

coevolution. Parasites, by reducing host fecundity and survival, strongly affect population size of the host, which very often is their only ecological niche. Already in the 1920s Lotka and Volterra showed that antagonistic interactions between species would lead to interdependent oscillations in their population size. However, most of the current models of host-parasite coevolution ignore population size changes or use a deterministic approach which cannot realistically imitate the finite nature of real populations. Similarly, in most experimental studies on host-parasite coevolution the population size is kept constant as a matter of good practice. To enhance a more realistic understanding of the coevolutionary dynamics, we performed laboratory-controlled evolution experiments with the model nematode host *Caenorhabditis elegans* and its microparasite *Bacillus thuringiensis* and specifically varied the factor population size. Here, we will show our results on temporal changes in host fitness and parasite virulence under different population size regimes.

Poster / Bacteria. Wednesday, 16:30. **BA-24**

An *in vivo* experimental evolution system for analyzing bacterial adaptation and evolution of *Bacillus cereus sensu lato* in an insect model

Rafael Patiño Navarrete^{1,2}, Isabelle Jehanno^{1,2},
Christina Nielsen-Leroux^{1,2} and Vincent Sanchis^{1,2}

¹INRA, UMR1319 Micalis, F-78350 Jouy-en-Josas, France

²AgroParisTech, UMR Micalis, F-78350 Jouy-en-Josas, France
Address for Correspondence: Rafael.patino@jouy.inra.fr

The continuous exposition of a pathogenic bacterium in a host during a serial passage experiment (SPE) may drive the fixation of mutations that favour its growth and multiplication in the host environment¹. These changes that are usually associated with an increase in virulence, can be now traced during an SPE by whole genome sequencing of the evolved variants². Here we describe the set up and initial results of a SPE using a *Bacillus thuringiensis* crystal minus strain (Bt407 Cry-) ³ using *Galleria mellonella* larvae. A new infection protocol has been established which permits bacterial multiplication inside the intestine following force-feeding with spores. The genomes of experimentally evolved bacteria that show significant changes in virulence or persistence will be sequenced and compared with the initial parental strain. Such a global genome based approach of pathogen evolution analysis should allow us to describe the history of the events which arose during the evolution of the *B. cereus* group in one of its natural hosts and explain phenotypic variations based on genotypic differences.

DISEASES OF BENEFICIAL INVERTEBRATES

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-1-STU**

Identification and Characterization of Immune Inhibitor A Metalloprotease of the Honey Bee Pathogen *Paenibacillus larvae*

Birte Arlt^{1,2}, Gillian Hertlein¹; Lena Poppinga¹;
Eva Garcia-Gonzalez¹; Elke Genersch^{1,3}

¹Institute for Bee Research Hohen Neuendorf, Friedrich-Engels-Str. 32, 16540 Hohen Neuendorf, Germany; ²Technische Universität Berlin, Institute of Biotechnology, 13355 Berlin, Germany; ³Freie Universität Berlin, Institute of Microbiology and Epizootics, 14163 Berlin, Germany
Address for Correspondence: elke.genersch@rz.hu-berlin.de

Honey bees (*Apis mellifera*) are essential pollinators of various agricultural crops and fruit but also of many wild plants. Therefore, it is crucial to maintain honey bee health and prevent or cure diseases. The most contagious and fatal bacterial disease of honey bee brood is American Foulbrood (AFB) caused by *Paenibacillus larvae*, a Gram positive, spore-forming bacterium. Infection spreads among the whole hive, eventually leading to the loss of entire colonies resulting in considerable losses in apiculture. Despite the enormous impact of this disease and intensive research, molecular mechanisms involved in the pathogenesis are still not fully understood. Recently we have identified and characterized four genotypes of *P. larvae* (ERIC I-IV) which differ, among other factors, in virulence. Here we present our data on immune inhibitor A (InhA), a metalloprotease which is exclusively secreted by *P. larvae* ERIC II. In homologs of other pathogenic bacteria, InhA has been shown to have multiple functions such as degradation of antimicrobial peptides and cleavage of tight junctions. Here we functionally characterize InhA of *P. larvae* by combining transcriptomic, proteomic and histological studies as well as *in vivo* exposure bioassays with wild type and mutant *P. larvae*, the latter being deficient in InhA expression.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-2**

Awareness and Concept of Insects in a Korean Population

Sung Min Bae, Tae Young Shin, Jae Bang Choi,

Won Seok Kwak, Yong Oh Ahn, See Nae Lee,

In Hui Kim, Ra Mi Woo, Dong Jun Kim and Soo Dong Woo

Department of Agricultural Biology, Chungbuk National University, Chungju, Korea

Address for Correspondence: sdwoo@cbnu.ac.kr

To investigate the degree of individuals' concept and awareness of insects, a survey study was conducted with students and adults living in Korea. The misconception rate for insects was about 50% for both students and adults, but it was lower for students and people who had experienced insect-related events than for adults and those who had not. The highest misconception rate was obtained in answer to a question about the basic structure of an insect. Most people had a high preference of insects. Significant differences and correlations for the preference of insects were found between students and adults, men and women, people who had experienced insect-related events and those who had not. The experience of an insect-related event most influenced preference of insects. These results suggest that increasing people's interest in insects and utilizing insects in treatment situations may be beneficial for the field of mental healthcare.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-3**

Virus Epizootiology in Managed and Native Bee Populations

John P. Burand¹; Matthew Boucher²; Anne Averill³

Departments of ¹Microbiology, ²Biology and ³Environmental Conservation, University of Massachusetts - Amherst, Amherst, MA 01003, USA

Address for Correspondence: jburand@microbio.umass.edu

The possible cross host-genus transmission of several honeybee viruses into native bee populations has recently been proposed. Given current pollination practices and the number as well as high levels of different viruses found in honeybees, the cross genus transmission of these viruses could have a dramatic impact on the health of native bees. In order to examine this possibility we initiated a study of the prevalence of the two honeybee viruses; deformed wing virus (DWV) and black queen cell virus (BQCV) in *Apis* and *Bombus* sp. where *Apis* was maintained under different conditions. These included sites

where stationary or migratory *Apis* hives were present, and sites where no or few *Apis* were present. Both viruses were found in both bee species in sites where *Apis* hives were present. The level of BQCV was significantly higher than DWV in all sites in both bee species when present. While BQCV reached level of 100% in *Apis* and 80% in *Bombus* in both migratory and stationary sites, DWV levels were only at 60% in *Apis* and 30% in *Bombus* in these sites. In the no or few *Apis* sites, BQCV reached levels of up to 65% in *Bombus* and DWV was never found in more than 10% of these bees. We are currently examining gene sequences of viruses recovered from the different bee species collected at each site to determine if they cluster by bee species or by collection site thereby providing further evidence on the interspecies transmission of these two viral pathogens.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-4**

Honeybee Virus Epizootiology in Bee Populations in Connecticut, USA

John P. Burand¹; Shuning Zheng²; Kimberly Stoner³
¹Department of Microbiology, ²Graduate Program in Molecular and Cellular Biology, University of Massachusetts - Amherst, Amherst, MA 01003, USA and ³Connecticut Agricultural Experiment Station, New Haven, CT 06504, USA
 Address for Correspondence: jburand@microbio.umass.edu

We examined the prevalence of Black Queen Cell Virus (BQCV), and Deformed Wing Virus (DWV) in bee pollinators found foraging on pumpkins (*Cucurbita* sp.) on four farms in Connecticut. The three main groups foraging on pumpkins, *Apis mellifera*, *Bombus* sp. and *Peponapis pruinosa*, were sampled 5 times at each site from early June to late September. Sampling included approximately 20 bees of each group when available. Our initial analysis has focused on BQCV which is the most prevalent of the viruses in bees we have examined to date. Of the ~ 1,000 bees we have analyzed to date, 46.3% were found to be infected with BQCV. This virus was the most prevalent in *Apis* with 73.2% being infected, while the *Bombus* and *Peponapis* were infected at 37.7% and 3% respectively. The level of virus-positive bees of any species from the different farms ranged between 2.3% and 91.9% and overall our results suggest a correlation between the level of this virus in honey bees and the level of infection of other bee species. On the two farm sites where we found honey bees infected with BQCV at 95% and 75%, *Bombus* bees were at 91% and 40% respectively. At the site where we found only 10% of *Apis* infected with BQCV we were able to detect only 9.5% BQCV infected *Bombus*, suggesting that the infection of *Apis* and *Bombus* is clustered and may be connected in some way.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-5**

High-throughput sequence analysis of the change in expression profile of Ig2-, Ig3- and Ig7- variant domains in *Carcinus maenas* Down Syndrome Cell Adhesion (*CmDscam*) mRNAs in response to pathogenic infection

Chris Hauton¹; John A. Hammond²
¹School of Ocean and Earth Sciences, University of Southampton, National Oceanography Centre, European Way, Southampton, Hants, SO14 3ZH, UK;
²Immunogenetics Group, The Pirbright Institute, Ash Road, Pirbright, Woking, GU24 0NF, UK
 Address for correspondence: ch10@noc.soton.ac.uk

Previously, we have identified a DSCAM gene (*CmDscam*) within the shore crab *Carcinus maenas*. This gene codes for a pattern recognition protein and has alternately spliced Ig2-, Ig3- and Ig7- domains and multiple different 3' UTRs. In other decapods evidence that these variable domains are alternately spliced during an immune response has been used to support a

concept of specificity within arthropods. However, these data have been generated using conventional Sanger sequencing of a limited number of clones. This approach has insufficient depth to confirm unequivocally that the transcript profile is changed specifically through infection. Herein we present the first high throughput sequencing comparison of the variant Ig2-, Ig3- and Ig7- domains in response to Gram-negative or Gram-positive bacterial challenge. Haemolymph from individual crabs was sampled before and after a single sub-lethal inoculation with either bacterium to produce a deep haemocytopenia through haemocyte degranulation. Amplicons from each sample were then deep sequenced to test the hypothesis that bacterial infection specifically alters the transcription of *CmDscam* during the immune response. Data are discussed in light of new theories of specificity and memory within the innate immune system of decapods.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-6**

A novel pathogenic *Paenibacillus* strain of *Biomphalaria glabrata*, an intermediate host for schistosomiasis

David Duval^{1,2}; Richard Galinier^{1,2}; Gabriel Mouahid^{1,2}; Eve Toulza^{1,2}; Anne Rognon^{1,2}; Nathalie Arancibia^{1,2}; Jean Francois Allienne^{1,2}; Guillaume Mitta^{1,2}; André Théron^{1,2}; Benjamin Gourbal^{1,2}
¹CNRS, UMR 5244, Ecologie et Evolution des Interactions (2EI), Perpignan, France
²Université de Perpignan Via Domitia, Perpignan, France
 Address for Correspondence: david.duval@univ-perp.fr

Schistosomiasis is the second most widespread tropical parasitic disease after malaria. To achieve the objective of schistosomiasis eradication in a decade, various research strategies and treatment programs were recommended and supported by WHO. One of these applicable approaches is based on the control of snail vectors in endemic area. Previous field studies have shown that competitor or predator introduction could be effective but no systemic investigation has ever been conducted to identify snail microbial pathogen and evaluate its molluscicide effect. In our laboratory, infectious agent was isolated on white nodules from unhealthy *Biomphalaria* snails. Only one bacteria was characterized and identified as *Paenibacillus* sp closely related to *P. alvei* through 16S and rpoB DNA analysis. Histopathological examination has shown massive bacterial infiltration leading to an overall disorganization of snail tissues. Exposure of healthy snails to *Paenibacillus* infected snails led to a massive mortality. Moreover, the number of hatched snails was significant lower in exposed snails than in control whereas the spawning appeared to be unaffected. Embryonic lethality is correlated with the presence of this pathogenic bacteria in eggs. This study reports the first description of a novel *paenibacillus* strain as snail microbial pathogen by affecting both adult and embryonic stages.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-7**

Venom from the ectoparasitic wasp *Habrobracon hebetor* activates calcium-dependent processes of haemocytic degradation in *Galleria mellonella* larvae

Natalia A. Kryukova¹; Ekaterina A. Chertkova¹; Alexandra D. Semenova²; Yuri I. Glazachev²; Irina A. Slepneva²; Victor V. Glupov¹
¹Institute of Systematics and Ecology of Animals, Siberian Branch of the Russian Academy of Sciences, Frunze Str.11, Novosibirsk, 630091, Russia; ²Institute of Chemical Kinetics and Combustion, Siberian Branch of the Russian Academy of Sciences, Institutskaya str., 3, Novosibirsk, 630090, Russia
 Address for Correspondence: dragonfly6@yandex.ru

The influents of *Habrobracon hebetor* venom on the cellular and humoral immune reactions of the wax moth larvae (*Galleria*

mellonella) by the naturally envenomation were analyzed. A strong decrease of phenoloxidase (PO) activity in the haemolymph and the number of haemocytes with PO activity of envenomated larvae were recorded. The capsule melanization in the envenomated larvae was twofold less than in control. Production of reactive oxygen species in the haemolymph of envenomated larvae also decreased. The main immune reactions (capsule formation, phagocytosis and coagulation of the lymph) are directly related by emission of calcium ions (Ca^{2+}) into the cytosol and in the pericellular space of haemocytes. The cytosolic calcium concentration in the haemocytes of *G. mellonella* larvae on first and second day after envenomation from *H. hebetor* female was measured (fura - 2 AM used). The increase of Ca^{2+} concentration and phospholipase C activity in haemocytes were registered for two days after envenomation. The addition of the parasitic venom *in vitro* (final concentration of protein 6,2 µg/ml) have induced the decreasing of viability and adhesive capacity of the haemocytes during one hour. The membrane potential was measured with a fluorescent probe. The changes of trans-membrane potential of hemocytes were investigated both *in vitro* and *in vivo* experiments. The degree of trans-membrane potential was in direct dependence of the added venom concentration. The envenomated insects exhibited the decreased potential values.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-8**

Histopathological analyses of different tissues of diseased honey bees (*Apis mellifera*)

Lena Poppinga¹, Heike Aupperle², Elke Genersch¹

¹Institute for Bee Research, Molecular Microbiology and Bee Pathology, Hohen Neuendorf, Germany; ²Laboklin GmbH & Co KG, Bad Kissingen, Germany

Address for Correspondence: elke.genersch@rz.hu-berlin.de

The western honey bee (*Apis mellifera*) is threatened by numerous infectious pathogens (bacteria, viruses and fungi), affecting different life stages of the honey bee and various tissues. This work aims to compare diseased and healthy honey bee tissues in order to detect the pathogens' specific localization and to identify tissue alterations caused by various etiologic agents. For this purpose honey bee larvae were infected with *Paenibacillus larvae*, the causative agent of American Foulbrood (AFB), a notifiable epizootic, by feeding first instar larvae with *P. larvae* spores of different genotypes. Also, white eyed pupae were infected with deformed wing virus (DWV) by injection of virus particles. Adult worker bees were infected with *Nosema apis* and *Nosema ceranae* by the oral uptake of food supplemented with defined spore concentrations. Diseased and control animals were collected at various time points post infection, fixed in formalin and embedded in paraffin. Thin sections of the different body parts were analyzed by fluorescence *in situ* hybridization (FISH) using specific fluorescence dyes labeled oligonucleotide probes for each pathogen and following recently established protocols. *In situ* visualisation of infected cells and tissues will in the end help us to understand the pathogens' life cycles during pathogenesis.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-9**

New findings in genome of *Apis mellifera* filamentous virus Lukasz Rabalski¹, Urszula Grzeda², Grazyna Topolska², Martyna Krejmer¹, Boguslaw Szewczyk¹

¹Department of Recombinant Vaccines, Intercollegiate Faculty of Biotechnology of the University of Gdansk and Medical University of Gdansk, Gdansk, Poland; ²Laboratory of Bee Diseases, Department of Pathology and Veterinary Diagnostics, Faculty of Veterinary Medicine, Warsaw University of Life Sciences, Warsaw, Poland

Address for Correspondence: lukasz.rabalski@biotech.ug.edu.pl

The honey bee plays an extremely important role as a pollinator of crops and wild plants. Honey bee colony losses noted worldwide since 2006 can heavily impair not only global food production but also ecosystem and biodiversity maintenance. One of the possible causes of this situation is the co-infection of bee colonies with different pathogens including *Nosema apis/ceranae*. This microsporidium is often associated with viruses like Black queen cell virus, Bee virus Y and *Apis mellifera* filamentous virus (*AmFV*). The life span of bees infected with *Nosema* and viruses is shorter than of bees infected with *Nosema* alone.

AmFV is a DNA virus. The size of the enveloped particle is 150-450 nm x 150 nm. On the basis of morphological features, *AmFV* was considered to be related to baculoviruses. In 2012 the first fragment of *AmFV* genome was sequenced (822nt long) and submitted to the GeneBank. Phylogenetic analysis of this fragment supports previous assumptions of similarity to baculoviruses.

In our studies we use the Illumina Next Generation Sequencing approach to sequence much longer fragments of genome of *AmFV*. One of the contig that contains the full sequence of previously described BroN gene comprises another gene, which sequence is highly similar to baculoviral ribonucleotide reductase. Other findings about genome structure and possible theories concerning origin of elusive *AmFV* will be presented during the conference.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-10**

Development of prototypes of rapid molecular diagnostic tests for pathogens of honeybees (*Apis mellifera* L.) on chromatographic NALF platform (Nucleic Acid Lateral Flow)

Adriano Ragni¹, Francesca Tabarrini¹, Mario Carucci¹, Claudio E. Lorenzetti¹, Antonella Cersini², Silvia Puccica², Valeria Antognetti², Marcella Milito², Alessandra Giacomelli², Giovanni Formato², Francesco Panara³

¹RAPID BIOTECH Strada Sperandio 9 I-06125 Perugia; ²Istituto Zooprofilattico Sperimentale del Lazio e della Toscana Via Appia Nuova, 1411, 00178 Roma;

³ENEA - Centro Ricerche Trisaia S.S. 106 Ionica - Km 419+500 75026 Rotondella Matera, Italy

Address for Correspondence: info@rapidbiotech.com

Honeybees are of inestimable value as agents of cross-pollination and also as workinsect for beekeeping. Honeybee populations have been decreasing globally in recent years because they are affected by environment, human activities, moreover they are susceptible to many pathogens.

Viroses and nosemosis are widespread in honeybees, but despite the serious economic losses they can cause, these are underestimated by the beekeeping industry. An early diagnosis of the causative agents has great importance for the management of the disease and in the establishment of measures to guide therapy and prophylaxis.

We present the development of diagnostic tests based on the NALF (Nucleic Acid Lateral Flow) technology for the detection of the following pathogens of honeybees: Deformed Wing Virus (DWV), Israeli Acute Paralysis Virus (IAPV) and the microsporidian *Nosema (Nosema ceranae)*.

DNA and RNA of the pathogen are amplified by isothermal reactions using LAMP (Loop-mediated Isothermal Amplification) in the presence of at least one primer conjugated to Gold Nano Particles (GNPs) that are used to label the molecules of interest. The result of the isothermal reaction is detected by naked eye, in a few minutes, by means of a NALF device.

The assay has the same sensitivity and specificity of a molecular test but being at the same time quicker, cheaper, waste friendly, adapted to basic laboratory equipment and accessible to ordinary technical personnel.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-11**

What Kind of Insects Do You Like?

Tae Young Shin, Sung Min Bae, Jae Bang Choi,
Won Seok Kwak, Yong Oh Ahn, See Nae Lee, In Hui Kim,
Ra Mi Woo, Dong Jun Kim and Soo Dong Woo
Department of Agricultural Biology, Chungbuk National
University, Chungju, Korea
Address for Correspondence: sdwoo@cbnu.ac.kr

Insect constitute the largest and most diverse group of animals on world and also serve as the hosts or nutrient sources. In addition, several insects have a strong influence on people's emotion. To utilize the preference and interest of insects in the field of mental healthcare, a survey study was conducted with individual living in Korea. As results, the most people had a high preference and interest of insect, but some were disagreeable to the insect itself. The preference and interest of insect were high on male, adult and practitioner experienced insect-related events than female, student and non-practitioner, respectively. The most favored insects were familiar or pet insects such as *Papilio xuthus*, *Lucanus maculifemoratus*, *Allomyrina dichotoma* and Lampyridae. These results may be useful to develop a healing program for mental healthcare using insects. Further research is needed to determine the effects of these insect in the mental therapy for this purpose.

Poster / Dis. Ben. Invertebr. Wednesday, 16:30. **DB-12**

A muscle-infecting microsporidium infecting pink shrimp (*Pandalus montagui*) from Europe: closing in on the type species of *Thelohania*?

Stentiford, G.D., Ross, S., Kerr, R., Bateman, K.S.
European Union Reference Laboratory for Crustacean Diseases,
Centre for Environment, Fisheries and Aquaculture Science
(Cefas), Barrack Road, Weymouth, Dorset DT4 8UB, United
Kingdom
Address for Correspondence: grant.stentiford@cefes.co.uk

The type species of the genus *Thelohania*, *T. giardi* was described infecting European brown shrimp (*Crangon crangon*) in the late 1800's. Although never rediscovered, recent work describing *T. butleri*, a similarly octosporous microsporidium infecting Canadian pink shrimp (*Pandalus jordani*), provided evidence that *Thelohania* (containing parasites of marine shrimp, freshwater crayfish, and ants) is polyphyletic and in need of significant revision. This work led to proposals that only marine forms should be considered as true members of the genus and that effort should be applied to rediscover the type species. In this study, we describe a novel microsporidium infecting another pandalid shrimp, *P. montagui* from Europe using histological, ultrastructural and phylogenetic data. Although the parasite does not display the characteristic morphological features of either *T. giardi* or *T. butleri* (8 spores contained within each sporophorous vesicle), phylogenetic analysis places it closest to *T. butleri* (91% similarity, 100% coverage of 937bp fragment of SSU rDNA gene) within the broader microsporidian tree. Previous work from our laboratory has focussed on the potential for morphological plasticity within Microsporidia infecting the musculature of marine crustaceans. To this end, we propose that despite divergence in form from the type species of *Thelohania*, the close phylogenetic relationship to *T. butleri* suggest that the parasite in *P. montagui* is a species of *Thelohania*. In addition, we provide further evidence that closely related taxa can display wide morphological variance and, that marine thelohanids may display a level of intra-generic plasticity which nullifies the use of morphology in their taxonomy.

FUNGI

Poster / Fungi. Wednesday, 16:30. **FU-1-STU**

Monitoring of entomopathogenic fungi in *Metarhizium* and *Beauveria* treated fields

Emese Balog, Do Van Hung, Zoltán Mayer, György Turóczy
Szent István University, Plant Protection Institute,
Gödöllő, Hungary
Address for Correspondence: Emese.Balog@mkk.szie.hu

Application of entomopathogenic fungal strains for the control of cockchafer grubs was investigated in sour cherry orchards. Safety like possible effect of the inoculum on natural soil microbiota as well as efficacy and fate of these fungi need to be investigated. The applied fungal strains have wide host range, thus we have to determine the risks of their use during repeated long-term applications. Different inoculation methods were compared and the persistence of inoculum was monitored in the soil and on target and non-target organisms. One year after treatments we collected soil samples and grubs from un-treated and treated areas and re-isolated the fungi on selective media. Furthermore we applied PCR analysis for the identification of our *Metarhizium anisopliae* strains. According to Ya Li & Shuang Hu-Cai (2011) we used a species-specific primer for the detection of fungus. We were able to detect the presence of *Metarhizium* strains. Neither another entomopathogens (*Beauveria*, *Lecanicillium*), or other fungi like fusaria gave positive signal with the *Metarhizium*-specific primers. Furthermore, the presence of *M. anisopliae* was detected in about 10 percent of untreated soil samples. It proves that *Metarhizium anisopliae* can be found in the original soil mycobiota, although at a very low frequency. Research was supported by the grant **GOP-1.1.1-11-2012-0059** „Development of environment friendly product with the use of entomopathogenic organisms”.

Poster / Fungi. Wednesday, 16:30. **FU-2**

Distribution of insect-pathogenic soil fungi in agricultural and forest ecosystems in Georgia

Medea Burjanadze¹, Richard Humber²,
Mariam Arjevanidze¹, Tea Abramishvili¹, Giuli Tsereteli¹,
Manana Lortkipanidze³
¹ Agricultural University of Georgia, Department of Forest
protection, Georgia; ² USDA-ARS BiolPM Research, RW Holley
Center for Agriculture and Health, Ithaca, NY., USA;
³ Ilis State University Institute of Zoology, Georgia.
Address for correspondence: medeabu@yahoo.com

Entomopathogenic fungi naturally occurring in the soil represent a reservoir of antagonists to insect pest. Local strains of such fungi may be adapted to their environment and are of particular interest for usage in biological control. Georgia has a high diversity of altitudes, eco-systems and cropping system and may offer special opportunities for studies of insects pathogens. Soil samples were obtained in 2012-2013 from 8 different geographical sites at different altitudes (600-2200 m a.s.l.), representing different agricultural and forest ecosystems, National parks of Georgia. A total 161 soil samples representing 45 locations were analysed using the insect bait method (Waxworm, *Galleria mellonella* L. and Mealworm *Tenebrio molitor*). The following entomopathogenic fungal taxa were found: *Beauveria bassiana* s.l., *Beauveria brongniartii*, *Metarhizium* spp., *Lecanicillium* sp. *Isaria* sp. Also, we isolated *Aspergillus flavus*. The most abundant species was *Beauveria bassiana* (41,4%) and *Metarhizium* sp. (49,4%) from the total number of isolates. Three isolates of both *Metarhizium* and *Lecanicillium*