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OP-089 [Bee Biology]

Implementation of an extended SNP Panel for the genetic monitoring of honeybees and its application to A. mellifera mellifera and A. mellifera carnica samples across Europe

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A number of methods have been established for the routine genetic monitoring of honeybees. These mainly focus on the estimation of hybridization between subspecies, as introgression is a major threat to the genetic integrity of native subspecies, leading to the replacement of locally adapted forms and the loss of species' genetic diversity through homogenization. Given this focus, intra-subspecies diversity of markers is limited, making them less suitable for the estimation of other measures relevant in a conservation monitoring scheme, such as genetic diversity, inbreeding and effective population size.

In this project, we evaluate a new tool for the genetic monitoring of honeybees, a 70K SNP-chip based on Jones et al. (2021). This has the advantage of including markers identified in previous studies that reflect phenotypic differences, such as variation in immune response or associations with traits such as hygienic behaviour, honey production and varroa tolerance. It also includes previously published marker sets for the estimation of introgression. The inclusion of markers that show intra-subspecies variation of functional relevance, as well as the higher marker density compared to previous honeybee SNP-chips, makes this a promising tool including a wide range of applications. These are the estimation of genetic diversity, inbreeding and effective population size, parentage analysis and possible genomic selection in breeding programs. Further, the analysis of introgression was optimized to distinguish between six clusters comprising of the A-, O- and Y-Lineages, A. mellifera mellifera, A. mellifera carnica and A. mellifera ligustica, using a comprehensive database of 1270 reference samples, built considering a total of 20 subspecies and ~4600 samples across Europe, the Middle East and Africa.

Here, we report on the optimization and validation of these applications on the basis of the 70K SNP-chip and present results on ~4200 samples targeting A. m. mellifera and A. m. carnica across 20 European countries.