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*Universitatea de Științe Agricole și Medicină Veterinară Cluj-Napoca*

**Calea Mănăștur, nr.3, 400372 Cluj-Napoca**

Tel. 0264-596384

Fax. 0264-593792

E-mail: [eap@usamvcluj.ro](mailto:eap@usamvcluj.ro)

## Understanding the French honeybee populations by whole genome sequencing of haploid drones

Dave Wragg, Benjamin Basso, Maxime Beguin, Kamila Canale-Tabet, Cecilia Costa, Aleš Gregorc, Kaspar Bienefeld, Alice Pinto, Melanie Parejo, Laurent Gauthier, Andrew Abrahams, H el ene Delatte, Johanna Cl emencet, Jean-Pierre Bidanel, Yves Le Conte and [Alain Vignal](#)

GenPhySE, Universit e de Toulouse, INRA, INPT, INP-ENVT, Castanet Tolosan, France

**E-mail:** [alain.vignal@toulouse.inra.fr](mailto:alain.vignal@toulouse.inra.fr)

The endemic honeybee subspecies *Apis mellifera mellifera* has gradually been replaced in many beekeeper operations in France by other subspecies and by hybrids between *A. m. ligustica*, *A.m. caucasica*, and *A. m. mellifera*, which were found to be more efficient producers of honey and royal jelly, and also to be less aggressive. In order to understand the impact of these practices on the genome makeup of bee populations, we sequenced over 600 haploid drones, each from one colony belonging to various populations including black bee conservatories, queen breeders (honey and royal jelly production) as well as a few out-groups from various European locations. Results show that sequencing haploid individuals allows high confidence genotyping at a low cost, yielding millions of SNP. Chromosomal regions highly differentiated between populations are observed, presumably as a response to artificial selection on traits such as honey or royal jelly production, but also to other unknown events such as pathogen pressure and other environment variables. Varying degrees of admixture between the local black bee *Apis mellifera mellifera* (M mitotype) and C-type sub-species that were imported by beekeepers are observed.