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ORTHOPTERA IN A CHANGING WORLD

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12TH INTERNATIONAL CONGRESS OF ORTHOPTEROLOGY

PLENARY LECTURES

BIRTH AND EARLY CHILHOOD OF ORTHOPTEROLOGY IN SOUTH AMERICA WITH EMPHASIS ON NATIVE TAXONOMISTS.

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THE South American fauna is one of the most poorly known in the world, and the case of the invertebrate one, knowledge is still much more fragmentary than that of vertebrates. The situation for terrestrial invertebrates could perhaps be qualified as rudimentary. The size of the subcontinent, its landscape heterogeneity, the rich variety of vegetation types, presence of large areas of megadiverse tropical and subtropical forests and other factors, combined with the lack or insufficiency of taxonomists for many groups contribute for the extant paucity of faunal knowledge. In what concerns the order Orthoptera, knowledge on taxonomic diversity seems slightly skewed towards the Caelifera, group to which some genus-level revisions have already been presented mostly by native researchers from Argentina and Uruguay. Several European, North American, and a few native specialists have done the bulk of descriptions in both sub-orders. The purpose of this lecture is to present a brief compilation of the history of orthopterology in South America focusing on the role played by native taxonomists.

Key Words: History, Orthopterology, South America

ORTHOPTERAN SYSTEMATICS: PAST, PRESENT, AND FUTURE

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THE Orthoptera are the most diverse order among the polyneopteran insect lineages, with more than 26,000 described species. The Orthoptera consists of two monophyletic suborders, the Ensifera and Caelifera. The Ensifera consist of two infraorders, the Gryllidea and Tettigoniidea, and are characterized by long, flagellate antennae that are often longer than the length of the body, and a sword-like or needle-like female ovipositor. The Gryllidea include the superfamilies Grylloidea and Gryllotalpoidea, whereas the Tettigoniidea include the Schizodactyloidea, Rhaphidophoroidea, Hagloidea, Stenopelmatoidea, and Tettigonioidea. Collectively, the Ensifera include about 14,000 described species. The Caelifera also consist of two infraorders, the Tridactylidea and Acrididea, and are characterized by shorter antennae and the female ovipositor with only two valvular pairs. The Tridactylidea include The Tridactyloidea, whereas the Acrididea include eight superfamilies: Tegtrigoidea, Eumastacoidea, Proscopioidea, Tanaoceroidea, Pneumoroidea, Trigonopterygoidea, Pyrgomorphoidea, and Acridoidea. The Caelifera include more than 11,000 described species. With recent advances in phylogenetic studies, the higher-level relationships among different superfamilies in the Orthoptera are now relatively well resolved.

While higher-level relationships among major superfamilies are established, we are far from understanding lower-level relationships. In this presentation, I briefly review different phylogenetic hypotheses proposed by the pioneers of orthopteran systematics of the 20th century. Then, I highlight some of the major advances made using modern molecular data and contrast with previous hypotheses. I also highlight several clades that will require additional studies in order to fully understand their phylogenetic relationships and challenges in achieving the full resolution. Finally, I discuss about the promises and pitfalls of new genomic and transcriptomic data in resolving phylogenetic relationships of Orthoptera.

Key Words: phylogenetics, molecular data, taxonomic impediments

SURVIVAL IN FRAGMENTED LANDSCAPES – EFFECTS OF LAND-USE AND CLIMATE CHANGE ON ORTHOPTERA IN EUROPE

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ORTHOPTERA are important bioindicators of the effects of global change. Moreover, they are of high functional importance to open and nutrient-poor terrestrial ecosystems, e.g. as a crucial food resource for many vertebrate species.

However, these formerly widespread habitats are nowadays, due to land-use intensification or abandonment in most parts of Europe, often restricted to small and isolated remnants. Recently, climate change has become an additional factor that influences Orthoptera habitats and the distribution of the species.

The aim of this plenary talk is to disentangle the effects of current land-use and climate change on the long-term persistence of Orthoptera in European landscapes. Based on extensive field and laboratory studies ranging from the microhabitat and habitat to the landscape scale level, the most important drivers are highlighted. A special focus will be on the effects of habitat quality, habitat heterogeneity, patch size and landscape connectivity on Orthoptera diversity and dispersal. The presented examples cover research from semi-natural grasslands, heathlands and floodplains all across Europe (Fig. 1). Evaluations of habitat restoration to counteract the negative effects of global change are also shown. Based on the current knowledge I will give recommendations for the management of species-rich Orthoptera habitats in times of global change.

Key Words: Conservation management, Dispersal, Habitat quality, Landscape connectivity, Restoration, Semi-natural habitat

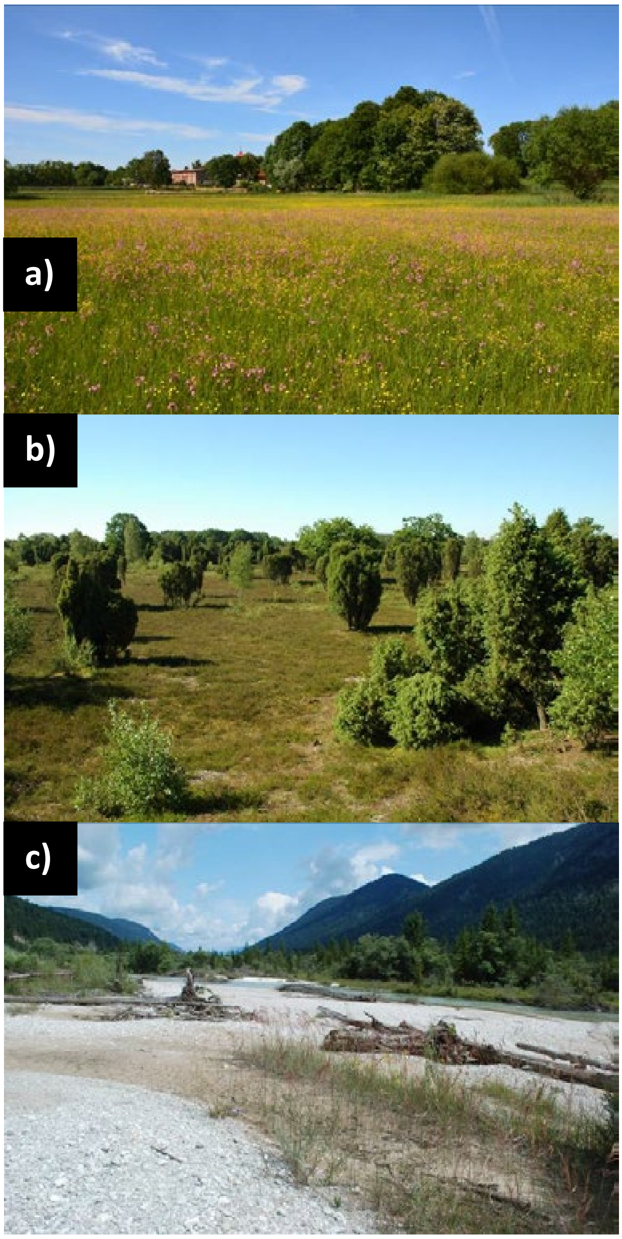

Figure 1. Semi-natural grasslands such as wet grasslands (a), heathlands (b) or natural floodplains (c) are important habitats for Orthoptera in Europe.

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NEW METHODS IN POPULATION GENETICS AND THEIR EMPIRICAL ASSESSMENT IN GRASSHOPPERS

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THE talk will successively present then demonstrate on observed data two new methods in population genetics.

First, in the field of inferential genetics, model choice and parameter estimation are pivotal statistical treatments to reconstruct population histories or processes from molecular data (e.g. invasion routes). These statistical treatments have greatly benefited from the development of approximate Bayesian computation (ABC). Pudlo et al. (2016; in prep.) proposed a new approach, named ABC-random forest (ABC-RF), to reliably choose among historical models and estimate demographic parameters, at a low computational cost and without having to choose among a large set of statistics summarizing genetic information. We here used the ABC-random forest method (ABC-RF) to unravel the evolutionary history of the African arid-adapted pest species, *Schistocerca gregaria*. We found that the processes that have shaped the present geographical distribution of the species in disjoint northern and southern regions of Africa were relatively recent, i.e. 4.7Ky (90%CI: 2.0 – 12.9). ABC-RF inferences also supported a southern colonization of Africa from a low number of founders of northern origin. Interestingly, such a young divergence history is better explained by the peculiar locust biology that involves a density-dependent swarming phase with some exceptional spectacular migrations rather than recent climatic and biogeographic mechanisms in Africa.

Second, in the field of landscape genetics, graphical visualization of genetic variation is a key initial step to uncover spatial structure and underlying landscape features (e.g. conservation of endangered species). This exploratory treatment has greatly benefited from the development of spatial networks based on pairwise (distance) metrics. Piry et al. (2016) proposed a new approach, named MAPI, to reliably map averaged pairwise information in variation surface that can be overlayed on land cover, without confounding effects resulting from isolation-by-distance and incorporating a reliable statistical test for spatial genetic structure. We here used the MAPI method to assess the genetic variation of *Prionotropis hystrix rhodanica*, a protected species endemic to the 'Crau' steppe in southern France. We found that the fragmentation of the landscape due to orchard fields impacted its genetic structure at a fine spatial scale.

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THE ENVIRONMENTALLY FRIENDLY TECHNOLOGY SYSTEMS FOR THE CONTROL OF LOCUSTS AND GRASSHOPPERS IN CHINA

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LOCUSTS and grasshoppers are a serious threat to stable food supply world-wide because of their voracious damage to crops when they outbreak. More than 1000 species of locusts and grasshoppers have been recorded in China, of which over 60 species are of great economic importance. Locust control has been playing an important and special role in plant protection. In fact, the battle between outbreak and control of grasshoppers and locusts has been lasting more than 3000 years. It is believed that the history of plant protection in China started from locust and grasshopper control thus making it the model system for other types of plant protection in terms of organizing and action patterns. Here we present a primary introduction to locust plagues and control in ancient China, then describe the locust control in the past century of which the recent progress in environmentally friendly controls has gained most emphasis in this paper. Finally, a prospect on application in the field is discussed.

1. Primitive locust and grasshopper control in ancient China

1.1. The earliest record on locusts in China can be traced to about 16 century B.C. until 1950s locust plague was recorded more than 800 times. Locust plague, as drought and flood, was one of the three most serious disasters in ancient time. The most harmful species in that time was *Locusta migratoria* which distributed mainly in central China, such as Shandong, Henan, Hebei, Jiangsu, Anhui, Shanxi, Guangxi provinces.

1.2. The descriptions about plagues in ancient records: ‘Locust migrated from east the swarms covered the sky, fed all of crops and grasses’ in 223 A.C., and other ‘Locust swarms migrated from east, covered the sun more than 10 days, locusts fed crops and plants, run out of food, people die of hunger.’

1.3. The primitive methods for control were manually: catching with hands or nets, swatting locusts with brooms, burning, and burying locusts. It is worth noting that ancient people conducted locust control in organized teams. From farmers to premier even emperor were involved in locust plague control. Moreover, a law for locust control had even been issued as early as Song Dynasty (1075).

1.4. The knowledge about locust plague was described non-experimentally with a lot of superstition in the ancient times. At the very beginning, people believed that locust plague was a punishment sent from heaven due to the evils people or governments did. Then in the subsequent centuries, it was a popular belief among folks that locusts were transformed from shrimps or other things although there already had some scientific descriptions on locusts. This interesting belief is based on the Hua-sheng (Organisms Transforming- Producing) Theory, meaning everything can transform from/to other things.

1.5. Features in this long period. Chinese people have suffered from locust plagues over 3000 years. In ancient times they observed and described many aspects of locust biology, though superstitious beliefs were more dominant. Locust controls were limited to manual actions, such as catch, burn, bury and swat. It is worth noting that it was always the governments that organize the fighting against locust plague.

2. Reforming breeding regions and chemical control (1930s-1980s)

2.1. In this period, locust plague outbreaks occurred frequently and infested widely.

2.2. After 1950s new strategies for controlling locust plague were proposed that focused on reforming locust breeding regions and chemical control. The locust control was mainly based on spraying chemical pesticides (from DDT to malathion) with hand and ground sprayers, and aircrafts started to be used in this process. The main reforming methods of the locust breeding regions included fixing riverways of Yellow river and Huai river, planting trees alternative to weeds, and establishing ponds for raising fish, etc. About 3.6 million ha locust breeding regions were reformed.

2.3. Several scientific research projects were conducted on locust biology and breeding region ecology, which greatly promoted understanding of locust outbreak and control.

2.4. A permanent locust control system has been established since then. The area of locust breeding regions was decreased by 1.5 million ha after reformed. There were only very few serious locust plagues though locust outbreaks still occurred every now and then. In 1985, locust swarms migrated from Tianjin to Hebei.

2.5. The technologies of monitoring and controlling the dynamics of locust and grasshopper populations had been all manual, mainly by excessively spraying chemical pesticides. As a result, monitoring and controlling were passive and inefficient, bringing environmental pollution and high chemical pesticide residues on agricultural products at the same time. This will not meet the requirements to establish an environmentally friendly and sustainably developed agriculture in China.

3. Environmentally friendly control systems (1990s-present)

3.1. The threat from locust plague still exists nowadays and more than 60 species of locusts and grasshoppers are recorded to be economical pests, including *Locusta migratoria, Oedaleus asiaticus, Oxya chinensis,* and *Calliptamus italicus* which are widely distributed in 1100 counties in 20 provinces of China. However, very few locust serious outbreaks actually occur at present. Since 1990s new strategies for environmentally friendly monitor and control technologies based on information technology, insect pathology, insect behavior, and molecular biology have been proposed and developed. The basic principle is to change the ecological system of locust breeding region, priority use of biological control and enhancement of biodiversity, combined with information technology, the control of locust and grasshopper outbreaks becomes more efficient.

3.2. The most striking progresses in locust control benefit from the development of biological control. Biopesticides, including protozoa, *Antonospora locustae* (former, *Nosema locustae*), fungus (*Metarhizium*), have already been widely used to this day. Some of these biopesticides from plant extracts, such as azadirachtin or matrine are also applied for control.

3.3. The conservation of natural enemies, including birds (*Strunus roseus*) etc. is applied in Northwest of China. Increasing biodiversity in the locust breeding regions by planting Chinese jujube, alfalfa and cotton to replace weeds (reed) is widely applied in Central and Eastern China.

3.4. The handset with customized software as well as auto-monitoring traps for monitoring locusts and grasshoppers have been rapidly developed and widely applied. An information platform has been established for integrating and analyzing information gained from different sources to improve the accuracy of forecast, which will greatly contribute to the real-time command and dispatch system as part of intelligent management of locust and grasshopper outbreaks. Based on GIS and GPS technologies precision spraying technology has also been developed with aircrafts.

3.5. All of these technologies have been integrated into 5 ecological regions and formed regionally specific technology systems for locust and grasshopper outbreaks management. The systems have been demonstrated to be effective and widely applied, covering more than 300 million ha in recent 20 years. The application of biological control increased to over 30% by now from less than 10% in 1988. The information platform has been widely used in over 95% of the agricultural regions in China. The efficiency of control increased over 30%, and 50% of labor was saved. Since 2009 large scale locust or grasshopper outbreaks have never occurred, whereas it used to be one outbreak/1.5 year before. Overall, the control of locusts and grasshoppers in China has been reformed to be environmentally friendly, intelligent and precise.

4. Prospects

4.1. Knowledge on locust and grasshopper biological features should be further explored to develop new methods based on new molecular targets.

4.2. Utilization of new natural enemy resources, such as parasitoids and new fungus need to be developed.

4.3. Novel methods, such as behavioral control, nanotechnology in biological control and unmanned aerial vehicle have now been studied, which prospectively exhibit potential in locust and grasshopper control.

4.4. Information technology and precision control are expected to be widely used.

Key Words: Conference, ICO2016, Brazil

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WORKSHOP

ORTHOPTERA SPECIES FILE: BEYOND A TAXONOMIC DATABASE

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THE Orthoptera Species File (OSF, http://orthoptera.speciesfile.org/) is a taxonomic database of the world's Orthoptera (grasshoppers, locusts, katydids, crickets), both living and fossil, updated daily with the most recent references. It has synonymic and taxonomic information for more than 27450 species, 44660 scientific names, 13400 references, 85400 images of type and alive specimens, 1490 sound recordings, and 93500 specimen records. Nowadays, the classification of Orthoptera shown in OSF is being used worldwide as the general reference for the group.

The workshop will be focused on the basic features of the public interface of OSF; information and contents of the database and the different types of search; features of the editing interface (adding images, specimens, changes related to the rank and status of taxon names; showing the way the program prevents changes that conflict with the rules of nomenclature). The potential of using OSF as a tool for producing systematic studies as a way of integrating many of the most recent cybertaxonomic tools with species descriptions will be presented in this workshop. An introduction to “Taxon Works” the new platform that will integrate the best features of Species Files software with other software (mx and 3i) will be presented. The possibilities of developing regional field guides with the information content in OSF will also be shown.

Key Words: OSF, cibertaxonomy, Taxon Works

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New generation sequencing (NGS) methods
RNA IN ORTHOPTERA INSECTS: INTRODUCTION TO THE RNA-SEQUENCING (RNA-SEQ) DATA ANALYSIS USING A CRICKET

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ADVANCES in sequencing and other data-intensive technologies are rapidly transforming life science, in particular by the introduction of the problem of "big data" storage and analysis. Some of the key large-scale research approaches in the biology of Orthoptera include the RNA-sequencing (RNA-seq) based transcriptome assembly and annotation, and gene expression analysis. RNA-seq has a wide variety of applications, but there is no optimal pipeline for the variety of different applications and analysis scenarios in which RNA-seq can be used. Scientists plan experiments and adopt different analysis strategies depending on the organism being studied and their research goals. For example, if a reference genome or transcriptome is available for the studied organism, it should be possible to identify transcripts by direct mapping RNA-seq reads onto this reference and identify these reads based on their homology with reference transcripts. By contrast, for organisms without reference genome or transcriptome, as is the case for the majority of Orthoptera taxa, first assembling reads *de novo* into contigs and then mapping these contigs onto the published genomes and/or transcriptomes would achieve the identification of homologous transcripts and their quantification. Using our results on an *Amphiacusta* cricket (Phalangopsidae), we introduce some primary steps in RNA-seq data analysis, including sample preparation, quality control of the reads, read alignment, gene ontology (GO) analysis, and quantification of transcript and gene levels. For this purpose, we use the portal "Discovery Environment" (DE), on CyVerse (ancient iPlant) cyberinfrastructure (http://www.cyverse.org/), which provides an accessible virtual workbench that enables all levels of expertise, ranging from students to traditional biology researchers and computational experts, to explore, analyze, and share their data. We highlight some challenges associated with each step. Finally, we discuss the outlook for novel technologies that are changing the state of the art in transcriptomics and in the study of Orthoptera biology.

Key Words: RNA-sequencing, CyVerse, transcriptome, homology, gene ontology (GO), gene expression, Orthoptera

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RECORDING AND SIGNAL PROCESSING

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ANIMALS use acoustic signals for communication using a wide range of frequencies in water, soil and air. Sometimes, these signals are not "sound" in the narrow sense of the word (i.e. mechanical compression waves that propagate through a medium and are detectable by the human ear). Various Orthoptera insects, katydids for example, communicate using sounds with frequencies higher than 100 kHz (100-150 kHz), far into the ultrasound range. Bats usually use ultrasound lower than these insect extreme frequencies (20-70 kHz for most species, but some up to 120 kHz). On the other side of the frequency spectrum are low frequency-vibrations, often not detected by hearing organs, but with other, less specialized sense organs. The examples include ground vibrations produced by elephants whose principal frequency component is around 15 Hz, and low- to medium-frequency substrate-borne vibrations used by many insects, usually in the range of 10-30 Hz. However the acoustic signals of many animal species lie within the frequency range detectable by a human ear, between 20 and 18,000 Hz. Mechanisms for sound production and detection are just as diverse as the signals themselves.

Given such a wide range of sound properties and the diverse media used to transmit the signals, specialized recording equipment may be required instead of the usual microphone: hydrophones for underwater sounds, ultrasound sensitive microphones for high frequencies in air, accelerometers or vibration meters for low frequency infrasound, or a laser vibrometer for vibrating surfaces. Computers are used for storing and analysis of recorded sounds. Specialized sound-editing software is used for describing and characterizing signals according to their intensity, frequency, duration and other parameters.

When recording acoustic signals in the lab or the field, not only the choice of recording equipment is important but also the proper calibration and the recording circumstances. The calibration and the circumstances (distance from source, temperature, humidity, etc.) can be used during data analysis to produce meaningful quantitative results for the comparison of sound signals, e.g. when comparing the overall amplitude (or sound power) of various insects recorded under different conditions. Equipment calibrations can also be used to correct for variations in frequency sensitivity to produce spectro-temporal analyses approaching the real signals.

In this workshop, we will describe and present some of the techniques used in our lab to record a range of audible and ultrasound signals from choosing the right equipment, performing calibrations, to digitizing, processing and presenting the signals in meaningful ways.

Key Words: ICO2016, Brazil, Ilhéus

• corresponding author

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SYMPOSIUM

- The orthopteran systematics in a changing world
- Orthoptera Conservation
- Locust and grasshopper control: Efficacy, Economics and Environment. Can all three E's be achieved simultaneously?
- Morphology, molecules and evolution in Orthoptera
- Phylogeography and speciation
- Acoustic and vibrational communication in Orthoptera
- Orthopterology in a changing Brazil

TOWARDS A CLEANER, EASIER AND INFORMATIVE TAXONOMIC PRACTICE: A NOTATION SYSTEM TO EXPRESS ORTHOPTERA MERISTIC CHARACTERS IN DESCRIPTIVE AND REVISIONARY WORK

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ALL taxonomic descriptions must be treated seriously, the descriptor having in mind colleagues who will study his work in the future. When describing species, we have specimens in front of our eyes or under the microscope, *i.e.*, real, touchable, elements of physical nature, not just concepts as supra-specific taxa are. All information present in classifications comes from specimens, so, examining them to define a species is a crucial task. Every species description must be: 1- thorough, as detailed as possible: all traditional structures observed- as well as the innovative ones- must be characterized by words and/or illustrations (or measurements and counts), even if their shapes do not vary among the other species belonging to that genus. 2- clean and not excessively wordy: a "telegraphic-style" writing, free of unnecessary verbs, doubt-leading colloquialisms and vague or imprecise terms is very important. If one or more species is already known (described or being described at the moment) in that genus, all efforts must be made to provide a comparison of diagnostic features among all species; if it happens that previously known species were poorly described, one's article will suffer from that gap. History has shown us how much bad descriptions, *i.e.*, too brief and devoid of without illustrations ones, can be so limiting. For obvious reasons we must excuse the old 18th and 19th centuries taxonomists for their short descriptions, but persisting in this practice nowadays is not excusable. A description must be envisaged to be helpful in the future. If a thorough and clean description is to be the target, the problem still remains when we imagine colleagues, in the future, trying to pick up information from within the texts of several or many descriptions to build up a table or compile an identification key for a taxonomic revision. I believe that in certain cases we can help them in advance, and explain how to do it is the purpose of this presentation. Orthoptera meristic characters like spurs, spines, teeth, chevron marks (on the hind femora of several groups), ovipositor armature, etc., are normally located serially along certain lines that can be easily identified, no matter if they are located on limbs' segments or other parts of the body. Since these elements are queued, not chaotically distributed, I have thought of two notation methods to represent them which will promptly allow comparisons of their type and numbers between two or more species or higher taxa. One of the methods is a graphical one, a drawing showing the distribution of elements- spines, spurs, teeth- on a given body part of a taxon; to compare the condition of each body segment in different taxa all one needs is to place the drawings next to each other. The other method consists of representations of meristic characters by formulae after coding the different types of elements and their quantities by using letters, numbers and a few diacritical marks, all available from a regular computer keyboard. With this method, the character type and numbers will be readily visible for one or more taxa in subsequent lines of text or displayed in a spreadsheet table. Comparisons are straight forward; colleagues in the future will not need to scavenge through the text to compile information.

Key Words: Formulas, Meristic characters, Notation system

PHYLOGENETIC AND BIOGEOGRAPHIC STUDIES WITHIN THE NEOTROPICAL ROMALEINAE (ORTHOPTERA, ACRIDOIDEA, ROMALEIDAE)

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THE subfamily Romaleinae (Acridoidea, Romaleidae), with the largest and most colorful representatives within Acridoidea, comprises 264 species in 69 genera (Eades *et al*., 2016). This group of grasshoppers is distributed in the Americas and mostly represented in the Neotropical Region in a wide range of habitats. Most of the hypotheses agree on a southamerican tropical origin of the subfamily (Amedegnato, 1977; Carbonell, 1977, 1986). However, inconsistencies with this hypothesis arise from the idea that northamerican romaleids seem to be more primitive than southamerican ones (Amedegnato, 1977; Rowell, 2013). Following the current classification adopted by the "Orthoptera Species File" online (OSF, Eades *et al*., 2016), ten valid tribes are included in Romaleinae. This study aims to reconstruct a phylogeny of the group based on molecular and morphological evidence. We included 75 ingroup taxa representing all the tribes of Romaleinae and 6 outgroups representing the tribes included in Bactrophorinae. The morphological matrix consisted on characters from external morphology, coloration, external and internal male genitalia, and morphometric characters. Molecular data included fragments of three mitochondrial loci [Cytochrome c Oxidase subunit 1 (COI) and subunit 2 (COII), and the 16 Subunit of ribosomal RNA (16S)] and one nuclear loci [Histone 3 (H3)]. Phylogenetic analyses were performed employing Bayesian (BA) and maximum parsimony (MP) searching criteria. We performed analyses based on each independent data set and total evidence analyses. We carried out a dispersal–vicariance analysis (DIVA) to trace the biogeographic patterns and analyze the diversification processes that may have occurred within the group. We discuss the results of our phylogenetic analyses and test them against the previous classification schemes and propose a new classification for the group. We provide detailed information on conflictive groups and incongruence among the different data sets, pointing out where the focus of future research needs to be directed. Based on our phylogeny, we also test and discuss the biogeographic hypotheses postulated for the group.

Key Words: Lubber grasshoppers, Phylogeny, Americas

• corresponding author

CURRENT KNOWLEDGE OF PYRGOMORPHIDAE SYSTEMATICS USING MORPHOLOGICAL AND MOLECULAR DATA

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USING morphological data we present the first phylogenetic hypothesis of Pyrgomorphidae based on 28 out of the 31 currently known tribes. Specifically, we aim to test the monophyly of the family and subfamilies and to describe phylogenetic relationships among major clades within the family. We recognize four main clades and we provide extensive discussion about phylogenetically important morphological characters in light of the phylogenetic analysis. This study is intended to establish a strong foundation for future studies on the evolution of Pyrgomorphidae. Using molecular data we focus on the origin of New World Pyrgormorphidae. Only 32 out of the 482 species of Pyrgomorphidae are distributed in the New World, while the majority of tribes, genera and species are distributed only in Africa and Asia. Currently, it is not clear if the origin of Pyrgomorphidae was Africa, Madagascar or Tropical Asia. In the New World, only 30 species in 13 genera from 4 tribes are found. The tribes Ichthiacridini (3 genera; 10 spp.) and Ichthyotettigini (4 genera; 7 spp.) are exclusively distributed in Mexico. The tribe Omurini (3 genera; 4 spp.) distributes exclusively in South America. The fourth tribe, Sphenariini, has a peculiar geographical distribution: 3 genera; 9 spp. in Mexico, Central America and Dominican Republic, 3 genera; 3 spp. in Eastern Africa and Madagascar and 3 genera; 10 spp. in China. Currently, there are two hypotheses about the origin of New World Pyrgomorphidae: 1. The family colonized the Americas (through North America) at least two or three times from Southeast Asia. 2. Pyrgomorphidae together with Pamphagidae, Tristiridae and Lentulidae originated in Asia then dispersed to Africa and then in minor degree to South America. However both hypotheses have never been tested in a phylogenetical framework. Using next generation sequencing we generated 22 complete mitochondrial genomes from 10 out of 13 genera from the New World and 12 genera from Africa, Asia and Australia, as well as three additional pyrgomorph mtgenomes from the Genbank. As outgroups we included genera of the families Pamphagidae, Tristiridae and Lentulidae. We reconstructed a robust phylogeny that allowed us to answer the following questions a) Does New World Pyrgomorphidae form a monophyletic group? b) Did they come from different places/times? c) Is Sphenariini monophyletic? d) What is the sister group of Caribbean *Jaragua*?

Key Words: Pyrgomorphidae, New World, Next Generation Sequencing

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MORPHOLOGICAL PHYLOGENY OF NEOTROPICAL PHALANGOPSIDAE (ENSIFERA, GRYLLOIDEA) WITH SPECIAL REFERENCE TO MALE GENITAL CHARACTERS

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THE family Phalangopsidae is one of the most important families of Grylloidea, in terms of number of species and ecological diversity, comprising around a thousand species grouped in six subfamilies distributed throughout tropical and subtropical zones. This taxon reaches its highest diversity in Neotropical region, where the subfamily Luzarinae emerges as the largest lineage of Phalangopsidae, with at least 290 known species. However, the taxonomic knowledge of these taxa is incipient, with a lot of unknown genera and species to be described. Besides, there is still a debate about the number of suprageneric lineages and taxonomical classification. The systematics knowledge, from a phylogenetic point of view, is still more incipient.

Here, I present the results of a morphological study on the male phallic complex of phalangopsid crickets and the first phylogeny proposed for this family, based on morphological characters. This study aimed to understand the evolutionary relationships of its lineages, to test the monophyly of Luzarinae, and to propose a suprageneric classification of Luzarinae based on the results of the analyses.

The male genitalia of Luzarinae crickets presents a general morphological pattern, mainly regarding the pseudepiphallus, and the main characteristics are the modification of pseudepiphallic parameres in two lobes (dorsal and ventral) and the development of pseudepiphallic arms – the latter is the main synapomorphy of the subfamily. These characters of the pseudepiphallus, as well as the main characters regarding the ectophallic invagination and the endophallus will be discussed.

The cladistic analysis was performed using 142 characters (83 genital + 59 morphology), for a total of 60 species of the two Neotropical subfamilies: Phalangopsinae (10 spp.) and Luzarinae (45 spp.). Five species of Gryllidae, of 3 subfamilies (Gryllinae, Eneopterinae, and Podoscirtinae), were included as outgroup.

The set of characters studied were both male and female general morphology and the morphology of male genitalia – characters regarding female genitalia and other male's potentially informative set of characters as wing venation and metanotal glands were not studied.

The analyses were performed using both equal weights and implied weights for the dataset of morphological + genital characters, and only genital characters.

I'll discuss the results of the analyses, focusing on the internal relationships of the subfamily Luzarinae. Furthermore, I'll discuss the general morphology, the main structures on the male genitalia, and the impact of the genital characters on the analyses.

Acknowledgments: This study was supported by the University of São Paulo, the Programa de Pós-Graduação em Zoologia (Zoology Graduate Program) of the University of São Paulo, and the "Coordenação de Aperfeiçoamento de Pessoal de Nível Superior"(CAPES), Proc. 5568-13-7.

Key Words: phylogeny, cricket, evolution

EXPANDING THE BOUNDARIES OF THE NEW MORPHOLOGICAL FRONTIER: EXPLORING FUNCTIONALITY IN 3D (ORTHOPTERA: ACRIDIDAE: MELANOPLUS: PUER GROUP)

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A morphology renaissance is underway, revolutionized by powerful imaging technologies being used in novel ways, particularly in examining insects, and the frontier in greatest need of exploration is functional morphology, which can now be done in improved ways. One such way is via micro-computed tomography (micro-CT) that enables non-invasive investigations of both external and internal morphology by creating an image stack that can be virtually reconstructed in three dimensions (3D) (Fig. 1). We synergized micro-CT with two additional imaging methods, digital single lens reflex (DSLR) camera photography with focal stacking and scanning electron microscopy (SEM), to gain a better understanding of genitalia evolution. Specifically, we examined the interacting genitalia of a male and a female of the flightless grasshopper species *Melanoplus rotundipennis* (Scudder, 1878) frozen rapidly during copulation to determine the role of the genital components of each sex. Many hypotheses have been suggested for the function of these components, but few have been tested in a copulation framework. Additionally, we wanted to assess the general value of this synergistic approach and determine if it is the most efficacious method for examining genitalia morphology and function in at least grasshoppers. Detailed descriptions are given for each genitalia component, including relative position to other parts, and were based on 3D reconstructions using micro-CT data (Fig. 1), and DSLR and SEM images. We were able to assign a function(s) to all observed genitalia components of both sexes except for the male's furculae and follow-up studies are needed to further investigate the functions of some components. The value of this synergistic approach is immense in terms of the resulting knowledge gained and we think this method is highly effective for examining the morphology and function of insects, especially body regions or events that are difficult to access and understand otherwise, as shown here with genitalia and copulation. We thank Benjamin Wipfler of the Jena Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem-must at Friedrich-Schiller University in Germany for the micro-CT scanning.

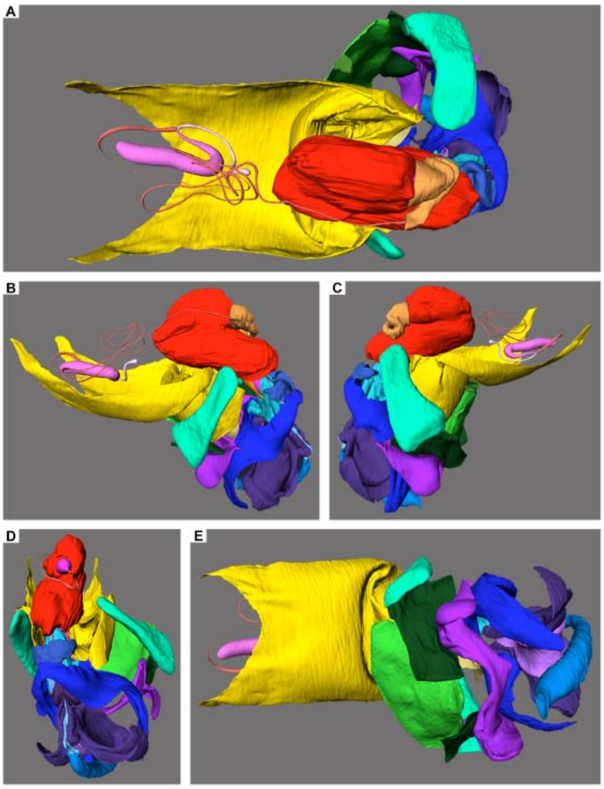

Figure 1. Five views of the 3D reconstruction created from micro-CT scans of male and female genitalia (and components of the greater reproductive system) during copulation: A) dorsal; B) left lateral; C) right lateral; D) posterior; E) ventral.

Key Words: functional morphology, anatomy, genitalia, copulation, sexual selection, *Melanoplus*

• corresponding author

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IDENTIFYING SOUTH AFRICAN KATYDID (ORTHOPTERA: TETTIGONIOIDEA) HOTSPOTS

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SOUTH Africa is one of only seventeen recognized megadiverse countries in the world, harboring a large proportion of the world's endemic species in three global biodiversity hotspots: Cape Floristic Region, Succulent Karoo and Maputaland-Pondoland-Albany. Biodiversity hotspots are selected as such on the basis of two criteria: (1) they contain significantly levels of biodiversity (traditionally estimated on the basis of plant diversity alone); and (2) they experience high levels of threat of transformation from humans. Although animal diversity is not considered for designation of biodiversity hotspots, the global biodiversity hotspots have been shown to harbor a significant proportion of the Earth's mammals, birds and other vertebrates. However, little is known regarding whether the biodiversity hotspots are equally as effective at protecting invertebrate diversity. In this study, we aimed to define hotspots of katydid diversity in South Africa, and to determine the extent to which katydid hotspots overlapped with biodiversity hotspots. In 2014, all South African katydid species were added to the IUCN's Red-List. Using this newly available data, katydid hotspots were delineated in two ways: (1) as areas with the highest species richness counts of total, endemic, threatened and sensitive species; and (2) as areas with the highest mean scores when ranking species on their perceived vulnerability to change. The two types of katydid hotspots were compared with each other and with recognized global biodiversity hotspots. There was a great degree of overlap between katydid and biodiversity hotspots, with an additional katydid hotspot in Limpopo Province, in South Africa's subtropical northeastern region. Grid cells within biodiversity hotspots had significantly more threatened, less widespread and less mobile katydid species than grid cells outside of biodiversity hotspots. Taking species composition into account in hotspot delineation is recommended for future practice and wider application. More distribution records are necessary in order to pinpoint fine-scale areas of high conservation value for South African katydids.

Key Words: biodiversity, conservation, endemism

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ORTHOPTERA CONSERVATION IN MEXICO, CURRENT STATUS AND CHALLENGES

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MEXICO is a megadiverse country and harbors approximately 10% of the known flora and fauna. This high diversity is due to the fact of the confluence of the Neartic and Neotropical regions, plus a complex topography. According to Orthoptera Species File, there are more than 27,000 valid species of Orthoptera. Currently for Mexico there are more than 1,100 described species, meaning that approximately there are 1,500 undescribed species for Mexico. Of the described species, around 45% corresponds to Ensifera and 55% to Caelifera. In Ensifera, Tettigoniidea accounts for 60% and Gryllidea for 30%. In Caelifera, Acridoidea accounts for 80% of diversity. There are regions poorly studied such as Baja California Peninsula, The Northwestern (Sierra Madre Occidental mountain range) and Yucatan Peninsula. In 2014, a recently described grasshopper (*Liladownsia fraile*) was assessed for the IUCN Red List of Threatened Species and due to its small geographic distribution, the low number of localities and continuing decline of its habitat caused by grazing and forestry, it was assessed as Endangered. This is so far the only species assessed for Mexico. The main challenge is to assess more species for the coming years. The suggested target taxa to start this challenge are the mountain endemic grasshoppers in the group Melanoplinae, selected recently described species of Tettigoniidea and the charismatic and well known species of edible grasshoppers of the genus *Sphenarium*. Mention apart is to focus in two evolutionary important taxa of Caelifera. The first one is the family Tanaoceridae, which is the only group of grasshopper where the antennae are longer that body. Its distribution is restricted to California in the United States and Baja California Peninsula in Mexico. There are only three species in two genera and very little is known about them. The second one is the family Xyronotidae which is endemic to mountains in Central Mexico (Veracruz and Oaxaca). Its closest relative is the Family Trigonopterygidae which is found only in the Indo-Pacific region. There are only four species in two genera. Mexico has good policies in conservation and the assessments of more species for the IUCN will help to protect the areas they inhabit.

Key Words: Conservation, Mexico, Orthoptera

HOW NEW INFORMATION TECHNOLOGIES CAN CONTRIBUTE TO ORTHOPTERA CONSERVATION

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NEW information technologies such as crowd-sourced web databases, in combination with accessible hardware such as smartphones, generate Terabytes of natural history data consisting of geo-referenced pictures, videos and sounds. In addition, historic publications, fieldbooks and labeled specimens are now accessible in digital format.

The Global Information Facility (GBIF: www.gbif.org) federates many (but not all!) of these distinct datasets. GBIF contains an impressive number of 733,922 georeferenced Orthoptera recordings, with 240K from (museum) specimens, and a major part from observations from regional recording schemes, such as the Swiss National Orthoptera Databank (doi:10.15468/bcthst), which holds records of various origins, assembling literature data, digitized collection data and recent observational records. In contrast, the low number of type specimens (<1,000) and images (6,483) accessible via GBIF indicates still limited coverage. Images are not shown directly, but only after drilling into the original data source. However, images are needed to validate records by experts, especially from citizen science recording schemes. GBIF is a powerful data aggregator, but it is still evolving and needs more feedback from experts.

Orthoptera Species File (OSF: Eades, D.C.; D. Otte; M.M. Cigliano & H. Braun. Orthoptera Species File. Version 5.0/5.0. [04/10/2106]. <http://Orthoptera.SpeciesFile.org>) provides images for 11,552 taxa, many of which include singletons, which means that the species is only known from one type specimen, representing only one sex. Many of these are from endangered habitats such as tropical rainforests, where the type locality habitat is destroyed or severely degraded. Such species could be red-listed as Data Deficient, and experts could initiate targeted search projects, involving citizen naturalists. An example is *Eulophopyllum thaumasium* Hebard, 1922, a phaneropterine species which is only known from one female collected at Labuan island (Borneo) around 1900. A dedicated search by experts using social media, www.flickr.com, or www.youtube.com can be backed up by iNaturalist tagging tools (http://www.inaturalist.org/taxa/flickr_tagger) and picture similarity search tools (https://www.tineye.com/).

As a stand-alone platform, Observado (www.observado.org) is frequently used for Orthoptera assessments. However, conservation has to go beyond red-listing! Identification of potentially endangered habitat and monitoring of protected areas is facilitated by remote sensing and web-based Geographic Information Services, which are now accessible to the general public, such as www.loggingroads.org in combination with http://www.openstreetmap.org/

In synthesis, a workflow is presented for identification, prioritization and protection of endangered Orthoptera, combining the aforementioned databases with habitat GIS layers, botanical data and the Global Strategy for Plant Conservation (http://www.plants2020.net/).

Key Words: Databases, Conservation, Red List

THE CONSERVATION STRATEGY OF THE CRAU PLAIN GRASSHOPPER – PRACTICAL IMPLEMENTATION, FIRST RESULTS AND OPEN QUESTIONS

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THE Crau Plain Grasshopper *Prionotropis rhodanica* is a Critically Endangered grasshopper species endemic to a Mediterranean stone steppe, the Crau steppe in Southern France. A strong population decline occurred within the last decade. The formerly wide distribution in the Crau steppe is nowadays restricted to three remaining populations which are spatially separated. Reasons for the decline are unknown. A workshop under the supervision of the Species Conservation Planning Sub-Committee (SCPSC) and the Invertebrate Conservation Sub-Committee (ICSC) of the International Union for Conservation of Nature (IUCN) in 2014 resulted in a conservation strategy for the species. The strategy includes habitat management activities, research topics (habitat preferences, population ecological aspects, field experiments concerning threat analysis, genetic analysis) and the development of a captive breeding project (Fig. 1). The close collaboration between science and reserve management is essential for answering the leading questions of the conservation strategy. The presentation will give an overview on the structure and the current state of the project and summarize the results of the first two fieldwork seasons. Employing a conservation strategy for preserving and protecting invertebrate species is a rather new approach. Thus the exchange about the project-based experience is valuable in order to develop similar projects for different species.

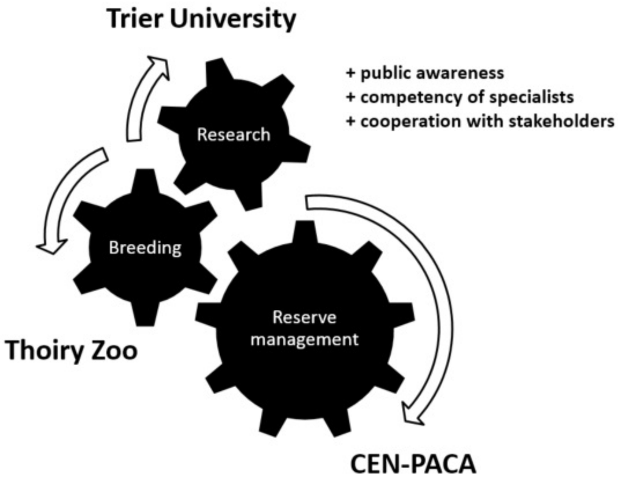

Figure 1. Principle of the Conservation strategy.

Key Words: Conservation strategy, Threat analysis, Endemic species

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THE CONSERVATION STATUS OF EUROPEAN ORTHOPTERA – RESULTS FROM THE FIRST CONTINENTAL RED LIST ASSESSMENTS

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A complete assessment of the conservation status of European Orthoptera has been conducted during the last two years. These assessments have shown that one quarter of the European Orthoptera are threatened by extinction. The major threats are agricultural land use changes, such as intensive farming or grazing, but many species are also threatened from the use of pesticides, touristic development, wildfires, climate change and drainage. Here, I present the results of the IUCN Red List assessments to discuss the distribution of threatened taxa and the major gaps in our knowledge.

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CHARACTERIZATION OF ZONES OF HIGH AND LOW FREQUENCY PRESENCE OF THE DESERT LOCUST *SCHISTOCERCA GREGARIA* (FORSKÅL, 1775) POPULATIONS IN MAURITANIA USING SATELLITE IMAGERY

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TO understand the environmental factors favorable for breeding of Desert locust *Schistocerca gregaria* in its solitary phase and its gregarization, a two-year long study was conducted in two geographically close areas, one of high frequency and one of low frequency of reproduction and gregarization. The static components of habitats such as climate, geomorphology, and vegetation, were linked to locust presence or absence. Remote sensing (satellite imagery) was used to generalize the observations and categorize the sites. Fifteen geomorphological classes where correspondence analysis linked the presence of locust nymphs to the geomorphological classes were identified through photo interpretation. These results may have profound and beneficial impact on the strategy of surveillance and preventive and curative Desert locust control in Mauritania and beyond.

Key Words: Desert locust, geomorphology, high frequency zone, low frequency zone, meteorology, phase change, remote sensing, vegetation, Mauritania.

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DEVELOPMENT OF THE 2015-16 PLAGUE OF THE SOUTH AMERICAN LOCUST, *Schistocerca cancellata* (Serville, 1838) IN ARGENTINA

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DURING 2015 and 2016, Argentina suffered from the worst locust plague in the past 60 years. Even though there were very few locusts detected during 2014, by July 2015, there were many swarms of the South American locust, *Schistocerca cancellata* (Serville) in western Argentina. In spite of substantial locust control campaigns against adult swarms between August and October 2015, many bands and swarms were present during the 2015-16 season. The life cycle of *S. cancellata* in Argentina is characterized by having an overwintering adult diapause, with there normally being two generations during the late spring to late summer breeding season. This locust outbreak coincided with an El Niño event, which is characterized by above average temperatures and rainfall in Argentina. Evidence will be presented which demonstrates that the resulting warm wet conditions allowed *S. cancellata* to have three generations per year instead of the normal two during both the 2014-15 and 2015-16 locust seasons, leading to substantial population increase. Given that a locust generation is completed in 2-2.5 months from late spring until early autumn, the fact that nymphs of various stages were present for a total of 7 months, from November 2015 until the following May, indicates that there were three generations during 2015-16. Following August and October rains, there were hatchings of nymphs during November 2015, which led to first generation adults by January. Second generation adults (January to March) were observed laying eggs in late March, which was followed by hatchings and young nymphs of the third generation in April. Adults of a given generation lay eggs for a protracted period, so that as the season progressed, locust development was less and less synchronized so that by late in the 2015-16 season (March), locusts were observed at all stages of development. During the 2014-15 season, there is only indirect evidence of three generations because very few locusts were detected until swarms suddenly appeared during July 2015 in Santiago del Estero province of western Argentina. However, temperatures were above average during October 2014 and for some months thereafter, which would have allowed three generations during 2014-15. The implications for locust outbreaks during the warmer periods expected with climate change and during El Niño years will be discussed.

Key Words: plague, *Schistocerca cancellata*, Argentina

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GRASSHOPPER CONTROL IN NORTH AMERICA: RECENT TRENDS

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GRASSHOPPERS (Orthoptera: Acrididae) are the predominant herbivores in North American prairies. As an intrinsic component of the grassland biome, they stimulate plant growth, participate in nutrient cycling and play an important role in food chains. About 20 out of 450 North American grasshopper species are important rangeland pests in 17 western U.S. states and in western provinces of Canada. Annually they destroy about 25% of above-ground rangeland forage at an estimated cost of almost one billion U.S. dollars per year. During outbreaks, grasshoppers inflict severe damage to rangeland and crops and require large-scale applications of broad-spectrum insecticides to control them. Federal, state and private landowners annually expend considerable resources for grasshopper control. For example, during the 1986-88 outbreaks in the U.S., over eight million ha of rangeland were treated with five million liters of neurotoxins at a cost of over $75 million. Currently, the preferred strategy of rangeland grasshopper control in North America is the Reduced Agent and Area Treatments (RAATs). RAATs is an integrated pest management (IPM) strategy 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 Insect Growth Regulator which acts by ingestion. It provides three to four week protection from grasshopper pests and has lower non-target impacts than conventional pesticides. RAATs reduce the cost of control and the amount of insecticide used by more than 50%. In 2010, over 2.4 million ha were treated by RAATs in a single state of Wyoming at an average cost of only 3.60 U.S. dollars per protected ha. This successful control program resulted in significant savings for Wyoming agriculturists and had no detected negative environmental impacts. Besides RAATs, research is ongoing to develop biological options of grasshopper control, which include applications of liquid or solid bait formulations of fungal pathogens.

Key Words: Grasshopper, control, North America

LOCUST CONTROL IN AUSTRALIA: HITTING THE RIGHT TARGET

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THE history of locust control in Australia over the past 100+ years provides numerous examples of practices with questionable effectiveness and limited regard for the off-target impact of these. From isolated physical intervention by individual landholders through to indiscriminate large-scale use of non-selective and persistent insecticides, these practices have provided a basis from which the current Australian Plague Locust Commission (APLC) has learnt what not to do. Since its creation over 40 years ago, APLC has applied considerable resources to addressing the trident of efficiency, effectiveness and the environment. Over the past 15 years, APLC has invested at least as much in its environmental research program as it has in maximising the effectiveness of locust control. Demonstrating that APLC can deliver against these three objectives concurrently is not, however, without its own challenges – not least of which is the perceptions of stakeholders at either end of the spectrum.

Key Words: Australia, Locust, Control

THE USE OF BIOPESTICIDES AS PART OF IPM OF LOCUSTS AND GRASSHOPPERS

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THE search for alternatives to the widespread use of chemicals to control locusts and grasshoppers (Orthoptera: Acrididae) has led to the development of mycoinsecticides having the active ingredient *Metarhizium acridum* (Hypocreales: Clavicipitaceae). During the 1990's, isolates of *M. acridum* from Australia and Africa were intensively studied and since then isolates have been studied in many countries. The isolate from Australia has been formulated as the product Green Guard®, which was first used operationally in the year 2000 as part of IPM of the Australian plague locust, *Chortoicetes terminifera* (Walker). More than 100,000 ha has been treated with Green Guard® since then, mainly in Australia, but also in Timor Leste and Indonesia against the migratory locust during 2007. Under the very hot conditions (maxima 37-42ºC) of summer, Green Guard has been shown to cause >90% mortality of locusts within 6-10 days. Against locusts and grasshoppers in milder conditions during spring, mortality is often slightly less (80%) and occurs more slowly (2 weeks or so). The isolate from Africa has been formulated as the product Green Muscle®, and has been used operationally against a number of species including the Red locust and Migratory locust. Trials with *Metarhizum* in Mexico with both the Australian and local isolates has led to local *Metarhizium* biopesticides being used in some locust and grasshopper control programs. However, the country in which the use of biopesticides has increased dramatically in the past few years is China. Both *Metarhizium acridum* and *Antonospora (Paranosema) locustae* (Protozoa: Microsporidae) are used extensively in both locust and grasshopper control. While *Antonospora* was developed much earlier than *Metarhizium,* its moderate levels of mortality had limited its use, but in recent years, improved formulation and application techniques have led to *Antonospora* giving relatively high levels of mortality. The result has been that both *Metarhizium* and *Antonospora* are an important part of IPM of locusts and grasshoppers in China.

Key Words: biopesticides, IPM, locusts, grasshoppers

CAN WE FURTHER IMPROVE DESERT LOCUST'S PREVENTIVE STRATEGY?

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THE Desert Locust is one of the major crop pest with devastating consequences on food security in Africa and Asia. The current strategy to manage this pest is early warning and preventive control. It consists in locating and destroying the locusts starting to change behaviour from solitarious individuals to dense group of gregarious. Over the past 50 years, the Desert locust control programme, coordinated by FAO, has reduced the frequency of plagues and allowed to better manage desert locust infestations.

Several lines of research are possible to further improve this preventive strategy. They concern our knowledge on the locust ecology, its environment and the behavior of the multiple stakeholders involved in the Desert Locust control strategy. Significant improvements have recently taken place in all these areas.

(1) Much progress has been made in the understanding of the dynamics of solitary populations, much mobile and abundant than was previously assumed. The gregarization thresholds has been determined - in the field - both for larvae and adults. The risk of gregarization - according to locust density, vegetation cover and phenology - has been defined, allowing preventive control teams to have more precise information on the population density justifying chemical treatment to reduce the risk of gregarization and hence invasions.

(2) Remote sensing data are now widely used to locate, in real time, where convenient environmental conditions occur and facilitate locust outbreaks and upsurges. The use of remote sensing data steadily improves during the past few years. The combined use of historical prospection data of Desert locust observations and spatio-temporal statistics of a vegetation index gathered by remote-sensing, help to derive a predictive model of probability of finding locusts in specific areas. The methodology developed should help in more efficiently focusing survey efforts on specific parts of the gregarization areas based on the predicted probability of locusts being present.

(3) The anti-locust management start to be considered as an adaptive complex system and the behavior of the various actors involved in the Desert Locust preventive control begins to be better taken into account, in particular by the use of agent-based modeling techniques. Multi-agent modelling could allow exploring the interactions between the various stakeholders of locust preventive management. Promising results have already been obtained. Thus, using a multi-agent model developed for locust control, it was possible to demonstrate, in a parsimonious way, that a dynamic of progressive failure to remember the importance of preventive management is enough for generating the invasion cyclicity observed. The funding institutions could clearly make the preventive management more efficient by increasing by just few percent their base of support to the control units.

All these developments should enable a more sustainable strategy as well as earlier and more accurate interventions. It is likely that an even earlier intervention strategy should further reduce the duration and extent of plagues of this species and could entirely prevent some of them.

Key Words: Desert locust, early warning, pest management, preventive control, complex adaptive system.

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EACH MUSICIAN HIS INSTRUMENT: 3-D IMAGING REVEALS STUNNING CONVERGENCES IN CRICKETS, KATYDIDS AND THEIR ALLIES (ORTHOPTERA)

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ORTHOPTERA are well known for their capacity to emit and perceive sounds, having developed a high diversity of morphological structures and acoustic behaviors unrivalled in other animal groups. In Ensifera (crickets, mole crickets, prophalangopsids, katydids), signals are mainly produced by complex anatomical structures located on the veins, at the very basal part of the forewings (FWs). When the forewings come to overlap by a lateral movement of opening - closing, the ventral face of one FW, bearing a row of teeth called the file, rubs the thickened rim (scraper) of the other FW. The generated vibrations are propagated by a resonator, which amplifies the intensity and the frequency of the signal. The main controversy regarding these acoustic structures concerns the homology of the file, and the identity of the veins that shape the resonators, i.e. the cricket harp and the katydid mirror.

Two main hypotheses coexist to explain the origin of the FW acoustic apparatus in Ensifera: either they originate from an ancestral design of common single origin, which would explain their similarity and unique function of stridulation in modern taxa; or they would result from convergent occurrences in different groups of Ensifera. The issue still remains controversial because of different and competing interpretations of wing venation. We performed the first 3D reconstruction of the structures at the extreme bases of orthopteran FWs. This allowed the resolution of the widely and long debated homology of orthopteran wing venation, previously considered only in a 2D context. Remarkably, the stridulatory apparatus is found to be nonhomologous, i.e., it is organized with different veins in crickets, mole crickets, katydids and prophalangopsids. In the light of the most recent phylogenetic evidence, the stridulatory apparatus developed at least four times in modern Ensifera. The acoustic structures in Ensifera illustrate an extraordinary case of convergent evolution between closely related clades, by far exceeding the number of evolutionary steps ever proposed for calling ability in this group. Genomic studies will now be performed to understand the complex evolution of these intricate structures.

Key Words: Orthoptera, venation, homology

• corresponding author

RNA IN POLYNEOPTERA INSECTS. *DE NOVO* TRANSCRIPTOMIC INSIGHTS INTO THE MOLECULAR SUBSTRATE UNDERLYING EVOLUTIONARY ADAPTATIONS IN *Amphiacusta* CRICKET (ORTHOPTERA, PHALANGOPSIDAE)

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THE molecular substrate underlying evolutionary adaptations and relationships inside the Polyneoptera remains controversial despite the molecular and morphological studies done until now. The study of evolution within this group is hindered mainly by the high structural complexity of its genetic material. This structural complexity is expressed at the functional level of the genome, and the NGS methods offer invaluable opportunities for its investigation. Here, we present results from our analysis of the transcriptome of *Amphiacusta* cricket (Orthoptera, Phalangopsidae) having no raw reads available at present in databases such as GenBank, ENA and DDBJ. The transcriptome, which was assembled *de novo,* represents a strong potential for future comparative evolutionary and ecological studies based on differentially expressed genes, in variable environmental conditions.

PHYLOMORPHOLOGY OF PSORODONOTUS: ECOLOGY EXPLAINS MORPHOLOGICAL CONSERVATISM

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THE genus *Psorodonotus* (Orthoptera, Tettigoniidae) ranges over Anatolia, Caucasus and the Balkans. This genus has 14 species which were assigned to three species groups on the basis of their morphologies: *P. specularis*, *P. caucasicus* and *P. venosus* groups. However, homoplasy may be common in morphology and evaluating existing phenotypic characters using phylogenies may allow us to understand the rate of evolution per characters. This study aims to compare the rates of morphological and genetic divergence in species of *Psorodonotus*. To estimate morphological divergence rates we studied the four morphological structures. To estimate genetic divergence rates we used sequences of two mitochondrial segments (COI and 12SrDNA-tRNAval-16SrDNA) from 52 populations representing 14 species of the genus. We arrived to following conclusions: (i) although both kind of data confirm existing species, phylogenetic trees do not retrieve species groups, (ii) as the ancestral lineages restricted to present Euxinic vegetation this area possibly represent origin place and ecological preference of ancestral stock, (iii) terminal clades are ranged almost totally outside the ancestral place, thus, radiation in the genus possibly triggered by dispersing out of ancestral area, (iv) there are three species pairs distributed in Euxinic zone, each pair constitute one of three basal branches, thus, their morphological similarity is phylogenetic because of morphological conservatism caused by ecological conservatism, (v) male cerci is the most rapidly diverged morphological structure partly because of sexual selection, and (vi) stable ecology results in morphological conservatism while ecologic shifts lead to rapid divergence and speciation.

Keywords: *Psorodonotus*, ecological conservatism, speciation

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SEARCHING NUMTS IN GIGANT GENOME OF ORTHOPTERA: LENGTH AND FREQUENCY OF PARALOG COPIES OF COI

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MITOCHONDRIAL COI is one of the most widely used genetic marker in phylogenetic, phylogeographic and taxonomy researches. Especially, a 600-700bp of the gene is using in barcoding of life (Folmer region). Nuclear copies (Numts) of this gene are the main handicaps of such studies and reported in gigantic genome of Orthoptera too. In this study it is aimed to search for presence/absence of numts in total DNA using different primer pairs targeting five segments of COI of different length (named I.-V. regions) and to determine their commonalty and frequency. For this purpose, total DNA extracted from representative taxa of Orthoptera and five different approaches were used to determine possible numt copies of COI. Studies yielded no PCR products to be sequenced for region I. Numt percentage per suborders are as following for the other regions: for region II 45% in Ensifera and 75% in Caelifera; for region III 80% in Ensifera and 85% in Caelifera; for region IV 8% in Ensifera and 44% in Caelifera; and for region V 2% in Ensifera and 35% in Caelifera. The following conclusions were arrived at: (i) Numts are common in Orthoptera and reported for Ensifera for the first time in this study, and more common in Caelifera than in Ensifera, (ii) possibility of amplifying numts decreases with increasing length targeted gene in Ensifera but not in Caelifera, and (iii) the Folmer region of COI which is using in DNA barcoding seems less functional in Orthoptera, especially in Caelifera.

Keywords: ***Pseudogenes*****, Orthoptera, Folmer region**

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THE INGNORED MODEL BUDDING SPECIATION: LIGTHS FROM PSORODONOTUS VENOSUS (ORTHOPTERA, TETTIGONIIDAE) SPECIES GROUP

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THE budding species model has remained theoretical until recently as it defined by fuzzy criteria. Although the model is easily applicable to island population it is unclear especially for the terrestrial lineages. The mountainous *Psorodonotus venosus* species group (PVG) distributed in Anatolia and Caucasus offered potential to test and revise the predictions of the model. Sequences of two mitochondrial fragments including four loci (12S rDNA + tDNAval + 16S rDNA and COI) and a nuclear fragment including three loci (ITS1-5.8S rDNA-ITS2) were obtained and used in phylogenetic reconstruction , time estimation, population genetics and demographic analyses. Monophyly of the PVG was supported by phylogenetic analyses while that of each of the species in PVG not. The molecular chronograms indicated radiation of the group throughout the Pleistocene. Demographic analyses suggested constant population sizes for the populations in the centre of the range but a significant departure from constancy in peripheral populations. Genetic diversity is significantly reduced in peripheral populations but not in others. In the light of genetic and phenetic data we concluded that *P. venosus* is the ancestral species and *P. rugulosus*, *P. tendurek* and *P. hakkari* are bud species, as their haplotypes are nested within *P. venosus* in phylogenetic trees. Considering the PVG as a model group the main criteria defining budding speciation model can be defined as; (i) in contrast with ancestral species, genetic diversity is reduced, and there are signs of departure from constant population size in bud species; (ii) bud species have isolated and restricted ranges, while the ancestral species does not, (iii) the relative ages of ancestral and bud species are the most reliable data to confirm the model, and (iv) budding speciation renders ancestral species to paraphyly. Besides, major climatic transformations of the Pleistocene are possible driver of budding speciation.

Keywords: Budding speciation, *Psorodonotus venosus* group, Orthoptera

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DYNAMIC BIOGEOGRAPHY OF ACRIDID OUTBREAKS IN THE PALAEARCTIC REGION

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BIOGEOGRAPHERS usually try to describe more or less static distribution patterns or to operate very long temporal periods (thousands and millions of years). However, we know those distribution patterns of populations, species, assemblages, and biotas change continuously. These changes are very important both for theoretical estimations of prospective evolutionary and ecological changes and for forecasts of pest upsurges in different areas. The Palaearctic Region occupies the northern parts of Eurasia and Africa. It includes huge areas where grasshopper outbreaks occur and where levels of acridid diversity are relatively high. There are a lot of pest acridid species including several locusts. Although the history of acridid upsurges is relatively long, the well documented period is limited to last two centuries. In the 19th century, the situation with grasshoppers in the Palaearctic Region (especially in the Russian Empire) was relatively calm. Many acridid outbreaks were registered in 1821–1830 and 1841–1850. The situation changed in the next century. Extremely serious outbreaks were in 1921–1940. From 1940 until 1990 upsurges occurred quite often. At the end of the century, outbreaks became extremely serious and common. Huge acridid outbreaks were registered every year from 1992 until 2004. These outbreaks were associated with both locusts (Italian, Migratory, Moroccan) and solitarious grasshoppers. During the last decade, outbreaks of Migratory and Moroccan locusts were observed in the North Caucasus, and upsurges of the Moroccan locust were often in different parts of Central Asia.

A relatively detailed pattern can be described for the second half of the last century for the Italian locust. In the North Caucasus — Lower Volga area, there were four main outbreaks (1954–1957, 1972–1974, 1982–1984, 1992–1998). In the southern part of West Siberia, the outbreaks occurred in 1952–1956, 1967–1971, 1977–1982, and 1999–2002. Thus, the outbreaks of the Italian locust do not exactly coincide in different part of its range. In many cases, outbreaks in West Siberia began earlier then in the North Caucasus — Lower Volga area. However, the last huge outbreak began in 1992 in the Lower Volga and by 1996-1998, the outbreak region occupied a waste area from the Azov Sea to the eastern part of Kazakhstan. By 1999–2001, the outbreak area moved further northward and eastward and by the last stage (2002–2004), this outbreak became smaller and was limited to the territory from the Ukraine to the Caspian Sea.

Thus, the population dynamics of the Italian locust differs significantly in the different part of its range. The same pattern may be described for other pest species. Biogeographically the dynamics of their upsurges looks like a kind of a pendulum. Besides that, the areas of outbreaks of potential acridid pests are often associated with acridid foci of diversity. This fact indicates serious problems related to population management of both common and rare species. All that means we should take the biogeographic patterns into account for forecasting and management.

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Key Words: Grasshopper, Palaearctic region, outbreak, pest, dynamic biogeography, forecast, diversity

THE IMPORTANCE OF CAPTURING UNBIASED SPECIES HISTORIES FOR TESTING PHYLOGEOGRAHIC HYPOTHESIS AND THE PROMISE OF NEXT GENERATION SEQUENCING DATA

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STATISTICAL phylogeography has played a vital role in our understanding of historical and ecological processes shaping evolutionary history of species. These methods, which are based on the coalescent, have been used to estimate effective population sizes, levels of gene flow, divergence times and also for testing complex demographic hypothesis. However because these estimates are heavily influenced by genealogical stochasticity results will very much depend on the subset of loci used or in other words on the number of unique genealogical histories captured. Therefore statistical phylogeographic methods are most powerful when inferences are based on a high number of un-linked loci. With the advent of next-generation sequencing technologies it is now possible to sequence hundreds of thousands of loci spread throughout the genome from virtually any organism. As such we now have the framework for conducting phylogeographic inferences using an un-precedented amount of genomic data. However, even though phylogenetic and phylogeographic studies utilizing genomic data is rapidly growing most studies have not taken advantage of the sheer number of independent loci available for hypothesis testing opting instead for analysis based on concatenated sets of super matrices. However, concatenated data sets will result in a loss of information as individual gene histories, which might carry vital information, are averaged over. Here we show, using examples from endemic Anatolian crickets, how hundreds of thousands of independent loci captured by reduced genomic representation can be used for testing phylogeographic hypothesis based on the multi-species coalescent. These methods not only result in more accurate parameter estimates but allow for determining the range of values parameters take under different genealogical histories allowing for pinpointing genomic regions that are more heavily influenced by ecological or evolutionary factors. Moreover by re-conducting analysis using multiple independent sets of randomly chosen loci we show a simple way for testing the repeatability and overall robustness of results under random genomic subsets.

Key Words: statistical phylogeograhy, next generation sequencing, Orthoptera

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INTEGRATING PHYLOGENETICS AND NICHE MODELING TO ELUCIDATE THE DIVERSIFICATION PROCESSES IN SOUTH AMERICAN GRASSHOPPERS (ACRIDIDAE: MELANOPLINAE)

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Integrating phylogenetic hypotheses with geographic and ecological data has revealed new insights on the factors that influence the evolution and distribution of species. The spatial and temporal distribution of a species is shaped by its fundamental niche, which determines the potential distribution. Incorporating environmental and ecological data in a phylogenetic context allows the identification of phylogenetic signals in niche dimensions. These analyses provide a measure of niche similarity between related species, which can be used to build hypotheses on niche and range evolution and help to elucidate radiation mechanisms. Most attempts to infer diversification processes have compared geographic ranges in relation to phylogenies without considering the environmental space occupied. Inclusion of an environmental dimension in these analyses can allow us to assess whether ecologically mediated divergent selection is associated with speciation. The grasshopper genus *Scotussa* together with the remaining taxa of the Scotussae group are mostly distributed in Brazil, Paraguay, Uruguay and Argentina occurring in the Chacoan and Parana dominions of South America.

Contrary to the general pattern observed within the tribe Dichroplini, *Scotussa* species are highly variable in the structure of their ovipositor valves. Besides, it has been shown an association between the structural changes that occurred in the ovipositor of species of *Scotussa* with their oviposition habits. However, it was never tested if this association was related to the diversification processes occurred within the genus. In this study, we analyze the phylogenetic relationships among species of *Scotussa* adding new molecular data and use environmental variables to (1) predict the potential distribution of each species (2) quantify geographical and environmental niche overlap among species, and (3) analyze niche evolution combining phylogenetic information and georeferenced occurrence records in order to investigate the diversification of the species.

Key Words: Scotussae, biogeography, Speciation

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SONG ANALYSIS REVEALS TWO SPECIES OF THE *Stenobothrus eurasius*-GROUP (ACRIDIDAE: GOMPHOCERINAE) INHABITING RUSSIA AND ADJUCENT COUNTRIES

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IN the territories of Ukraine, Russia, Kazakhstan and Kyrgyzstan, two subspecies of *Stenobothrus eurasius* are recognized: *eurasius eurasius* (Zubovskii 1898) and *eurasius hyalosuperficies* (Vorontsovskii 1928). *S. eurasius eurasius* Zub. is suggested to inhabit southern regions of Siberia reaching the Transbaikal to the east, Kazakhstan and mountains of Kyrgyzstan; *S. eurasius hyalosuperficies* Vor. is suggested to occur in southern regions of Ukraine and European Russia. We have recorded and analyzed calling and courtship songs of the specimens from Ukraine, Russia and Kazakhstan. Not only the sound but also the movements of the hind legs during stridulation (Fig. 1) were recorded with a unique opto-electronic device. The specimens from one locality of Saratov, from Orenburg region and Kazakhstan generated sound by two different mechanisms: hind-leg striduation, which is typical for gomphocerine, and wing clapping, which was previously described only for the *S. rubicundulus*-group. The calling song was only produced by wing stridulation, which was performed on the ground. The courtship song started with the low-amplitude leg movements, which generated single or double soft pulses (element I) (Fig. 1). An element II was produced by the high-amplitude leg strokes, which accompanied by conspicuous movements of antennae. In a developed courtship, groups of 4-7 soft pulses generated by legs alternated with a loud sound generated by wing beats (element III). The specimens from Ukraine and another locality of Saratov generated sound by only hind-leg stridulation. During calling, the males produced a single phrase consisting of complex syllables. The first half of each syllable was produced by faster vibrations during the leg up-stroke, whereas the second half of each syllable – by slower vibrations during the leg down-stroke. As a result, each syllable included pulses of different rate and duration. The courtship song started with groups of 3-5 soft pulses, which were gradually transformed into a sound, resembled the calling song syllables. In the developed courtship, the vibrating up-stroke of a syllable was replaced by an abrupt, high-amplitude up-movement of the hind legs. On the basis of the strong differences in songs, we propose to classify the two subspecies, *eurasius eurasius* and *eurasius hyalosuperficies*, as different species.

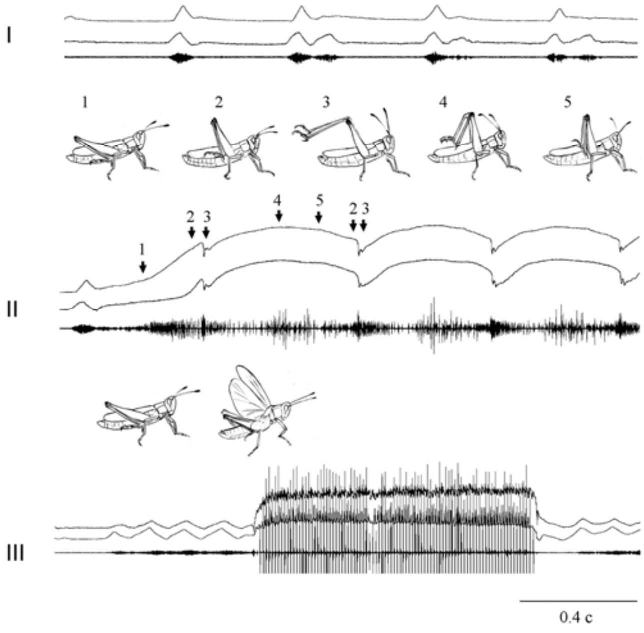

Figure 1. Courtship song of *Stenobothrus eurasius eurasius* Zub. I, II, III – different elements of courtship.

Key Words: grasshopper, courtship, stridulation

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HEARING MECHANISMS IN TREE CRICKETS

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MALE tree crickets broadcast a highly directional, tonal call to attract potential mates. Females orient towards and locate males based on this call which varies both in amplitude and frequency content according to environmental conditions; for instance a higher ambient temperature causes an increase in the frequency content of the call, which in cluttered habitats, is also subject to attenuation by leaves and other obstacles to acoustic transmission. To ensure signal detection, the female receiver must therefore be tuned to calls across a range of frequencies with a high dynamic sensitivity range. Recent work on receiver mechanics has shed light on how the *Oecanthinae* achieve this. Tree crickets, like most vertebrates, have active auditory systems whereby the response of the anterior tympanal membrane is nonlinear[1,2]. They exhibit a lack of tuning at high amplitudes, only becoming tuned as stimulus amplitude decreases. When tuned, the membrane responds best to the frequency content of conspecific male calls, indicating sender-receiver matching only at low amplitudes. This low-amplitude frequency tuning of the tympanal membrane, along with the neuronal frequency response, increases with increasing temperature, matching changes in male call frequency[3]. Active auditory mechanics are thus given an adaptive function in the *Oecanthinae* to maintain sender receiver matching under variable environmental conditions, allowing detection and selection of mates over large distances and a range of ambient conditions.

Key words: Tree cricket, hearing, auditory mechanics, mating call

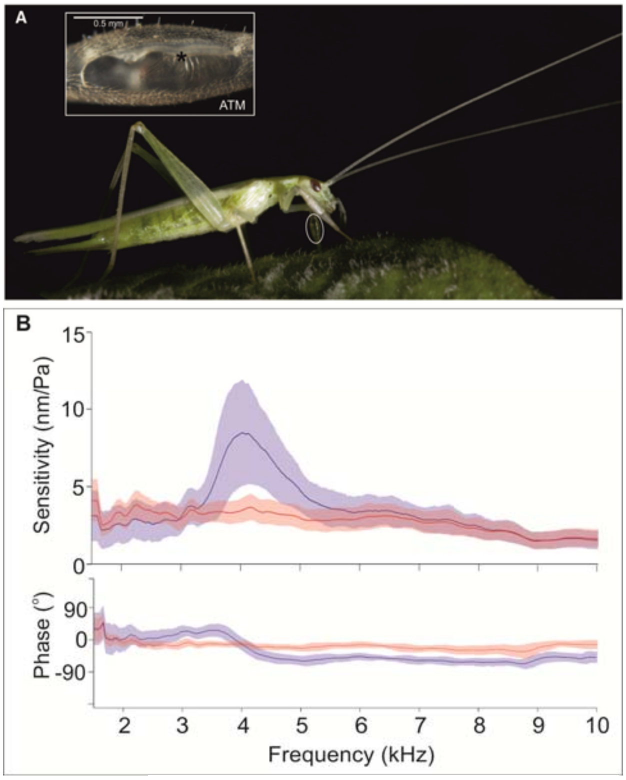

Figure 1. (A) The position of the auditory organ on the foreleg of a female O*ecanthus henryi*. The larger anterior tympanal membrane (ATM) is depicted (inset), with an asterisk marking the position of laser Doppler measurement. From Mhatre & Robert (2013). (B) Mechanical sensitivity (top) and phase (bottom) response of the ATM in live *O.nigricornis* at 36 dB SPL (red, n = 9) and 66 dB SPL (blue, n = 13). From Morley & Mason (2015).

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DATA MINING SOUNDSCAPES FOR ORTHOPTERA SONGS: BIG DATA OR DATA DELUGE?

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AUTOMATIC recording of soundscapes has become a standard monitoring tool, generating Petabytes of acoustic data. Bats, birds, frogs or overall bioacoustics indices are targets of ecoacoustic monitoring projects, some of which running for years. Orthoptera are a dominant element in most recordings, but there are few examples for a comprehensive analysis. Examples from the author´s acoustic monitoring projects in (1) Hymettos (Attica, Greece: http://www.amibio-project.eu/) and (2) Kinabalu Park (Borneo - Sabah, Malaysia), and data-mining of freely accessible soundscapes demonstrate the potential for generating distribution data and species discovery.

(1) For the Greek site, 24 distinct song types could be attributed to known species thanks to an existing well-curated song library (www.systax.org). Distribution data depended heavily on microsite selection, with a strong dominance of Caelifera in open habitats. (2) The tropical rainforest site at Borneo revealed about 60 song types, of which only 15 could be identified to species level, thanks to reference recordings of captured individuals, some of which represented new species to be described. Surprising convergence between microhylid frogs and tettigoniid calls (e.g. *Metaphrynella* Parker, 1934 vs. *Tympanophyllum arcufolium* (Haan, 1843)) impeded unequivocal classification of Orthoptera songs. Data mining of accessible soundscape recordings from other projects (e.g. Purdue soundscape ecology http://centerforglobalsoundscapes.org/) provided valuable information about presence-absence and phenology of Orthoptera. In summary, acoustic recordings can reveal effects of global change on threatened species, effectiveness of conservation measures, or contribute to species discovery. However, the workflow for annotation and data mining of huge acoustic files is still time-consuming. Another bottleneck for determination of Orthoptera species in soundscapes are incomplete reference song libraries. A dedicated search for well-referenced Orthoptera sound recordings (preferably connected to a voucher specimen) in Orthoptera Species File (http://orthoptera.speciesfile.org/) resulted in a total of only 786 species (of 27425), with a strong regional bias for Europe and North America (Tab. 1). Note that regional species numbers do not add up to world's total.

Table 1. Regional percentage of species with songs in OSF (accessed July 2016)

Area	N songs	N species	percent
Temp Asia	194	5424	3.6
Trop Asia	125	6262	2.0
Europe	370	1185	31.2
Africa	60	5572	1.1
N America	127	2231	5.7
S America	89	6056	1.5
Australasia	18	1650	1.1
Pacific	5	728	0.7

Several ongoing OSF projects intend to fill this huge gap, but a concerted action involving authors working on bioacoustics, publishers and major sound archives is needed to overcome this bottleneck within a reasonable timeframe.

Acknowledgments: Supported by OSF grant "Grasshopper songs from Southern South America (SSA): Digital recordings for Orthoptera Species File (OSF)"

Key Words: Bioacoustics, soundscapes, songs

LET ME SEE WHAT YOU HEAR: TRANSPARENCY IN KATYDID AUDITORY SYSTEMS

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LIKE mammals, katydids (Tettigoniidae) exhibit a sophisticated hearing system that includes an outer, middle and an inner ear. The katydid hearing organ, however, is located in the forelegs, with the inner ear being uncoiled and protected only by a layer of exoskeletal cuticle. In mammals the coiled shape and osseous protective material make the inner ear difficult to access without altering its integrity. In-vivo measurements of travelling waves (TW) and frequency spatial mapping (FSM) have only been done through small openings in the scala tympani or other isolated places. Additionally, spatial frequency response on the basilar membrane has been calculated through computational models, or estimated from auditory afferent nerve fibres at selected points. Using non-invasive Laser Doppler Vibrometry (LDV) and intact specimens, FM-Z measured TW and FSM in the ear of the katydid *Copiphora gorgonensis*. The same protocol was repeated on other species, however it was not possible to visualise auditory processes in all species tested. As a result, we proposed that cuticle transparency determines the viability of LDV measurements. Tettigonids' cuticle pigmentation varies among species, from dark colours to light tones (Fig. 1). Lightly pigmented cuticles have a translucent appearance, and in some species it is even possible to see their internal organs. Therefore, species with transparent cuticle should be further investigated as they represent experimental systems in which cochlea-like organs can be accessed with non-invasive techniques (e.g. LDV). The aim of this study is to quantify cuticle transparency across different species (Fig. 2), and to correlate this property with LDV measurements of auditory activity (Fig. 3). The results showed that TW and FSM could be measured only in species with high levels of light transmittance in the exoskeleton. Species with transparent cuticle and non-invasive experimental techniques are key elements for assessing auditory phenomena otherwise impossible to measure in intact acoustic systems.

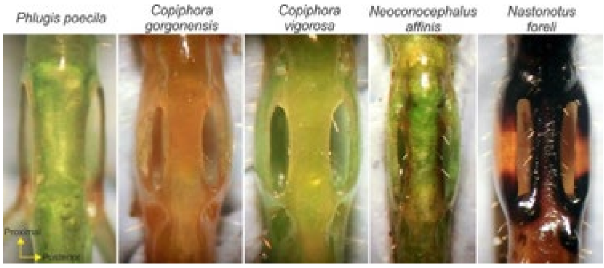

Figure 1. Cuticle pigmentation across species.

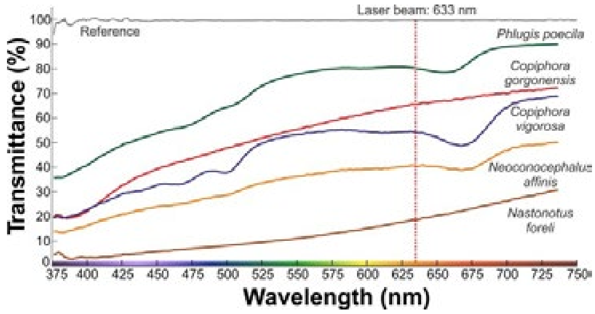

Figure 2. Cuticle transmittance measurement.

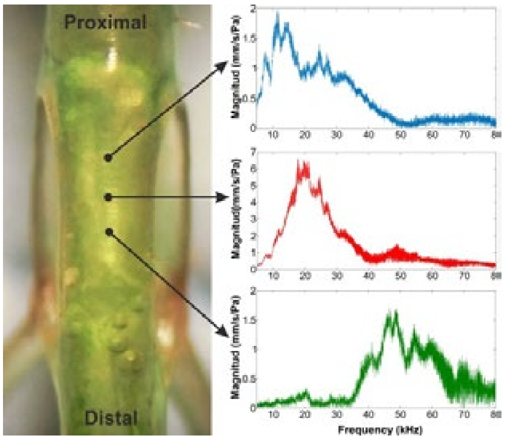

Figure 3. LDV measurement of the auditory activity of the katydid's inner ear.

Key Words: Transmittance, Traveling wave, Tettigoniidae.

• corresponding author

CONTEXT-SPECIFIC SIGNALING WITH DIFFERENT CARRIER FREQUENCIES - THE CASE OF THE BUSH-CRICKET GENUS *Gonatoxia* Karsch 1889

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BUSH-CRICKETS typically communicate by sound to find a mate. In most groups the males produce species-specific song patterns, which attract phonotactically approaching females. The carrier frequencies of the song depend on the morphology of the stridulatory organs and typically do not change while singing. In few groups of tettigonioids (mainly Phaneropterinae and Bradyporinae) males and females engage in acoustical duets. In these cases males and females show very different song patterns, but in many species both sexes use the same frequencies (Heller et al. 2015). The males often sing at large intervals as long as there is no female responding, and avoid thus being detected by predators and parasites. However, if a female responds, the male has to defend his duet against conspecific satellites which could approach the responding female without singing. Many phaneropterine species have complicated songs, parts of which are best understood as imitating female responses and aiming to confuse satellites. In few phaneropterine species, however, males and females have different carrier frequencies, and their auditory neuronal networks are tuned to the signals of the opposite sex (e.g., *Ancistrura nigrovittata*; see Stumpner & Nowotny 2014). In such species, imitating females acoustically seems to be impossible. In the East African phaneropterine genus *Gonatoxia* the narrow-banded songs of males and females differ in peak frequency by up to a factor two, the females being lower than the males. In one species, the males often produce supposedly rival-confusing signals - at about the time when a female response is to be expected: 250 ms after his song (Fig. 1) - with their own high frequency. The males of another species, however, emit at that time a signal with the typical low frequency of a female, while the other parts of their song have the male-specific high frequency (Fig. 2). For the production of these sounds the male uses a bi-parted stridulatory file, not found in any other *Gonatoxia* species. This unique behavior, where only in a clearly defined context a special frequency is produced, will be discussed concerning its function and evolution.

Figure 1. Oscillogram of a *Gonatoxia* duet

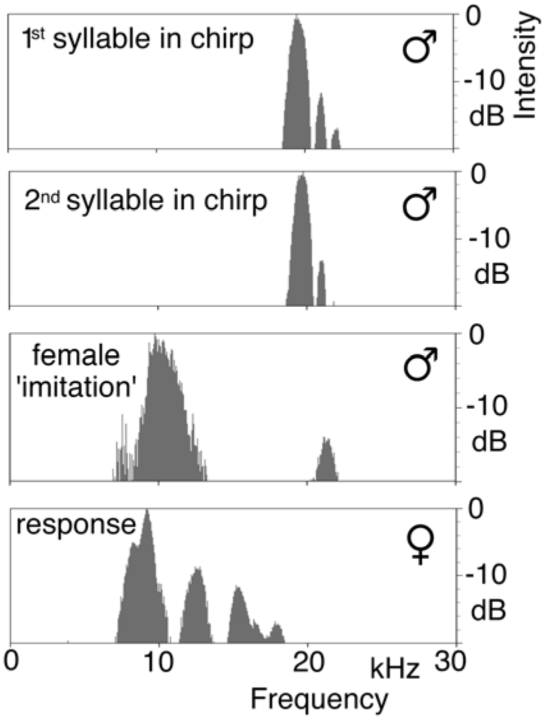

Figure 2. Power spectra of male and female sounds.

Key Words: acoustic communication, duetting, Phaneropteridae

• corresponding author

SOUNDS FROM THE PAST:
FROM FOSSIL TO SONG IN ENSIFERA

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ENSIFERA (Orthoptera) are amongst the earliest terrestrial arthropods to develop acoustic communication; probably as early as the lower Triassic. Extant male katydids (Ensifera, Tettigoniidae) are known to produce loud courtship songs by tegminal stridulation, i.e. the rubbing together of specialized structures on the forewings, namely the file (a serrated vein) and the scraper (a plectrum-like, hardened region). The songs are further amplified by modified and specifically resonating wing cells and detected by other katydids via pressure-sensitive tympanal organs located in the front tibiae. The general biomechanics and bioacoustics of this system are well understood in modern katydids, where it was found that a high proportion of species communicate with signals in the ultrasonic frequency range (20-150 kHz). However, earlier research provided evidence to suggest that the origins of tettigoniid courtship songs lie in audible, much lower frequency signals (<7 kHz). Here, we describe how detailed understanding of the anatomy and biophysical function of the auditory communication system in living bush-crickets and the use of modern imaging techniques, comparative methods and multiphysics finite element modelling of the signal producing and receiving structures in fossils can help to gain insight into the evolution of singing in Ensifera. By incorporating results from experiments using laser Doppler vibrometry on ears and wings of extant species with morphological 3D models, we can build refined finite element models recreating the bioacoustic properties of these structures (Fig. 1). By applying the same models to 3D reconstructions of fossilized wings and ears, we will then be able to infer the resonances of these systems. Combined with anatomical data from fossilised files, the likely frequency ranges used in acoustic communication by these extinct taxa can be obtained. Similar methods can be used to determine the auditory range of extinct species when the tympanal ears are preserved. A more detailed understanding of the evolution of singing in Ensiferans will enable us to shed light on changes in the sensory physiology and the palaeoecology of these insects and their predators through time.

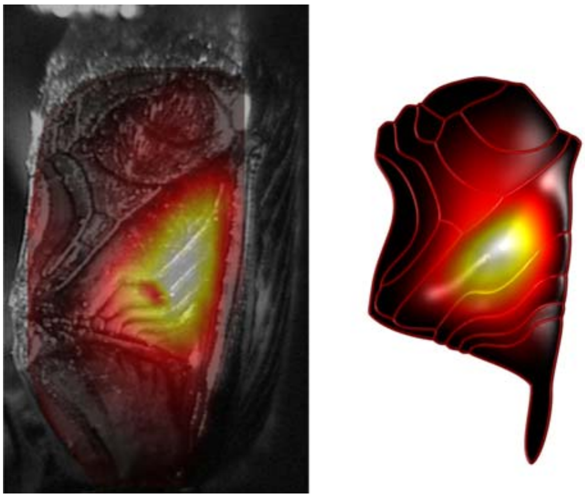

Figure 1. Vibration pattern at first resonant mode (ca. 5 kHz) of a *Gryllus bimaculatus* wing measured with laser Doppler vibrometry (left) and recreated through finite element modelling, based on wing venation pattern (right)

Key Words: katydid, acoustic communication, fossils, finite element modelling

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• corresponding author

A NEW SYSTEM OF COMMUNICATION IN CRICKETS DERIVED BY SENSORY EXPLOITATION OF ANTI-PREDATOR BEHAVIOR (ORTHOPTERA, GRYLLIDAE, ENEOPTERINAE)

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IN the standard system of communication of crickets, which was derived from the study of field crickets (Gryllinae), males are emitting calling signals to attract females at long distances, and females find males by phonotaxis. As new information emerges from the exploration of cricket diversity with multidisciplinary studies, it seems that the standard "field cricket" model is hiding multiple communication systems. Diverse systems of communication may have emerged during the long evolutionary history of crickets to adapt their diverse habitats and contexts of communication.

New communication signals can evolve by sensory exploitation if signaling uses existing sensory biases in receivers. For mate attraction, signals are typically similar to attractive environmental cues such as food, which amplifies their attractiveness to mates, as opposed to aversive stimuli like predator cues. In field crickets, the females approach the low-frequency calling song of males, whereas they avoid high-frequency sounds like predatory bat calls. In one group of crickets (Eneopterinae: Lebinthini), however, males produce exceptionally high-frequency calling songs in the range of bat calls, a surprising signal in the context of mate attraction.

We found that female lebinthines, instead of approaching singing males, produce vibrational responses after male calls, and males track the source of vibrations to find females, which have lost phonotaxis. We also demonstrated that field crickets, which are closely related to Eneopterinae, show an acoustic startle response to high-frequency sounds that generates substrate vibrations similar to those produced by female lebinthine crickets. Therefore, the startle response is the most likely evolutionary origin of the female lebinthine vibrational signal.

In field crickets, the brain receives activity from two auditory interneurons; AN1 tuned to male calling song controls positive phonotaxis, and AN2 tuned to high-frequency bat calls triggers negative phonotaxis. In lebinthine crickets, however, we found that auditory ascending neurons are only tuned to high-frequency sounds, and their tuning matches the thresholds for female vibrational signals. Our results demonstrate how sensory exploitation of anti-predator behavior can evolve into a new communication system that benefits both senders and receivers.

Key Words: high frequency, vibration, sensory exploitation

• corresponding author

TWO MYSTERIOUS LITTLE KATYDIDS FROM THE ECUADORIAN ANDES AND THEIR ULTRASONIC CALLING SONGS

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TWO very small katydids living in cloud forest and elfin woodland on the eastern cordillera of the Andes in south Ecuador feature a confusing mixture of morphological characteristics, each typical of a different subfamily. Most puzzling are the unconcealed tympana combined with tiny auditory spiracles. The tegmina of the males are reduced to the stridulatory apparatus and are completely covered by the posteriorly inflated pronotum (Fig. 1). The soft costal margins fit the tegmina snugly to the insect's back and probably prevent acoustic short-circuiting, while the thin and almost transparent pronotal metazona might act as sound radiator. Females are practically apterous. In conclusion, these curious katydids seem to belong to the Hexacentrinae, apparently representing a sister tribe to Ecuanedubini. The males of one species produce at night one or two short calls per minute, the ones of the other species repeat incessantly long calling sequences. Both have similar carrier frequency ranges at about 20-30 kHz. With an ultrasound detector the presence of these species can easily be ascertained, especially with the second one, distinguished by the very conspicuous calling song (Fig. 2). This allowed an acoustic assessment of the altitudinal distribution of the two nocturnal katydids. The first species lives in upper montane rainforest between 2450 and 2850 m, and the other one in patches of elfin forest between 2700 and 3200 m, this being the uppermost record of a katydid in the investigation area. The moderately broad carrier frequency spectrum of the songs is probably sufficient for distance ranging by differential degradation of higher versus lower frequencies. This is especially important for females at higher elevations, where suitable habitat is very fragmented, with small patches of woodland separated by areas with very low vegetation which provides little protection against the harsh weather conditions. Approaching a male calling from too far away would be hazardous. Acoustic monitoring after sunset should be extended over undisturbed high-elevation woodland on other sites of the tropical Andes, to determine the distribution ranges of the two as well as other still unknown species. Perhaps it would also be possible to study distribution shifts along altitudinal gradients caused by global warming.

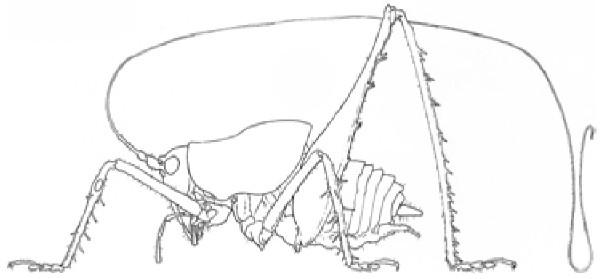

Figure 1. Male of one of the species belonging to a new genus, coloration is dark brown with light green (body length including cerci 12 mm).

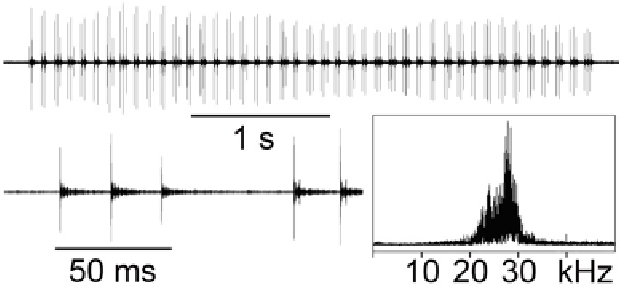

Figure 2. Song of species from Fig. 1: oscillogram of complete calling sequence, below two pulse groups and linear spectrogram (field recording, 5°C).

Key Words: acoustic monitoring, bioacoustics, Tettigoniidae

AUDITORY MECHANICS IN KATYDIDS: DUAL SOUND INPUTS IN THE PRESSURE DIFFERENCE RECEIVER

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THE ear of the bush-cricket *Copiphora gorgonensis* consists of a system of paired eardrums (tympana) on each foreleg. In these insects, the ear is backed by an air-filled tube, the acoustic trachea (AT), which transfers sound from the prothoracic acoustic spiracle to the internal side of the eardrums. Both surfaces of the eardrums of this auditory system are exposed to sound, making it a directionally sensitive pressure-difference receiver. A key feature of the AT is its capacity to reduce the velocity of sound propagation and alter the acoustic driving forces at the tympanum. The mechanism responsible for reduction in sound velocity in the AT remains elusive, yet it is deemed to depend on adiabatic or isothermal conditions. To investigate the biophysics of such multiple input ears, we used micro-scanning laser Doppler vibrometry and micro-computed X-ray tomography. We measured the velocity of sound propagation in the acoustic trachea, the transmission gains across auditory frequencies, and the time-resolved mechanical dynamics of the tympanal membranes in 10 males and 11 females *Copiphora gorgonensis*. Tracheal sound transmission generates a gain of ~15 dB SPL, and a propagation velocity of *ca*. 255 m/s, a ~25% reduction from free field propagation. Modelling tracheal acoustic behaviour that accounts for thermal and viscous effects (e.g., Eq 1)

$$v = c\cdot\left(1-\frac{1}{r_v\sqrt{2}}-\frac{\gamma-1}{r_t\sqrt{2}}\right) \qquad (1)$$

(c = sound velocity in free field air (343 m/s), r_v and r_t terms for the viscous and thermal boundary layers and γ = ratio of specific heats), we conclude that reduction in sound velocity within the acoustic trachea is explained by heat exchange between the sound wave and the tracheal walls.

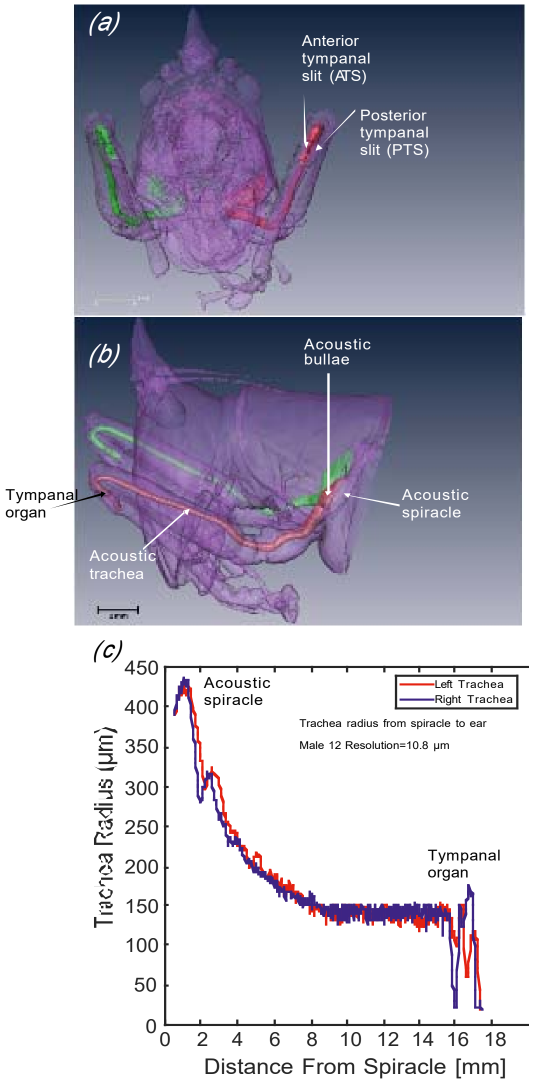

Figure 1. Anatomy of the katydid outer ear. (a,b) Transparent frontal and lateral views of head and thorax showing tracheal tubes on left and right body sides. (c) Variation of the tracheal radius from the spiracle to the tympanal organ.

Key Words: Tympanum, bush-cricket, sound propagation, acoustic trachea

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• corresponding author

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- Orthopterology in a changing Brazil

THE ECOLOGICAL NICHE OF FOREST LITTER CRICKETS (ORTHOPTERA: GRYLLOIDEA)

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TROPICAL forest litter is a high productivity microhabitat, due to the dynamics of litterfall of dead and living leafs, fruits and twigs. Litter fauna includes detritivores, predators and omnivores. Crickets are abundant and diverse in this habitat but we are still lacking formal explanation for such a coexistence. When in equilibrium, coexistence of species in the same trophic level depends on resource replacement. Alternatively, there has to be some sort of resource partitioning, so as to reduce diet overlap among the co-occurring species. Our hypothesis was that cricket species manage to co-occur by segregating their trophic niche. Here we evaluated the trophic niche of nine species of crickets distributed along six forest fragments. In each fragment, a subgroup of three to four of those species co-occur. Diets exploited by crickets were inferred from concentrations of stable carbon and nitrogen isotopes in their bodies, obtained by measuring $_{13}$C/$_{12}$C (hereafter called δ_{13}C) and $_{15}$N/$_{14}$N (δ_{15}N) ratios. Cricket species diet overlapped in all fragments, revealing no segregation in the delta space among co-occurring species. Cricket species in a given community explored a continuum of diets, comprehending up to three trophic levels. Comparing trophic niche of different sites for each species, evidenced that the cricket species could have an intraspecific diet amplitude of up to three trophic levels. The most striking examples was *Melopsis doucasae* (Phalangopsidae) and *Phoremia zefai* (Trigonidiidae: Nemobiinae), both collected in five sites, with different ranges of δ_{15}N in each site. At the δ_{13}C dimension, trophic niche overlap was almost complete. Values of δ_{13}C ranged from -30 to -22‰, evidencing consumption of resource originated from C3 plants. The intraspecific variation of δ_{15}N ranges among sites, evidenced that the same cricket species could vary from mixed detritivorous, to strict carnivorous. Thus, our results evidenced that there is no trophic niche segregation among co-occurring litter cricket species, and that litter crickets have great diet amplitude (omnivory) and flexibility. This suggests that availability of feeding resource for forest litter crickets is not limited. Trophic flexibility observed for litter cricket community as a whole, as well as among sites within species, allows to infer that the organization of litter cricket trophic niche is driven by local resource availability, rather than by specific preferences or limitations. In other words, litter crickets are sufficiently flexible to change resources when necessary.

Key Words: Stable isotopes, trophic niche

• corresponding author

JUMPING AMONG DINOSAURS: (RE)DISCOVERING THE ORTHOPTEROFAUNA OF EARLY CRETACEOUS FROM THE CRATO FORMATION, BRAZIL

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THE Santana and Crato Formations are located at the Chapada do Araripe, on the borders of the states of Ceará, Pernambuco and Piaui (Northeastern Brazil), in the Brazilian Caatinga.

These formations are known world-wide as one of the richest Cretaceous (112 m.a.) fossil Lagerstatten. The Crato Formation is considered as one of the most important study areas of fossil arthropods due to its huge diversity, mainly insects.

This high diversity is represented by at least 18 insect orders and over than 350 described species. One of the main taxonomists that studied part of that diversity was the Brazilian paleoentomologist Rafael Gioia Martins Neto, who described the majority of the fossil taxa.

However, several fossil types described by Martins-Neto were not found by sistematists in Brazilian collections. Considering the major importance of Orthoptera fossils for phylogenetic studies and the understanding of the evolution of this important insect lineage, I made a search in some Brazilian collections in order to locate these types.

Thus, here I present some interesting (re)discoveries. I’ll show the 26 types (holotypes and paratypes) described by Martins-Neto and deposited in the collection of the Laboratório de Paleontologia Sistemática (Laboratory of Paleontological Systematics) of the Instituto de Geociências (Geosciences Institute) of the University of São Paulo (IGC-USP).

Moreover, I’ll present the great amount of new, not studied material from Crato Formation deposited at the collection of IGC-USP. These materials are composed by hundreds of well-preserved Orthoptera fossil, with several undescribed taxa.

I´ll also discuss the importance of these new amounts of fossils for systematic studies and the understanding of Orthoptera evolution, and the perspectives for the paleoentomology in Brazil.

Key Words: fossil, Cretaceous, evolution

A COMPARED MORPHOLOGY OF THE STRIDULATORY REGION OF TEGMINA IN TETTIGONIOIDEA Krauss (ENSIFERA)

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MALES of the suborder Ensifera (Insecta: Orthoptera), produce specie-specific sounds during the opening and closing of both tegmina. A tegmen slides under the other, rubbing a row of teeth with the scraper. Various structural components are involved in this mechanism (Cu´s and annals veins, mirror and harp). The quantity of symmetry of the morphological components of left and right tegmina differs broadly within Tettigoniidae. There are species with very symmetric tegmina, and species with completely asymmetric tegmina. But the origin and evolution of the asymmetry pattern of the stridulatory apparatus is a focus of controversy; if these morphological patterns have been acquired by convergence or have a unique origin from a common ancestor.

It were studied tegmina of 132 species from Colombia and Brazil, belonging to the following six Neotropical subfamilies: Pterochrozinae, Conocephalinae, Listroscelidinae, Meconematinae, Phaneropterinae y Pseudophyllinae. It was carried out geometrical morphometric analyses on the tegminal components and analyses on the number of teeth of the stridulatory files. Additionally, to propose an evolutionary scenario for morphological tegmina changes, it was made a cladistics analysis using cytochrome c oxidase subunit II and 18S ribosomal RNA. The molecular sequences correspond to the same species and genus studied in the morphological analyses. Listroscelidinae and Pterochrozinae have more symmetrical tegmina, with well-developed left and right stridulatory files. Both subfamilies form a clade in the cladistics analysis. Species of Pseudophyllinae have the more asymmetrical tegmina and correspond to the more derivate clade. Through a PGLS model ($R^2=0.99$ p-value <0.0001; K=3.00 p-value <0.001), it was found that the right row of teeth were lost at the expense of the left row, showing a process of evolutionary retrocession in derivative groups. On the other hand, the asymmetry of the shape of the stridulatory complex exhibits a significant phylogenetic signal (Kmult = 0.8394 P-value <0.01).

It is demonstrated for Tettigoniidae that differences of symmetry and asymmetry of components of the tegmina can be traced through the lineages. These differences can be attributed to biological factors or evolutionary conservatism explained under a model of Brownian motion. However, the changes of the form in an evolutionary scenario are complex, as more of an evolutionary force can produce a particular pattern.

• corresponding author

GRYLLINAE GROUP IN THE NEOTROPICAL REGION: STATE OF ART AND FUTURE PERSPECTIVE

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THE subfamily group Gryllinae is a non-systematic grouping that comprises six extant subfamilies of uncertain phylogenetic relationship, with 181 genera and 1640 species. This group is formed by the subfamilies Gryllinae Laicharting, 1781; Gryllomiminae Gorochov, 1986; subfamily Gryllomorphinae Saussure, 1877; Itarinae Shiraki, 1930; Landrevinae Gorochov, 1982 and Sclerogryllinae Gorochov, as well as seven genera of uncertain position. The Neotropical region has species of two of these subfamilies (Gryllinae and Landrevinae) and of two genera of uncertain position. The number of these species are 133, which corresponds to only 8 percent of the total number in the group. The subfamily Gryllinae is the largest of the group and currently has 1139 species, 118 genera and 7 tribes, with three of these tribes occurring in the Neotropics. The Cophogryllini tribe has 47 species in three genera, but only one species of Cophogryllus occur in the Neotropics. The Modicogryllini tribe has a total of 333 species and 26 genera, and these genres occur in the Neotropics: *Faguagryllus* (one species), *Geogryllus* (20 species), *Gryllodes* (one species), *Kazuemba* (one species) and *Miogryllus* (20 species). The Gryllini tribe has 452 species in 49 genera, and the following genera occur in the Neotropics: *Gryllus* (26 species), *Anurogryllus* (25 species), *Megalogryllus* (two species), *Scapsipedus* (three species) and *Tarbinskiellus* (one species). Besides, two Gryllini genera of uncertain position also occur in the Neotropics: *Zebragryllus* (six species) and *Hispanogryllus* (two species). The subfamily Landrevinae currently has 170 valid species, distributed in 38 genera and three tribes. The Odontogryllini tribe is exclusively Neotropical and has 3 genera: *Brasilodontus* (six species), *Odontogryllus* (11 species) and *Valchica* (one species). The Landrevini tribe comprises 27 genera and 136 species, but only two monotypic genera are Neotropical: *Yarrubura* and *Xulavuna*. Besides that, the genus *Landreva* has one Neotropical species in Costa Rica, while the other species of the genus occur in Asia. The Neotropical genera *Paranurogryllus* and *Neogryllodes* are allocated in the grouping although not in any subfamily, and they have respectively, two and one species. The numbers regarding the Neotropics diversity of the subfamily group Gryllinae show us that this group is underestimated in the region compared to other families and subfamilies. This group requires an effort in the formation and training of human resources to improve the knowledge of the cricket biodiversity.

Key Words: taxonomy, biodiversity, cricket

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Anurogryllus Saussure, 1878 (GRYLLIDAE: GRYLLINAE) FROM SOUTHERN BRAZIL: NEW SPECIES AND NEW RECORD

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THE genus *Anurogryllus* Saussure, 1877 comprises 26 valid species distributed throughout the Americas, with occurrence from Argentina to United States. These crickets dwell open habitats, whether natural or anthropized, and have underground habits and subsocial behavior. Despite the larger number of newly described species (13 in the last decade), only four have information about your calling sounds.

The aim of this work is to describe two new *Anurogryllus* species from southern Rio Grande do Sul State, Brazil, based on morphological and genital characters as wells as calling song descriptions. Besides that, we also provide new records for *Anurogryllus toledopizai* (de Mello, 1988), with acoustic data and genital figures.

The specimens were collected in the following municipalities in southern Rio Grande do Sul State, Brazil: Capão do Leão (31°46'52.7"S 52°35'20.8"W; 31°48'03.4"S 52°25'05.8"W), Canguçu (31°28'00.0"S 52°57'00.0"W; 31°20'57.0"S 52°43'54.3"W) and São Lourenço do Sul (31°17'39.43"S 52°09'02.76"W). Holotypes and paratypes were deposited in the Museu de Zoologia of the Universidade de São Paulo (MZUSP).

Anurogryllus tapes sp. nov. is diagnosed by the ocelli arranged almost in a crossbar, median ocello slightly below the lateral ocelli; tibia I with large and elongated external tympanum and without internal tympanum; ectophallic arc wide, basal concavity accentuated and semicircular, apical convexity more pronounced in the central region, right in apical direction when in lateral view; ramis connected at the basal portion, rectangular, longer than wide, apical end simple; pulse period 12.26 - 12.59ms, pulse rate between 80 - 82p/s; dominant frequency between 5340 - 5510Hz.

Anurogryllus patos sp. nov. is diagnosed by the ocelli arranged almost in line, forming a concave arc; tibia I with oblong external tympanum and internal tympanum small and oval; ectophallic arc wide and short, basal concavity attenuated, apical convexity attenuated, straight and diagonal apical when in lateral view; ramis connected in the basal portion, rectangular, as long as wide, apical end simple; continuous trill with pulse period between 6.91 - 7.61ms, pulse rate between 130 - 146p/s; dominant frequency between 4990 - 6020Hz.

The calling sound of *Anurogryllus* species have a similar structure, with almost all species singing in a continuous trill, allowing a little time of variations. Nevertheless, the calling sound becomes very useful to differentiate species which occur in the same habitat.

Key Words: Gryllini, calling song, cricket

• corresponding author

ANALYSIS OF THE MITOCHONDRIAL AND NUCLEAR NUCLEOTIDE SEQUENCES AS THE APPROACH TO THE PHYLOGENETIC SYSTEMATICS OF ACRIDIDAE GRASSHOPPERS

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FOR a long time, taxonomy, the phylogenetic relationships and understanding of the evolution of Acrididae family were based mainly on comparison analysis of key morphological structures of recent and fossil species. However, on subfamily level, the problems of convergence and parallelism are rising up for these insects. One of the most effective methods of establishing phylogenetic relationships is the analysis of various DNA markers. In present work, we conducted molecular phylogenetic analysis of complete mitochondrial sequences (Fig. 1), mitochondrial (COI, COII, CytB) and nuclear (ITS2, 28S rRNA) markers of more than 220 species of Acrididae grasshoppers from 26 subfamilies. The data on nucleotide sequences from these insects were obtained experimentally and from NCBI database. All original DNA marker sequences will be in a free access in the NCBI database. Phylogenetic trees for different combinations of these markers were obtained using maximize likelihood and Bayesian methods. The complete sequence of mitochondrial genomes currently set for 42 species only belonging to the 12 subfamilies. The phylogenetic tree constructed on these sequences, contains three major groups. The first group includes three subfamilies: Gomphocerinae, Oedipodinae, and Acridinae. Both the second and the third groups consist of several clusters, which include the representatives of 17 and 9 subfamilies, subsequently. Phylogenetic trees constructed based on the analysis of COI, COII, Cytb, ITS2 and 28S rRNA sequences are largely clarify and complement the results obtained on analysis of complete mitochondrial genomes sequences. As the result of the work done, we found out that all studied species under discussion grouping up into 13 phylogenetic clusters. Phylogenetic relationships between them are presented in cladogram form and will discuss. Five out of 26 subfamilies (Acridinae, Oedipodinae, Gomphocerinae, Oxyinae and Catantopinae) found to be polyphyletic in present study. An analysis of the geographical distribution of different branches of polyphyletic groups show, that external similarity is a result of homoplasy in evolution of some subfamilies, belonging to Acrididae family.

Acknowledgment. Sequencing procedures have been carried out at SB RAS Genomics Core Facility (Novosibirsk, Russia, http://sequest.niboch.nsc.ru)

Key Words: Acrididae, molecular phylogeny and systematics

• corresponding author

EVOLUTION OF THE NEO-XY SEX CHROMOSOME DETERMINATION IN PAMPHAGIDAE GRASSHOPPERS

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THE karyotype structure of grasshoppers is very conservative. For instance, the modal male karyotype of Acrididae grasshoppers consists of 22 acrocentric autosomes and an acrocentric X chromosome. In Pyrgomorphidae and Pamphagidae, the modal karyotype consists of 18 acrocentric autosomes and an acrocentric X chromosome. The sex chromosome system in the vast majority of species is XX♀/XO♂. In the karyotype evolution of some grasshoppers species the X chromosome enters into centric fusion with an autosome, which leads to a neo-XX♀/neo-XY♂ sex chromosome system. Neo-XY sex chromosome determination is a rare event in short horned grasshoppers, but it appears with unusual frequency in the Pamphagidae family. We perform here karyotyping and molecular cytogenetic analyses in 25 Pamphagidae species from Central Asia, Caucasus, Transcaucasia, and Anatolian plateau. Among the species studied vest majority consisted of 16 acrocentric autosomes and a neo-XY sex chromosome system (2n♂♀=18, neo-XX♀/neo-XY♂). The submetacentric neo-X derived from centric fusion between an ancestral medium sized acrocentric X chromosome and an ancestral acrocentric autosome, and the high similarity in size and morphology of the neo-X chromosome between all species analyzed. Two different types of the neo-Y chromosomes were found. One of them was typical for three species of the *Glyphotmethis* genus and for three species of the *Asiotmethis* genus from Thrinchinae subfamily, and showed a neo-Y chromosome being similar in size to the XR arm of the neo-X, with the addition of two small subproximal interstitial C-blocks. In the second type, the neo-Y chromosome was smaller and more heterochromatinized than the XR arm, and was typical for all Nocarodeini species studied belonging to *Nocaracris, Nocarodes, Paranocaracris, Paranocarodes, and Saxetania* genera (Pamphaginae subfamily). Localization of telomeric and ribosomal DNA in the sex chromosomes suggests that translocation of an autosome and the X chromosome was followed by the loss of the autosome fragment. It can be assumed that the deletion is the primary reason in the loss of structural homology between autosome arm of the neo-X chromosome and neo-Y.

Our results show more high frequency of neo-XY sex chromosome systems in Pamphagidae grasshoppers inhabiting the Anatolian region, with at least two different lineages. In Trinchinae species neo-Y chromosomes have scarcely evolved in respect to their autosomal ancestral condition, and we can consider that they are at the initial stage of heterochromatinization and differentiation. In Nocarodeini species (Pamphaginae) the neo-Y chromosome was conspicuously smaller than that of the XR arm of the neo-X chromosome, and its proximal third is heterochromatic. All these features indicate that these neo-XY sex chromosome systems are old and thus the neo-Y is highly modified. In this model of Pamphagidae chromosomes evolution are still many missing links, but our analysis showed that these links should be found in the West Asia.

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Key Words: Pamphagidae, chromosomes

• corresponding author

EXPLORING THE TAXONOMIC DIVERSITY OF THE WEST INDIAN GRASSHOPPER GENUS *Dellia* Stål, 1878 (ACRIDIDAE: COPIOCERINAE)

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MOUNTAINS in island archipelagos are systems in which speciation by isolation (allopatry) has been a major factor in the production of biodiversity. The complex geological and biogeographic history of the Antilles has resulted in a rich and diverse fauna with high levels of endemicity in each one of the major islands. *Dellia* Stål, 1878 is a genus of colorful arboreal and flightless grasshoppers partially associated to mountains, each species being endemic to a single island. *Dellia* is restricted to some of the Greater Antilles (Cuba, Hispaniola and Jamaica) and the Bahamas (San Salvador Island), where it has undergone considerable speciation. *Dellia* have been found from very humid environments to relatively dry forests from sea level to nearly 1500 m above sea level, always perched in a variety of small trees and shrubs less than 4 meters above the ground.

This research pursues several objectives:

1) Resolve the identity of the genotypic species *Dellia insulana* Stål, 1878, described from an unknown locality in Cuba. This implies establishing the present distribution of this species and evaluating the validity of its synonymy with *D. multicolor* Carl, 1916.
2) Taxonomic description of several new Cuban species from diverse parts of the island. Specimens borrowed mostly from the collection of the Instituto de Ecología y Sistemática (La Habana) and more recent collections, suggest that *Dellia* has multiple undescribed species in Cuba.
3) Better evaluate the diversity of *Dellia* in Jamaica. Partial evidence suggests the existence of more than the three known species.
4) Six species of *Dellia* have so far been described from the Dominican Republic, island of Hispaniola. Specimens of *Dellia* from Haiti are needed to expand the taxonomic coverage to the whole island.
5) The taxonomic description of the *Dellia* sp. known to be in San Salvador Island. Fresh specimens are desired for a characterization of their natural coloration.
6) Evaluate the validity of each morphological species using DNA barcodes, as well as the taxonomic position of species like *Dellia viridissima* Perez-Gelabert & Otte, 2012, whose coloration and morphology suggest it is an outlier in the *Dellia* radiation.
7) DNA barcodes will also be used in phylogenetic analysis to evaluate whether the genetic diversification has occurred mostly within islands and whether the relationships of species groups follows the hypothesized geological relationships between islands.

PRELIMINARY PHYLOGENY OF THE TRIBE PODISMINI (ORTHOPTERA: ACRIDIDAE: MELANOPLINAE) IN JAPAN BASED ON MITOCHONDRIAL CYTOCHROME C OXIDASE I GENE SEQUENCES

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THE Podismini, one of the six tribes of the subfamily Melanoplinae (Orthoptera: Acrididae), is distributed in the Palearctic region. The aim of this study was to clarify relationships between Podismini in Japan by analyzing cytochrome c oxidase I (COI) mitochondrial gene sequences. Forty-seven individuals representing sixteen podismine species and ten genera as well as two outgroup species were used in the analyses. Our preliminary phylogenetic analyses using maximum likelihood and Bayesian Inference confirmed earlier hypotheses that Podismini is paraphyletic (Fig. 1). The Podismini were divided into two lineages B1 and B2. A monophyletic group was recovered for genera: *Fruhstorferiola*, *Podisma*, *Zubovskya*, *Sinopodisma*, and *Tonkinacris.* The members of the genus *Parapodisma* included in this analysis do not seem to be monophyletic according to molecular or morphological data. We discovered several subgroups in *Parapodisma.* Our study showed that the *Podisma* was not placed in basal position. The present study is an initial step towards understanding fully the phylogenetic relationships between the members of the tribe Podismini from Japan. A comprehensive molecular analysis of these Melanopline taxa will be the subject of the next-step studies, where more species and genes will be included. This could shed further light on the circumstantial evolutionary history in Podismini and will thus provide useful information for the understanding of speciation process in grasshoppers.

This work has been supported in part by JSPS KAKENHI Grant Numbers 15F15762, 25291088, and 25304014.

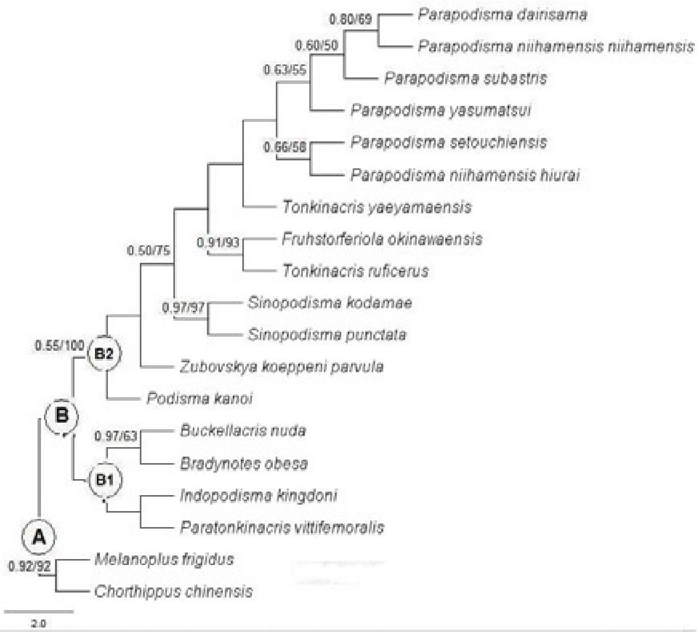

Figure 1. Phylogenetic tree of the Podismini based on BI analysis of concatenated COI sequences. BI posterior probability (PP) and maximum likelihood bootstrap (B) values are shown near resolved branches (only support values above 50% are shown) as PP/B. The respective branches are marked with a circle and a capital letter as follows: "A" – outgroup species; "B" – Podismini species.

Key Words: grasshopper, phylogeny, DNA

• corresponding author

TAXONOMY AND CLADISTIC ANALYSIS OF *Eidmanacris* Chopard, 1956 (GRYLLOIDEA, PHALANGOPSIDAE)

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GYLLOIDEA has undergone several taxonomic discrepancies over the years probably due the lack of scientific studies on this group, mainly taxonomic and systematics. The current number of described species is still much underestimated. The first phylogenies of crickets were based on groups as models of speciation, acoustic communication and diversification of stridulatory apparatus. Recently, some molecular phylogenies of Orthoptera, Ensifera and Grylloidea, began to clarify their relationships. Understanding lower level taxa could help to resolve phylogenies of higher level groups. Until now, no phylogenetic hypothesis has been proposed for the genus *Eidmanacris* Chopard, 1956. It comprises 20 described species, and is mostly distributed in Atlantic Forest and Cerrado areas, extending from south, southeast and center-west Brazilian regions, as well as in Bolivia and Paraguay. Active at night, the species inhabit burrows, hollow trees trunks, cavities in rocks and caves. The aims of this study were to review the genus *Eidmanacris*, with redescription of poorly known species and description of new species, as well as to carry out a phylogenetic analysis to test the monophyly of the genus and to infer the species relationships based on morphological characters. The material examined were from: Muséum national d"Histoire Naturelle (MNHN); Museu de Zoologia da Universidade de São Paulo (MZSP); Museu de Zoologia da Universidade Estadual de Feira de Santana (MZUEFS); Departamento of Zoology, Institute of Biosciences, São Paulo State University, Botucatu Campus (UNESP). Eight species are redescribed (*E. larvaeformis, E. alboannulata, E. dissimilis, E. fusca, E. ultispinosa, E. tridentata, E. bidentata* and *E. corumbatai*); three new combinations are proposed (*Endophallusia minuta*, *Endophallusia endophallica* and *Phalangopsis speluncae*); and five new species are described. For the phylogenetic analyses, 38 terminals were examined, 12 in the outgroup. We constructed 98 morphological characters, with searches using parsimony optimization. We obtained 11 most parsimonious trees. A second analysis was performed without *E. paramarmorata* (94% of missing data). Just one most parsimonious tree was found. Both analyses showed *Eidmanacris* as a monophyletic taxon including the genus *Endophallusia*, with seven synapomorphies: 1 - presence of latero-posterior projections of male supra anal plate; 2 - presence of anterior projection of pseudepiphallic sclerite; 3 - not sclerotized connection between pseudepiphallic parameres 1 and 2; 4 - ectophallic fold entirely membranous; 5 - endophallic apodeme crest form; 6 - medio-posterior projection of endophallic sclerite long, through ectophallic fold; 7 - presence of latero-posterior lobes of endophallic sclerite. These relationships could be the beginning of biogeographical, behavioral or even evolutionary studies, becoming *Eidmanacris* as a good model to understand these questions.

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Key Words: cricket, morphology, systematics

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ALTITUDINAL DISTRIBUTION PATTERNS OF ORTHOPTEROIDEA IN THE WEST SAYAN MTS.

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ALTITUDINAL distribution patterns of different taxa of Orthopteroidea were described for several mountain systems. The main part of these publications was associated with species distribution along the altitudinal gradient of some mountain ridges and with evaluation of biological diversity levels and endangered species disposition. The distribution patterns of biogeographic boundaries were also revealed in several publications. However, general patterns of orthopteran altitudinal distribution remain unclear. The main aims of this publication are to analyze and to compare the altitudinal distribution patterns of Orthopteroidea in the West Sayan Mts. These mountains are in the central part of the mountains of South Siberia and form their northern border. At least three orders of Orthopteroidea, namely terrestrial Orthoptera and Notoptera and amphibiotic Plecoptera, are known from this area. Qualitative and quantitative data were collected from 1995 until 2016 for Orthoptera and from 2013 until 2016 for Plecoptera. We tried to study all habitats applicable for local Orthoptera, Notoptera, and Plecoptera. Besides our own data, some published and unpublished data were used. We analyzed distribution of species and assemblages over main altitudinal belts: mountain tundra (1,600–2,400 m); alpine and subalpine meadows (1,400–1,700 m); mountain taiga (800–1,500 m); mixed forests with intermountain steppes (500–800 m); mixed forests with forest-steppes (200–600 m). In the mountain tundra, the levels of species diversity and abundance of Orthoptera were very low. *Gomphocerus sibiricus* (L.) was the most common species. The only local member of the order Notoptera was found here. There were no stoneflies. In the alpine and subalpine meadows, the dominant species were *Zubovskya mongolica* Storozhenko and *Pteronarcys reticulata* (Burm.). In the mountain taiga, the levels of taxonomic diversity slightly increased, the orthopteran abundance was low, the plecopteran biomass was high. In the mixed forests with the intermountain steppes, 39 species of Orthoptera were found. Several forms are associated with the East Asia (*Chorthippus hammarstroemi* (Mir.) *et al.*) or with the Mongolian steppes (*Myrmeleotettix palpalis* (Zub.)). The level of orthopteran abundance was high. One species of stoneflies was found in the local stream. In the mixed forests with forest-steppes, the levels of taxonomic diversity and abundance of Orthoptera were relatively low. 17 species were found, mainly associated with the northern part of Eurasia. One of four local species of stoneflies (*Nemoura sahlbergi* (Morton)) was also very abundant. Thus, the altitudinal distribution patterns of Orthoptera and Plecoptera in the West Sayan Mts. resemble the same in the North Altay Mts. (Sergeev et al., 2013). Almost all species of both orders are associated with relatively low altitudes. 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.

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Key Words: Orthopteroidea, altitudinal distribution, West Sayan Mts.

• corresponding author

COMPOSITION AND VERTICAL STRATIFICATION OF KATYDIDS (TETTIGONIIDAE) COMMUNITY IN A URBAN PATH OF THE BRAZILIAN SAVANNA

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IN structure and composition of katydids, is highlighted the organization of species in relation to height within a specific location, which affects directly the sound communication. The species and community organization from the Cerrado in the central-western region of Brazil is almost unknown. This domain is a biodiversity hotspots and one of the most threatened and over-exploited region in this country. There are few studies on Orthoptera from this domain. In the state of Mato Grosso do Sul (MS), only eight species of katydids have been registered. The aim of this study is to describe the composition and the vertical stratification of the community of katydids in an urban path of Cerrado in the state of MS. The path is a continuous remaining with 36,5 ha of cerrado and "Cerradão" phytophysionomies. Katydids where sampling from July 2015 to June 2016. Representative specimens of each species were collected and dry preserved. Additionally, during eight nights between February and March of 2016 from 19:00 to 21:00 hours, was registered the height (cm) on the hosts plants for each observed specimen. Estimated richness index and rarefaction curve were used to describe the community and to verify the vertical stratification was used direct ordering analysis. All tests were realized in R software. There were collected and preserved 36 specimens belonging to 11 species. The Jackknife 1st order index estimated 14.68±1.28 species, associated with the rarefaction curve. Thus was sampled most of katydids fauna in the area (87.5%). There were recorded five species of Phaneropterinae, four of Conocephalinae, one of Pseudophyllinae, and one Meconematinae. Then, species are showed in order of number of decreasing records: *Homotoicha similis* (175), *Euxiphidion* sp. nov. (65), *Neoconocephalus ferreirai* (34), *Copiphora producta* (26), *Mendesius albosignatus* (14), *Conocephalus saltator* (9), *Phylloptera callosa* (5), *Hyperophora cerviformis* (4), *Gongrocnemis* sp. (3), *Topana aguilari* (1), *Phlugis* sp. nov. (1). Eight of the founded species are new records for the state. The species *C. mandibularis* was collected only one time in July 2015. In relation to vertical stratification there were registered 174 occurrences from ten more abundant species. Conocephalinae have 134 records, Phaneropterinae 36, and Pseudophyllinae 3. The community is structured by the vertical stratification with different katydid species located at different heights. The individuals are distributed on the vertical gradient, from 10 to 320 cm of height. Phaneropterinae was found in a wide gradient of height on shrubbery and short trees, Conocephalinae species, excepting for *C. producta*, were found on low vegetation. The latter species was registered in median and high heights on median and high trees, and this feature along with the distance between individuals (data not shown here), may be related to their loudly calling song. Individuals of *E. subapterus*, *C. saltator*, and *N. ferreirai* are gregarious and share similar vertical strata. The difference in vertical position could be related to sound communication and behavior.

Key Words: Cerrado, distribution, occurrence

• corresponding author

CORRELATIONS OF ORTHOPTERA SPECIES AND HABITAT DISTRIBUTION PATTERNS IN THE PANNONICUM

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IN the Orthopteran Fauna of Hungary the following faunal elements show high frequencies: European and Eurasian (4.6 and 32.5 %), Continental (35.7 %), Mediterranean (27.2 %). Several taxa being important from aspects of biogeography are indicator of habitat condition, degradation and disturbances. In our study area (Hungary) we examined relations between distribution of habitat-specialist species of the Pannonicum Region and distribution of their potential habitats occurring on patches of the landscape-structure being characteristic in climate, topography and soil. We ordered the known data into the Hungarian quadrates of Central European Flora Mapping (CEU) system. Our database had the following variables: presence, absence data of the examined Orthopteran species; presence, absence and frequency (3: high, 2: medium, 1: low) of the potential Orthopteran habitats. Analyses revealed several positive and negative correlations between the distribution pattern of the Orthopteran species having biogeographical importance and their potential habitats characterized different ecological circumstances. Our results showed that distribution of sand- and saltsteppe preference species as *Acrida ungarica, Calliptamus barbarus, Oedaleus decorus, Gampsocleis glabra, Platycleis affinis* are strongly determined by the cover of habitats as open sand steppes (Fig. 1), salt meadows, Artemisia salt steppes etc. Distribution of the typical steppe species as *Stenobothrus eurasius* and *Saga pedo* showed strict positive correlations with the distribution of calcareous open rocky grasslands and calcareous rocky steppes. Our analyses did not point out any relation between species related to small, hardly confinable habitats (e.g. *Pholidoptera aptera*) and the involved potential Orthopteran habitats. Based on these preliminary results we confirmed that exploration and mapping of Orthopteran habitats help a lot in investigation of sensitive species. Over the cover of potential Orthopteran habitats the importation of other limiting parameters (e.g. macroclimate) into the "Orthogeographical" researches is needed in the future.

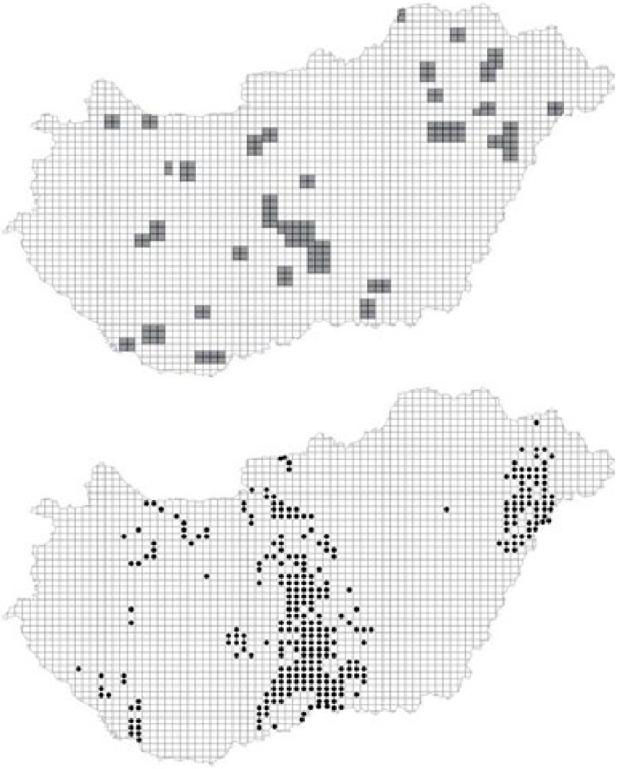

Figure 1. Distribution of *Oedaleus decorus* (above) and open sand steppes (below)

Acknowledgements: Our thanks go to Zsolt Molnár, Ferenc Horváth and group of Á-NÉR authors for the compilation of the habitat data.

Key Words: habitat-preference, distribution pattern

• corresponding author

IMPACTS OF SOME CLIMATE PARAMETERS ON POPULATION SIZE OF *Isophya costata* (Brunner von Wattenwyl, 1878)

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ISOPHYA COSTATA is a postglacial, subendemic species of the Carpathian Basin (Central-Europe). It is strictly protected species in Hungary and Natura 2000 species in the EU. Occurrences of *Isophya costata* are known just from Hungary and some neighbouring areas (Austria: Viennese Basin; Romania: Transylvania).

Previous summaries contain significant contradictions concerning the choice of habitat of the species (liquidation of habitats, abandonment of hayfields etc.). Opposite this, in the last decades several new stands of the species have been discovered thanks for the systematic fieldwork.

Isophya costata related to mesophytic hayfields, loess and steppe grasslands and mesotrophic wet meadows being rich in dicotyledonous plant species. It originally was a species typical of loess grasslands and closed steppe grasslands, but later the species adapted to the anthropogenic hayfields, which contain dicotyledonous plant species with high frequency. By this time hayfield has become the main habitat of the species.

We examined population and local habitats of *Isophya costata* occurring near Lake Fertő, in the Western-Pannonian Region till 2007. Annual size of the population showed considerable deviation from 2007 to 2014.

We hypothesized that these differences are caused by the weather during hatching and larval states.

We analyzed relations of (a) population size of *Isophya costata* and microclimate data; (b) vegetation-structure and microclimate data; (c) population size of *Isophya costata* and macroclimate data; (d) vegetation-structure and macroclimate data; (e) population size of *Isophya costata* and vegetation-structure.

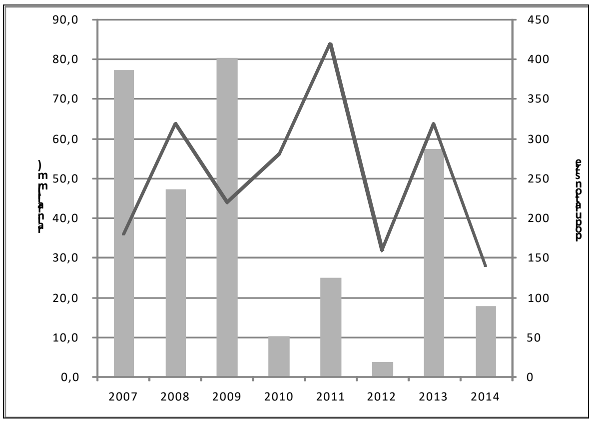

Figure 1. Changes in population size and rainfall in March

Our results showed that annual population size of *Isophya costata* is hardly affected by (I) overall cover of mesophytic dicotyledonous plant species; (II) macroclimate parameters of March. We found that less than 25 mm and more than 55 mm rainfall in March are both unfavourable for hatching and larval development of the species (Fig. 1).

Acknowledgements: Our special thanks go to the Fertő-Hanság National Park Directorate and to Gábor Takács for the permanent supporting.

Key Words: macroclimate, vegetation

• corresponding author

SURVIVAL IN A CHANGING ENVIRONMENT – EFFECTS OF LAND-USE AND CLIMATE CHANGE ON ORTHOPTERA IN MONTANE GRASSLANDS

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THE ongoing global biodiversity loss is one of the most severe current problems. In terrestrial ecosystems, land-use change has the greatest influence on biodiversity. More recently, climate change has become another important driver of biodiversity changes. Orthoptera respond sensitively to environmental alterations and, therefore, are well-suited model organisms to study the effects of global change. In Central Europe, many Orthoptera species have experienced a strong decline due to the transition from traditional land-use practices to modern agriculture. However, in the last two decades some species have shown rapid range expansions and there is increasing evidence that these shifts are caused by global warming. In our study, we analyzed the effects of land-use and climate change on Orthoptera in grasslands of a low mountain range in Central Europe. Therefore, habitat patches which have been surveyed in 1994 were resampled in 2015. Over the last two decades, there has been a significant increase of the mean annual temperature in the study area. Furthermore, the grassland patches were particularly affected by abandonment. However, in some patches traditional land use was reintroduced. Overall, we detected a significant increase in species richness (Figure 1). This increase was especially attributed to a rapid expansion of mobile habitat generalists. In contrast, in habitat specialists there were nearly no changes in patch occupancy.

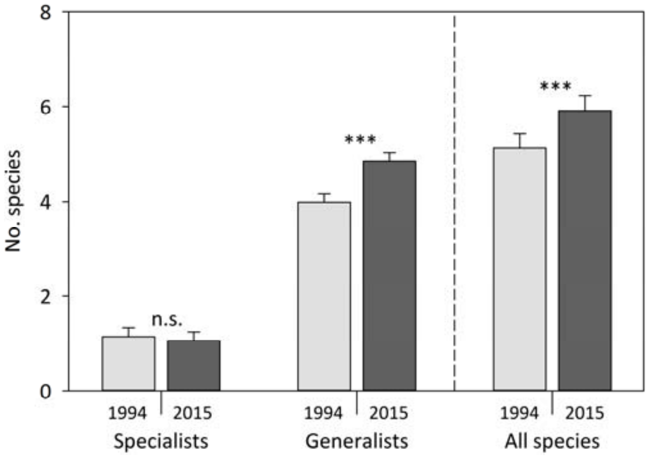

Fig. 1: Mean number of Orthoptera species in all studied grassland patches in 1994 and 2015. n.s. not significant, *** $P < 0.001$.

However, the patterns differed between habitat and land-use types. The increase in species richness was especially high in managed habitats without land-use alterations, whereas at abandoned patches Orthoptera species numbers decreased. Our results clearly indicate that the recent increase in Orthoptera diversity is influenced by climate warming. However, in the long run a low-intensity grassland management is indispensable for the preservation of Orthoptera biodiversity in these grasslands. The presented study was funded by a scholarship of the German Federal Environmental Foundation (DBU).

Key Words: Central Europe, Global Change, Habitat management

• corresponding author

THE STONEFLIES (PLECOPTERA) ASSEMBLAGES IN THE MOUNTAIN RIVERS OF SOUTH SIBERIA: DIVERSITY AND ALTITUDINAL DISTRIBUTION

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THE spatial distribution of stoneflies assemblages in the mountain streams of South Siberia is discussed. In 2009–2013 the assemblages were investigated along 15 rivers and streams: Sema, Pestshanaya, Anuj, Cherga, Sarasa (North Altay); Ona, Kebezh, Tashtyp, Idzim (West Sayan Mts.); Koltyrak, Froliha, Suenga, Tarsma, Poldennay, Kinterep (Salair Mts.). Sampling sites were distributed over 200-meters altitudinal intervals. Each site included three collecting stations. All data were obtained in the middle of summer. 178 sites were sampled. At each station all invertebrates were collected in different microhabitats with a Surber sampler over an area of 0.3 m^2. The specimens were fixed in 75% ethanol. For each sampling station the main environmental parameters were recorded: altitude (m.a.s.l.), flow velocity (m/s), flow volume (m^3/s), water temperature (°C), depth and width of the channel (m), amount of dissolved oxygen (mg/l), type of substratum, presence or absence of macrophytes. In the laboratory, the stonefly nymphs were identified and preserved in 80% ethanol. The dry biomass was evaluated both for the stoneflies assemblages and for all benthic community. After that, a degree of Plecoptera presence was measured for each community at each site. The paired group hierarchical clustering analysis was used to verify differences between the plecopteran faunas of North Altay, the Salair Mts and the West Sayan Mts. The Shannon index of diversity was calculated for the stoneflies assemblage of every sampling site. The multiple factor ANOVA was used to distinguish the main factors, their effects and interactions. In general, 26 species of stoneflies were found. There were 21 species in North Altay, 20 — in the West Sayan Mts. and only 6 — in the Salair Mts. The Perlodidae family is the most common family of the order (37% of species diversity). The comparative analysis of the Plecoptera fauna of West Sayan and North Altay revealed great similarity, however, the fauna of Salair was quite different. The altitudinal distribution of several species, namely *Alloperla rostellata* (Klapálek, 1923), *Eucapnopsis brevicauda* (Claassen, 1924), *Capnia atra* (Morton, 1896) was characterized by preference for high altitudes (more than 1200 m.a.s.l.). *Paraleuctra zapekinae* (Zhiltzova, 1974) and *Amphinemura borealis* (Morton, 1894) inhabited only the middle parts of the streams from 400 to 670 m. *Isoperla altaica* (Šámal, 1939*), Isoperla lunigera* (Klapálek, 1923), *Arcynopteryx polaris* (Klapálek, 1912), *Leuctra fusca* (Linnaeus, 1758) were randomly distributed along waterflows. The most diverse assemblages of Plecoptera were at the upper and middle parts of the metarhithral zone of streams. The Shannon index calculated for assemblages at these sites varied from 1.6 to 1.9. Of the parameters considered, the altitude, the amount of oxygen, and the type of the substrate were the most important factors affecting the spatial distribution of the stonefly nymphs.

These studies were financially supported by the Russian Foundation for Basic Researches (13-04-91163, 16-04-00706, 16-34-00632).

Key Words: Plecoptera, mountain stream, South Siberia

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EVALUATION OF DENSITY THRESHOLDS OF DESERT LOCUST GREGARIZATION IN MAURITANIA

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THE Desert locust, *Schistocerca gregaria*, preventive control strategy adopted by FAO and locust affected countries is focused on early warning and early reaction system which is assumed as a way to decrease the frequency of plagues by monitoring and controlling population's size in seasonal breeding areas. The present work aimed to better define the desert locust density threshold for gregarization in natural environments. Indeed, the density threshold of gregarization remains a major tool in determining intervention criteria for minimizing the locust invasion risks. The influence of environmental factors on the gregarization phenomenon has never been tested in the field. The study was conducted in two parts. The first part involved a statistical analysis of historical database of Desert locust survey operations of National Center for Locust Control in Mauritania. The information recorded in this database was used to examine the influence of the locust adult's density and vegetation on the probability of observing gregarious populations. The second part performed vegetation measurements, hoppers densities and phase determination during and shortly after two successive rainy seasons allowing field sampling in seasonal breeding areas of Mauritania. These samplings permitted an assessment of Desert locust hoppers density thresholds of gregarization in field conditions. For the adult desert locusts, the results showed the change in the threshold of gregarization according to the cover and status of the vegetation. Low cover and dry vegetation led to a low density threshold of gregarization due to high probability of individuals to touch each other. Dense and green vegetation favored a high threshold of gregarization due to a dispersion of the individuals and a low probability of individual encounters. For hoppers, the field sampling provided a critical density value around 2.45 hoppers m^2 above which gregarious hoppers were expected to be seen more frequently in nature. Hopper density was confirmed as the main factor explaining the presence of gregarious individuals. Vegetation parameters were not helping in explaining the observation of gregarious hoppers compared with hopper density. These findings should help the management of locusts and decision making during control operations. Indeed, field workers could assess easily the gregarization risks depending on the numerical values of density (and vegetation situation for adults). Using these, the field workers would control with pesticide only when it is necessary. Hence, this should contribute to safeguard environment and human and animal health in general and improve cost-effectiveness of Desert Locust control operations.

Key words: Vegetation, Density, Phase polyphenism

• corresponding author

FAO’S COMMISSION ENSURES SUSTAINABILITY OF DESERT LOCUST PREVENTIVE CONTROL IN WEST AND NORTHWEST AFRICA (CLCPRO, 2016)

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THE Commission for controlling the Desert locust in the Western region (CLCPRO) has successfully put in place mechanisms that ensure the long-term sustainability of the preventive control strategy in the Western Region (WR): (i) CLCPRO member countries have developed a strong sense of ownership that resulted in tripling the amount of annual contributions to the Commission’s Trust Fund from USD 227 000 to USD 639 000 starting from 2011 – Figure 1-, (ii) a new sustainable financing system for Desert Locust preventive control in the WR was adopted by the ten member countries,(iii) the organization of periodical ministerial meetings that bring together all CLCPRO members in order to check and review the CLCPRO track record and determine strategic orientations.

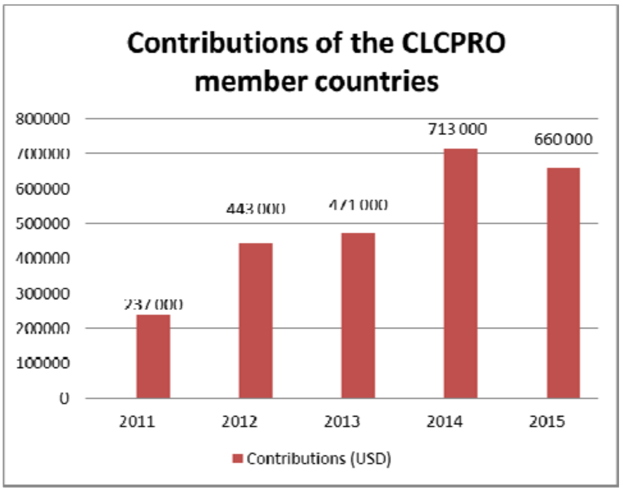

Figure1

The cost of the last Desert Locust upsurge in the WR, in 2003-2005, was estimated at USD 570 million. Its control required spraying 13 million liters of pesticides with associated risks to human health and the environment that were already vulnerable due to drought and climate change. CLCPRO estimates that the curative cost of USD 570 million was equal to 170 years of preventive control in the same ten member countries without using substantial amounts of pesticides. Since 2006, five Desert Locust outbreaks have been contained. The management of the major one, Locust threat (major outbreak) in the Sahel (2012-2013) was fast and efficient and brought the situation under control and prevented an upsurge. Several important lessons were learned from managing this emergency: (i) resources were mobilized in 1-2 months, (ii) the lead time for releasing external funding varied from country to country, showing the need to have country requests prepared at the earliest stages of the threat to speed up the process, (iii) equipment procurement and delivery took much longer than expected, (iv) cooperation between countries facilitated by FAO allowed to meet pesticide requirements without having to purchase additional ones, and (v) more advocacy is needed to support faster donor involvement. Overall, the rapid and organized response led to a lower use of pesticides over a much smaller area, causing less adverse impact on the environment than in 2003-2005. Sustainability of the preventive control strategy is on track, but countries are facing critical challenges especially due to the increasing insecurity in the WR Region that could jeopardize good results obtained so far. New approaches are being investigated in close collaboration with the Desert Locust Information Service in order to get timely locust and habitat information, essential for early warning and rapid response.

Key Words: Preventive control, Desert Locust, Western Region, outbreaks, Upsurge.

• corresponding author

MAPPING AND MONITORING LOCUST HABITATS IN THE ARAL SEA REGION BASED ON SATELLITE EARTH OBSERVATION DATA

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LOCUSTS (*Orthoptera: Acrididae*) are a major threat to food security worldwide. They harm agricultural production on every continent except Antarctica, hence represent a threat to 10 % of the world's population. Permanent breeding areas for the Asian Migratory locust [*Locusta migratoria migratoria* Linnaeus, 1758 (LMI)] are reed stands (*Phragmites australis)*, as they are present in the Amudarya River delta south of the Aral Sea in Karakalpakastan, Uzbekistan. Identifying these reed stands and thus locust risk areas, which can help ground survey personal to improve their work, is the central goal of this study. This task requires maps with sufficient spatial detail showing such potential risk areas.

Hence, the primary objective of this study was to test the utility of Landsat-5 and Terra MODIS satellites at 30 m and 250 m spatial resolution (pixel size), respectively for identifying and mapping reed beds in the Amudarya Delta. The secondary objective was to estimate the area of the reeds and to develop a locust-risk map based on the degree of suitability for locust habitats. For the years 2006, 2007, 2008 and 2009, images from the Landsat-5 and Terra MODIS satellites were fused to create a synthetic data set with a very high spatial and temporal resolution via the ESTARM algorithm. The synthetic data sets were classified with a Random Forest algorithm to create land cover maps (Fig. 1, top) and based on these, a locust-risk map was created (Fig. 1, bottom) based on the degree of suitability for locust habitats (Tab. 1).

Table 1. Final classes and their designated locust-risk stages.

Land cover classes	Locust risk
Dry reed	High
Reed (partly flooded), shrubland (partly with reed)	Medium
Bare area, salt soils, crops, water	Low

The classification accuracies of the maps were reasonable high (>80%), although they had some difficulty in separating other vegetation when it was mixed with reeds. However, this does not diminish the utility of this tool for locust habitat monitoring. The maps show the spatial and temporal patterns of locust-risk with a high spatial detail, even capturing narrow bands of reeds along irrigation canals. Using the synthetic data set will allow reed distribution maps to be produced every year. Furthermore, multiyear information can be used to gain insights about annual changes in reed distribution. Locust risk maps can enable survey teams to specify their surveys on high risk areas and thus save money, labour and time. Further, the spraying of broad spectrum insecticides could be applied more target-oriented and therefore relief the environment and the people living in these areas from harmful side-effects coming along with uncontrolled spraying operations.

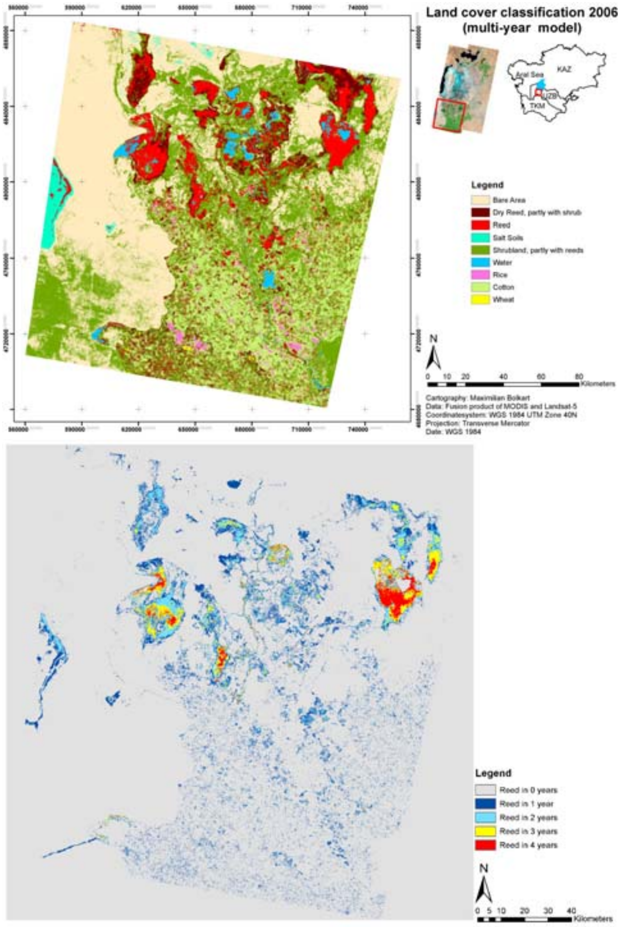

Figure 1. Annual land cover map from 2006 (top). Locust risk-zones (multi-year; bottom).

Key Words: Locust management, Central Asia, Satellite earth observation

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• corresponding author

THE CENTRAL AMERICAN LOCUST *Schistocerca piceifrons piceifrons* (Walker, 1870): ITS FORECASTING AND MANAGEMENT IN THE YUCATÁN PENINSULA, MEXICO

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THE Central American Locust (CAL) *Schistocerca piceifrons piceifrons* Walker (Orthoptera: Acrididae) is a harmful phytophagous species that causes a great deal of damage to crops in Central America. The CAL has two subspecies: *S. piceifrons piceifrons* from Mexico to North Costa Rica and *S. piceifrons peruviana* in Perú, Ecuador, Colombia, Venezuela, Panamá and Trinidad and Tobago. The Yucatán Peninsula in Mexico has an important gregarious zone for *S. piceifrons piceifrons*, where the formation of swarms and damage to various crops is frequent; losses of corn crops have a big impact on local communities as this grain is one of their main food sources. The Yucatán Peninsula has several characteristics of vegetation and soil type that hinder CAL Management: the large area that can be infested, an area of about 4,200 ha where walking surveys are difficult, the presence of soil holes and stones, and the occurrence of dangerous animals (snakes). In an "outbreak year", the swarm migrations cause additional problems: the swarms tend to "stay" in the ecological reserves where field officers can not do any control, or the swarms invade cities and so change from an "agricultural pest" to an "urban pest".

A most important question is: when will there be an "outbreak year"? A good tool for CAL management is being able to forecast an "outbreak year" to allow preparation for control including good coordination between different authorities. We analyzed the frequency of non-outbreak (0= low population) and outbreak (1= high population) years for each decade beginning in 1964. The probabilities for each period were estimated by determining the proportion of times that the system moved from one state to another (e.g. 0→0, 0→1, 1→0, 1→1): a two-state Markov chain was used to describe the probability of CAL outbreak in the 51 years. A great deal of variation was found in CAL outbreak probabilities in the different decades.

Table 1. Markov chain probabilities for the CAL outbreaks for the 51-year period.

Year periods	**0→0**	**0→1**	**1→1**	**1→0**
1964-1975	57.1	42.8	0	100
1975-1985	75	25	0	100
1985-1995	57.1	42.2	0	100
1995-2005	52.9	47.1	0	100
2005-2015	41.7	58.3	46.2	53.8

We found that in the first period 1964-1975, the probabilities of 0→0 (no outbreak followed by no outbreak) was higher than 0→1 (outbreak beginning) and all outbreaks lasted only one year (100% 1→0). However, there was a change in outbreak characteristics in the last period 2005-2015, where the probability of an outbreak beginning (0→1) was higher, and many outbreaks lasted more than one year (1→1).

The model provides information about the probabilities of CAL outbreaks that can be incorporate into economic models to improve management decisions about control strategies.

Key Words: Markov chain, probabilities, Central American Locust

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• corresponding author

TOWARD OPERATIONAL MONITORING OF ASIAN MIGRATORY LOCUST HABITATS USING SATELLITE EARTH OBSERVATION – A CASE STUDY IN THE AMUDARYA DELTA, UZBEKISTAN

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THE Asian Migratory locust (*Locusta migratoria migratoria* L.) is a pest that continuously threatens crops in the Amudarya River delta near the Aral Sea in Uzbekistan, Central Asia. Its development coincides with the growing period of its main food plant, a tall reed grass (*Phragmites australis*), which represents the predominant vegetation in the delta and which cover vast areas of the former Aral Sea, which is desiccating since the 1960s. Current locust survey methods and control practices would tremendously benefit from accurate and timely spatially explicit information on the potential locust habitat distribution. To that aim, satellite observation from the MODIS Terra/Aqua satellites and in-situ observations were combined to monitor potential locust habitats according to their corresponding risk of infestations along the growing season. A Random Forest algorithm was applied for classifying image time series of MODIS enhanced vegetation index from 2003 to 2014 at an 8-day interval. Land cover maps were created (Fig. 1A) and risk levels of habitat susceptibility to locust infestation were associated to certain land cover classes, according to the vegetation type. Results are instrumental for predicting potential locust outbreaks and developing well-targeted management plans. The method offers positive perspectives for locust management and treatment of infested sites because it is able to deliver risk maps (Fig. 1B) in near real time, with a classification accuracy of 80% in April–May which coincides with both locust hatching and the first control surveys. Such maps could help in rapid decision-making regarding control interventions against the initial locust congregations, and thus the efficiency of survey teams and the chemical treatments could be increased, thus potentially reducing environmental pollution while avoiding areas where treatments are most likely to cause environmental degradation.

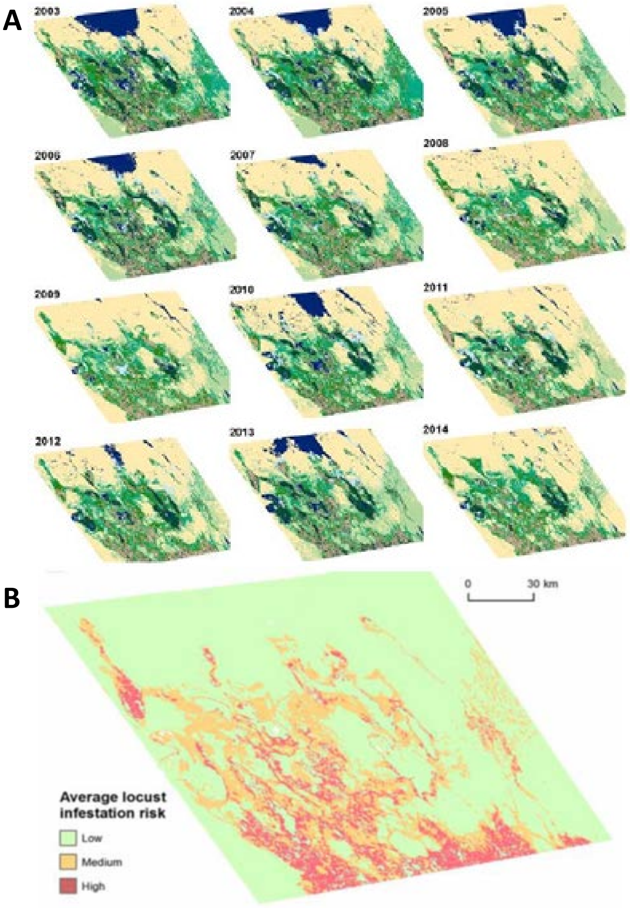

Figure 1. A: Annual land cover maps. B: Average locust infestation risk.

Key Words: Locust management, Central Asia, Satellite earth observation

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FIRST EVIDENCE OF *WOLBACHIA* INFECTION IN POPULATIONS OF GRASSHOPPER *Podisma sapporensis* (ORTHOPTERA: ACRIDIDAE)

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THE brachypterous grasshopper, *Podisma sapporensis* Shiraki, is distributed throughout the Sakhalin, Kunashir and Hokkaido Islands. Cytogenetic analysis of *P. sapporensis* populations has revealed that this species consists of two major chromosomal races with different sex chromosome systems. The XO/XX and XY/XX races are allopatrically distributed, and each race contains several distinct local populations (chromosome subraces) characterized by different compositions of chromosomal inversions. Field and laboratory experiments on the crosses of different populations (chromosome subraces) involving the XO and XY races have shown that most of the embryos developed parthenogenetically. One possible factor in parthenogenetic development of embryos is endosymbiotic *Wolbachia* bacteria that are widespread throughout various species of insects. Here we first report that *P. sapporensis* is infected with different strains of *Wolbachia*. We focused on two different loci, *wsp* and *gatB*, and found three different variants in *wsp* but all *gatB* sequences corresponded to the *gatB-9* allele. Characterizations of *Wolbachia* in the cells such as shape and distribution were also examined. According to the constructed phylogeny based on the NJ method, the *wsp* sequences were split into three distinctive variants, wSap-1, wSap-2 and wSap-3, supported by high bootstrap values. Individuals of XO/XX and XY/XX chromosomal race constituted the wSap-1 variant, and wSap-2 and wSap-3 comprised the XO/XX chromosomal race only. It was also revealed that the population of Mt Teine (XO/XX race) included at least two markedly different types of *Wolbachia*. The sister group of the *wsp* genes of *Wolbachia* in *P. sapporensis* was *Drosophila forficata*, not the same orthopteroid group *Chorthippus* sp. (Figure 1). The results obtained by electron microscopy confirmed the presence of *Wolbachia* that was inferred from the molecular technique and revealed the distribution of the bacteria in head, thorax and abdomen of *P. sapporensis* embryos.

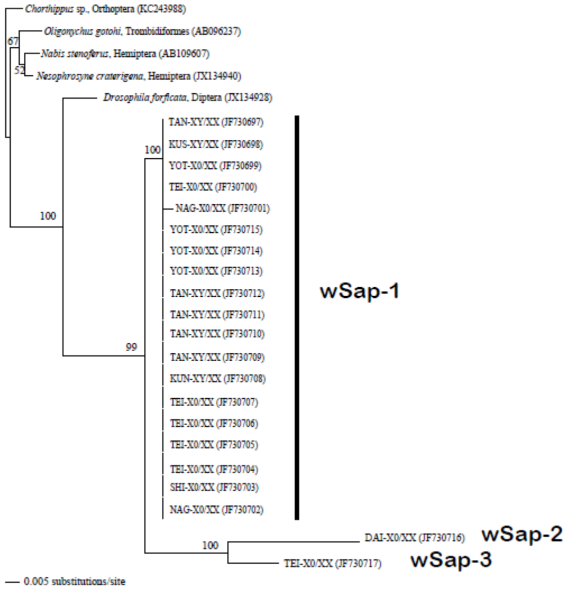

Figure 1. Neighbor-joining tree of 21 individuals of *Podisma sapporensis* and other five invertebrate species. Bootstrap confidence levels of major clades calculated based on 1,000 replications are described near branches.

ACKNOWLEDGMENTS
This work was supported by the Program of Basic Research of the RAS Presidium "Biodiversity" and an OPTEC grant for young scientists and JSPS KAKENHI Grant Numbers 25291088.

Key Words: *Podisma sapporensis*, *Wolbachia*, parthenogenesis

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• corresponding author

MORPHOLOGICAL, ACOUSTIC AND GENETIC DIVERGENCE IN THE BLADDER GRASSHOPPER *Bullacris unicolor* (Linnaeus, 1758)

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ALTHOUGH the processes that promote biodiversity remain poorly understood, geographic variation resulting from selection and/or neutral processes is thought to be a precursor to allopatric speciation. An examination of intraspecific divergence in multiple traits and their co-variation is an essential part of understanding the origin of new species. Here we investigate patterns of geographic variation in acoustic, morphological, and genetic characters of allopatric populations of the bladder grasshopper *Bullacris unicolor*. Individuals were sampled from five locations along the west coast of South Africa (Fig. 1). Morphological measurements were taken from both males and females and compared across locations. In addition, sound recordings of male advertisement calls were analysed for their acoustic properties. We found significant geographic variation in both temporal and frequency components of male advertisement calls, as well as in morphological variables of males and females. However, acoustic characters were much more strongly differentiated between populations than were morphological characters. Furthermore, analysis of the mitochondrial DNA marker cytochrome *c* oxidase I indicated strong genetic structuring, pointing to genetic isolation among populations, in the absence of isolation by distance. Furthermore, we found support for a genetic correlation with morphological differentiation, but not acoustic differentiation. The high levels of variation in male advertisement calls between populations, as well as the lack of association between acoustic and genetic distance, suggests that divergence in acoustic traits cannot be attributed to genetic drift, and is more likely due to alternative selective pressures, such as mate choice or the ecological environment.

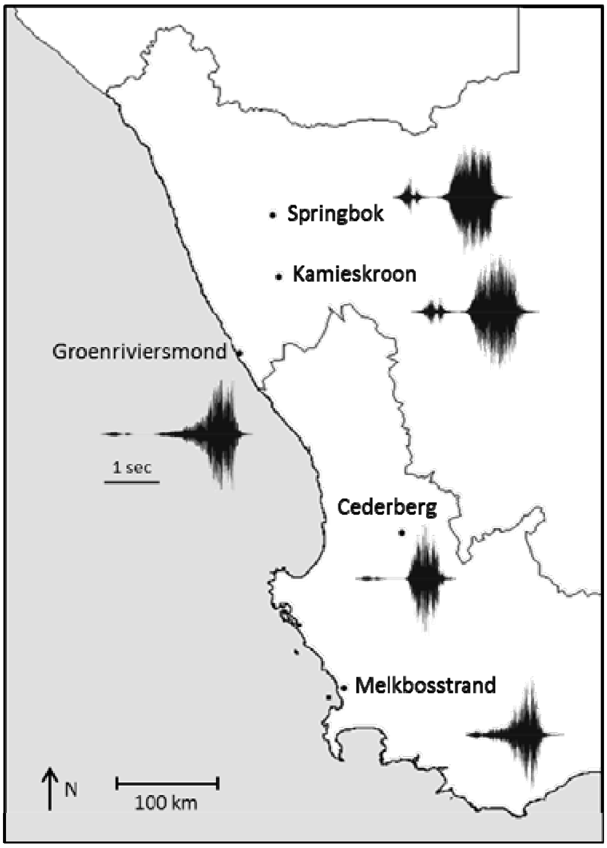

Figure 1. Map of the west coast of South Africa showing sampling localities and oscillograms of male advertisement calls.

In conclusion, our findings suggest a high degree of phenotypic and genotypic divergence within *B. unicolor*. However, relationships between morphology, acoustics, genetics and geography were fairly complex, highlighting the intricate nature of the forces behind allopatric divergence, and the importance of considering multiple traits when examining intraspecific variation.

Key Words: Advertisement call, COI, morphology, population divergence, Pneumoroidea

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• corresponding author

POST-EMBRYONIC DEVELOPMENT, REPRODUCTION AND SURVIVAL OF *Atractomorpha acutipennis* (Guerin-Meneville, 1844) (ORTHOPTERA: PYRGOMORPHIDAE)

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ATRACTOMORPHA ACUTIPENNIS (Guérin-Méneville, 1844) (Orthoptera: Pyrgomorphidae), is an agricultural pest which attacks the leaves of cotton, rice, sweet potato, market gardenings, tobacco and alfalfa. *A. acutipennis* has a continuous reproduction with two to three generations per year. To improve the search of fighting against *A. acutipennis*, this study is aimed at describing the post-embryonic development, survival and reproduction of *Manihot esculenta* in the laboratory. The adults were captured in Nkolbisson (Yaounde) using a sweep net. The couple of adults reared allowed us to obtain the stage 1 larvae which were monitored. The results showed that the development of nymphs passed through five (for male) and six (for female) instars after hatching. The average durations of development of the larvae of 1st, 2nd, 3rd, 4th, 5th and 6th stages in the male were respectively 17.14±0.62, 12.91±0.62, 13.45±0.69, 13.80±0.68, 15.23±0.55 days for male and of 16.18±0.54, 13.13±0.59, 12.49±0.42, 13.19±0.58, 14.58±0.61, 16.57±0.68 days for the female (Tab. 1). The survival rate increases from stage 1 larvae to the adult stage. A sexual size dimorphism was highlighted. After the final moult, the females of *A. acutipennis* spent averagely 18±15.42 days to start mating. We observed about 1 to 4 mating before oviposition. The oviposition appeared averagely at 19.33± 5.33 days after the first mating. The number of ootheca deposited by female varied from 2 to 5 (an average of 3.67±2). Each ootheca produced almost 30.77±10.5 eggs and one couple 40-122 larvae.

Table 1. Nymphal developmental duration (days)

S	L1	L2	L3	L4	L5	L6
M	5-28 (65)	6-26 (64)	4-28 (60)	3-26 (56)	5-24 (47)	/
F	10-29 (60)	6-26 (60)	7-22 (59)	4-22 (54)	7-23 (50)	7-25 (42)

S=sex, M=male, F=female, L=larva

Key Words: ***Atractomorpha acutipennis*, morphology, post-embryonic development, reproduction.**

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EFFECTS OF PHYSIOLOGICAL STATUS AND VEGETATION ON LOCUST'S COLLECTIVE MOVEMENT

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THE behaviour of locusts groups in front of food (vegetation) was studied experimentally, using group of marching *Schistocerca gregaria* hoppers reared in the laboratory. Two different physiological states were studied: 24 h fasted locust, and locusts fed ad libitum. Patches of food were introduced in circular arena where the groups of locusts were marching. Two different distribution of food were tested in the arena: a uniform distribution and a clustered distribution. We used Ctrax (Caltech multiple fly tracker, Branson et al. Nature Methods 6, 451 – 457, 2009), to analyse the collective motion of locusts groups in the arena and their average speed. Results did not show any difference in the effect of food distribution on the oriented motion and in the average speed of groups. However, the physiological state of individuals had a strong effect on group's movement patterns. Oriented motion and the average speed of fed groups were not influenced by the introduction of vegetation. On the contrary, the fasted groups' oriented motion was immediately affected and their speed dropped after introduction of vegetation. After feeding, the individuals took a rest- time of 30 min to 60 min. This period serves probably to the individuals to digest and update their energy status. After the rest- time the groups speed increased gradually and the collective movement started again in the same direction as before the introduction of food. The difference in the behaviour of locusts in front of food is a result of the difference in the individual's priorities caused by the physiological status. Thus, the priority for hungry individuals is first to eat and upgrade their energy level in their body. While sat individuals do not need to feed. Thus the priority of feeding is lower than the priority of aligning with the group for sat individuals.

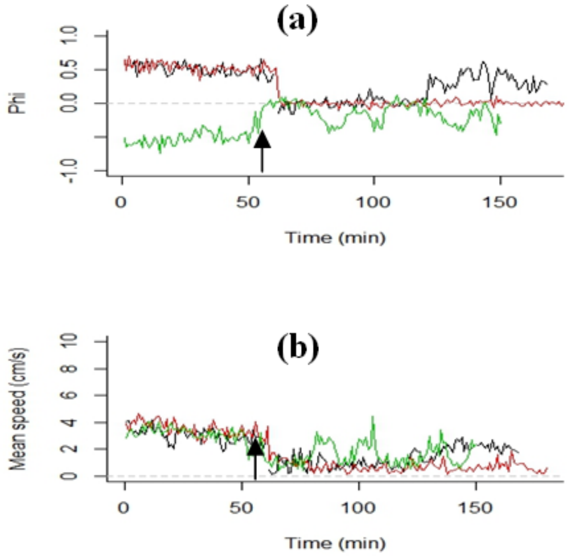

Figure 1. Exemple of the effect of food on the collective movement (a) and the average speed (b) of fasted locusts groups in circular arena. The three colors represent the tree replicates for the same test.

Key Words: ***Schistocerca gregaria*, physiological status, collective movement**

• corresponding author

MANIPULATING BUSHCRICKET GENITALIA SHOW THEIR MULTIPLE FUNCTIONS TO STIMULATE FEMALES AND OVERCOME MATING RESISTANCE
(ORTHOPTERA: ENSIFERA: TETTIGONIIDAE)

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GENITALIA are morphological structures that evolve rapidly and are generally considered to be subject to sexual selection. In several bushcrickets species males possess “titillators”, sclerotized internal genital devices.

We compared a range of bushcricket species that either had or lacked titillators.

Additionally, a range of hypotheses for the role of these devices have been proposed. These include that they (a) are used for sperm removal; (b) are needed as anchors to secure matings; (c) are stimulating females during copulation; and/or (d) assist spermatophore transfer.

The bushcricket *Metrioptera roeselii* (Hagenbach, 1822) was used as a model organism. To investigate the possible function of titillators during copulation we undertook a range of observations and experimental manipulations. We also compared the relationship between male body mass, spermatophore mass, copulation duration, and the size and morphological complexity of titillators.

Firstly, video recordings of unrestrained copulating pairs were taken to observe behaviour. Secondly, copulating pairs were snap-frozen and scanned by X-ray micro-computed tomography to determine the position of titillators during mating. Finally, the influence of multiple male characters including titillators on the mating success in *M. roeselii* was studied.

Additionally we recorded synchrotron X-ray videos which show the titillator movements live inside the female’s genital chamber during mating.

Across species we found that species possessing a titillator exhibited longer copulation duration compared to those without, whereas the complexity of the titillator had no influence.

The manipulation of titillators in *M. roeselii* led to a reduction in correct spermatophore attachment due to females exhibiting resistance behaviour if mated with manipulated partners.

We conclude that titillators are tools used both to stimulate conspecific females and to place the spermatophore accurately during copulation.

Key Words: Genitalia, Sexual selection, X-ray synchrotron video

REANALYZING THE CALLING SONG OF *Eneoptera surinamensis* (De Geer, 1773)

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SOUND of crickets is produced by males rubbing the forewings to attract females. The calling song dominant frequency usually ranges from 2 to 8 kHz (Fd), and many crickets recorded to date sing that way. Originally the calling song of *E. surinamensis* was shortly described by Robillard & Dessuter-Grandcolas 2005), and later by Miyoshi et al (2007), from records of two populations in Brazil. These studies found the calling song frequency was ranging a classical cricket low frequency band (2325 to 3445 Hz). Nevertheless other Eneopterinae crickets are also known to communicate with high-frequency sound (>10 kHz). The tribe Lebinthini from South-East Asia and the Pacific, were the first crickets known to use ultrasounds (26–28kHz) for example (Vicente et al, 2015). More importantly, the species *Eneoptera guyanensis*, known to alternate low and high frequency song parts (Desutter-Grandcolas, 1998; Robillard & Dessuter-Grandcolas 2011), was recently found to use a combination of low and high frequency in the whole song (Robillard et al. 2015), suggesting that the song of *E. surinamensis* needed careful reanalysis with materials allowing recording of high frequencies. We have recorded new males and reanalyzed the calling song at Orthoptera Lab, Universidade Federal de Viçosa in Minas Gerais, Brasil. The present was made on July of the current year, in a breeding room with controlled conditions at 22.5°C, Relative Humidity 40% and 12/12hrs photoperiod, constant during each recording. We used a modified Condenser ultrasound microphone Avisoft-Bioacoustics CM16/CMPA and a Fostex 2FR recorder. Four males were recorded for the present ten times each one. Song was analyzed with the software Audacity (Audacity Team, 2016) and Avisoft SASlab Pro (Specht, 2015). We found that males of *E. surinamensis* start singing with an intro as heating way that could last six minutes until begining a continuous trill that could last from some minutes until about an hour when the male is not interrupted. More interestingly, all the syllables of this song's spectrum show simultaneously a low frequency component 2-4 kHz (LF) as well as a loud, very high-frequency component (23-33 kHz) (HF), the latter being broadband.

We concluded that this high frequency is in fact an ultrasonic signal which is an acoustic novelty for *E. surinamensis* giving more clues about the acoustic behavior for the neotropical side of this subfamily. It particularly raises questions about how such a high-frequency band is produced by the stridulatory system and for what use in the communication system of this common, yet understudied, cricket species.

Key Words: Insecta, Orthoptera, High Frequency, Ultrasonic signals.

• corresponding author

THE OPPORTUNITY FOR SEXUAL SELECTION DOES NOT EXPLAIN THE EVOLUTION OF COMPLEX GENITALIA IN BUSHCRICKETS

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IT is believed that animal genitalia evolve rapidly under sexual selection. We test this hypothesis using data from 45 species of tettigoniid bushcrickets. Males in various bushcricket families develop sclerotised copulatory organs called “titillators.” These, like other genital structures exhibit great variation between species. Additional mating traits, such as the refractory period and polyandry, are also very different between bushcrickets species.

Using data on the mean polyandry (‘lifetime number of matings for females’) and refractory periods of males and females we tested the hypothesis (Simmons 2014, *Austral Entomol* 53: 1-17) that genitalia complexity increases with the number of matings. To reflect the complexity found in copulatory organs across species we developed a ranked system for classification and developed an analytical model.

We found a high degree of variation in the species mean polyandry for females; ranging from 28 down to 1.5 matings during a female’s lifetime. Titillator complexity and polyandry were not related. Among species the male refractory period was highly labile. The complexity of the titillator predicted neither differences in refractory periods between females and males nor the refractory period in males.

We conclude that our results cannot support the hypothesis of post-copulatory sexual selection being a driver for the evolution of genitalia in male bushcrickets.

Key Words: Genitalia, Polyandry, Sexual selection

• corresponding author

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RESEARCH LINE ON "BIOACOUSTICS OF GRASSHOPPERS IN URUGUAY: ITS APPLICATION TO SYSTEMATICS"

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THIS research line has been developed by our working group since 1997, having started financially supported by the "Agencia Española de Cooperación Internacional para el Desarrollo" (AECID) and providing results up to now. The objectives of this contribution is to present a summary of the current state of knowledge on Bioacustics of grasshoppers, the species studied up to now, publications generated, sound and video archive obtained, future prospects and current needs. Up to now, samplings were conducted in different locations belonging to 15 departments of Uruguay, South and North of Río Negro (Montevideo, Canelones, Maldonado, Lavalleja, Rocha, Florida, San José, Salto, Minas, Flores, Colonia, Paysandú, Tacuarembó, Soriano, Durazno). Sound recordings were made in the field and at the laboratory of Entomology (Faculty of Sciences, University of the República), under controlled conditions, using an Uher 4000 and an Uher 6000 analogical tape recorders at a tape speed of 9.5 cm/s attached to an Uher M518 and Uher M655 dynamic microphones. Observations of the communicative and interactive behavior and the general activity of the studied specimens were recorded in writing. Some of these sequences of behavior were also recorded with a video-camera for subsequent analysis. Sound recordings were studied with a Mingograph 420 System at the Laboratory of Orthoptera of the University of Murcia. Selected sounds were digitized and studied with Avisoft® SASLab Pro PC software. Specimens and recordings are kept at the "Colección de Entomología de la Facultad de Ciencias de la Universidad de la República", Uruguay, and at the "Colección del Área de Zoología de la Universidad de Murcia", Spain. The work carried out so far has led to about 23 hours of sound recordings, a similar number of hours of videotape recordings and countless hours of observation and recording of behavioral data, both in the field and in captivity. Different types of sound, corresponding to different behavioral situations of 28 species, 26 belonging to the family Acrididae (16 Gomphocerinae, 7 Acridinae, 2 Copiocerinae, 1 Melanoplinae) and 2 to the family Romaleidae, have been recorded. As a result of these studies five papers in scientific journals, plus one in review, and a book chapter have been published, and 17 contributions have been presented in scientific meetings. Some species have been studied as part of a postgraduate thesis (PEDECIBA). As a result, some species have been distinguished using new taxonomical features, based on the sound characteristics, to be added to the traditional ones. All those, together with results of molecular methods, recently incorporated, provide elements to solve taxonomical problems. Acquisitions of new equipment to record and digitize sounds as well as to properly classify the recordings from the current collections are one of the most pressing current needs. A correct preservation of the sounds is required since in a few years they will become irrecoverable due to technological changes, and it will enhance the development of a regional sound archive by exchanging materials with other sound archives. As future perspectives, it is expected to study the recordings not yet processed, to continue the bioacoustics studies in other acridomorph species of Uruguay, to extend the research to the Orthoptera Ensifera, still poorly studied, and to train students in this field.

Key Words: Acridoidea, acoustic behaviour, taxonomy

• corresponding author

SING ME AN OLD FASHIONED SONG: FOREWING RESONANCES IN THE RELICT KATYDID *Cyphoderris monstrosa* (INSECTA: ORTHOPTERA: PROPHALANGOPSIDAE)

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MALE bush-crickets, grigs, and crickets generate acoustic signals to attract females primarily by tegminal stridulation; the rubbing together of specially modified forewings acting as sound generators. Bush-crickets (Tettigoniidae) usually have asymmetric wings, and only one wing bears the main sound radiator, the ‘mirror’, which alone dictates parameters of frequency and quality in the acoustic signal. In contrast, crickets (Gryllidae), a separate lineage with symmetric wings, use another cell for sound radiation, the harp, with reduced mirrors on both wings playing a secondary role. The grigs (Propholangopsidae), an ancient lineage more closely related to bush-crickets than crickets, have retained a more pleisomorphic wing anatomy. They exhibit symmetrical wings and weakly delimited wing cells including the harp and mirror. This relict group therefore is of major importance to investigate the early. This research investigates whether wing biophysics in grigs is more similar to that of bush-crickets or crickets. Using direct evidence from Laser Doppler Vibrometry, this study confirms the mirror cell as a tuned acoustic resonator in the relict species *Cyphoderris monstrosa* (Fig.1), and also observes as-one vibrations of the mirror and harp area. Properties of the mirror in dictating the frequency of the signal are considered in relation to sound production in bush-crickets (Fig.2). Bush-crickets and crickets diverged some 240 million years ago, with each lineage developing unique characteristics in sound generator morphology. These results further our understanding of the role of wing veins in delimiting functional cells, and the evolution of acoustic characters in this diverse group.

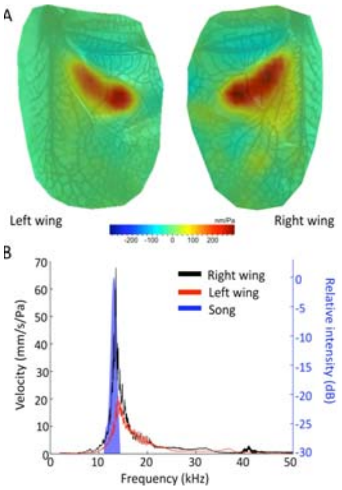

Figure 1. (A) Displacement maps of vibration compliant areas and (B) resonant tunings of *C. monstrosa* forewings.

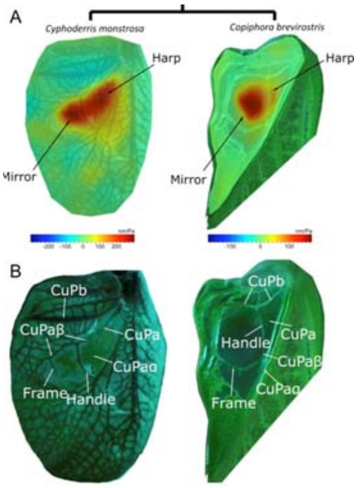

Figure. 2. Comparison of (A) displacement maps and (B) wing venation patterns between *C. monstrosa* and the bush-cricket *Copiphora brevirostris*

Key Words: Grig, Bush-cricket, sound generation, wing vibration

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• corresponding author

INFLUENCE OF WEATHER VARIABLES IN TEMPORAL VARIATION OF DENSITY OF *Dichroplus maculipennis* (MELANOPLINAE) AND *Borellia bruneri* (GOMPHOCERINAE), PEST SPECIES IN THE PAMPAS

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GHASSHOPPERS are important invertebrate herbivores in grasslands worldwide. The composition and abundance of species in each community and the dynamics of populations respond to a combination of interacting abiotic and biotic factors that vary spatially and temporally. Extensive research has been conducted on grasshopper dynamics to understand the underlying mechanisms promoting outbreaks. It is well known that weather is one of the most influential factors in the population dynamics of the different species of grasshoppers. Since late 2005 to the present monitoring is being conducted in representative plant communities of the southern Pampas, an area affected by grasshopper pests. Major outbreaks of the *Dichroplus maculipennis* and the *Borellia bruneri* were recorded from late 2008 to 2010 affecting a variety of crops and natural grasslands in an area of *ca* 2.5 million ha. The main objective of this study was to evaluate the relationship between temporal variation in density of *D. maculipennis* and *B. bruneri* with climatic variables associated with precipitation and temperature. To carry out this study, specific density data obtained from sampling carried out during December and January 2005-2015 (Ten consecutive years) in natural grasslands of Laprida (Buenos Aires province) were considered. In order to achieve the proposed objective and assuming independence between density of each season, an ANCOVA was performed using as covariates those environmental variables that minimized CME (Mean Square Error) in a multiple linear regression modeling as response the density of species. The variables included in the analysis were: 1) Mean September temperature (prior to sampling), 2) Mean October temp, 3) Mean November temp., 4) Mean December temp, 5) Cumulative rainfall until October, 6) Rainfall of sampled month, 7) Rainfall over the year, and 8) Number of rainy days (from September to sampling date). The regression model that best adjusted for *D. maculipennis* included variables 1, 2, 3, 5, 6, 7, and 8. While it was observed that all variables significantly affected density, some coefficient variables resulted near to zero and dependence between them was observed. According to ANCOVA, significant differences between the samples of 2008 and 2010 occurred. The variables that better explained the observed density increase for *D. maculipennis* were the accumulated rainfall in the year ($p < 0.05$) and the number of rainy days ($p < 0.05$). The regression model that best adjusted for analysis of *B. bruneri* included variables 1, 2, 3, 4, 5, 7, and 8. According to ANCOVA, variables 5, 7, and 8 best explain the significant increase in density observed during the 2008-2010 seasons ($p < 0.05$). Our results suggest that among the climatic variables analyzed, those related to precipitation appear to have the greatest influence in density increases of both *D. maculipennis* and *B. bruneri.*

Key Words: *Dicrhoplus maculipennis*, *Borellia bruneri*, temperature, rainfall, density

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• corresponding author

INTERANNUAL VARIABILITY AND PHENOLOGY OF *Borellia bruneri* (Rhen 1906) IN GRASSLANDS OF SOUTH-CENTRAL REGION OF URUGUAY

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GRASSHOPPERS (Orthoptera: Acridoidea) are native insects that inhabit Uruguayan grasslands. Populations are usually in equilibrium, but when conditions are favorable an unusual population increase can be recorded, as occurred in the 1950' and in 2008/09, causing significant economic losses. The aims of this paper were to describe the interannual variability and phenology of *Borellia bruneri* (Rehn, 1906) in grasslands of south-central region of Uruguay. Population was monitored during five seasons (2009-2014) on sites located in the departments of Florida and Durazno. Five nymphal instars were determined, easily distinguishable based on the development of the wing pads, external genital and the major diameter of the eye, head and hind femur length. Insects collected were categorized into young nymphs (I, II and III), older nymphs (IV and V), and adults. At each sampling time, data from the different sites were grouped to calculate the percentage of each category. Based on the interannual variability of Constance of presence (C) and absolute and relative specific abundance, it was possible to identify and characterize outbreak, transition and non-outbreak periods. In 2009/10 (outbreak) *B. bruneri* was the only species classified typified as "constant"(*$_1$) and it was the most abundant species (A=58,08±12,99) (*$_2$). During 2010/11 - 2011/12 (transition), it remained predominant, it was typified as “very common” species, but absolute abundance decreased significantly (A=3,12±0,85; 2,67±0.92). During 2012/13 and 2013/14 (nonoutbreak), value of C and relative abundance decreased significantly, it was typified as "rare" species. In the period analyzed, one generation per year was recorded. The first births occurred in October. Young nymphs began to be recorded in late October (O-2), and most hatching occurred until early December (D-1). Hatchings were recorded until February although the percentages were considerably lower (Fig.1).

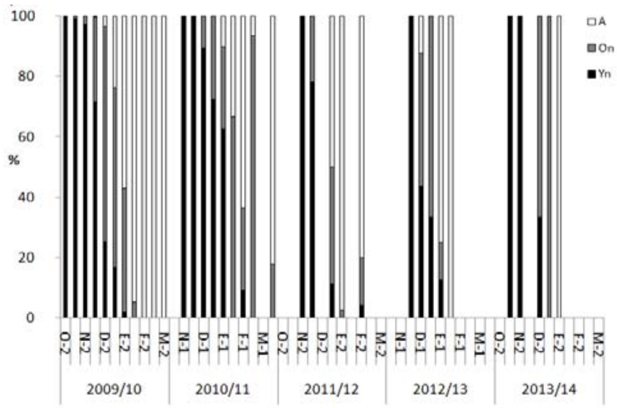

Figure 1. Phenology of *B. bruneri* in the south-central region (2009-2014), October to March. A: adults; On: older nymphs; Yn: young nymph

Older nymphs were first recorded in November-1 until March. This category was predominant in December. First adults were recorded in December and were the predominant development stage since the end of January. In the seasons following the 2009/10 outbreak there was a delay in the moment when the first specimens of the different categories were recorded. These results indicate that in the grasslands of South-Central region of Uruguay, the prevalence of *B. bruneri*, would be indicators of a transition period to an outbreak, and are the basis for establishing a monitoring plan. In order to determine the need for control and to avoid irreparable loss, samples must be intensified from the beginning of November to the beginning of December, when the young nymphs are no longer predominant.

Key words: Grasshopper, Temporal variation, Outbreak

(*$_1$) I: Constant, present in more than 75% of the collections, II: very common, present between 50 and 75% of the collections, IV: rare, present between 12 and 25% of the collections. (*$_2$) Absolute abundance: number of individuals collected/ 200 sweeps.

• corresponding author

PREFERENCE OF PLANTS BY GRASSHOPPER *Cornops frenatum frenatum* (Marschall, 1836) (ORTHOPTERA: ACRIDIDAE: LEPTYSMINAE) AS A FOOD SOURCE

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C*ORNOPS FRENATUM FRENATUM* (Marschall, 1836) is a herbivorous insect that deserves special attention because of having high capacity of defoliate. It is distributed in some Latin American countries, including Brazil. Presents phytophagus feeding habits, being commonly found associated with *Heliconia* spp., and on this plant, considered preferred by this grasshopper, it has its life cycle and provides a suitable substrate for its endophytic oviposition. The aim of this study was defined through laboratory tests, the food preference of *Cornops frenatum frenatum* (Marschall, 1836) by different plants species. Twelve species of plants were individually offered to groups of 10 nymphs during 12 days, which were: *Alpinia purpurata* (Vieill) K.Schum, *Brassica oleracea* (Linnaeus), *Canna indica* (Huber), *Etlingera elatior* (Jack), *Lactuca sativa* (Linnaeus), *Maranta arundinacea* (Starch), *Strelitzia reginae* (Banks), *Zingiber spectabile* (Griff), three varieties of banana trees (*Musa* spp.) micropropagation (cv. Thap Maeo, cv. Galil 18 e cv. Maravilha) and as control, we used the natural host of *C. f. frenatum,* the species *Heliconia psittacorum* L.. The plants most accepted in the initial test were selected for the preference test (free choice), which lasted 72 hours. At the acceptance test of the 12 plants offered, three proved to be well accepted by insects: *C. indica* and *M. arundinacea* (both with 96% in nymphs alive) and *S. reginae* (with 63% survival at the end of 12 days). For preference test, *C. indica* stands out from other species differing considerably (Fig. 1). Therefore, *C. indica* e *M. arundinacea,* may turn out to be its alternative host, because these were part of the food diet of *C. f. frenatum* in the absence of its natural host, since the species *B. oleracea* and *L. sativa* are considered to be harmful to this insect.

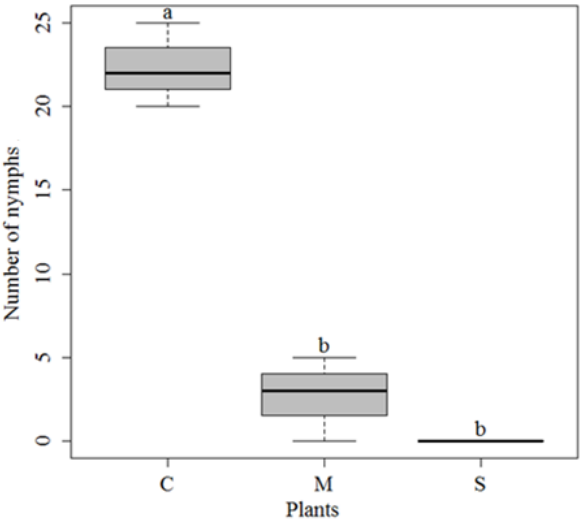

Figure 1. Nymphs observed feeding plants; M = *Maranta arundinacea*; C = *Canna indica*; S = *Strelitzia reginae*.

Key Words: nymphs, survival, mortality

• corresponding author

SURVEY OF NATURAL ENEMIES GRASSHOPPER *Cornops frenatum frenatum* (Marschall, 1836) (ORTHOPTERA: ACRIDIDAE: LEPTYSMINAE) IN *Heliconia* spp. L. (HELICONIACEAE)

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A number of Orthoptera species are of great economic importance, causing agricultural losses worldwide. Regarding their natural enemies, studies report that the entomopathogenic fungi are the main, although there are also nematodes, spiders, birds, ants, parasitic wasps and even some predatory grasshoppers from the Tettigoniidae family, commonly known as katydids. In this sense, the aim of this study was a survey of the main natural enemies species associated with the grasshopper *Cornops frenatum frenatum* (Marschall, 1836) in commercial plantations of *Heliconia* L. situated in a farm producing tropical flowers in Conceição do Jacuipe (Bahia state, Brazil). The study was conducted over a period of 18 months. Six species have been identified as natural enemies (Table 1). One species belonging to the genus *Entomophaga* (Batko, 1964) was found over different periods and two species infected in the adult stage, while one species of the genus *Mermis* (Dujardin, 1842) was found during the same sampling period on two kinds of adults. On the collected nymphs, no pathogenicity or parasitism was observed. Predation was recorded in the field by one species of the genus *Phlugis* sp. (Stål, 1861) (Orthoptera: Tettigoniidae), and by spiders of the Salticidae family.

Key-words: grasshopper, natural enemies, predator, pathogen, parasite

Table1: List of natural *C. f. frenatum predators* in *Heliconia* spp. crops

Order: Family	Species	Type	Attacked phase
Fungi: Hypocreales: Cordycipitaceae	*Beauveria bassiana*	Pathogen	Adult
Fungi: Entomophthorales: Entomophthoraceae	*Entomophaga* sp.	Pathogen	Adult
Orthoptera: Ensifera: Tettigoniidae	*Phlugis* sp.	Predator	Nymphs
Mermithida: Mermithidae	*Mermis* spp.	Parasite	Adult
Araneae: Saltícidae	-	Predator	Nymphs
Orthoptera: Ensifera: Conocephalinae	-	Predator	Nymphs

• corresponding author

POSTEMBRYONIC DEVELOPMENT AND REPRODUCTIVE ASPECTS OF *Borellia bruneri* (ACRIDIDAE: GOMPHOCERINAE) UNDER LABORATORY CONDITIONS

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BORELLIA BRUNERI (Rehn) is one of the most common species of Gomphocerinae of grasshopper communities inhabiting the Pampas grasslands of Argentina and one of the most harmful in the Pampas of Uruguay. It is a univoltine species with obligatory embryonic diapause and shows a wide geographic distribution, occurring in southernmost Brazil, much of Argentina, Chile, and Uruguay. *B. bruneri* is one of the 18 grasshopper species considered to be of actual or potential economic relevance as pests in Argentina. Several studies have been recently conducted on population dynamics of *B. bruneri* in the Pampas region but important aspects related to the life cycle development are still unknown. Because of this, the central objective of this study was to determine different biological and reproductive parameters of *B. bruneri* in the laboratory under controlled conditions.

Biological and reproductive aspects of *B. bruneri* were estimated by monitoring three cohorts of the first generation (F1) of individuals born in captivity from grasshoppers collected in the South of Buenos Aires province, Argentina, and held under controlled conditions (30° C, 14 light – 10 dark; 40% RH).

Five nymphal instars were recorded for both females and males. Total duration of nymphal development was 50.6 ± 0.44 (47-63) days: No significant differences were registered in the duration of the nymphal cycle between different cohorts (ANOVA $p>0.05$). The average longevity of female adults was 56.6 ± 1.35 days, and in males it was 54.4 ± 0.98 days. There were no significant differences between longevity of males and females ($p>0.05$). The number of egg-pods per female was 3.5 ± 0.2 (1-5) and the amount of eggs per egg-pod was 10.8 ± 0.6 (7-14). Mean fecundity was 37.9 ± 1.8 eggs per female with an oviposition rate of 1.20 ± 0.2 eggs/female/day. The highest reproductive value of females were reached in the fourth week leaving a number of egg-pods significantly higher ($p <0.0001$) than registered in the following weeks. These results and future studies about demographic parameters and vital statistics of pest species constitute a basic tool for the development of control strategies.

Key Words: *Borellia bruneri*, cycle nymphal, longevity, fecundity.

• corresponding author

CHROMOSOME NUMBER IS USEFUL TO DIFFERENTIATE BETWEEN THE GENERA *Euxiphidion* BRUNER, 1915 AND *Conocephalus* THUNBERG, 1815 (TETTIGONIIDAE: CONOCEPHALINI)

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CONOCEPHALINI is a katydid group worldwide distributed, comprising 21 genera and 220 species. Cytogenetically, only four genera (19%) and 15 species (6,8%) were studied up to now. This study presents for the first time, karyotype data on four *Conocephalus* species, collected in the Base de estudos do Pantanal of the Universidade Federal de Mato Grosso do Sul (UFMS), in the municipality of Corumbá; Reserva Particular do Patrimônio Natural (RPPN) of the UFMS, in the municipality of Campo Grande, and in the municipality of Coxim, Mato Grosso do Sul, Brazil. Additionally, this is the first chromosomal study on *Euxiphidion*, namely *Euxiphidion subapterus* Bruner, 1915, collected in the RPPN/UFMS and Fazenda Sossego, Campo Grande, Mato Grosso do Sul, Brazil (Tab. 1). The gonads were treated with colchicine (0,16%, 2 h), hypotonic solution (tap water, 15 min), and fixed with a mixture of methanol and acetic acid (3:1) during a minimum of 30 min. Cell suspensions were obtained by the dissociation of the organs in a drop of 60% acetic acid on the microscope slide surface, and drying on a heating plate. Some of the slides were stained with 3% Giemsa and others were treated with telomeric fluorescence in situ hybridization using a peptidic nucleic acid probe (PNA-probe) complementary to the invertebrate $(TTAGG)_n$ motif (PNA Bio, Inc). The diploid number observed in spermatogonial and oogonial cells of the four *Conocephalus* species studied here (Tab. 1) are the same found in all other 15 Conocephalini species already karyotyped, which belong to the genera *Chortoscirtes*, *Conocephalus*, *Orchelimum* and *Phlesirtes* and differs of the 2n♂=31 registered for the genus *Euxiphidion* (Tab 1).

Table 1. Diploid number, sex chromosome system and number of specimens examined.

Species	Karyotype	Specimens
C. saltator	33,X♂/34,XX♀	3♂/1♀
Conocephalus sp. nov.	33,X♂/34,XX♀	1♂/2♀
C. versicolor	33,X♂/34,XX♀	1♂/3♀
E. subapterus	31,X♂/32,XX♀	2♂/3♀

Whilst in the three *Conocephalus* species analyzed here monoarmed autosomes are only among the smallest of the complement, in *Euxiphidion*, monoarmed autosomes are also found among the largest ones. In all four species studied here, the X chromosome is metacentric, as described previously for all Conocephalini, except *Conocephalus melaenus* (Haan, 1843). The X chromosome length, when described, is the largest element of the karyotype. Diplotene cells allowed to confirm the X0♂/XX♀ sex chromosome system, due to the conspicuous X chromosome, which is a positively heteropycnotic univalent. This is the first telomeric FISH in Conocephalini, revealing signs only at the chromosome ends of all elements. No interstitial telomeric sites, indicative of chromosome fusions, were detected, which can be interpreted as a consequence of karyotypes similarity to that found in the Conocephalini ancestor. In sum, the diploid number and chromosome morphology proved to be valuable cytotaxomical characteristics to differentiate between the genera *Euxiphidion* and *Conocephalus*.

Key Words: Conocephalinae, mitosis, meiosis

• corresponding author

Neoconocephalus KARNY, 1907 (CONOCEPHALINAE: COPIPHORINI): HIGH CHROMOSOME DIVERSITY AND A RARE X_1X_2Y SEX CHROMOSOME SYSTEM IN TETTIGONIIDAE

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NEOCONOCEPHALUS (128 spp.) is one of the most taxonomically problematic Tettigoniidae genera on the morphology point of view. Thus, characteristics as the karyotype, can be useful. This study presents for the first time, chromosomal data on *Neonocephalus* from four localities at Mato Grosso do Sul state, Brazil: 1) Fazenda Sossego, 2) Reserva Particular do Patrimônio Natural (RPPN) of the UFMS, both in the municipality of Campo Grande, 3) Furnas do Dionísio, municipality of Jaraguari, 4) municipality of Coxim. Only *Neoconocephalus ferreirai* (Piza, 1971) was identified at species level. The gonads were treated with colchicine (0,16%, 2 h), hypotonic solution (tap water, 15 min), and fixed with methanol/acetic acid (3:1) (30 min). The organs were dissociated in 60% acetic acid on the microscope slide, which was dried on a heating plate. Some slides were stained (3% Giemsa) and others were hybridized with a peptidic nucleic acid (PNA) probe complementary to the invertebrate telomeric motif $(TTAGG)_n$. The observed chromosome numbers are in Tab. 1.

Table 1. Chromosome number, sex chromosome system and number of specimens examined.

Species	Karyotype
Neoconocephalus sp. (Sossego)	2n=23,X(1♂)/2n=24,XX(1♀); 2n=25 (1♀)
Neoconocephalus sp. (Furnas)	2n=23,X(2♂)
Neoconocephalus sp. (Coxim)	10 bivalentes + 1 trivalente ($10II+X_1X_2Y$) (1♂)
Neoconocephalus ferreirai (RPPN-UFMS)	2n=27 (1♀)

Taken into account only the diploid number and the sex chromosome system (SCS), the specimens from Sossego and Furnas are more similar to each other and to *Neoconocephalus* sp. (Mexico), previously karyotyped (2n♂=23,X). One female from Furnas deviates of the expected 2n♀=24, presenting 2n♀=25. Considering that females always have an even number of X chromosomes, an odd diploid number indicates a supernumerary, as also occurs in the female of *N. ferreirai* (2n♀=27). Unfortunately, the analyses of males do not reveal the diploid number in *N. ferreirai*, but there is only one X chromosome on spermatocytes I. Further analyses can confirm if this species possess 2n♂=25,X/2n♀=26,XX. The 2n♂=25,X was not recorded yet in *Neoconocephalus*. The second species of the genus already karyotyped, *N. infuscatus* (Scudder, 1875) presented 2n♂=27. The telomeric hybridization was fundamental to solve the SCS found in the male from Coxim, because revealed a trivalent in diplotenes (X_1X_2Y), similar to that found previously in *Letana atomifera* (Brunner von Wattenwyl, 1878) and *Odontura aspericauda* Rambur, 1838 (Phaneropterinae), also X_1X_2Y. Thus, our study presents the third occurrence of an X_1X_2Y in Tettigoniidae, and the first one in Conocephalinae. Interstitial telomeric sites, suggesting chromosome fusions, were found in the centromeric region of at least three chromosomes in males from Furnas. The chromosomes are predominantly biarmed, contrasting with only eight biarmed chromosomes on previously karyotyped *Neoconocephalus*, probably due to difficulties in determining the morphology of the small elements in older papers. In sum, the *Neoconocephalus* presented high karyotype diversity, including a rare X_1X_2Y SCS.

Key Words: katydids, telomeres, meiosis

• corresponding author

NEW SPECIES AND DISTRIBUTIONS DATA OF A PYGMY UNICORN *Metopomystrum* GÜNTHER, 1939 (INSECTA: ORTHOPTERA: TETRIGIDAE: METRODORINAE) FOR BRAZIL

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METOPOMYSTRUM Günther, 1939 is a South American genus that is characterized by medium size, tegmina and wings present or absent, and fastigium pronounced and concave. The main objective of this work is describing a new species of *Metopomystrum* from Atlantic Forest (Brazil) and including distribution data. This tetrigid was sampled by the "Biota de Orthoptera do Brasil" research group, in 21-23/January/2013, at Estação Serra do Ouro, municipality of Murici, state of Alagoas (Brazil), with pitfall traps containing ethanol fuel killing solution. This news species can be distinguished from the other species of *Metopomystrum* by the following combination of characters: (i) long and acute fastigium, greater than the vertical length of eye; (ii) forehead and gena yellowish; (iii) yellowish posthumeral spots in the pronotum; (iv) tegmina and wings absent; (v) lateral lobes of pronotum with yellowish band and rounded spine of lateral lobe and (vi) sternomentum shaped necklace brown and with yellowish spots. The genus *Metopomystrum* exhibits a very peculiar distribution for its species. It is reported for Colombia and for the northeastern Brazil, with no report for the large area that includes all Brazilian Amazon. Why aren't there any reported *Metopomystrum* species for all the northern Brazil area? We consider two hypotheses for that: (i) the genus does occur in that area, but its species haven't been sampled yet or (ii) the genus really doesn't occur in this area. For the first hypothesis, we think that the species could not have been sampled yet due to limited zoological expeditions focusing on grasshopper collection on that area. For the second hypothesis, we consider two possibilities. The first is that in the diversification of the genus, the two groups of species (the northeast and the northwest species) would have been restricted to the areas they occur. Maybe the species that occurred in the more central area of the north were naturally extincted. The second possibility is that the species or populations that eventually occurred in that central area were extincted due to intense deforestation rates in rainforests. In last December (2015), 175 km^2 of forest in Amazônia were deforested to other alternative land uses and between 2013 and 2014 the Atlantic Forest lost 183 km^2 of its remaining areas. Thus, for now the available data about *Metopomystrum* indicated that this genus distribution is certainly discontinuous. This abstract has benefited with grant aid and facilities from the CNPq/Universal (Proc n° 461854/2014-7), SISBIOTA Brasil (Edital MCT/ CNPq/MMA/MEC/CAPES/FNDCT e FAPEMIG – Ação Transversal/FAPs 166 nº 47/2010, Proc. 563360/2010-0) and PROTAX/CNPq (Proc. n° 440664/2015–2).

Key Words: Tetrigids, Brazil, Distribution

• corresponding author

TAXONOMIC STUDY OF LOCUSTS (ORTHOPTERA, CAELIFERA) IN THE REGIONS OF KASSERINE, GAFSA AND TOZEUR IN TUNISIA

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A comprehensive inventory and a taxonomic study of the locusts belonging to order Orthoptera and suborder Caelifera have been conducted in the regions of Kasserine, Gafsa and Tozeur during the spring 2016. The survey method is derived from Duranton *et al.* (1982) and consists in counting over three quadrants of 100 m² area chosen randomly. In each quadrant, locusts are collected, or observed, on 3 areas of one square meter. The surveys were conducted from the end of March until May 2016. In Kasserine, we reported five genus: *Pyrgomorpha, Vosseleriana, Anacridium, Pamphagus* and *Calliptamus.* The first four are grasshoppers, the latter is a locust outbreak at a density ranging from 35 to 50 individuals per m² according to the different sites explored. In Gafsa, ten genus of grasshoppers were reported: *Vosseleriana*, *Acrotylus*, *Sphingonotus*, *Acrida*, *Aiolopus*, *Anacridium*, *Oedipoda, Paratettix*, *Eyprepocnemis* and *Dericorys*. In Tozeur, 11 genus were reported: *Ochrilidia*, *Pyrgomorpha*, *Vosseleriana*, *Acrotylus*, *Sphingonotus*, *Acrida*, *Aiolopus*, *Anacridium, Paratettix*, *Eyprepocnemis* and *Dericorys*. The first one presents an outbreak of 50 individuals/m² in the site of Degach; the last one is considered as a rare genus. Totally, 14 genus were identified in these areas. We note that *Pamphagus* and *Calliptamus* are typical genus of Kasserine, *Oedipoda* feature of the Gafsa region; *Paratettix*, *Eyprepocnemis* and *Dericorys* are characteristics of Tozeur region. According to previous studies, 30 grasshopper species have been recorded in our study area (Chopard, 1943; Orthoptera.SpeciesFile.org).

Key Words: Taxonomy, Caelifera, Tunisia.

• corresponding author

TAXONOMICAL STUDY OF THE AFRICAN GENUS *Gemeneta* Karsch, 1892 (ORTHOPTERA: CATANTOPINAE) INCLUDING INTERNAL GENITALIA STRUCTURE

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THE genus *Gemeneta* created by Karsch in 1892, has two described species, *Gemeneta terrea* Karsch, 1892 and *G. opilioniodes* (I. Bolivar, 1905). This African genus is one of the less diversified genera of the subfamily Catantopinae. They are forest species: *G. terrea* extends over East and West Africa, while *G. opilioniodes* is endemic to the Congo Basin forests including Cameroon and Equatorial Guinea. The taxonomy, biology and ecology of these species are poorly known. Very little literature exists on the taxonomy of the genus *Gemeneta* including the recognition of the species *G. opilioniodes*. Thus the existing work on this species is insufficient, difficult to access and limited to the description of external morphological characters. These endemic species are becoming increasingly rare, their populations are highly threatened in the Congo Basin forests because of the accelerated deforestation due to increased human activities. This work presents a morphological description of the two species of the genus *Gemeneta* including internal genitalia structure. The specimens of *G. terrea* and *G. opilioniodes* described here have been collected in two villages (Ngutadjap and Zamakoe) in the forests of the south Cameroon plateau. *G. opilioniodes* has an integument strongly granulated and dotted with epicuticular wax in some parts of body, and it is larger, greenish colored and mottled with dark brown. The median inner areas of the hind femora are greenish mottled with brown dark. The integument of *G. terrea* is less granulated and is smooth in some parts of body, and it is smaller, brownish, with median inner areas of the hind femur blackish. A study of the internal genitalia structure of these species will be in conducted in order to complete the characterization and identification key of these forest grasshoppers.

Key words: Catantopinae, *Gemeneta*, species, genitalia structure, taxonomy

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• corresponding author

VALUE OF ENTOMOLOGICAL COLLECTIONS FOR ORTHOPTERA: TETRIGIDAE (CAELIFERA) CASE IN BRAZIL

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THE natural history museums in the world are facing a critical situation due the progressive loss of economic investments and in Brazil, this situation isn't different. Generally, species are described by taxonomists based on a type specimen and the specific details published in a scientifically recognized publication (e.g. Zootaxa, Zookeys, Nature). The published scientific name and the official description which define the characteristics of the species are then permanently associated with this type specimen. Type specimens form part of biological collections maintained by museums where they can be accessed by other scientists. In Brazil, the main biological and entomological collection are stored the Museu Nacional do Rio de Janeiro (MNRJ); INPA (Instituto Nacional de Pesquisas da Amazônia); Museu Paraense Emílio Goeldi and Museu de Zoologia da Universidade de São Paulo (MZUSP). Recently we found one male of *Rehnidium verutum* Grant, 1956 (Fig. 1) deposited in the Orthoptera collection of the Museu de Zoologia da Universidade de São Paulo. *Rehnidium* Grant, 1956 has a distribution known only from the Orinoco Amazonian basin and the eastern of the Andes. In the northeastern part of its range it is found in Venezuela (Barinas) and Dutch Guiana (Paramaribo), while to the south it is recorded only from central and western South America in Brazil (Mato Grosso) and Bolivia (La Paz). In the western area, the genus extends as far as Peru (Huanuco) and Ecuador (Tungurahua). *R. verutum* is recorded for the first time in Brazil, at Aldeia Yavaruha, Pará (XII/1964 Borys Maikin col.). Six decades after the original description, this new information reinforces the relevance of research in museums and indicates that new information may arise from stored material for Orthoptera as other groups. This abstract has benefited with grant aid and facilities from the CNPq/Universal (Proc n° 461854/2014-7), 165 SISBIOTA Brasil (Edital MCT/ CNPq/MMA/MEC/CAPES/FNDCT e FAPEMIG – Ação Transversal/FAPs 166 nº 47/2010, Proc. 563360/2010-0) and PROTAX/CNPq (Proc. n° 440664/2015–2).

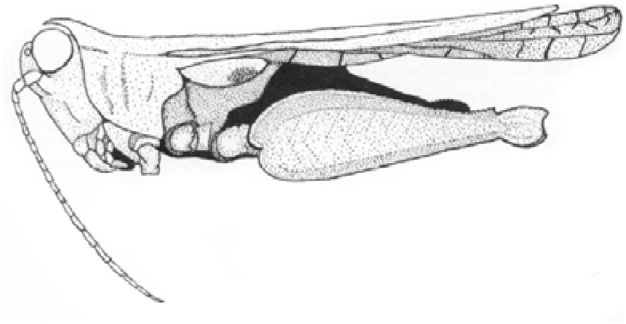

Figure 1. left lateral aspect of *Rehnidium verutum* Grant, 1956.

Key Words: Tetrigids, Collections, Brazil

• corresponding author

PERCEPTION AND INDIGENOUS KNOWLEDGE OF GRASSHOPPERS BY THE LOCAL COMMUNITIES OF SOUTH CAMEROON RAINFORESTS

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THE concept of sustainable development is now emerging as an alternative to conventional development as part of reducing poverty in the third world. Sustainable development is consistent with the need to conserve ecosystems and agro-systems for improved development in the medium to long term. Historically and to date, local communities in different parts of Africa have continued to rely on indigenous knowledge to live in harmony with nature, and develop significant tools for the conservation of natural resources and their use in education, health and as a food source. The increased attention in recent years to health, food security, landscape degradation, biodiversity conservation and climate change should bring together conventional scientists and indigenous scientists to share their knowledge systems for better outcomes. The aims of the present work are to assess the perception of grasshoppers by the local peoples of south Cameroon rainforests, especially (1) pest grasshoppers, (2) all the beneficial uses of grasshoppers in health and as a food source; and (3) the use of grasshopper diversity as a criterion of the level of forest degradation. Three hundred forty-one (341) persons were interviewed individually in different villages in the Center, South, East and Littoral regions of Cameroon between February 2016 and June 2016 using a rapid rural appraisal method (RRA) on 23 questions in a semi-structured survey form. Identification of species by people has been enhanced using some photos of many grasshoppers of these regions. 99% of people say know grasshoppers, their identification is generally made by color (83.0%) and shape (63.9%). Crop fields are the most cited landscape in terms of abundance of grasshoppers, followed by fallow; forest is rarely mentioned. Generally villagers claim that grasshopper abundance increases with forest degradation. The typically forest species most cited are *Parapetasia femorata* I. Bolivar, 1884, *Gemeneta terrea* Karsch, 1892 and *Mazea granulose* Stål, 1876. Abundances vary little seasonally but they are generally higher in the long dry season season. 84.2% of people consider grasshoppers to be both useful and harmful, 51.0% believe that all species may ravage crops, but the species most cited is *Zonocerus variegatus* (Linnaeus, 1758) (33.1%). The most attacked crops are cassava (71.6%), corn (69.2%) and groundnut (48.38%). Industrial crops such as cocoa, coffee and bananas are not cited as ravaged by grasshoppers. The most effective methods used against grasshoppers are insecticides (54.3%), hand collection (14.1%) among the traditional methods, spreading ash (15.3%) and smoke (7.9%). 85.9% of the villagers eat grasshoppers, 58.7% sell them and 11.4% use them to treat diseases. Grasshoppers are consumed fried or braised especially *Z. variegatus* and *Oxycatantops congoensis* (Sjostedt, 1929). Diseases such as rate, angina, tuberculosis, burns and painful menstruation are treated using *Z. variegatus* and *O. congoensis.*

Key words: Indigenous knowledge, grasshopper, south Cameroon, forest, health, food security

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CYCLIC LOCUST INVASIONS EXPLAINED THROUGH A MULTI-AGENT MODEL

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LOCUSTS are grasshoppers able to form devastating swarms. The strategy of preventive control of locust plagues consists in locating and destroying the locusts starting to change behaviour from solitarious individuals to dense group of gregarious. Preventive management of locust plagues works in some areas or species but still fails elsewhere. The role of funding institution awareness was questioned as potential facilitating factors of cyclic locust plagues.

We designed a multi-agent system to represent theoretically 1) the natural stochastic events of locust plagues development and 2) a hierarchical management system with three levels: a funding institution, a national locust control unit and field teams surveying and controlling locusts. We used a pattern-oriented modelling approach to adjust locust dynamics and agents' behaviours in order to reproduce time series of observation of Desert locust swarms on its distribution area. A sensitivity analysis of the model was conducted to identify the potential limits and improvements of the management system.

The model generated cyclic locust plagues through a decrease of awareness of funding institutions. The funding institutions could clearly make the preventive management more efficient by increasing by just few percent their base of support to the control unit. The control unit should avoid hiring too many field teams when the plagues bring money to be able to assure maintenance of surveys in recession times. And finally, the more information about the natural system the field teams can have, the more efficient they are. The current situation in Western Africa with improvements of information systems, stability of national anti-locust centres and rapid fund release support our findings. Some other locust-affected countries are counter-examples and our model depict well the vicious cycles of locust plagues they are confronted with. Given the specificities and complexities of each locust affected region, we argue that anti-locust management should be considered as an adaptive complex system.

Key Words: pattern-oriented model, preventive control, phase polyphenism, early warning, complex adaptive system, pest management, Desert locust, Migratory locust

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• corresponding author

LOCATION AND CHARACTERIZATION OF BREEDING SITES OF SOLITARY DESERT LOCUST USING SATELLITE IMAGES LANDSAT 7 ETM+ AND TERRA MODIS

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THE desert locust, *Schistocerca gregaria* (Forskål, 1775), is a dreaded insect because of the extent of damage it can inflict on agricultural production and of the socio-economic disruptions that may result. This insect can be effectively managed by the application of a preventive control strategy based on the monitoring of its outbreak areas, i.e. potential areas for reproduction and gregarization. These areas are large, often in remote places difficult to access, and need to be physically assessed by survey teams. An ongoing challenge is to better localize these outbreak areas, and to be able to guide where and when prospection surveys should occur depending on local meteorological and vegetation conditions. The use of satellite remote sensing technology can allow, firstly, to better locate and map these outbreak areas, and secondly to identify in real time the appearance in these areas of suitable ecological conditions for breeding (rain, runoff and development of green vegetation), well before the first signs of gregarization.

In this study, conducted in the southern Algerian Sahara, populations of the desert locust have been monitored during the past 43 years (1965-2008). On a limited study area, the use of remote sensing data from Landsat 7 ETM+ and Terra MODIS, coupled with the locust population database, allowed the identification and mapping of solitary desert locust breeding areas during remission periods. These sites, where the first outbreaks can occur, are mainly located in wadis and in areas of accumulation/spreading of rainwater. The joint use of remote sensing data and of locust data collected over a long period proved to be crucial. These locust data helped to prioritize the different areas according to their interest for the locust ecology. They allowed us to focus only on areas of major interest for the preventive control of this species. The methodology developped should be extended to all gregarization areas in Algeria and probably to other countries in the region containing outbreak areas, in order to improve the preventive management of this pest.

Key Words: Desert locust, early warning, remote sensing, pest management

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SUSCEPTIBILITY OF *Cornops frenatum frenatum* (Marschall, 1836) NYMPHS AND ADULTS (ORTHOPTERA: ACRIDIDAE; LEPTYSMINAE) TO *Beauveria bassiana* fungi- lineage CG1303

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THE entomopathogenic fungi have proven to be promising agents for the control of insect pests. This alternative method is considered effective and inexpensive, and do not leave residues in food and the environment, they increase biodiversity and are safe to humans and other organisms. Thus, this study aimed to evaluate the susceptibility of nymphs and adults of the grasshopper *Cornops frenatum frenatum* (Marschall, 1836) to the fungus *Beauveria bassiana* (Bals.) Vuill under laboratory conditions. This work includes four treatments with three repetitions each: T1 and T2 distilled water, T3 and T4 the fungal formulation in water at a concentration 2x10^8 conidia/mL. We used groups of 15 insects in each repetition. With a Potter tower, we sprayed 2 mL of the fungal suspensions or distilled water on grasshoppers (adults and nymphs). After applying the treatment, the insects were kept in plastic pots with food in a climatized chamber at 25±1°C and 70±10% UR. Mortality was checked every 12 hours for 14 days. Adults of *C. f. frenatum* had a mortality rate (50%) higher than nymphs (26%) (Fig. 1), suggesting that adults of *C. f. frenatum* are more susceptible to the fungus than the nymphs. Therefore, *B. bassiana* could be a promising fungus for the control of adults *C. f. frenatum,* which is considered a pest of *Heliconia* crops, a commercial flower.

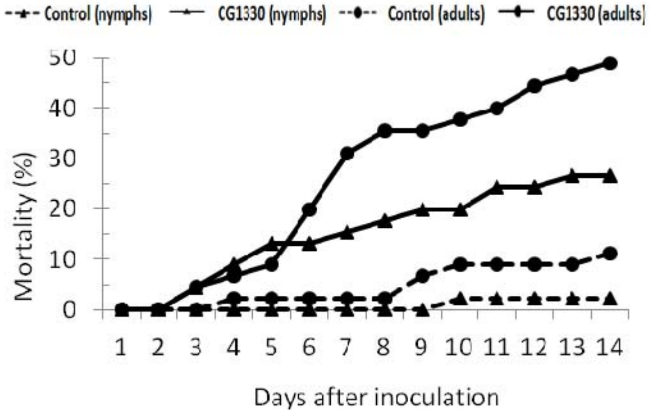

Figure 1. Mortality of *C. f. frenatum* nymphs and adults, in the Potter tower spray by fungus *B. bassiana* at a dose of 2x10^8conidia/mL.

Key Words: conidia, inoculation, Plague, pathogen, control

• corresponding author

FORAGE LOSS CAUSED BY *Dichroplus maculipennis* (ACRIDIDAE: MELANOPLINAE)

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GRASSHOPPERS are among the major groups of herbivorous insects in most grassland ecosystems. In many situations, they are considered harmful insects because they compete with livestock for available forage. The melanopline *Dichroplus maculipennis* (Blanchard) occurs in Argentina, Uruguay, Chile and Brazil. It is a polyphagous and univoltine species that presents obligatory embryonic diapause. *Dichroplus maculipennis* is considered the main grasshopper pest in Argentina, especially in areas of the Pampas and Patagonia regions, causing damage in grasslands and a wide variety of important crops. A major outbreak was recorded in the south of Buenos Aires province from late 2008 to early 2011 in an area of approximately 2.5 million ha. The aim of this study was to evaluate the forage loss caused by different densities of *D. maculipennis* under field conditions. Estimation of forage losses (plant material consumed + destroyed) was carried out with last (sixth) instars and adults. These developmental stages were selected because in most grasshoppers they tend to produce most of the damage. The study was conducted in Tandil, Buenos Aires province, in a pasture of *Festuca arundinacea*, the forage grass most commonly used in cultivated pastures of Argentina. Twelve aluminum-framed cages with wire-screened walls (70 x 50 x 50 cm) were placed, three replicates for each density tested (8 ind/m^2, 16 ind/m^2, and 32 ind/m^2) and three cages without grasshoppers (0 ind/m^2) as a control. The insects were placed in a 1: 1 male to female ratio. The experiment was carried out for a month. Weather conditions favored pasture growth. Both, average precipitation and temperature of January were higher than the historical average values for the area. The pasture in absence of grasshoppers (control cages) increased approximately five times its biomass within one month from 68.2 ± 5.5 gr/m^2 to 337.8 ± 7.5 gr/m^2. In presence of grasshoppers, a significant difference in the amount of biomass at the end of the experience was recorded. The reduction of plant biomass produced by *D. maculipennis* at the three tested densities was significantly different from control ($p<0.001$). The forage loss caused by a density of 32 ind / m^2 was 183.16 ± 8.09 gr/m^2, significantly higher than the other two densities ($p <0.05$). Although the forage loss caused by a density of 16 ind/ m^2 (110.2 ± 4.93 g / m2) was higher than caused for a density of 8 ind / m^2 (74.9 ± 9.63 g / m^2) the difference was not significant. On average, forage loss caused by an individual per day was 0.236 ± 0.02 gr. Our results represent the first quantitative assessment of plat biomass loss due to the action of *D. maculipennis*. Given that the impact of grasshopper damage is usually heavier when conditions for plant growth are unfavorable, further studies should be conducted under such conditions.

Key words: *Dichroplus maculipennis*, Forage loss, density, adults, Pampas region

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• corresponding author

EVALUATION OF DENSITY THRESHOLDS OF DESERT LOCUST GREGARIZATION IN MAURITANIA

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THE Desert locust, *Schistocerca gregaria*, preventive control strategy adopted by FAO and locust affected countries is focused on early warning and early reaction system which is assumed as a way to decrease the frequency of plagues by monitoring and controlling population's size in seasonal breeding areas. The present work aimed to better define the desert locust density threshold for gregarization in natural environments. Indeed, the density threshold of gregarization remains a major tool in determining intervention criteria for minimizing the locust invasion risks. The influence of environmental factors on the gregarization phenomenon has never been tested in the field. The study was conducted in two parts. The first part involved a statistical analysis of historical database of Desert locust survey operations of National Center for Locust Control in Mauritania. The information recorded in this database was used to examine the influence of the locust adult's density and vegetation on the probability of observing gregarious populations. The second part performed vegetation measurements, hoppers densities and phase determination during and shortly after two successive rainy seasons allowing field sampling in seasonal breeding areas of Mauritania. These samplings permitted an assessment of Desert locust hoppers density thresholds of gregarization in field conditions. For the adult desert locusts, the results showed the change in the threshold of gregarization according to the cover and status of the vegetation. Low cover and dry vegetation led to a low density threshold of gregarization due to high probability of individuals to touch each other. Dense and green vegetation favored a high threshold of gregarization due to a dispersion of the individuals and a low probability of individual encounters. For hoppers, the field sampling provided a critical density value around 2.45 hoppers m^2 above which gregarious hoppers were expected to be seen more frequently in nature. Hopper density was confirmed as the main factor explaining the presence of gregarious individuals. Vegetation parameters were not helping in explaining the observation of gregarious hoppers compared with hopper density. These findings should help the management of locusts and decision making during control operations. Indeed, field workers could assess easily the gregarization risks depending on the numerical values of density (and vegetation situation for adults). Using these, the field workers would control with pesticide only when it is necessary. Hence, this should contribute to safeguard environment and human and animal health in general and improve cost-effectiveness of Desert Locust control operations.

Key words: Vegetation, Density, Phase polyphenism

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