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Statistical Imputation of Queen Genotype from Pool Sequencing of Workers

Bertrand Servin, Sonia Eynard, Fanny Mondet, Lucie Genestout, Olivier Bouchez, Alain Vignal

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PLANT & ANIMAL GENOME CONFERENCE XXVIII
The Largest Ag-Genomics Meeting in the World.
January 11-15, 2020
San Diego, CA
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W622: Statistical Imputation of Queen Genotype from Pool Sequencing of Workers

Wednesday, January 15, 2020
03:10 PM - 03:30 PM
Pacific Salon 4-5 (2nd Floor)

Characterising the genetic diversity of populations allows to better understand their demographic history and their adaptation to selective pressures. In honey bees, this characterisation is facilitated by a relatively small genome size, but is hindered by the fact that often the unit of observation and sampling is the colony rather than a single individual. Moreover, performing large scale genetic analyses of honey bees is a real challenge, due to the specific reproduction mechanism including multi-male insemination, making the genotype of a bee colony a mixture of contribution from the queen and the mating drones. In this work we propose an approach to characterise the genotype of a colony based on pool sequencing of worker bees. We introduce statistical models for the analysis of pool sequence data allowing to reconstruct jointly individual queen genotypes of colonies and allele frequencies in bee populations. We demonstrate the performance of our approach using data on 1500 colonies collected throughout three years within the FranceAgriMer funded, BeeStrong project. Population admixture, in terms of queen sub-species composition, validation was accomplished using information on geographical and sociological organisation of the beekeepers. In addition to a better understanding of the population dynamics of honey bees, our approach to genotyping bee colonies promises to facilitate the genetic analysis of complex traits, and can be used for genome wide association studies on phenotypes of interests, for instance to assess Varroa resistance in honey bee populations.

Authors

Bertrand Servin
GenPhySE, INRAE, ENVT, ENSAT

Sonia Eynard
GenPhySe, INRAE, ENVT, ENSAT

Fanny Mondet
Abeilles et Environnement, INRAE

Lucie Genestout
EVOLUTION

Olivier Bouchez
INRAE GeT Genomics Facility

Alain Vignal
GenPhySE, INRAE, ENVT, ENSAT

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