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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Agenda

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<tr>
<td>17.05.2012 (Thursday)</td>
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<tr>
<td>10:00 - 12:00</td>
<td>Welcome and organizational matter</td>
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<tr>
<td>12:00 – 13:30</td>
<td>Presentation on the results from microsatellites analysis on the samples used in the GEI experiment.</td>
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<tr>
<td>13:30 – 15:00</td>
<td>Lunch</td>
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<tr>
<td>15:00 – 17:00</td>
<td>Discussion on the results from microsatellites analysis on the samples used in the GEI experiment.</td>
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<tr>
<td>17:00 – 19:30</td>
<td>Visit the centre of Athens</td>
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<td>20:00</td>
<td>Welcome dinner</td>
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<tr>
<td>18.05.2012 (Friday)</td>
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<tr>
<td>09:00 – 10:30</td>
<td>Presentation on the results from isoenzymic analysis on the samples used in the GEI experiment.</td>
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<tr>
<td>10:30 – 11:00</td>
<td>Coffee break</td>
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<tr>
<td>11:00 – 13:30</td>
<td>Discussion on the results from isoenzymic analysis on the samples used in the GEI experiment.</td>
</tr>
<tr>
<td>13:30 – 15:00</td>
<td>Lunch</td>
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<tr>
<td>15:00 – 19:00</td>
<td>Presentation on the results from geometric morphometry analysis on the samples used in the GEI experiment.</td>
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<tr>
<td>20:00 – open</td>
<td>Social dinner</td>
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### 19.05.2012 (Saturday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09:30 – 11:00</td>
<td>Discussion on the results from geometric morphometry analysis on the samples used in the GEI experiment</td>
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<tr>
<td>11:00 – 11:30</td>
<td>Coffee break</td>
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<tr>
<td>11:30 – 13:30</td>
<td>Discussion on the progress of mitochondrial DNA analysis and classical morphometry analysis on the samples used in the GEI experiment.</td>
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<tr>
<td>13:30 – 15:00</td>
<td>Lunch</td>
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<td>15:00 – 16:00</td>
<td>Conclusions</td>
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<tr>
<td>16:00</td>
<td>End of the workshop</td>
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**Local Organizer:** Dr. Maria Bouga
Completion of genetic analysis data

Meixner Marina ¹*, Kryger Per ², Evgeniya Ivanova ³, Bouga Maria ⁴

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³ Department of Developmental Biology, University of Plovdiv, Bulgaria
⁴ Lab of Agricultural Zoology & Entomology, Agricultural University of Athens, Greece

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

University of Plovdiv “Paisii Hilendarski”, Faculty of Biology, Department of Developmental Biology, Section of Genetics 24, Tzar Assen Str. Plovdiv 4000 Bulgaria

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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 heterozygositites, 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

<table>
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<tr>
<th>Name</th>
<th>Country</th>
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<tbody>
<tr>
<td>Bouga</td>
<td>Maria</td>
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<tr>
<td>Ivanova</td>
<td>Evgeniya</td>
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<tr>
<td>Kryger</td>
<td>Per</td>
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<tr>
<td>Meixner</td>
<td>Marina</td>
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