In partnership with

RNSBB 2024 Spring-Workshop

Bilbao, 13 March 2024

Proceedings

Edited by Melanie Parejo and Cecilia Costa

Genotyping by sequencing

Karina Kalmayer Jaquet[1], Jamal Momeni[1], Per Kryger[2]

Author Affiliation

1) Eurofins Genomics Europe AgriGenomics Products and Services A/S; 2) Department of Agroecology, Aarhus University (DK)

Abstract

Molecular biology is increasing our possibilities to study honey bees. Here we present a new option to study honey bee genetic diversity at more depth. During the past three decades, we have moved from mitochondrial DNA, over microsatellite loci, and whole genome sequencing to develop SNPs that can be studied with microarray.

One major challenge for understanding the genetics of honey bees, is the complex interactions between individuals, that share 75 % of their heritage within the same patriline, and individuals that merely share 25 %, since they originate from different drones. Studies on the influence of genetics on the division of labour, on kin selection, and on disease susceptibility have largely been performed with the help of patriline data. How much each of these components contribute has not been quantified. However, queens that mate with a more diverse set of drones, produce fitter colonies.

DNA microsatellite provided a unique tool to study the multiple mating of queens due the many alleles available at multiple loci. In contrast SNPs are only dimorphic due to the limitation of standard methods of measuring diversity in Illumina setups. These challenges can be overcome, by combining hundreds of SNPs to the analysis with complex bioinformatic tools.

Here we present data from MGI genomic sequencing of individual bees, enabling us to read the number of repeats in already known and previously used DNA microsatellites. We believe it will open new possibilities for the study of relationships amongst bees, within and between colonies.