



Action FA0803



COLOSS Work Shop

Genetic discrimination

17.-19.05.2012

Lab of Agricultural Zoology & Entomology

Agricultural University of Athens

75, Iera Odos Str, 11855, Athens, Greece.

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AGRICULTURAL UNIVERSITY OF ATHENS

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Agenda

TIME	
17.05.2012 (Thursday)	
10:00 - 12:00	Welcome and organizational matter
12:00 – 13:30	Presentation on the results from microsatellites analysis on the samples used in the GEI experiment.
13:30 – 15:00	Lunch
15:00 – 17:00	Discussion on the results from microsatellites analysis on the samples used in the GEI experiment.
17:00 – 19:30	Visit the centre of Athens
20:00	Welcome dinner
18.05.2012 (Friday)	
09:00 – 10:30	Presentation on the results from isoenzymic analysis on the samples used in the GEI experiment.
10:30 – 11:00	Coffee break
11:00 – 13:30	Discussion on the results from isoenzymic analysis on the samples used in the GEI experiment.
13:30 – 15:00	Lunch
15:00 – 19:00	Presentation on the results from geometric morphometry analysis on the samples used in the GEI experiment.
20:00 – open	Social dinner

19.05.2012 (Saturday)	
09:30 – 11:00	Discussion on the results from geometric morphometry analysis on the samples used in the GEI experiment
11:00 – 11:30	Coffee break
11:30 – 13:30	Discussion on the progress of mitochondrial DNA analysis and classical morphometry analysis on the samples used in the GEI experiment.
13:30 – 15:00	Lunch
15:00 – 16:00	Conclusions
16:00	End of the workshop

Local Organizer: Dr. Maria Bouga

Completion of genetic analysis data

Meixner Marina ^{1*}, Kryger Per², Evgeniya Ivanova³, Bouga Maria ⁴

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One of the main goals of COLOSS WG 4 is to establish a common protocol for the discrimination of honey bee populations. In Europe, different methods are used to determine the subspecies origin of honey bees. In WG4, different methods have been applied to analyze samples of the colonies that are part of the common GEI experiment. Data are obtained from different approaches: geometric and classical morphometry analyses, microsatellite, mtDNA and isoenzymic analyses. The data obtained from each different method have been statistically proceeded in order to discriminate the samples of the common GEI experiment. Each method will be accordingly estimated and a protocol with the potential of common use will be provided.

Genetic variability of honey bee origins used in the GEI experiment

Evgeniya Neshova Ivanova

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Different methods are used to determine the subspecies origin of honey bees. COLOSS WG4 “Diversity and vitality” has the purpose to find common approaches for discrimination of honey bee populations in Europe. In this aspect, in common GEI (genotype – environment – interactions) experiment of COLOSS WG4, data of enzyme analysis will be combined with microsatellite and mitochondrial DNA data, and classical and geometrical morphometrics in order various methods to be compared.

In this investigation, genetic variation in 15 honey bee populations of *Apis mellifera mellifera*, *A. m. carnica*, *A. m. ligustica*, *A. m. macedonica* and *A. m. siciliana* located in different regions in Europe was studied on different enzymic systems. Allozyme analysis revealed that studied loci were polymorphic in all populations studied. Three to six alleles were detected at the loci investigated. The allele frequencies, the mean number of alleles per locus, the observed and expected heterozygosities, mean F_{ST} value and genetic distance were calculated.

Data from this study will contribute to the documentation of the subspecies genetic origin involved in the common experiment and to the establishment of a published and accessible reference data-base that will be valuable for scientists and apiculturists working in the field of European honey bee biodiversity and conservation.

List of participants

Name		Country
Bouga	Maria	Greece
Ivanova	Evgeniya	Bulgaria
Kryger	Per	Denmark
Meixner	Marina	Germany