventional pesticides by environment protection agencies in many countries.

In North America, about 20 out of 450 non-swarming grasshopper species are important rangeland pests in 17 western U.S. states and in central and western provinces of Canada. Annually they destroy about 25% of above-ground rangeland forage at an estimated cost of almost one billion dollars per year (Hewitt & Onsager, 1982). During outbreaks, grasshoppers inflict severe damage to rangeland and crops and require large-scale applications of broad-spectrum insecticides to control them. For example, during the 1986-88 outbreaks in the U.S., over eight million ha of rangeland were treated with five million L of neurotoxins at a cost of over \$75 million (Lockwood & Schell, 1997).

In the late 1990s Jeff Lockwood and his colleagues from the University of Wyoming, in collaboration with federal and state pest management agencies, developed the Reduced Agent and Area Treatments (RAATs) to manage rangeland grasshopper infestations (Lockwood and Schell, 1997). RAATs is a strategy of integrated pest management (IPM) for rangeland grasshoppers in which the rate of insecticide is reduced from traditional levels and untreated swaths (refuges) are alternated with treated swaths. RAATs work through chemical control, meaning grasshoppers are killed in treated swaths and as they move out of untreated swaths, and conservation biological control, which allows predators and parasites preserved in untreated swaths to suppress grasshoppers. The most widely used pesticide in RAATs programs is diflubenzuron, an IGR which acts by ingestion, allows for three to four week protection from grasshopper pests and has lower non-target impact than conventional pesticides. RAATs reduces the cost of control and the amount of insecticide used by more than 50%

(Lockwood et al., 2000). Currently, RAATs is the preferred grasshopper management option by both, federal and private pest managers. In 2010, over 2.4 million ha were treated by RAATs in a single state of Wyoming (McNary et al., 2011) at an average cost of only USD 3.60 per protected ha (Shambaugh, 2011). This successful control program resulted in significant savings for Wyoming agriculturists and had no detected negative environmental impacts.

Are constant advances required to overcome increasing restrictions on the use of chemical pesticides?**Hunter, DM***Consultant to BASF in Locust Control, 125 William Webb Drive, McKellar, ACT 2617, Australia*

While some success has been achieved in the reducing the frequency and extent of outbreaks, substantial efforts continue to be required in the management of locust and grasshopper populations worldwide. Chemical pesticides form an important part of control programs but higher and higher standards have been required for both environmental safety and human health. Consequently, as new chemicals have been developed, they have faced increasing scrutiny leading to restrictions in some countries on organo-phosphorous compounds and on the more recent phenylpyrazoles and neonicotinoids. High development costs mean fewer new products are becoming available so we must use the products we have most efficiently and effectively, avoiding unwanted side effects. Side effects are more likely when infestations are large and directly threaten crops since there is then a great deal of pressure to do whatever is required. Furthermore, any side effects are likely to be detected because the widespread nature of infestations means their control will draw a high level of attention and scrutiny. Wherever possible, treatment programs need to be preventive in that populations are substantially reduced well before they reach crops not only to reduce crop damage but also to ensure that funding organizations and the local populace continue their support. Preventive control involves a strategy of early detection and rapid intervention where treatment begins early in outbreaks: locust populations are smaller and so treatments can involve the more judicious use of chemical pesticides. In addition, control programs should seriously consider including a biological alternative such as *Metarhizium* as part of their repertoire, because without a biological alternative, the increasing standards for environmental safety along with lower residue limits in foodstuffs can lead to important populations having to be left untreated, jeopardizing the success of preventive control. Finding infestations early in outbreaks requires close monitoring of locust populations, which can be aided by more accurate forecasting based on computer modeling of weather parameters and locust development. New techniques may well be required, but in many instances, adapting the advances already discovered in one region into control programs elsewhere will be sufficient. And adopting the latest techniques and standards in the use of pesticides is becoming essential in a world of increasingly globalized trade, where a country will need to meet the standards of the importing country if it wishes to sell its agricultural products. To meet the higher standards will require the use of an increasingly restricted range of chemical pesticides at the lowest possible dose and include more environmentally friendly methods of treatment. Chemical use can be reduced by beginning treatments early while infestations are smaller with the aim of reducing the need for widespread control of locusts directly attacking crops. The dose required for effective treatment can also be reduced through application by ULV equipment where there is more control of droplet spectra so less product is wasted in very large and very small droplets. Applying products in treated strips alternating with untreated areas can further reduce the amount of chemical used. Of course, for a strategy of preventive control to succeed, the chemical and biological products used and methods of their application will have to be adapted to the biology of the pest and be appropriate to the country concerned.

Integrating the ecology of phase change and collective movement into preventative locust management

Sword, GA

Department of Entomology, Texas A&M University, College Station, Texas, USA, 77843

Locusts are defined by the expression of density-dependent phase polyphenism and mass movement. Knowledge of the underlying mechanisms and relationships between phase polyphenism and mass movement has advanced considerably, providing multiple opportunities to apply this understanding to improve locust management practices in the field. Preventative locust management involves scouting potential habitats for early warning and rapid response against the first gregarious populations in an effort to limit additional population growth and mass movement to new areas. In pre-outbreak populations, the relationship between local population density, resource distribution patterns and resource abundance can be used to predict locust phase state. This information, in turn, can be used to prioritise populations for management actions based on their relative risk of gregarization. Locust survey operations currently assess local locust population densities in areas that are known historically to seed locust outbreaks, and also assess overall vegetation abundance. Incorporating local assessments of resource distribution and abundance patterns of key host plants is a simple addition to locust survey protocols that could provide much more predictive power in terms of quantifying gregarization risk. Once gregarization occurs and migratory bands form, insights into the self-organization and collective movement dynamics of these groups can potentially be used to predict their movement patterns, thereby improving the efficiency with which they can be monitored and controlled in the field.

Application of *Paranosema locustae* (Microsporidia: Nosematidae) to Control Grasshopper (Orthoptera: Acrididae) Populations in the Inner Mongolia Rangeland, China

Ban LP¹; Sun, YP² and Zhang, J¹

¹College of Animal Science & Technology, China Agricultural University, Beijing;

²College of Agriculture and Biotechnology, China Agricultural University, Beijing

E-mail: lipingban@cau.edu.cn

Paranosema locustae, which was originally described by Canning (1953), is a microsporidium of the adipose tissue of orthopterans. It was developed in the USA and was one of the earliest biological agents studied and used for grasshopper and locust control. We conducted field trials to evaluate the efficacy of wheat bran bait formulations of *Paranosema locustae* and *Metarhizium anisopliae* for controlling grasshoppers in Inner Mongolia during July (the rainy season), 2012. The Inner Mongolian grasslands are typical steppe and we investigated the main vegetation formations, *Stipa krylovii*, *Cleistogenes squarrosa*, *Leymus chinensis* (Chinese wildrye), *Artemisia frigida* and *Serratula centauroides*. We used a sweeping method to survey the population structure: the predominant grasshopper species were *Oedaleus asiaticus*, *Dasyhippus barbipes*, *Calliptamus abbreviatus* and *Myrmeleotettix palpalis*.

Moderately good control of grasshoppers has been obtained by direct applications of $2-5 \times 10^9$ *P. locustae* spores per mu ($3-7.5 \times 10^{10}$ spores per hectare), but because of the high cost of the product, lower doses were tested with and without *Metarhizium* in combination with bran bait. Treatments consisted of 1×10^7 spores *P. locustae* per mu, 1×10^7 spores *P. locustae* + *M. anisopliae* per mu or 5×10^8 spores *P. locustae* per mu, mixed with 0.2kg wheat bran. Using a 1m² sampling frame, we estimated the population density on the day of application, and subsequently at 3-day intervals until day 21. At each site, we sampled 5 points, with 3 replicate estimates at each point. We found that the 1×10^7 spores per mu *P. locustae* + *M. anisopliae* combination resulted in a 29.15% decline in grasshopper numbers, which was similar to the 33.15% decline caused by the fifty times higher dose of *P. locustae* alone (5×10^8 spores per mu). The treatment using 1×10^7 *P. locustae* spores per mu alone had no significant effect. These promising results suggest that further tests should be conducted to determine how the combination of *P. locustae* + *M. anisopliae* could reduce the dose required for grasshopper control.

Recent experience in large-scale locust campaigns and lessons learnt

Monard, A

UN FAO, Rome, Italy

Since the 10th International Congress of Orthopterology held in 2009, FAO assistance was required by its member countries to assist in dealing with two major locust threats. These threats were due to two different species, occurring in quite different geographical areas and that are still persisting but at a different scale. In one case, a long-term approach to develop and implement a sustainable locust preventive strategy was applied: a locust outbreak developed in insecure areas but was properly managed. In the other case, failure in applying the preventive strategy on a regular and sustainable manner, and in carrying out appropriate monitoring and then in controlling an upsurge at an early stage, resulted in the development of this upsurge into a plague.

For decades, FAO has been advocating the locust preventive strategy and has put it in place effectively from the late 90s through its programme “Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases” (EMPRES). The features of this strategy, as well as its limits and ways to anticipate and minimize them, will be presented to explain the general framework in which large-scale control campaigns are carried out. Then the recent examples of the two above-mentioned threats will be detailed against their respective context. It will provide the opportunity to show how recent innovations in a wide range of fields, and lessons learnt from previous campaigns, have been introduced into routine activities as part of improving locust control. It will also allow highlighting of the main and common characteristics of events, even with those that initially might appear quite different, and to underline lessons that have been learnt by all stakeholders to better manage locust issues in the future.

An assessment on *Nosema* spp. isolated from grasshoppers in Xinjiang province as a potential agent against the migratory locust

Zhang, PF¹; Zhang, AB¹; Chen, ZH² and Zhang, L^{1*}

¹*China Agricultural University, Beijing, 100193, China;*

²*Hei Long Jiang University, Harbin, 150080, China*

**Corresponding author: E-mail: locust @ cau.edu.cn*

Evaluation of *Nosema* spp. (Microsporida) isolated from naturally infected grasshoppers collected from Xinjiang Uygur autonomous region as a potential agent against *Locusta migratoria manilensis* was conducted in laboratory. The results revealed that the mortalities of locusts caused by *Nosema* spp. increased with the concentration, and reached 36%, 47%, 50% at 1×10^7 conidia/mL, 1×10^8 conidia/mL, 1×10^9 conidia/mL respectively after 14 days post-inoculation and 56%, 78%, 90% after 19 days post-inoculation. Concentration-dependent response was clearly demonstrated. The LT_{50} was significantly shorter than a strain of *Nosema locustae* in our laboratory. It showed potential as a biocontrol agent to control the locusts and grasshoppers.

Microsporidia as grasshopper control agents in Argentina

Lange, CE

Centro de Estudios Parasitológicos y de Vectores (CEPAVE), Comisión de Investigaciones Científicas (CIC) de la provincia de Buenos Aires – Universidad Nacional de La Plata (UNLP) – CCT La Plata CONICET

Research cooperative projects between scientists of La Plata National University (UNLP) and the United States Department of Agriculture (USDA) in the late 1970's and early 1980's prompted the study of microsporidia as possible biocontrol agents of grasshoppers in Argentina, a previously unexplored field of research in the country. Microsporidia are spore-forming, unicellular eukaryotic obligate parasites of which insects as a whole are one of the main host groups. As in other parts of the world, absolute reliance on chemical insecticides against some of the 10-15 pest grasshopper species of the country provided the justification underlying the search for more environmental-friendly alternatives of control. Prior to the implementation of the projects, no reports on grasshopper microsporidia were available in Argentina. Since then, three nativemicrosporidia have been fully described (*Liebertmannia dichroplusae*, *Liebertmannia patagonica*, *Liebertmannia covasacrae*), several other *Liebertmannia*-like isolates have been detected and are under study, and the fate of the introduced microsporidium *Paranosema locustae* was monitored for years in the Pampas, and to a lesser extent in two other introduction areas in Patagonia. The presentation will review the state of knowledge on the microsporidia associated with grasshoppers in Argentina. None of the native species so far discovered appear to be useful for control purposes due to constraints in transmission, host range, and pathogenicity. By contrast, *P. locustae* which is well established in the western Pampas and in Loncopué, Neuquén province (north-western Patagonia), seems to be of value as a long-term control factor. Simultaneously, some non-target grasshopper species may be negatively affected, particularly those belonging to subfamilies of recognized susceptibility and having small populations and restricted geographic distribution. However, in spite of the apparent usefulness of *P. locustae* against grasshoppers in Argentina, aside from some incipient interest by organic farmers and a few provinces, what has been called "the chemical paradigm" still prevails.

Design and implementation of a GIS, RS and GPS based information platform for locust control**Li, L***China Agricultural University, Beijing, China*

To monitor and control locusts efficiently, an information platform for locust control based on global positioning system (GPS), remote sensing (RS), and geographic information systems (GIS) was developed. The platform can provide accurate information about locust occurrence and control strategies for a specific geographic location. The platform consists of three systems based on modern pest control: a field ecology (locust occurrence) and GIS in a mobile GPS pad, a processing system for locust information based on GIS and RS, and a WebGIS-based real-time monitoring and controlling system. This platform was run at different geographical locations for three years and proved to facilitate locust control in China with high efficiency and great accuracy.

Climate change and anthropogenic impacts on grasshopper distribution in Mongolia

Batnaran, Kh¹; Ganbold, E¹; Dorjderem, S¹ and **Batkhuuyag, B²**,

¹*Entomological Laboratory of Plant Protection Research Institute;*

²*WWF Mongolia Programme Office*

Mongolia occupies a critical ecological transition zone where the Siberian taiga forest, the Central Asian steppe, the high Altai Mountains and the Gobi desert converge. Pastures, which are a sparse mix of grasses, herbaceous and woody ground plants and other species, cover roughly 124.3 million ha (approximately 80% of the country) and support the traditional semi-nomadic lifestyle that provide employment for over 40% of the work force. On this rangeland are an assemblage of diverse species that include many endemic and globally endangered species like snow leopard, Mongolian gazelle etc. The orthopteran fauna of the country include over 180 species from orders Blattodea, Mantodea and Orthoptera. The latter has the most diverse and rich representation that includes some 126 species from superfamily Acridoidea, 45 species from Tettigonoidea, 3 from Grylloidea, 2 from Tridactyloidea.

The traditional subsistence economy, based on semi-nomadic herding, trod lightly on the land and thus problems with grasshopper outbreaks were never recorded prior 20th century. The very first grasshopper outbreak was linked with the Russian settlements and crop cultivation in the northern part of the country in middle of 1920s. The first chemical control of grasshoppers using Sodium arsenate took place during 1926-1932 by Russian expedition in these areas. The rapid expansion of crop farms during the collective farm period resulted in the establishment of Plant protection and Quarantine section within the Ministry of Agriculture of Mongolia in 1958. Collective farming also led to localized overgrazing of rangeland which resulted grasshopper and field vole outbreaks: starting from 1964 Mongolia also began chemical control work in pastureland areas to suppress grasshopper and field vole outbreaks.

The collapse of centralized economy in early 1990s has resulted privatization of livestock and long-term lease of croplands. Within 20 years, the number of livestock has doubled, reaching as high as 45 million livestock and becoming the main factor of land degradation in the country. Between 2006 and 2009, ~110,000 square kilometers of land, approximately 7% of Mongolia's territory, was degraded each year, and in the absence of sound legal environment and market mechanisms there is little prospect of halting the process in the near term. As well, climate change is impacting the pastures through increasing average temperatures and number of warm days as well as through changes in rainfall patterns and the distribution of water resources. The Mongolian Assessment report on Climate Change (2009) highlighted that due to climate warming, Mongolia will have the semi-desert zone pushed into the steppe zone to the north, especially by 2080. It also predicted that by 2080 the forest-steppe and steppe areas would decrease, caused by reduced rainfall and increased temperatures during the growing season. The report also highlights that the percentage of desert will tend to expand to the north because the increased amount of precipitation is more than offset by increased evaporation.

The field research work carried out in forest steppe zones of Mongolia during 2005-2007 recorded, for the first time, the distribution of three typical representatives of steppe or desert steppe ecosystems and oases in the forest steppe zones of the country. These species include *Bryodema orientale* (Bey-

Bienko, 1930) the typical representative of steppe and semi-desert steppe, *Epacromius tergestinus tergestinus* (Charpantier, 1825)– found in 1970s only in great lake depressions and in oasis in the western and southern Gobi deserts and *Epacromius pulverulentus* (Fischer-Waldheim) found only in great lake depression and oasis and around lakes and rivers in steppe and desert steppe zones of the country. In parallel the field work in 2011 revealed a distribution of *Locusta migratoria migratoria* (Linnaeus, 1758) in Uvs lake basin. The species distribution records prior 1970s were all confined to the oases of Alashan plateau and gobi deserts of Inner Altai. This new distribution range pushes the former area of distribution by 500 kms northwards in case of *L. migratoria*. While the distribution areas are still tied with the lakes and other surface water, the early distribution areas belonged, according to Jambaajamts (1989) to the moderately cold region of sharp dry-warm zone with sum of above active air temperature above 2500 degrees, while the recent distribution area of Uvs lake basin is considered as a severe cold region of sharp dry-warm zone with sum of active temperature ranging between 2000-2500 degrees. With *B. orientalis* B-Bienko, *E. tergestinus* Charp. and *E. pulverulentus* F-W, the northern boundary of new distribution range is around 200 kms further north. The earlier distribution areas of these species ranged between the cold region of the very dry-warm zone to the cold region of moderately dry-moderately cool zone with sum of active air temperature ranging between 2000-2500 degrees. The recent distribution area of these grasshoppers in general considered as a colder region of the moderately humid-cool zone with sum of active air temperature ranging between 1500-2000 degrees.

Our observations indicate that due to the combined impacts of climate change that increased the mean temperatures by 1.8°C between 1940-2003 and overall pasture degradation, some patchy ecosystems with steppe and desert steppe feature have already formed in the forest steppe zone of the country as grasshoppers are considered as one of the most prominent indicators of the ecosystem change. The finding highlights that Mongolia needs more in-depth research on the impacts of climate change on grasshoppers and other field pest species because expansion of distribution areas of world most damaging grasshopper *L. migratoria* L. and other species could lead to frequent outbreaks of pest species. The issues are especially important if we consider the fact that the extensive livestock system dependent on availability of standing grass and surface water will itself also undergo severe climate change induced stresses.

Management of Red Locust populations in Tanzania – are current survey and control techniques working?

Spurgin, PA

Australian Plague Locust Commission

The Red Locust, *Nomadacris septemfasciata* (Serville 1838) is an important pest of agriculture in eastern and southern Africa. It breeds once a year at the beginning of the rainy season in swampy grasslands often referred to as outbreak areas. There are eight of these areas in southern Africa; the Mweru-wa-Ntipa and Kafue Flats in Zambia, the Lake Chilwa Plains in Malawi and the Buzi-Gorongos Plains in Mozambique. Tanzania has four; the Ikuu-Katavi Plains, the Malagarasi, the Rukwa Valley and the Wembere Plains as well as one secondary area, the Bahi Swamp. Swarms that leave or escape from these areas can pose a serious threat to subsistence agriculture in surrounding districts and during major upsurges can migrate long distances and cross international boundaries.

Since the 1940s several organisations have worked to limit regional upsurges in Red Locust populations through surveillance and control operations in the relatively small outbreak areas (0.1 % of the 8 million km² invasion area). In 1970 the International Red Locust Control Organisation for Central and Southern Africa (IRLCO-CSA) was formed with a specific mandate to control significant populations of Red Locust in the outbreak areas to prevent swarm escapes. Since 1994 the Tanzanian outbreak areas have remained active and IRLCO-CSA has cooperated with the Tanzanian Ministry Of Agriculture and Food Security (MAFC) and attempted to strategically manage populations through regular survey and control operations.

Monthly rainfall in the Tanzanian areas is closely monitored by IRLCO-CSA and MAFC during the wet season and is used as a trigger for timing aerial surveys of the outbreak areas by helicopter (the areas are remote and usually inaccessible by ground). These surveys occur at the end of the wet season from January to March and are used to determine the success of breeding by the previous generation and the extent of populations of nymphs. If significant numbers of nymphal bands or small swarms of fledglings are located, aerial treatment is carried out to reduce the potential for swarm formation and breakouts. If swarm escapes occur they tend to happen during the March to May period and are associated with prevailing winds, the drying of vegetation in the plains and grassfires that contribute to concentrating scattered adult populations into cohesive swarms.

Later in the dry season during June-September further aerial surveys of the outbreak areas are effective at locating surviving adult populations that often reform into highly visible, dense swarms. Further control at this point assists in reducing the total adult population prior to breeding at the onset of the wet season and as a consequence can lead to a direct decrease in the following nymphal population. Lack of resources often jeopardises these adult control operations.

Control of nymphal bands and adults is by ultra low volume aerial spraying. Chemical pesticides (mainly organophosphorous pesticides) continue to be the main control agents applied but since 2003 the biopesticide Green Muscle TC® (containing the fungal entomopathogen *Metarhizium acridum* [IMI 330189]), is being used with some success in the environmentally significant Katavi National Park (incorporating the Ikuu-Katavi outbreak area). This management strategy has proved adequate in protecting food crops at risk from Red Locust in Tanzania but could be improved with ongoing funding commitment to support annual survey and control programs against both the nymph and adult stages.

Studies of *Nosema locustae* and *Metarhizium anisopliae* as a control agent of *Locusta migratoria migratoria* in the Jilin Boluohu natural conservation area of China

Wang, XW^{1,2}; Zhang, LX²; Wang, SX³; Fan, JS²; Ren, BZ⁴; Zheng, SF²; Sun, Y²; Zhang, K²; Chen, ZH² and Wang, GQ^{2*}

¹Forest School of Northeast forest University, Harbin 150040, China;

²College of Agricultural Resource and Environment, Heilongjiang University, Harbin 150080 China;

³Daqing Extension Center of Agricultural Technology, Daqing 163411 China;

⁴School of Life Sciences, Northeast Normal University, Changchun 130024, China

E-mail: gqwang53@126.com

The Boluohu natural conservation area is a 24915 hectare national nature reserve is located in Changchun City of Jilin Province of China. In recent years, due to climate warming, land salinization and desertification has increased year by year, resulting in the loss of rangeland ecological balance and frequent natural disasters in the western Jilin Province. Since 2000, the Boluohu natural conservation area has had Asian locust (*Locusta migratoria migratoria* L.) outbreaks that have been a serious threat to the local agricultural production. In this 2012 study, both *Nosema locustae* and *Metarhizium anisopliae* (NM) were assessed for their potential as control agents of Asian locust in the Boluohu natural conservation area. The field studies were undertaken to investigate the effects of control and the rate of population decline after application of *N. locustae* mixed with *M. anisopliae* in the treatment plots. The treatment areas were dominated by grasses (Gramineae) and sedges (Cyperaceae), with vegetation coverage is above 55%. Implementation of the treatment was conducted in June 21 2012, when most Asian locusts were at the third instar nymph stage. In each plot, locust population density was assessed before and after spraying and at seven day intervals over the next 3 weeks. The sprayed area was about 2000 acres.

The experimental results showed that the control effect was lower when only *M. anisopliae* was used than when only *N. locustae* was used. With *Nosema* baits for locust control, the effect was relatively slow, but after correction for changes in the untreated control, decreases of 43% to 96% occurred between 14-35 days after treatment with a concentration of 10^7 to 10^8 spores / kg of bait. After treatment with *M. anisopliae*, the decline, after correction for the control, was a 14.3% decline at 7d reaching as much as 85.7% after 35 d. Using 10^7 spores/kg of *Nosema* bait mixed with *Metarhizium* led to locust declines of 25.7% at 7d, increasing to 66.7% at 14d, and as high as 100% after 35d. Complementary application of the two biological agents showed a good synergistic effect. The results indicated that *N. locustae* mixed *M. anisopliae* as a control agent was important for developing integrated management of *L. migratoria migratoria* in the Boluohu natural conservation area.

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Using public reporting to assist monitoring locust activity during an outbreak of the Australian plague locust, *Chortoicetes terminifera* (Walker), in Victoria

Berg, GN

Department of Environment and Primary Industries Victoria, Australia

A substantial increase in populations of the Australian plague locust, *Chortoicetes terminifera* (Walker), occurred in inland areas of New South Wales and southwest Queensland following heavy drought breaking rainfall in November 2009. Nymphal bands developed in early December 2009 and adult migrations resulted in increased population density in far western New South Wales. Further widespread rainfall resulted in a third generation of gregarious populations during the 2009-2010 season. Despite controls applied in New South Wales by both the Australian Plague Locust Commission and state authorities, prolonged migration of dense swarms occurred southward in autumn 2010 extending into northern, central and western Victoria and South Australia. Extensive, dense egg laying (up to 1×10^9 eggs per hectare) occurred in Victoria.

It was anticipated that the locust hatching in the spring and summer of 2010/2011 was likely to be more widespread, intense and damaging than any outbreak seen in Victoria since 1973/1974 and prior to that 1934/1935. Approximately 9.6 million hectares was estimated to be affected to some degree, and of this total, some 2.4 million hectares was likely to be directly affected by locust hatchings during spring 2010. The Victorian Government, in collaboration with the Australian Plague Locust Commission and other states, committed substantial resources to prepare for and respond to the potential locust outbreak. The Victorian Premier chaired a taskforce overseeing the state response and the Victorian Government allocated \$43 million of additional funding for the program. It was the single-largest sustained emergency response undertaken by the Department of Primary Industries in Victoria with over 1200 staff deployed through more than 20 rotations across 35% of the state.

Because of the scale of the outbreak, it was recognised that response staff could not effectively monitor the large area affected without the assistance of landholders and the general public. A public engagement program that both informed the public about the impending outbreak, and encouraged and facilitated public reporting of egg laying, hatching, nymphal band development and adult activity was developed. The data generated aimed to assist mapping locust occurrence, planning, and the coordination of control activities for the response.

A comprehensive communications program was undertaken. This included conducting over 500 community meetings and the use of news media. The Department of Primary Industries' website was developed to include an online forum, interactive maps and on-line reporting mechanisms. Website information was updated on a daily basis during the response period. A Locust Hotline was activated which also captured public reports of locust sightings and provided information to landholders and managers. Spatial mapping systems were developed and integrated with the website and Hot-line reporting data to provide real time mapping of reports of locusts and locust life-stages.

Surveys showed that the communication and community engagement activities were successful in achieving increased awareness of and action in response to the threat posed by locusts. Over 10,000 stakeholders including land managers, agribusiness and government agencies attended community

engagement meetings across the state and there were over 4,000 TV, radio, newspaper, outdoor (billboards) and online advertisements placed in metropolitan and regional media in. The value of this activity was further leveraged by 'free' media exposure valued at over \$10 million including interviews by response staff. By March 2011 surveys indicated that 100% of Victorian farmers had become aware of the locust threat and the subsequent response program. Over 60% of farmers felt better prepared to meet future locust threats than they did previously.

About 20,000 reported sightings were received through the Locust Hotline and the website between July 2010 and March 2011. The public reporting of locust activity was highest during spring and early summer 2010, but lower than expected during late summer and autumn 2011. This lower level of reporting was in part attributed to factors such as: "reporter fatigue", "message fatigue", fewer locusts in the latter stages, and other emergency responses occurring in Victoria in early 2011 such as floods.

Selected public reports were followed up by field response teams for verification. Egg, locust and grasshopper specimens were collected for entomologists to confirm their identity, developmental stages, viability and level of parasitism. There was a low level of misidentification noted from public reports including other Orthoptera such as spur throated locusts, *Austracris guttulosa* (Walker), upolo meadow katydid, *Conocephalus upoluensis* (Karny), several species of field crickets and occasionally species from other insect orders such as bees and cicadas. There was some biasing of reporting (increased frequency of reporting in relation to land area and locust densities) near larger regional towns and in particular in the capital city of Melbourne. Overall these issues did not affect the usefulness of public reporting. The community engagement process ensured that the public was well informed and successfully promoted their involvement in the program. The public reports together with reports from field teams provided a clear indication of the spatial and temporal progression of the outbreak that would otherwise have been difficult to achieve for an outbreak of this scale. This information greatly assisted planning of controls and the overall success of the response program.

Public reporting, including the use of internet web-based and 'Hot-line' telephone reporting of locusts, during a major locust outbreak can provide valuable data for a response program. Mapping technologies can use the reports to provide real time information that both informs the public and assists the planning and coordination of response activities. On-ground verification of a subset of the public reports will inform the level of accuracy of these. In a prolonged response the longer-term effectiveness of public reporting may diminish due to issues of "reporter and message fatigue".

The pests on chickpea cropped in arid regions of Uzbekistan

Gapparov,FA; Tufliiev, NH and Kholliiev,AT

Uzbek Institute for Plant Protection

Chickpea is an annual that is resistant to dry conditions and is a thermophyte nutritive plant. Chickpea seeds are widely eaten and prepared as a meal in many countries. The seed consists of about 30% protein, 7% fat, 48-61% non-nitrogen extractive compounds and has a high content of minerals and vitamins. In Uzbekistan, chickpea is mainly cropped in arid lands near foothills and covers about 10,000 ha. At present, the average yield of in these arid areas is 500-600 kg/ha, but with agrotechnic machines yield may be increased to 800-1000kg. Because of its drought-resistant properties, the chickpea plant became popular in Uzbekistan since 1960, being cropped in arid areas near of foothills and hills in the Dzhizakh, Samarqand, Qashqadarya, Surkhandarya regions. One of important measures for good growth conditions and getting high yield is the development of pest management on chickpea fields.

Legumes, including chickpeas, can be attacked by 14 pest species during their growth. The most serious damage on chickpea plants grown in arid area is considered to be caused by locust species belonging to the order Orthoptera. According to P.A. Alimdzhanov's (1968) data the average annual yield loss on pea legumes because of this pest's attack was 15-36%; present indications are that that estimate needs to be increased substantially.

In 2012, research surveys were conducted on pea plants grown in arid parts of the Qashqadarya region. The results indicated that outbreaks of the locusts *Dociostaurus maroccanus* Thunb, and *Dociostaurus kraussi* Ingen, (Orthoptera: Acrididae) caused a yield loss about 30-40% in chickpeas, with up to 70% losses in some places. The chickpea plant was affected most by the Moroccan locust *D. maroccanus* and as result of pest development in arid places, locust feeding on all parts of the plant led to significant decrease of the crop yield.

In places where there were swarms of adult locusts, control was very difficult. For management of flying adult locust swarms, the use of preparations with manual or motor sprayers was not effective, and the field treatment should be conducted with a hang-glider or airplane. However for farmers, use of aircraft is very costly and not profitable. In order to avoid this situation, it was recommended that the leaders of farms and farmers growing the chickpeas in arid areas should conduct timely surveys on their fields for identification of locusts recently hatched from eggs (this time is complied with third ten days of March and first ten days of April). They should determine the location of pest locusts before the locusts reach the first to second instar stage and then report to the regional plant protection station or pest control workers so that pest management can occur in time.

Chemical control of small pest bands when the locusts were first to second nymphs was very effective and prevented their distribution over larger areas. This early treatment allowed for a high yield of seeds as well as hindering locust migration to other crops.

The Biological Effect of *Metarhizium* and Nomolt on Locusts and Grasshoppers under Laboratory Conditions

Hamroev, AI and **Gapporov, FA**

Uzbek Research Institute for Plant Protection

It is presently well known that special attention is paid to using microbiological control of locusts and grasshoppers that belong to the order Orthoptera. It should also be noted that there has been some success achieved in this way. As a result, many countries have started using the biopesticide made from strains of the fungus *Metarhizium*, and currently in these countries where this biological product being used against locusts and grasshoppers is known as Green Guard or Green Muscle.

The biopesticide made by Becker Underwood Pty based on Australian strains of the fungus *Metarhizium acridium*, was first tested against main species of katydids (*Tettigonia viridisima*) and white-fronted grasshoppers (*Decticus albifrons*) at the laboratory of the Uzbek Research Plant Protection Institute in Uzbekistan. About 18-20 4-5 day old grasshoppers were placed in special cages in the laboratory and were fed on naturally grown plants treated with *Metarhizium* combined with a 15 % suspension of Nomolt. Grasshoppers fed on grass treated with ordinary water served as the control.

Observations were made 1, 3, 5, 7, 14 and 19 days after treatment. No effect was seen on the day after treatment but there was 12.9% mortality after 3 days. The subsequent mortalities were: after 5 days - 24.3%, after 7 days - 44.7%, after 9 days - 63.7%, after 14 days - 88.0 % and mortality remained at 88.0% at 19 days. During observations it was noticed that grasshoppers became sick, their activity was very low, and legs tore off, with wings and bodies bent out shape.

In the control, it was observed that grasshoppers were moving, eating and living more than 30 days and naturally died. The samples of dead grasshoppers treated by *Metarhizium* were studied under a magnifying glass and microscope and this showed that they had died because of its application.

Chitin Metabolism Enzymes of *Locusta migratoria* and their Application in PestControl

Zhang, JZ¹; Li, DQ¹; Liu, XJ¹; Ma, EB¹ and Zhu, KY²

¹Research Institute of Applied Biology, Shanxi University, Taiyuan, 030006, China

²Department of Entomology, 123 Waters Hall, Kansas State University, Manhattan, KS 66506, USA

Chitin is widely distributed in epidermis and the peritrophic matrix of insects. The importance of chitin in insect development and the absence of chitin in vertebrates have led to a hypothesis of attacking the insect chitin biosynthesis pathway as a novel target for developing safe and effective insecticides. The process of chitin biosynthesis and degradation consists of at least eleven key enzymes, but the roles of these enzymes in insect development have not been well elucidated. Five important genes putatively encoding glutamine: fructose-6-phosphate aminotransferase (*GFAT*), glucosamine-6-phosphate *N*-acetyltransferase (*GNAT*), UDP-*N*-acetylglucosamine pyrophosphorylase1 (*UAP1*), trehalase 1 (*TR1*), and chitin synthase 1 (*CHS1*) have been identified to be involved in chitin biosynthesis in *Locusta migratoria*. In contrast, multiple chitinase (*Cht10*) genes and one β -*N*-acetylglucosaminidase(*NAG1*) gene have been identified to be involved in chitin degradation. By using RNA interference in different nymphal stages, we observed that nymphs injected with dsRNA of *LmGFAT*, *LmUAP1*, *LmCHS1*, *LmCht10* or *LmNAG1* developed slowly, failed to detach from the old cuticle during the molting process and has high mortality. When RNAi suppressed the expression of *LmCht10*, we found significantly reduced new cuticle development and cuticle thickness as compared with those of the dsGFP-injected controls. Our results suggest that *LmGFAT*, *LmUDP1*, *LmCHS1*, *LmCht10* and *LmNAG1* are essential for insect growth and development. The enzymes encoded by these genes could potentially serve as an excellent target for developing novel strategies for controlling this important pest.

Epizootics of entomopathogenic fungus, *Entomophaga grylli* regulating densities of grasshopper population in Northwest of China

Zhang, LW¹; Dawutijiang, Y²; Yang, JF⁴; Kuiban, A³; Deng, SX⁴ and Zhang, L¹

¹Department of Entomology, China Agricultural University, Beijing100193, China;

²Plant Protection Station of Xinjiang Uygur Autonomous Region, Urumqi830006, China;

³Agricultural College of Xinjiang Agricultural University, Urumqi830006, China;

⁴Regional Agri-Tech Extension and Service Center, Altay836500, China

Entomophaga grylli is one of the most important entomophagous fungi, playing key role in regulation of grasshoppers and locusts. In order to evaluate the role of *E. grylli* in grasshopper population dynamics in CHE, JDY and KAN of Xinjiang, northwest of China, we conducted consecutive field surveys and lab examinations within two years. We found that seven species of grasshopper, *Calliptamus italicus*, *Stauroderus scalaris*, *Gomphocerus sibiricus*, *Omocestus haemorrhoidalis*, *Chorthippus albomarginatus*, *Bryodemella sp.* and *Oedaleus sp.* were infected by this fungus. Two species of grasshoppers, *Stauroderus scalaris*, *Chorthippus albomarginatus*, *Bryodemella sp.* and *Oedaleus sp.* were first recorded as this pathogen hosts in China.

Table 1, infection rates (%) of *E. grylli* on various hosts in different survey sites during 2010

| | CHE | JDY | KAN |
|-----------------------------|------|------|------|
| <i>Calliptamus italicus</i> | 83.3 | 33.3 | — |
| <i>Stauroderus scalaris</i> | 0 | 40.7 | 77.3 |
| <i>Bryodemella sp.</i> | 0 | 33.3 | — |
| <i>Oedaleus sp.</i> | 1.4 | — | — |

Further analysis showed that the fungus shows different preferences in grasshopper species in different places. *Calliptamus italicus* was dominantly infected by the fungus in CHE, but *Stauroderus scalaris* and *Gomphocerus sibiricus* at JDY. As shown in Table 1, we found pervasively high infection rate of *E. grylli* in all sites: the highest was detected in CHE of *C. italicus* (83.3%), then in KAN of *S. scalaris* (77.3%) and the lowest infection rate about 1.4 % of *Oedaleus* grasshoppers in CHE, which demonstrate that *E. grylli* is playing a significant role in regulating grasshopper populations. Interests in basic biology and manipulation of this pathogen in grasshopper integrated pest managements are the stimulus for initiating long-term research project on the natural dynamics of the *E. grylli*.

Evaluation for Virulence and Potential Application of *Metarhizium* Strains against Tibet Migratory Locusts: *Locusta migratoria tibetensis* Chen (Orthoptera, Acridoidea)

Sali, YS^{1,2}; Nong, XQ¹; Wang, WF³; Sidike, ALM² and Zhang, ZH¹

¹Institute of Plant Protection, Chinese Academy of Agricultural Sciences, 100193 Beijing, China;

²Xinjiang Agricultural University, 830052 Urumqi Xinjiang, China;

³Tibet Academy of agricultural and Animal Husbandry Sciences, 850032 Lhasa Tibet, China

*Correspondence: xqnong@sina.com

The experiment aimed to evaluate the potential ability of *Metarhizium* strains, fungal entomopathogen, as biocontrol agent against Tibetan migratory locust: *Locusta migratoria tibetensis* Chen. Five *Metarhizium* strains (HK0101, 56096, 189, 801 and HC-5), known high virulence against oriental migratory locusts, were used for bioassay to 3rd instar nymphs of Tibet migratory locusts in lab. The conidia of these *Metarhizium* strains were formulated into baits at five gradient concentrations, 2.3×10^5 , 2.3×10^6 , 2.3×10^7 , 2.3×10^8 and 2.3×10^9 conidia/g, to feed the testing locusts. Mortality and infected cadavers were determined and compared. The highly virulent strain 189 was cultured and formulated into conidial oil suspension to control Tibet migratory locusts on plateau grasslands in Lhasa suburb and Nyingchi County of Tibet. Mortality and population development were investigated. The results showed that the five strains were all certainly virulent to Tibet migratory locusts with mortalities ranged 71%-100%. The higher concentration used, the more locusts died, as well significantly more infected cadavers. At the concentration of 2.3×10^9 conidia/g, all of the five strains caused more than 50% dead in six days, and exceeded 80% dead at 15th day. Virulence of strain 189, 801 and HK0101 arranged at the top three based on mortalities. Amount of them, the strain 189 presented the highest infected rate with 74% cadavers at 5th day. In field experiment, we did not find dead or infected cadavers in 15 days after conidial suspension application, however, our investigation showed that 4th instar and 5th instar nymphs accounted for more than 70% of the total population in the area of applied *Metarhizium*, while only 20%-26% of nymphs and other adult majority in the control area. It means that the population growth slowed down by *Metarhizium* application. On the other hand, we collected nymphs and adults from the areas after 5, 10 and 15 days of applying *Metarhizium* and brought them back to lab. The surprising results were that *Metarhizium* hyphae and conidia could grow out from 75%, 45% and 35% of these collected locusts which were killed by -20°C freezing and kept in moisture Petri dishes at room temperature. We speculate that the infection and virulence of applied *Metarhizium* were restricted by strong ultraviolet, temperature, humidity and other factors under plateau conditions. And we suggested that *Metarhizium* vitality must be effectively protected by appropriate formulation to ensure their successful infection to the locusts.

Microsatellite Analysis of Genetic Polymorphism in 14 Geographical Populations of Tibetan Migratory Locust: *Locusta migratoria tibetensis* Chen (Orthoptera, Acridoidea)

Sali, YS^{1,2}; Gao, S¹; Nong, XQ¹; Zhang ZH*

¹*Institute of Plant Protection, Chinese Academy of Agricultural Sciences, 100193 Beijing, China;*

²*Xinjiang Agricultural University, 830052 Urumqi Xinjiang, China*

*Correspondence: lgbcc@263.net (ZHANG Z. H.)

To explain the genetic characteristics of 14 geographical populations of *Locusta migratoria tibetensis* Chen, 9 pairs of fluorescent-labeled SSR primers were used to conduct PCR amplification for 14 geographical populations of *Locusta migratoria tibetensis*, and dendrogram was constructed using UPGMA method based on genetic distance. The result showed that 208 alleles were amplified with 9 primers. The average numbers of alleles and average efficiency numbers of alleles of per locus were 20 and 11.77 respectively. The observed heterozygosity ranged from 0.351 to 0.810 and the expected heterozygosity varied from 0.835 to 0.946, the mean heterozygosity of whole population was 0.669. The polymorphism information content varied from 0.810 to 0.9521, with average value of 0.902. There are closest relationship between Nagra and Xiangzi geographical populations, their genetic distance and similarity coefficients were 0.1677 and 0.8456. There are furthest relationship between Xiangcheng and Xiangzi geographical populations, their genetic distance and similarity coefficients were 2.8319 and 0.0589. The results showed that the genetic polymorphism of geographical populations of *L. migratoria tibetensis* Chen is abundant, and the genetic differentiation among the 14 geographical populations in Tibetan plateau were clearly defined. The Tibetan migratory locust was divided into two groups and 4 sub geographical populations. The group one include two sub geographical populations I and II, sub geographical population I was composed by **Gaer**, **Ritug** and **Baiba** geographical populations. And the sub geographical population II was composed by **Xiangzi**, **Naga** and **Sangri** geographical population. The group two include two sub geographical populations III and IV, sub geographical population III was composed by **Luhuo**, **Luoxu**, **Ganzi** and **Bamei** geographical populations. The sub geographical population IV was composed by **Rikaze**, **Zhanang**, **Sangri** and **Xiangcheng** geographical population.

Population dynamics and life history of Tibetan migratory locust: *Locusta migratoria tibetensis* Chen (Orthoptera, Acridoidea) in Lhasa river basin

Sali, YS^{1,2}; Nong, XQ¹ and Zhang, ZH^{1*}

¹*Institute of Plant Protection, Chinese Academy of Agricultural Sciences, 100193 Beijing, China;*

²*Xinjiang Agricultural University, 830052 Urumqi Xinjiang, China*

**Correspondence: lgbcc@263.net(Zhang Z. H.)*

To explain the occurrences of natural population of *Locusta migratoria tibetensis* in Lhasa river basin by field investigation of population dynamics and life history. Two perennial focus areas [meadow grassland (N: 29° 38' 04.77", E: 91° 01' 42.11", Altitude: 3641m) and Yangda farmland (N: 29° 40' 39.90", E: 90° 55' 05.34", Altitude: 3702m)] in Lhasa river basin was chosen as the sample area, and the population density was surveying every 4 days by no ground pattern box with chessboard sampling. Record the ecological type (phase gregarious and phase solitarious), female, male, developmental stages respectively. Because of difficult to distinguish the female and male before 3rd instar nymphs, so record the density of females and males after appears 3rd instar nymphs. Total of 33 times of field investigation work and survey since April 22 until August 29, in 2012. The occurrence time and population density of Tibetan migratory locust was significantly difference in different habitat. Locust eggs was hatched late April in meadow grassland, and late May in farmland, the incubation stages of eggs was appears mid to late may with temperatures rebound, young hoppers peak appeared in early June and the population density was 50±0.6 numbers/per square meter. But the average population densities were remaining around 5 umbers/per square meter, and gradually reduce from 6 June. The adult locust were appeared mid on June, and the eclosion stage was July, August and September was the copulation and spawning stage. The Tibetan migratory locust occurred incompletely two generation in a year in the meadow grassland and completely one generation per year in farmlands in Lhasa river basin.

Study on numerical characteristics of different populations of *Locusta migratoria tibetensis* Chen (Orthoptera, Acridoidea) in the Tibetan Plateau

Sali, YS^{1,2}; Gao, S¹; Nong, XQ¹ and Zhang, ZH^{1*}

¹*Institute of Plant Protection, Chinese Academy of Agricultural Sciences, 100193 Beijing, China;*

²*Xinjiang Agricultural University, 830052 Urumqi Xinjiang, China*

*Correspondence: lgbcc@263.net (Zhang Z. H.)

To explain the relationships between different geographical population of *Locusta migratoria tibetensis* in phase gregarious and solitarious. Nine geographical populations of *Locusta migratoria tibetensis* collected 1119 individuals from different regions in the Tibetan Plateau during 2007 to 2010 and were investigated the numerical characteristics of phases gregarious and solitary for by numerical analysis on the tegmen (elytron) length-E, posterior femur length-F, maximum width of head-C, E/f, F/C of female and male adults of the geographical populations. The results of Cluster analysis and principal component analysis were similar. Nine geographical populations were divided into three groups in the gregarious phase: Group I include the BBNT geographical population from Baiba Nyingchi Tibet in Brahmaputra River Valley (N: 29° 43' 23.06", E: 094° 18' 06.72", 3018m) and BDGS geographical population from Bamei Dawu Garze Sichuan in Yalongjiang River Valley (N: 30° 35' 42.50", E: 101° 26' 45.00", 3541m); Group II includes BNT geographical populations from Burang Ngari Tibet in Majiazangbu River Valley (N: 30° 31' 12.70", E: 101° 29' 75.30", 3485m), CST geographical populations from Chatang Shannan Tibet in Brahmaputra River Valley (N: 29° 14' 35.49", E: 091° 19' 59.25", 3584m), LSGS geographical population from Luoxu Serxfi Garze Sichuan in Jinshajiang River Valley (N: 32° 31' 02.00", E: 097° 49' 14.50", 3358m); Group III includes the GNT geographical population from Gar Ngari Tibet in Sengezagbu River Valley (N: 32° 26' 42.60", E: 079° 09' 06.10", 4225m), XZNT geographical population from Xiangzi Zanda Ngari Tibet in Langqinsangbu River Valley (N: 31° 07' 09.25", E: 079° 51' 53.70", 4029m), RNT geographical population from Rutog Ngari Tibet in Sengezagbu River Valley (N: 33° 09' 25.64", E: 079° 09' 34.27", 4154m), NZNT geographical population from Nag Zanda Ngari Tibet in Langqinsangbu River Valley (N: 31° 05' 33.70", E: 079° 07' 98.50", 3756m). The results showed that the morphological indicators elytron length, posterior femur length, maximum head width, tegmen length and posterior femur length ratio, posterior femur length and maximum width of head ratio can be used as parameters to analyze the gregarious phase of different geographical populations. It explained that there were strong geographic variations and species interactions in the gregarious phase. While it was significantly different with solitary phase of the nine geographical populations, and no obvious combinations were observed. Morphometric variations in the gregarious phase of nine geographical populations may attributed to climate, weather and habitat variations, the degree of isolation of the populations, as well as variations in their overall size and density.

Recent progresses of control technologies for locust plague in China

Zhang, L¹; Yang, PY²; Li, L¹; Lu, WG³; Zhu, JQ²; Zhang, J¹; Lin, YR⁴; You, YW⁵; Zhang, SM⁶; Lv, GQ⁷; Gao, Q¹; Zhang, ZW⁸; Wang, LM⁹ and Kuiban, A¹⁰

¹China Agricultural University, Beijing, 100193, China;

²Chinese National Agricultural Technology Extension Center, Beijing, 100026, China;

³Peking University, Beijing, 100191, China;

⁴The General Plant Protection Station of Shandong Province, Jinan, 25010, China;

⁵High - Tech Research Center, Shandong Academy of Agricultural Sciences;

⁶Hebei Plant Protection and Plant Quarantine Station, Shijiazhuang, 050011, China;

⁷Henan Plant Protection and Quarantine Station, Zhengzhou, 450002, China;

⁸Tianjin Plant Protect and Plant Quarantine Station, Tianjin, 300061, China;

⁹Chifeng Plant Protection and Plant Quarantine Station, Chifeng, 024000, China;

¹⁰Agricultural College of Xinjiang Agricultural University, Urumqi830006, China

Locust plague threaten to agriculture because it currently infests more than 2 million ha annually in China. There are many technologies have been developed since ancient time. But development of more efficient, green and intelligent control measures has been conducted to meet the need of ecologically sound and less labor locust control.

We first figure out the aim of locust plague control, that is green, higher efficient, precision, and intelligent. According to the aim, we divided our researches into four key links based on locust plague control process, forecasting, control measures, application measures, allocation, monitoring and assessment. We have developed novel measures or devices for each of the links.

We have screened three higher virulence strains of *Nosema locustae*, the strains exhibit 2 times higher in virulence than original. The mass producing technology for *N. locustae* spores has been highly improved, and *Nosema* two new water based formulations have been developed. In order to have more effective we combined both *Nosema* and *Metarhizium* spore at certain ratio, and found this can increase highly mortalities of locusts both in laboratory and field. We also found an attractant for gregarious nymphs. This attractant can significantly. Besides, we found two anti-feedants for locust based on the study on binding property of odorant binding proteins of locust. We performed an consecutive investigation on epizootics of *Entomophaga grylli* in Xinjiang province from 2010-2012, and found that this pathogen can cause very high infection in local grasshopper populations, by over 80% some time, and the threshold for infection is quite low, by 1 individual/m², indicating that this grasshopper disease is the predominant factor to regulate local grasshopper populations.

Recently we have develop a locust plague control information platform which plays important role in monitoring, forecasting and decision made assisting, and allocation of labor and materials for control, based on global positioning system, geographical information system and remote sensing system. This platform covered the whole locust breeding region of China. This platform consists of mobile device for colleting locust occurring information, analyzing system and real-time allocating system. And this provides easier and procession location service to users.

Besides, we have developed a procession auto-control airplane sprayer device. This device can

control automatically the switch to open or close the sprayer according to locust densities at GIS data. All of the technologies have been demonstrated for 6 years, covering 800,000 ha, and highly improved locust plague control level. This work was supported by the grant: public welfare fund for agriculture (200903021).

Functional Genomics & Molecular Biology

Molecular dissection of the circadian clock in the cricket, *Gryllus bimaculatus*

Tomioka, K; Uryu, O; Komada, S; Moriyama, S and Yoshii, T

Graduate School of Natural Science and Technology, Okayama University

Most insects show daily rhythms in their physiology, including general activity, responsiveness of the sensory systems, hormonal secretion, etc. The rhythm is driven by an endogenous timing mechanism, so-called circadian clock. Although the molecular oscillatory mechanism has been extensively studied in the fruit fly, *Drosophila melanogaster*, recent progress in molecular technology allows us to use crickets as a new model insect. We have investigated the molecular clock work in the cricket, *Gryllus bimaculatus*. We first made molecular cloning of clock and clock-related genes such as *period* (*per*), *timeless* (*tim*), *Clock* (*Clk*), and *cycle* (*cyc*), and found that *per*, *tim* and *cyc* showed a clear rhythm under light-dark cycle, and the rhythms for *per* and *tim* persisted in constant darkness. Unlike in *Drosophila*, however, *Clk* showed no clear rhythmic expression.

To examine the role of clock genes in circadian rhythm generation we adopted a RNA interference (RNAi) technology. RNAi is a natural process that cells use to turn down, or silence, the activity of specific genes. The RNAi is triggered by double-stranded RNA (dsRNA) molecules that enter a cell. We first tested the effectiveness of the RNAi using dsRNAs artificially synthesized from *per* and *Clk* genes. Results showed that dsRNAs effectively knocked-down mRNAs of the corresponding clock gene; higher concentrations of dsRNA principally yielded a more efficient knock-down of mRNA levels, and the effect of RNAi reached its maximal 1-2 weeks after the dsRNA injection, suggesting a slow and long-term effect of RNAi.

We then tested the effects of RNAi of clock genes on the circadian rhythms. The RNAi revealed that *per* and *Clk* play important roles in rhythm generation: Their RNAi resulted in a loss of the locomotor rhythm. The treated crickets also lost the molecular oscillation of all the clock genes tested. However, *tim* and *cyc* seemed not essential but play important roles in the rhythm generation because their knock-down never lead to a loss of the locomotor rhythm but shortened or lengthened the free-running period, respectively. Measurement of mRNA levels revealed that the molecular oscillation only partially disrupted. In *tim* RNAi crickets, the oscillation of *per* and *cyc* was disrupted but *cryptochrome 2* maintained a rhythmic expression. Interestingly, in *cyc* RNAi crickets, rhythmic expression was observed not only in *per* and *tim* but also in *Clk*. This fact suggests that the cricket circadian clock possesses mechanisms for oscillation of both *cyc* and *Clk*. In insects two types of expression pattern are known for *Clk* and *cyc*: only *Clk* is rhythmically expressed in some insects such as the fruit fly and the sandfly, while *cyc* does in others such as the honeybee and the monarch butterfly. Our results suggest that an ancestral insect probably possessed the oscillatory mechanisms for both *cyc* and *Clk* but in higher order insects either of these two clock genes might have lost its rhythmic expression in due course of evolution. This view is strengthened our recent finding that the firebrats show rhythms of both *cyc* and *Clk* in certain conditions.

For photic entrainment, we found that opsin genes expressed in the compound eye play important roles. In the cricket compound eye, three opsin genes, *opsin-UV*, *opsin-Blue* and *opsin-LW* are expressed in gene-specific regions. Knocking-down of each *opsin* gene by RNAi had specific effects

on the photic entrainment: *opsin-LW* RNAi decelerated but RNAi of *opsin-UV* and *opsin-Blue* both accelerated entrainment at least in advance shifts. The results suggest that the photic information affects the molecular oscillatory mechanism through opsin-specific pathways to cause phase shifts. On the basis of these results, the organization of the cricket circadian timing system will be discussed and compared with that of other insects including *Drosophila*.

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RNA interference in the desert locust, *Schistocerca gregaria*

Verlinden, H; Wynant, N and Vanden Broeck, J

Molecular Developmental Physiology and Signal Transduction, KU Leuven, Naamsestraat 59, P.O. Box 02465, B-3000 Leuven, Belgium

RNA interference (RNAi) is initiated by double-stranded (ds) RNA molecules in a cell's cytoplasm, where they interact with the catalytic RNA-induced silencing complex (RISC) component *argonaute*. When the dsRNA is exogenous, it is transported directly into the cytoplasm and cleaved in short fragments (short interfering (si) RNA) by the enzyme *Dicer*. These siRNAs separate in single strands and integrate into an active RISC, which will then base-pair to its target mRNA and induce cleavage.

The selective and robust effect of RNAi makes it a valuable, widely used research tool for suppression of specific genes of interest. A considerable number of successful systemic RNAi-experiments have been reported in insects, but different insect species do not show the same degree of sensitivity towards dsRNA. Therefore, we conducted a comprehensive study of the systemic RNAi-response in the desert locust, *Schistocerca gregaria*. Intra-abdominal injection of dsRNA for two housekeeping genes (*α -tubulin 1a* and *gapdh*) in the range of picograms per mg tissue induced a potent transcript knock-down which significantly increased in a 10 day period, although the male and female reproductive systems displayed a more moderate response. Tissue distribution analysis of the transcript levels of putative RNAi-related genes indicated reduced levels of two genes, namely *dicer-2* and *argonaute-2*, in the reproductive tissues. Decreased transcript levels of these two genes may be major determinants for the tissue-dependence of the RNAi-response in the desert locust.

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Can epigenetics explain the swarm?

Boerjan, B¹; Van Eynde, A²; Bollen, M²; De Loof, A¹ and Schoofs, L¹

¹*Research Group of Functional Genomics and Proteomics, Department of Biology, University of Leuven, 3000 Leuven, Belgium;*

²*Laboratory of Biosignaling & Therapeutics, Department of Cellular and Molecular Medicine, University of Leuven, 3000 Leuven, Belgium*

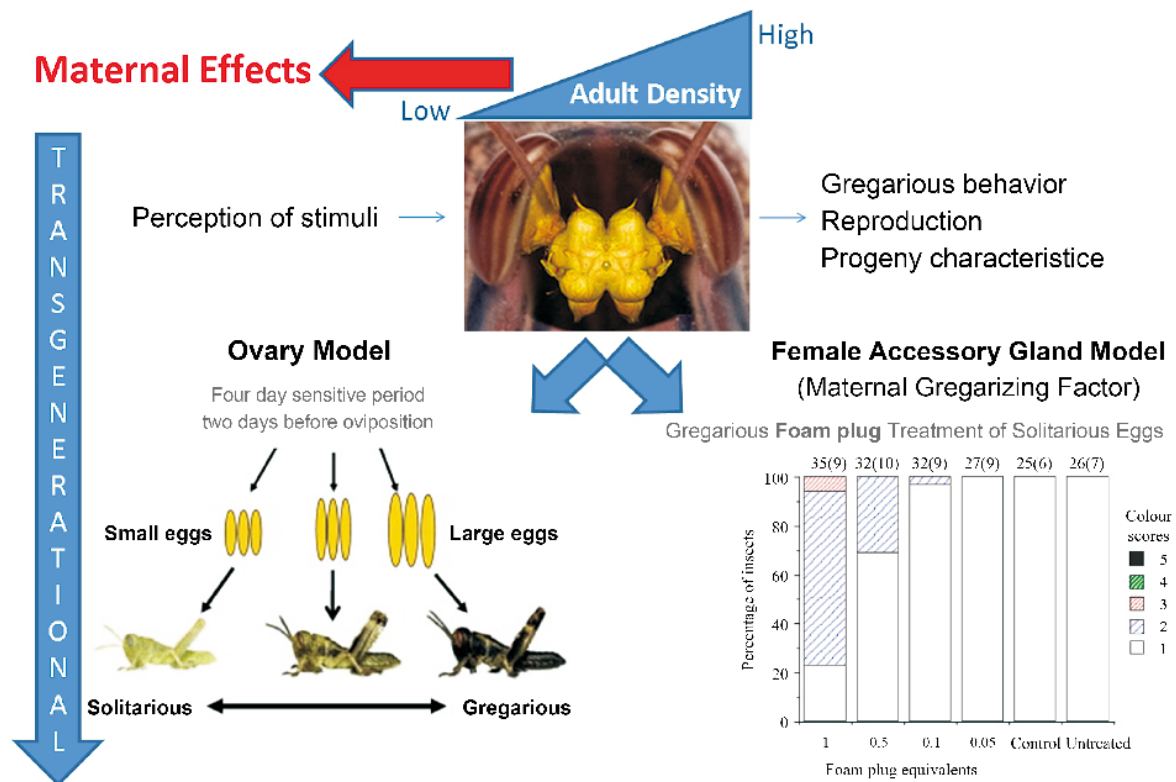
Our observation that longevity gets imprinted in very early life by crowding of young desert locust hatchlings points to a mechanism that is likely an addition to an endocrinological control. Furthermore, both juvenile hormone and ecdysone might be important but overlooked mediators of epigenetic control of gene expression, in particular at high hormone levels. Hence, we coined the term 'epi-endocrinology' to indicate that epigenetics may complement classical arthropod endocrinology. Trans generational, maternal and epigenetic transmission have been used in literature to describe the dynamics of progeny characteristics. Desert locust female adults respond to crowded conditions by changing fecundity and the body size and coloration of hatchlings. Two models, describing progeny behavior and/or coloration, have been proposed from an adult female's perspective.

Do epigenetic mechanisms account for trans generational effects on both longevity and fecundity in the desert locust? Recent experiments and collaborations have focused on gaining additional proof for this hypothesis and include both the study of DNA methylation and histone modifications. Initial proof for epigenetic machinery was mined through BLAST searches from a desert locust EST-database. Next, the existence and amount of 5mdC (5-methyl-deoxy-cytidine) had to be confirmed in order to continue our epi-endocrinological approach. A mass spectrometrical approach was used for the quantification of nucleosides from tissue extracts. Depending on the methylation status of the cytidine residue, 5-methyl-2'-deoxycytidine (5mdC) might be detected. In our quest for identifying more DNA methylation machinery, the Dnmt1 catalytic domain fragment was amplified from brain cDNA. Deep sequencing libraries were prepared from brain mRNA (transcriptome). Paired-end sequencing was performed on an Illumina HiSeq system. Preprocessed data were assembled around the Dnmt1 catalytic fragment. For a methylome characterization of the gregarious phase, a library for genome-scale bisulfite sequencing (Paired-end Illumina HiSeq) was prepared. Sequencing data have been deposited in the GEO database under the accession number GSE41214. In recent experiments we extended our approach the study of posttranslational histone modifications in relation to desert locust phase change. Here, different mouse or rabbit antibodies against modifications of humane histone H3 (Acetylation (Ac), phosphorylation (P), trimethylation (me3)) of histone 3 (H3) were tested and evaluated by means of immunoblot analyses.

BLAST searches in the EST-database revealed different components of both the DNA methylation and histone modification system. Searches with queries of Dnmt1 and 3 did not result in any significant hit. Initially, proof was found for both Dnmt1 and Dnmt2 expression in the desert locust. However, further analysis of the dnmt1 sequence we reported^[1] revealed that this sequence does not contain any of the conserved catalytic motifs of Dnmt1 enzymes. Further analysis of the *Tribolium* genome sequencing data, that provided our initial hit, strongly suggested that the predicted Dnmt1-like

gene with a cullin domain, hence, our first reported Dnmt1 sequence is an artifact from the genome assembly process. Besides the four standard nucleosides, a clear peak for 5mdC was observed in the LC-MS chromatogram. The percentage of methylated cytidines in different tissues varied between 1.3 and 1.9. Complementary, using genome-scale bisulfite sequencing we have shown that the *S. gregaria* methylome is characterized by CpG- and exon-specific methylation. We used this sequence information to calculate the total cytosine methylation level and found it to be 1.3% for brain tissue and 1.4% for metathoracic ganglia (MTG). The presence of a Dnmt1 homologue in *S. gregaria* was further confirmed by a transcriptome-scale shotgun cDNA sequencing approach and by a BLAST search for sequence fragments with significant homologies to *Apis* Dnmt1a. In contrast, no evidence for dnmt3 was found in the *S. gregaria* transcriptome sequencing data. We detected robust levels of rDNA methylation in brain and in MTG, suggesting that repetitive sequences are methylated. Further analysis revealed high methylation levels for both transposable sequences (e.g. mariner-like elements) and transposases. In animals, methylated genes are often characterized by a lower than expected density of CpG dinucleotides. CpG observed/expected (o/e) ratios analysis for all *S. gregaria* contigs revealed a characteristic bimodal distribution, with the two groups separated at 0.51 and a pronounced peak at low ratios. We also found that contigs with low CpG(o/e) ratios had substantially higher average methylation levels than contigs with high CpG(o/e) ratios. In subsequent experiments we have determined the mRNA expression levels for 6 contigs by quantitative RT-PCR (both high and low methylation level). The results showed that expression levels varied greatly among both unmethylated and methylated gene contigs. With this methylome characterization^[3] by means of deep sequencing, we have currently reached the limits of our desert locust methylome analyses without a reference genome. In a pilot scale immunoblot analysis, we evaluated the abundance of nine histone modifications in the adult brain of both phases (H3-S10P; H3-S28P; H3-T3P; H3-T11P; H3-K4me3; H3-K27me3; H3-K9me3; H3-K9Ac; H3-K27Ac). Differential analysis between brain extracts revealed differential phosphorylation with hyperphosphorylation in the brain of gregarious animals.

In honeybees, epigenetic mechanisms that regulate gene expression are undoubtedly linked to phenotypic plasticity (e.g. caste differentiation). Here, we show that all necessary components for this system to be operational in locusts as well, are present. Both DNA methylation and histone modification mechanisms are likely to be involved in different aspects of locust phenotypic plasticity. Because there is crosstalk between both epigenetic mechanisms, fixed epigenetic states at the histone level might be paralleled by a similar state at the methylome level. As we are approaching the boundaries of DNA methylation studies without the presence of a fully sequenced genome is available, future experiments will focus on how different histone modifications relate to locust phenotypic plasticity. Moreover, our pilot data might complement recent data^[4] where RNAi knockdown of a kinase (PKA), which has amongst his substrates amino acid residues of histone H3, counteracts gregarization. This might be reflected by the fact that hyperphosphorylation is observed in the gregarious brain.



Can Epigenetic Mechanisms Explain for Locust Phenotypic Plasticity?

DNA methylation versus Histone Modification

The ovary model, as forwarded by Seiji Tanaka and colleagues, states that the close relationship between egg size and the degree of melanization in hatchlings is pre-determined in the ovaries in a four day sensitive period two days prior to oviposition. The other model from Stephen J. Simpson and coworkers places the female accessory glands as key determiner of the progeny characteristics and states that solitary eggs are influenced by a small (<3 kDa), hydrophilic gregarizing factor that is produced in the female accessory glands and that is present in gregarious foam plugs. Later, this factor was analyzed by nuclear magnetic resonance spectroscopy and identified as an alkylated l-dopa analogue. Our work aims at revealing epigenetic mechanisms that might explain these trans generational phenomena and phenotypic plasticity in the desert locust.

New comparative genomic insights into Orthopteroid Insects

Chintauan-Marquier, IC^{1,2}; Grandcolas, P¹; Legendre, F¹; Desutter-Grandcolas, L¹ and Nichols, RA²

¹*Muséum national d'histoire naturelle, Département de systématique, évolution et biodiversité, UMR CNRS 7205, 57 Rue Cuvier, BP 50, 75231 Paris Cedex 05, France;*

²*Queen Mary University, School of Biological and Chemical Sciences, Mile End Road London E1 4NS, United Kingdom*

Comparative genomic approaches have great power to shed light on the function and organization of genomes, but these methods have mainly been applied in model organisms such as *Drosophila*, yeast and mammals, where sufficient genomic data has been available, or species of commercial or medical interest. With the advent of cheap, high-throughput DNA sequencing technology, this kind of data is being generated for non-model organisms, such as the “Orthopteroid” insects. Our team is applying both functional genomics and reverse genetic approaches to interrogate genome function and organismic complexity in eukaryotes by using taxa such as *Cryptocercus*, *Amphiacusta* and *Podisma*.

Inside the Melanoplinae: new molecular evidence for the evolutionary history of the Eurasian Podismini (Orthoptera: Acrididae)

Chintauan-Marquier, IC^{1,2}; Amédégno, C; Nichols, RA²; Grandcolas, P¹ and Desutter-Grandcolas, L¹

¹*Muséum national d'histoire naturelle, Département de systématique, évolution et biodiversité, UMR CNRS 7205, 57 Rue Cuvier, BP 50, 75231 Paris Cedex 05, France;*

²*Queen Mary University, School of Biological and Chemical Sciences, Mile End Road London E1 4NS, United Kingdom*

The Podismini are melanopline grasshoppers with a Holarctic distribution and well represented in the Eurasian fauna. To investigate their controversial taxonomy and evolutionary history, we studied 86%, 78% and 33% respectively of the Eurasian, European and Asian Palearctic genera (Otte, 1995; Eades et al., 2013). We reconstructed parsimony, maximum likelihood and Bayesian phylogenies using fragments of four genes (ITS1, 16S, 12S, CO2). We applied a Bayesian molecular clock to estimate the times of species divergence, and the event-based parsimony method to depict the biogeographic framework of the diversification. Our results suggest that the selected Eurasian Podismini constitute a monophyletic group inside the Melanoplinae, provided it includes the North American genus *Phaulotettix*. The clades proposed by the present study inside the Podismini do not fit the older morphological or cytological classifications, but are in agreement with more recent proposals. Furthermore, our results can be explained by a plausible biogeographic history in which the present geographical distribution of the Eurasian Podismini resulted from known changes, to the Cenozoic climate and vegetation, induced by major geological events including the genesis of high mountain chains (e.g., Himalayas, Altay, Alps) and large deserts (e.g., Gobi, Karakoum, Taklamakan), and the opening of marginal seas (e.g., Bering, Japanese and Yellow Seas).

A tree in the jungle: COI data in *Isophya***Grzywacz, B¹**; Chobanov, DP²; Heller, K-G³ and Warchałowska-Śliwa, E¹¹*Institute of Systematics and Evolution of Animals Polish Academy of Sciences Krakow, Poland;*²*Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria;*³*Grillenstieg 18, 39120 Magdeburg, Germany*

Isophya is one of the short-winged Palearctic genera of tribe Barbitistini in the subfamily Phaneropterinae (Orthoptera: Tettigoniidae). The intrageneric relationships are poorly understood and thus the groups of related species within the genus are still not defined. *Isophya* contains around 89 species in Central Europe and the Black Sea region (The Balkans, Asia Minor, Caucasus) and is characterized by high levels of endemism. Moreover, this genus includes a large number of morphologically similar species. Most taxonomic studies of *Isophya* species are based on classical morphological features and identification is oftentimes extremely difficult.

The main aim of the study is the analysis genetic variability between several taxa within the genus *Isophya* using the molecular data, cytogenetic information and revision of current taxonomic. The material studied consisted of 33 species, including 7 species from outside group belonging to the genera *Ancistrura*, *Andreiniimon*, *Barbitistes*, *Lepthophyes*, *Metaplastes*, *Phaneroptera* and *Tylopsis*. The molecular research based on mitochondrial DNA cytochrome oxidase subunit I. The total alignment of DNA fragment consisted of 650 base pairs. Genes were sequences to establish a phylogenetic tree by using Bayesian Inference.

Preliminary data disagreed more than they agreed with results from cytogenetics and morphology, which may indicate *Isophya* taxa are phylogenetically quite young and/or in the process of fast evolutionary change. Still, many problems arise when trying to explain the results obtained from molecular data in the light of our present knowledge on the systematics of the group and although some discrepancies with earlier data exist, the study may be the basis for future reconstructions of the relationships of *Isophya*.

Biogenic amine receptors in the desert locust and their role in behavioral gregarization**Vleugels, R;** Verlinden, H; Verdonk R and Vanden Broeck J*Laboratory for Molecular Developmental Physiology and Signal Transduction, Zoological Institute, KU Leuven, Naamsestraat 59, 3000 Leuven, Belgium*

Biogenic amines are known to play a crucial role in many key processes throughout the animal kingdom, including the regulation of mood and emotion, sleep, circadian rhythms, nutrition, behavior, development, learning and memory formation. Our research focused on the role of three major insect biogenic amines (octopamine, serotonin and dopamine) in the behavioral changes of the desert locust, *Schistocerca gregaria*. Desert locusts are known for their extreme, density-dependent phenotypic plasticity between a harmless solitary and a swarming gregarious phase. This phase transition is a multilayered process with a remarkable, very rapid switch in behavior from shy solitary animals to mutually attracted gregarious locusts. Studies have shown that these initial behavior changes are influenced by biogenic amines in several locust species, including *S. gregaria*.

Sequencing data from a recently assembled transcriptome of *S. gregaria* made it possible to amplify sequences of several biogenic amine G protein coupled receptors (GPCRs). Analysis with real-time PCR showed that these receptors are highly expressed in the central nervous system. Moreover, transcript levels of the receptors were differentially expressed in long-term gregarious locusts compared to long-term solitary locust. The very sensitive systemic RNA interference (RNAi) response in locusts allowed functional knockdown studies. The effect of a receptor knockdown on the speed of behavioral gregarization was investigated based on the performance of individual locusts in an observation arena before and after a period of forced crowding. Possible roles in the behavioral gregarization process could be assigned to different biogenic amine GPCRs. These behavioral data can form a link between biogenic amines and PKA, which were both shown to play a role in behavioural gregarization in *S. gregaria*. By activating receptors positively coupling to the adenylate cyclase (AC) – cyclic AMP (cAMP) – protein kinase A (PKA) pathway, the signal of biogenic amines can be passed on to PKA. The negative coupling of e.g. 5-HT₁ type serotonin receptors to the PKA-pathway can serve as a negative feedback mechanism to regulate phase-related behavior.

The whole genome sequence of the migratory locust, *Locusta migratoria***Wang, XH**; Yang, PC; Jiang, F; Zhao, DJ and Kang, L*State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences, Beijing, China*

Locusts represent the world's most destructive agricultural pests and a model system in entomology; however, the lack of genetic information has limited locust research. We sequenced the genome of a single eight-generation inbred female individual of *L. migratoria* using the Illumina HiSeq 2000 sequencing platform. We achieved a final assembly of 6.5 Gb with a length-weighted median (N50) contig size of 9.3 kilobases (Kb) and scaffold N50 of 320.3 Kb, which is the largest sequenced animal genome so far. We constructed further a genetic map containing eleven major linkage based on 8,708 makers using restriction-site-associated DNA sequencing (RAD-seq) data. We annotated the genome and predicted 17,307 gene models and identified over 2,639 different repeat families. Repetitive elements constituted ~60% of the assembled genome. Methylome and transcriptome analyses revealed a set of genes involved in phase change. We found significant expansion of gene families associated with long-distance flight capacity and phytophagy. We also provide a list of hundreds of potential insecticide target genes including cys-loop ligand-gated ion channels, GPCR, and 'lethal genes'. The *L. migratoria* genome sequence offers new insights into the biology and sustainable management of this pest species, and would promote its wide use as model system.

Barbitistini under the molecular eyeglass

Grzywacz, B and Warchałowska-Śliwa, E

Institute of Systematics and Evolution of Animals Polish Academy of Science in Kraków

The tribe Barbitistini (Orthoptera, Tettigoniidae, Phaneropterinae), sometimes considered as the subfamily Barbitistinae (Phaneropteridae), includes 15 genera and about 300 species widely distributed in the Western-Palearctic region. All members of the group are characterized with their high specialization for a settled way of life, narrowly connected with their food-plant. All species possess reduced wings with well-developed structures for sound production. Typical for the group is that most genera are clearly defined while the relationships between them are ambiguous and poorly understood. The typical Barbitistini (sensu Heller 1990) with few genera, e.g. *Barbitistes*, *Metaplastes*, *Ancistrura*, *Isophya*, *Poecilimon* and *Polysarcus* form a natural group of the most highly specialized taxa. More distant are the long winged genera of *Lepthophyes* and *Andreiniimon*.

The aim of the present study was the analysis of genetic variability of Barbitistini including representatives of as many genera as possible of this group and related outgroup taxa based on molecular data. Additionally, we will try to answer to question: "Do the molecular data confirm the monophyly of Barbitistini?" To clarify the molecular relationships we included 29 bush cricket species belonging to 8 genera of the tribe Barbitistini and 13 species as outgroup from 5 other tribes (*Phaneropterini*, *Tylopsini*, *Acrometopini*, *Ducetiini* and *Odonturini*) and other subfamily (Tettigoniinae). The genetic variability of all taxa was examined by using nuclear DNA sequences: 18S and internal transcribed spacer 2 (ITS2). In particular, we sequenced 1100 base pairs of two nuclear genes. Phylogenetic topologies were estimated using Bayesian inference. No polymorphism in nuclear DNA sequences was detected between specimens belonging to particular species and only single sequences (haplotypes) were used in analyses for each species. Six phylogenetic lineages were distinguished in the rDNA tree. The first, second and third lineages are represented by outgroup taxa. Clade fourth includes 6 *Poecilimon* species and 4 *Polysarcus*. In clade fifth two subclades are recognized: A represented by *Lepthophyes*, *Andreiniimon*, *Metaplastes*, *Ancistrura* and *Barbitistes*; and B comprising *Isophya* species.

Results were compared with cytogenetical data, the two analyses producing partly complementary and congruent conclusions. The monophyly of Barbitistini was supported based on topology of phylogenetic tree. The present study revealed a rather well resolved phylogeny at species level identifying a number of clades. Our study creates a basis for future investigations of monophyletic origin of tribe Barbitistini. Further studies should focus on the including more genes and longer sequences will contribute to a better understanding of the evolutionary processes of this bush cricket group.

**Analysis of whether non-functional or functional structures have more taxonomic value:
Geometric morphometric analysis of the variation in size and shape of the fore wing and hind
femur of *Sinopodisma* species (Orthoptera: Acridoidea)**

Huang NJ and Xu SQ*

Institute of Zoology, Shaanxi Normal University, Xi'an 710062 China

Taxonomic character selection is the core content of systematics, and it may affect species description, key editing, and phylogenetic analysis. Some taxonomists tend to prefer to use reproductive organs (such as genitalia) in systematics, while others like non-functional organs more than functional organs as they are less affected by environment. It is difficult to find out taxonomic characters from the continuous morphological structure but geometric morphometrics provides a new way to analyze the variation, and the taxonomic and phylogenetic value of morphological structures such as shapes and size. This study will use 137 male individuals of 14 micropterous grasshopper species of the genus *Sinopodisma* as material to distinguish whether non-functional or functional organs have more taxonomic value: we conducted geometric morphometric analysis of the *non-functional* degenerated fore wing and the *functional* powerful hind femur.

The results show that there is no obvious intraspecies size variation among fore wings and hind femurs, but there are significant interspecies differences. It appeared that the distal tip and posterior margin of fore wing plays more important role than the anterior margin in species differentiation. The most variable parts of hind femur were the widest part of the hind femur and the knee. We find that the non-functional degenerated fore wing had greater variation in size and shape than that of functional hind femur so that the forewing had more value taxonomically. A correlation analysis showed highly significant positive correlation between the size of fore wing and hind femur, which may be related to body size. The results of the UPGMA cluster analysis on species relationship using fore wing characters was not consistent with that resulting from using characters of the hind femur.

The gene expression profile during the development of solitary and gregarious phase of the migratory locust

Ma, ZY¹; Guo, XJ²; Xu, LL² and Kang, L^{1,2,*}

¹*Beijing Institutes of Life Sciences, Chinese Academy of Sciences, Beijing, China;*

²*State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences, Beijing, China*

The behavioral plasticity of locusts is a striking trait presented during the reversible phase transition between solitary and gregarious individuals of the migratory locust. However, the molecular mechanism of behavioral phase change during development of the migratory locust is less known. In this study, we applied microarray to investigate gene expression profiles during the development from the first to the fifth stadium of the migratory locust. Self organization map analysis reveals the specific gene clusters that potentially regulate the development of phenotypic traits associated with phase change of the migratory locust. During the development of gregarious nymphs, we found the largest number of differentially expressed genes in the transition from the first to the second stadium. During the development of solitary nymphs, we identified the largest number of differentially expressed genes in the transition from the fourth to the fifth stadium. The gene classes signalling transduction, RNA processing, molecular transport, cuticle protein and storage protein are highly active during the development of gregarious nymphs. In addition, the two-factor ANOVA analysis found 709 genes expressed differentially under interaction effect of phase and development. We found the gene classes signal transduction, RNA processing, molecular transport, cuticle protein and redox metabolism are active under the interaction effect. The specific gene classes identified during the development of solitary and gregarious nymphs are potentially involved in behavioral phase change of the migratory locust.

Transgenerational Epigenetic Inheritance of Population Density-dependent Phase Change Plasticity in the Migratory Locust

Chen, B¹ and Kang, L²

¹State Key Laboratory of Integrated Management of Pest Insects and Rodents, Beijing 100101 China;

²Institute of Zoology, Chinese Academy of Sciences, Beijing 100101 China

It is intriguing to know if environmental information experienced by parents can be inherited epigenetically to their next generation, i.e., the trans generational inheritance of environmental information. Population-dependent isolation and crowding are considered as social factors, critically affecting behavioral and physiological patterns. For example, the migratory locust, *Locusta migratoria* manifests remarkable phase change plasticity in which morphological, physiological and behavioral traits change in a population density-dependent manner. However, it is little known how the density alteration impacting on parents is inherited to their progeny. Here we undertook a study on the trans generational effects of density changes in the locust so as to answer: (1) what phase-related traits can be transmitted to progeny? (2) whether the traits are inherited by epigenetic mechanism? We established isofemale lines for gregarious and solitary locusts, and their isolated- and crowd-reared colonies, respectively. Strict matings were performed for the investigation on maternal and paternal effects of isolation and crowding. Phase traits in offspring eggs and hatchlings were analyzed by comparing the isolated- and crowd-reared lines and their control. Crowded-rearing of the solitary locusts or isolated-rearing of the gregarious locusts resulted in an apparent shift in the morphological characteristics in parents. Egg weights were significantly altered by parental crowding or isolation. Furthermore, nymphal weight and morphological trait (E/F) in the new hatchlings were also modified by parental density changes. Compared with controls, the trait variation resulting from crowding and isolation had been inherited to their progeny by both maternal and paternal effects. Our study demonstrated a density change-induced, both maternal and paternal, trans generational inheritance of phenotypic plasticity for which epigenetic mechanisms were proposed.

Using molecular markers in comparative cytogenetics of Pamphagidae grasshoppers with different types of the sex chromosome determination

Bugrov, AG^{1,2}; Jetybayev, IE^{1,3} and Rubtsov, NB^{2,3}

¹*Institute of Systematics and Ecology of Animals, SB RAS, Novosibirsk, 630091, Frunze str. 11*

E-mail: bugrov04@yahoo.co.uk;

²*Novosibirsk State University, Novosibirsk, 630090, Pirogov str 2;*

³*Institute of Cytology and Genetics, SB RAS, Novosibirsk, 630090, Academician Lavrentiev Avenue, 10*

E-mail: jetybayev@mail.ru; bugrov@fen.nsu.ru

It was believed that Pamphagidae grasshoppers have standard karyotype ($2n\♂=19$, and $2n\♀=20$ acrocentric chromosomes) with the $XO\♂/XX\♀$ mechanism of sex determination only (Camacho et al., 1981; Santos et al., 1983). However our comparative cytogenetic analysis of some Pamphagidae grasshoppers from Central Asia, the Balkan Peninsula, the Caucasus and Transcaucasia does not support the view of uniform karyotypes in Pamphagidae. At least two types of chromosome sets have been observed: 1) standard karyotypes with acrocentric chromosomes (*Asiotmethis muricatus* (Pall.), *Eremopeza festiva* (Sauss.), *Pezotmethis ferganensis*(Uv.), *Melanotmethis fuscipennis* (Redt.), *Thrinchus arenosus* B.-Bienko), *Strumiger desertorum* Uv., *Haplotropis brunneriana* (Sauss.) and 2) karyotypes with $2n\♂=16+\text{neo-XY}$ and $2n\♀=16+\text{neo-XX}$ (*Atrichotmethis semenovi* (Zub.), *A. turritus* Rme., *A. limbatus* (Charp.), *A. heptapotamicus* (Zub.), *A. zacharjini* (B.-Bienko), *Saxetania cultricolis* (Sauss.), *Paranocaracris bulgaricus* (Ebn. et Drenow), *P. rubripes* (F.-W.), *Paranocarodes straubei* (Fieb.), *P. chopardi* Peshev, *Nocaracris cyanipes* (F.-W.), *Paranothrotres opacus* (Br.-W.).

Using the method of fluorescence in situ hybridization (FISH) (Pinkel et al., 1986), we analyzed the distribution of rDNA, telomeric and original DNA probes generated by microdissection as molecular markers of chromosome evolution in Pamphagidae grasshoppers. The 18s rDNA probe hybridized with different regions of two, three or four chromosome pairs, including the sex chromosomes. In some cases, one of the large chromosomes demonstrated two sites of hybridization with the 18s rDNA probe. This is a specific feature of Pamphagidae karyotypes compared with another Orthoptera. Telomeric repeats (TTAGG) were located primarily on the ends of chromosome arms. The lack of a hybridization signal with this probe in the region of autosome-X-chromosome translocation (pericentromeric region of the neo-X chromosome) is probably the result of deletion of the euchromatic part of an autosome and its homologous neo-Y chromosome. It seems that deletion is the primary reason for the loss of homology between autosome and neo-Y chromosome.

The DNA probes were generated by micro dissection of sex chromosomes of different species. FISH of neo-Y DNA probe with chromosomes of the same species (*N. cyanipes*) revealed a strong signal in pericentric C-positive block on small neo-Y chromosome and a weak signal in other C-positive and euchromatic regions. The distal part of the neo-X chromosome of showed homology to the neo-Y DNA probe. Cross-hybridization of obtained probes showed no homology with the C-positive blocks on neo-Y chromosomes of close related species. We suggest that the reduction of the neo-Y chromosome size in Pamphagidae was due to deletion of the euchromatic part of the neo-Y chromosome accompanied by DNA amplification which led to formation of pericentric C-positive block. The lack

of a hybridization signal in pericentric C-positive regions of autosomes and the neo-X chromosome suggests that repeats in neo-Y chromosomes evolved independently from other C-positive regions. The presence of neo-Y chromosome at different stages of degeneration makes Pamphagidae a perspective model of sex chromosome evolution in animals.

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Chitin Metabolism Enzymes of *Locusta migratoria* and their Application in Pest Control

Zhang, JZ¹; Li, DQ¹; Liu, XJ¹; Ma, EB¹ and Zhu, KY²

¹Research Institute of Applied Biology, Shanxi University, Taiyuan, Shanxi 030006, China;

²Department of Entomology, 123 Waters Hall, Kansas State University, Manhattan, KS 66506, USA

Chitin is widely distributed in epidermis and the peritrophic matrix of insects. The importance of chitin in insect development and the absence of chitin in vertebrates have led to a hypothesis of attacking the insect chitin biosynthesis pathway as a novel target for developing safe and effective insecticides. The process of chitin biosynthesis and degradation consists of at least eleven key enzymes, but the roles of these enzymes in insect development have not been well elucidated. Five important genes putatively encoding glutamine: fructose-6-phosphate aminotransferase (*GFAT*), glucosamine-6-phosphate *N*-acetyltransferase (*GNAT*), UDP-*N*-acetylglucosamine pyrophosphorylase1 (*UAP1*), trehalase 1 (*TR1*), and chitin synthase 1 (*CHS1*) have been identified to be involved in chitin biosynthesis in *Locusta migratoria*. In contrast, multiple chitinase (*Cht10*) genes and one β -*N*-acetylglucosaminidase (*NAG1*) gene have been identified to be involved in chitin degradation. By using RNA interference in different nymphal stages, we observed that nymphs injected with dsRNA of *LmGFAT*, *LmUAP1*, *LmCHS1*, *LmCht10* or *LmNAG1* developed slowly, failed to detach from the old cuticle during the molting process and has high mortality. When RNAi suppressed the expression of *LmCht10*, we found significantly reduced new cuticle development and cuticle thickness as compared with those of the dsGFP-injected controls. Our results suggest that *LmGFAT*, *LmUDP1*, *LmCHS1*, *LmCht10* and *LmNAG1* are essential for insect growth and development. The enzymes encoded by these genes could potentially serve as an excellent target for developing novel strategies for controlling this important pest.

Molecular Cloning, Characterization and Functional Analysis of Glutathione S-Transferase genes from *Locusta migratoria***Ma, EB**; Zhang, XY and Zhang, JZ*Institute of Applied Biology, Shanxi University, P. R. China*

In this present research, 28 full length cDNA sequences of cytosolic GST genes were obtained based on the transcriptome database of *Locusta migratoria*. The NJ phylogenetic tree suggested that all these genes belong to 6 GST families, in which sigma and epsilon were the two biggest families. The expression patterns of ten glutathione S-transferase genes from nine different tissues, including foregut, midgut, gastric caecum, hindgut, Malpighian tubules, fatbodies, muscles, spermaries and ovaries, were analyzed, the results showed that most of genes were mainly expressed in midgut, gastric caecum, Malpighian tubules and fat bodies. The function of five glutathione S-transferase genes were studied by RNAi, and the results showed that the Sigma GSTs played an important role in both carbaryl and malathion detoxification.

Culture & Education

From St. Urho to Heavy Metals: Delivery of Orthopteran content to non-entomological audiences**Bomar, CR***Interim Dean, College of Science Technology, Engineering and Management, Executive Director, Orthopterists' Society, University of Wisconsin-Stout, Menomonie, WI 54751 USA**E-mail: bomarc@uwstout.edu*

The American view of Orthoptera varies historically and has had multiple influences. As a “melting pot” society, many cultures have provided both positive and negative contextual contexts for Orthoptera. As tokens of emergence and festival icons, they represent enormous cultural centerpieces. As educators, we have an opportunity to expose a wide array of learners to the wonders of Orthoptera and the value and influence they have had on our society. Integrating nontraditional Orthopteran content into coursework for science majors, as well as non-science majors, provides unique opportunities for student learning.

History of Cricket Culture in China

Shao, QM

BASF (China) Co. Ltd

There are estimated 3000 cricket species around the world. On the record there are 230 species of Grylloidea insect in China, which belong to 69 genera 10 families according to the morphology. To review the history about human utilization of folk insect, cricket is the most common insect found at different cultural field, such as science, literature, philosophy and art. Fighting cricket as a game was already very popular more than 1000 years ago. And the chirping of the crickets was also enjoyed by Chinese people long time ago. There are more than 20 books describe the color, the life habit, feeding mode and fighting behavior of crickets until now. Here, as a traditional Chinese cricket cultural, the fighting and the chirping of cricket from the ancient times to the present will be introduced.

Perception of Orthoptera in religion and culture

Babah Ebbe, MAO and Maeno, KO

Centre National de lutte antiacridienne, BP :655, Tinnessoueilem, Nouakchott, Mauritania.

E-mail: maouldbabah@yahoo.fr, otokomaeno@yahoo.co.jp

Among all *Orthoptera*, the locusts of the family Acrididae, particularly *Schistocerca gregaria*(Forskål, 1775), have always been feared for their adverse effects on agriculture and pasturelands. These locusts have been mentioned in many religions and cultures. Judaism, Christianity and Islam referred to these pests in their holy books (the Torah, the Bible and the Koran) more than 3000 years ago. They speak primarily, and almost in the same way, about locusts as the penalty that God imposed on the Pharaoh of Egypt after Moses' warning (the famous 8th plague of Egypt). But there are many other statements about locusts in the holy books. For instance, the resurrection of the dead after the Judgment Day is often described as being similar to a massive locust larval hatching in the Koran. The kosher or halal aspects of locusts are also discussed in these books, sometimes with great detail in the description of the characteristics of the different edible locusts such as in Torah. These descriptions from biblical times are consistent with the current dietary habits in some regions of Asia and Africa. In terms of culture, the term "locust" in literature and poetry is synonymous with abundance or greed. Finally, in Islam locusts are considered to be the last creatures that will disappear from this world. As a consequence, their presence reassures some people about the continuity of life. The proposed presentation will discuss all these aspects in detail.

Orthopteroids in Mexican Culture

Mariño-Pérez, R

Department of Biology, University of Central Florida, Orlando, USA

Mexico is a combination of indigenous people and Europeans, which causes the Mexican Culture to possess both “oriental” and “occidental” cultural approaches. Orthopteroids have played an important role and, apart from being used as food, they are present in myths, tales, and songs. The word “grasshopper” in Spanish is “saltamonte”, however, in Mexican Spanish the word “chapulin” is more commonly used. This word comes from nahuatl (the language spoken by the Aztecs): chapa(nia), which means “bounce” and ulli, or “rubber”, and, therefore, together, the word means “insect that jumps like a rubber ball”. This concept first appeared in the Florentine Codex (XVI century) and introduced different species with similar roots, like: “Acachapoli” (*Schistocerca* spp.); “Tiectli chapoli” (*Melanoplus* spp.); “Xopanchapoli” (*Sphenarium* spp.); “Cacatecuilichtli” (*Microcentrum* spp.) and “Colacachapoli” (*Taeniopoda* spp.).

In Mexico, both adult and nymph Orthoptera are eaten, mainly in the Acrididae family although species of the Pyrgomorphidae genus *Sphenarium* are widely eaten and harvested. 78 species belonging to 42 genera and 5 families are used as food, mainly in the southern part of Mexico. Also, in Mexico, the most popular and common name for a praying mantis is “campamocha”, which comes from the nahuatl phrase “kampa mo chantli”, which literally means “where is your home?” and makes reference to different tales in which people are lost and after finding a praying mantis, it indicated the correct direction to follow using its legs.

The common name in Mexico for walking stick insects is “zacatones” (dry grass) and there is a very common myth that when they, and praying mantids, are eaten accidentally by cattle and horses and they produce gas once inside the bellies of the farm animals, which inflates their bodies and causes death.

Lastly, the common name for earwigs in Mexico is “tjerillas” (small scissors) in reference to the posterior forceps and, as in other countries, there is a belief that an earwig enters into your different cavities (ears, nose) and causes damage by using its forceps.

Orthopterology and Jewish Tradition

Shor, N

The Jerusalem Academy of Jewish Studies, Dvar Yeroushalayim Yeshiva

Locusts have always been an important part of man's history. Traditions and stories about them are found in many cultures. Jewish tradition, based on the Bible and the Talmud, is particularly rich in such references.

According to Jewish tradition, locusts were created on the fifth day of Creation, referred to along with the Leviathan. The Talmudic commentary on this verse says that G-d created the Leviathan male and female, but had to kill the female, preserving her in salt for the saints to feast upon in the World to Come. If they had been permitted to multiply, the world could not have endured. In interesting parallel, Islamic tradition says Mohammed prayed that the grasshopper would have only 99 eggs, for otherwise, if it had 100, it would destroy the world.

To take the Jews out of Egypt, G-d sent ten plagues upon the Egyptians. The eighth, locusts, covered and destroyed all the food left in Egypt. Yet this brought joy to the Egyptians, for they salted these locusts and so, had much healthy food. G-d then said: "What! I sent them a plague and they rejoiced!" And He sent a wind that blew all the locusts into the Sea, including those which were salted.

As incredible as it sounds, the locusts of the Egyptian plague observed the Sabbath. In the Pentateuch, the Hebrew word for "and rested" are used only twice: once for these locusts and once for the fourth command, "Remember the Sabbath." Using the classical rules of interpretation of the Bible, the Sages understood from this that the locusts rested on the Sabbath day. The spies sent by Moses to explore the Land of Canaan told him they saw giants there, and that they felt "like locusts" in their eyes. Because they succeeded in discouraging their fellow Jews from conquering the Land, this date became a day of sorrow for the Jews from that time until the coming of the Messiah. In addition to the Egyptian plague, the prophecy of Joel also contains a beautiful description of a huge and destructive locust plague.

Locusts are the only insects that are kosher (allowed to be eaten by Jews). The Bible defines the sign to recognize kosher locusts: "Yet, these you may eat of every flying insect that goes upon four which have jumping legs above their feet, to leap with upon the earth; these of them you may eat: the *Arbeh* and its species, the *Salam* and its species, the *Chargol* and its species and the *Chagav* and its species." *Arbeh* corresponds to *swarms locusts*, *Salam* to *long-horned acridids*, *Chargol* to *katydid*s, and *Chagav* is both the individual species and the common name for locusts. There is a long discussion in the Talmud about this verse, in which the scholars attempt to define which locusts are kosher. Nowadays, only *Schistocerca gregaria* and *Locusta migratoria* are identified as kosher.

The supreme Jewish classical legal codification, the *Shulchan Aruch*, based on this Talmudic passage, definitively fixed the signs of kosher locusts:

- Four legs and four wings that cover most of the locust's length and the body circumference
- Two jumping legs for jumping on the earth
- The name of the locust must be *Chagav*, (or one must have a tradition that the name of the locust is *Chagav*).

Jews from Yemen, Morocco and Algeria still have the tradition of eating locusts. They all have the tradition (not written in *Shulchan Aruch*) that the kosher locusts bear on their thorax the Hebrew letter "n" (Heth) which is also the first letter of **Chagav**. In the tradition of Algerian Jews, locusts are very healthy for the heart. In Morocco, locusts were a component of the *Dafina*, the traditional Sabbath meal. In Yemen the Jews were very strictly orthodox, young men and women keeping separate. When there was a locust plague, however, they could meet. At night, groups of young men and girls left the fortified cities to collect the locusts early in the morning, and this was the opportunity to meet each other in order to get married.

According to the *Pirkei Shira*, every creation has a special song. The song of the locusts is: "I will lift up my eyes to the hills; from where will my help come? From G-d, Who made heaven and earth." Rabbi Chaim Kanievski explains this. Everyone tries to catch the locust: the sage, because by eating the locust in a special way, he will remember everything he learned; women, because it heals women's diseases; and children, because they play with them. Thus, since everyone wants to catch the locust, only G-d can save him. In Hassidic literature, the locust is the symbol of the vacated space needed by G-d, Who is not bound by time or space, to create this world, which is bound by time and space. "Locusts have no king," unlike ants or bees, and yet "they march in rank". There is Love and Unity between them. In Hebrew, each letter has a numerical value. *Chagav* (13) has the numerical value of Love and One (13). *Arbeh* (numerical value 208), the gregarious form of *Chagav*, is a multiplication of *Chagav* (13×4^2); maybe an allusion to the link between solitary and gregarious locusts 3,200 years before Uvarov !

At the time of the final Redemption, the Messiah will reveal the Secret of the Locust. Then all the veils that impede us from seeing the word in truth will fall away, and we will hear a new song of perfect melody. We all agree that locusts are very special creatures. They are not only plagues, they can be a blessing. Studying them in nature sometimes leads to unexpected uses. Studying them throughout human history can also bring important innovations in a variety of fields – for human and animal nourishment, for healing, in philosophy, faith and even, according to Jewish tradition to bring the Final Redemption.

Folk songs on Orthoptera in Turkish culture

Ünal, M

Abant İzzet Baysal University, Department of Biology, Bolu, Turkey

Grasshoppers and locusts have been effected people life in Anatolia for hundreds of years. Turkish people had been mostly subsisted on agriculture especially until last 50 years. Therefore the effect of the outbreaks of grasshopper and locust was very big. In Turkey people who subsisting on agriculture can pay their important expenses such as their debts and for weddings only after harvest and sell their crop. Especially the traditional weddings need much expenses and take three days. If the agricultural fields are harmed because of any reason such as climatic or grasshopper swarms, the farmers have to postpone their payment for debts or postpone the weddings next year. Besides in Ottoman Emperor time because of the grasshopper swarms some period extreme shortage of food in some region were occurred. These famines caused many death of people. These conditions influence deeply psychology of the people and especially the young couples. All of these negative effects caused to appear the anonymous folk songs on Orthoptera. Grasshoppers are negatively perceived, harmful and unlovable animals in Turkish culture. This negative perception is reflected to the lyrics of the folk songs. For example a quatrain in a song as follow:

Wing of the grasshoppers, What is this stubbornness, Bloody grasshoppers, Exterminated barley and wheat.

Another quatrain in a different song:

My grasshopper comes fly, Comes opening the wing, My big sized grasshopper, Comes mowing the crop

There are 4 folk songs recorded by the Turkish folk songs department of TRT (Turkish Radio and Television). These are: 1) My grasshopper comes fly, 2) Wing of the grasshopper, 3) The slipper of my locust, 4) I expelled locust to the field. All of these songs include people's negative opinions on grasshopper outbreaks. Grasshoppers are seen as nuisance, unpleasant problem and troublemaker animals. Besides some unlovable people are compared with grasshoppers because of their unguessable acts. For example there is a proverb that is said for people who frame up in secret: "Grasshopper jumps one time and second time, but captured in third time".

As it is seen grasshoppers are negatively perceived animals in Turkish culture. But, although the lyrics of the songs are mostly negative their lovable and dynamic musical sound make them very popular. They are played, singed in weddings or entertainments and are used to dance. It is an irony that these songs are very positively effected people's psychology. End of this study some examples of the folk songs are played.

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