


EurBee 9
9th European Congress of Apidology
20-22 September 2022
Belgrade, Serbia

Abstract Book





Alveis, a worldwide reference for the health and nutrition of honey bees



ApiLifeVar

Varroa treatment
based on
essential oils
(Thymol, Eucalyptus
Oil, Levomenthol,
Camphor)

Api-Bioxal

886 mg/g powder for beehive

Varroa treatment
based on oxalic acid.
Allowed both for
trickling and
vaporization

Api-Bioxal

62 mg/ml solution for beehive

Varroa treatment based
on oxalic acid with
glycerol

100% READY TO USE

Apifor

Varroa treatment
based on
formic acid 60%

All the treatments are

Allowed in
organic beekeeping



ALVEIS
By Chemicals Laif
Between Bees & Honey

✉ info@chemicalslaif.it  www.alveis.it  +39 049 626281  Italy



EurBee 9
9th European Congress of Apidology
20-22 September 2022
Belgrade, Serbia

Abstract Book

TABLE OF CONTENTS

WELCOME	4
COMMITTEES	6
PRACTICAL ISSUES	8
VENUE MAP	10
PROGRAM OVERVIEW	12
CONTENTS OF ABSTRACTS	17
34	PLENARIES
41	GENETICS AND GENOMICS
62	ECOLOGY AND BIODIVERSITY
88	PATHOLOGY
151	IMMUNITY
158	NUTRITION
176	MICROBIOTA
188	ECOTOXICOLOGY, PESTICIDES
226	POLLINATION AND BEE FLORA
253	PAN-EUROPEAN RESEARCH NETWORKS
273	QUANTITATIVE GENETICS, REPRODUCTION AND BEE BREEDING
290	COMMUNICATION AND CHEMICAL ECOLOGY
298	MONITORING BEES
339	OPEN
AUTHORS INDEX	361
SPONSORS AND PARTNERS	369

WELCOME

On behalf of the European Association for Bee Research (EurBee) I have the great honour and pleasure to invite you to attend the 9th European Congress of Apidology (EurBee 9) convened under the motto: “Save the bees for our future”.

The conference intends to promote knowledge exchange and international cooperation and to enable the further exchange of up-to-date scientific information on different aspects of managed and wild bees among researchers, teachers, students, experts in extension. EurBee has become the main European event for bee scientists studying how bees respond to climatic changes to discuss problems with bee health, conservation, ecology, diversity, pollination, beekeeping and colony losses.

The six world-renowned experts in bee’s science are invited to give keynote lectures to present the latest developments in their research fields. Each morning and afternoon will commence with a plenary lecture, followed by three parallel symposia. Scientists from Europe and far beyond are welcome to Belgrade to exchange recent advancements and ideas that emerge from basic and applied research.

The conference serves as a connection platform for top European research in Apidology and hosts the pan-European research projects and networks. EurBee 9 congress should contribute to identifying new approaches, tools, and techniques to meet future needs and challenges facing bee science.

We will do our best to make the EurBee 9 successful and enjoyable as possible and look forward with great anticipation to seeing you in Belgrade, Serbia, September 20-22, 2022.

Sincerely Yours,
Ljubiša Stanisavljević,
Host Committee President

COMMITTEES

HOST COMMITTEE

Ljubiša Stanisavljević , *Conference chair*

Nenad Zarić

Aleksandra Splitt

Jovana Bila Dubaić

Sladjan Rašić

Uroš Glavinić

Aleksandar Četković

Milan Plečaš

Nenad Lazarević

Srđan Dživdžanović

Jelena Stojanović

Nataša Grujičić

Mića Mladenović, *Honorary Members of Host Committee*

SCIENTIFIC COMMITTEE

Robert Paxton, *Martin Luther University of Halle-Wittenberg, Germany (Chair)*

Karl Crailsheim, *University of Graz, Austria*

Pilar De la Rúa, *University of Murcia, Spain*

Daniel Dezmirean, *University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Romania*

Dirk de Graaf, *University of Genth, Belgium*

Jevrosima Stevanović, *University of Belgrade, Serbia*

Ljubiša Stanisavljević, *University of Belgrade, Serbia*

EURBEE BOARD

Ljubiša Stanisavljević, *President, UBelgrade, Serbia*

Robert Paxton, *Secretary, UHalle, Germany*

FREE-LIVING VS. MANAGED HONEY BEES – A POPULATION GENETIC APPROACH

Davidović, Slobodan, Department of Genetics of populations and ecogenotoxicology
Institute for Biological Research “Siniša Stanković” – National Institute of Republic of
Serbia, University of Belgrade, Belgrade, Serbia

Patenković, Aleksandra, Department of Genetics of populations and ecogenotoxicology
Institute for Biological Research “Siniša Stanković” – National Institute of Republic of
Serbia, University of Belgrade, Belgrade, Serbia

Erić, Katarina, Department of Genetics of populations and ecogenotoxicology
Institute for Biological Research “Siniša Stanković” – National Institute of Republic of
Serbia, University of Belgrade, Belgrade, Serbia

Erić, Pavle, Department of Genetics of populations and ecogenotoxicology
Institute for Biological Research “Siniša Stanković” – National Institute of Republic of
Serbia, University of Belgrade, Belgrade, Serbia

Stanisavljević, Ljubiša, Center for Bee Research, Faculty of Biology, University of Belgrade,
Belgrade, Serbia

Tanasković, Marija, Department of Genetics of populations and ecogenotoxicology
Institute for Biological Research “Siniša Stanković” – National Institute of Republic of
Serbia, University of Belgrade, Belgrade, Serbia

The honey bee is one of the most economically and ecologically important species currently facing serious challenges. Its history is marked by strong anthropogenic influence and its local populations are rapidly changing while its diversity is constantly manipulated by beekeepers through the import of foreign queens, selection, and migratory beekeeping. The practice of queen importation caused one of the most disastrous events in the history of beekeeping when in the mid-20th century *Varroa* mite was accidentally imported to Europe. This infestation, combined with the degradation of natural habitats, was believed to have caused the disappearance of free-living populations throughout European forests. Recent studies challenge this view and demonstrate that honey bees are able to survive in nature without human interference.

To assess the genetic diversity of different honey bee colonies, we analyzed mitochondrial DNA and 14 microsatellite loci in samples collected from 102 apiaries (with 542 hives) and 55 free-living colonies (FC) from the urban and natural environments throughout Serbia.

Standard parameters of genetic diversity for both genetic markers showed that FC exhibit higher values compared to managed colonies (MC). Values of pairwise F_{ST} genetic distances were higher when FC were compared to MC from different parts of Serbia while MC exhibited somewhat lower values when compared among themselves. Relatedness estimates demonstrated that feral colonies are more related among themselves than they are to other MC and vice versa, implying the existence of a viable and stable free-living population of honey bees. A significant change in the distribution and diversity of mtDNA lineages among MC compared to the historical data for Serbia was detected while genetic analysis based on microsatellite data demonstrated a high genetic uniformity.

Our data confirmed the existence of a genetically diverse and distinctive free-living population of honey bees in Serbia worthy of protection as well as a significant change in the genetic diversity of managed honey bees that calls for immediate change in the current beekeeping practices so that genetic diversity of locally adapted populations could be preserved.

Keywords: genetic diversity, *Apis mellifera*, feral honey bees

DETECTION OF DIPLOID MALES IN *BOMBUS TERRESTRIS* FROM HIGH-THROUGHPUT SEQUENCES

Shah, Abhijeet; & Hasselmann, Martin; Department of Livestock Genomics, Institute of Animal Science, University of Hohenheim, Stuttgart, Germany

Diploid males in the buff-tailed bumble bee, *Bombus terrestris*, with a haplodiploidy in single-locus complementary sex determination system, represent significant costs in terms of colony growth and reproduction. Differentiating between diploid and haploid males requires morphological (sperm count and testis area), morphometric (wings) and genetic (microsatellite) analysis, and therefore specialized expertise. The presence of diploid males in a bumble bee colony presents a risk of inbreeding depression due to shared sex alleles, monogyny, and monandry. As *B. terrestris* is mass bred for commercial purposes, this poses a threat to commercial viability of breeding lines with high number of diploid males. With the help of high-throughput sequencing, we can assess ploidy levels in several datasets and studies to determine the prevalence of diploid males in natural populations and in commercial mass breeding lines. Here, we investigate the presence of diploid males in natural populations and a highly inbred colony using high-throughput short-read sequencing followed by alignment-based and alignment-free methods to estimate allele frequencies and k-mer frequencies. Alignment based methods such as NGSploidy rely on estimating the allele frequencies at many loci. The distribution and counts of these allele frequencies at a specific heterozygosity provides us with evidence of the ploidy level. K-mer based approaches such as KMC/GenomeScope2 rely on k-mer coverage and distribution modelling to make reliable estimations of ploidy levels. However, most previous studies have not considered these approaches to answer this question crucial to the buff-tailed bumblebee. We show that post-hoc high-throughput sequencing methods may also yield compelling evidence to identify ploidy levels in the buff-tailed bumblebee.

Keywords: *Bombus terrestris*, ploidy, genomics