SCIENTIFIC PROGRAMME
15-18 November 2017

EUROPEAN PhD NETWORK "INSECT SCIENCE"

VIII Annual Meeting
15-16 November 2017

GIORNATE CULTURALI DI ENTOMOLOGIA

Accademia Nazionale Italiana di Entomologia
Società Entomologica Italiana
17 November 2017

ACCADEMIA NAZIONALE ITALIANA DI ENTOMOLOGIA

General Assembly and Public Session
18 November 2017

FEDERICO II Convention Centre
Via Partenope 36, Napoli – Italy

Human based genetic tools to refine genetic populations structure of honey bees (*Apis mellifera ssp* L.) (Hymenoptera: Apoidea: Apidae) colonies at regional scale

Grégoire Noël[1,2]; Kridsadakorn Chaichoompu[3], Gil Leclercq[1,2], Edgar Fabre[1], Nicolas Gengler[2], Kristel Van Steen[3] & Frédéric Francis[1]

[1]*Functional and Evolutionary Entomology, Gembloux Agro-Bio Tech, University of Liege (ULiège), Belgium;* [2]*Animal Sciences Unit, Gembloux Agro-Bio Tech, University of Liege (ULiège), Belgium;* [3]*GIGA-R Medical Genomics - BIO3, University of Liege (ULiège), Belgium*

The native distribution of *Apis mellifera* covers Europe, Africa and western Asia. Thereafter, importations, globalization of commercial exchanges and human management has extended honey bees populations worldwide, excluding Antarctica. It has also led to the admixture of native subspecies, particularly in our temperate regions, and to the common use of managed hybrid populations. Understanding the population structure of hybrid colonies and the intensity of admixture at local and regional scale might help to guide conservation and breeding strategies. Single Nucleotides Polymorphisms (SNPs) data were generated with genotyping-by-sequencing method (GBS) on 285 samples of pooled honey bees workers from different apiaries in Wallonia region (Belgium) and Gabon (Africa). For fine-scale stratification of honeybees populations we employed a newly developed fine-scale SNP-based structure detection tool in humans, called IPCAPS, which was built on principles of iterative pruning Principal Component Analysis (ipPCA). We found that Gabonese honey bees populations are more genetically diverse than Belgian honey bees populations. However, by computing population genetic distance values (Fst) between samples, it seemed that our Gabonese honey bees belong to one clearly defined subspecies, whereas Belgian honey bees should follow an admixture gradient from two hypothetical ancestral groups (lineages). In conclusion, we believe that the cost-effective approach we adopted could help beekeepers and conservation policy makers to design evidence-based standards to preserve native subspecies as well as hybrid populations and to select specific honey bee populations of interest.