



Genetic mapping in the genomics era - the unusual genetic architecture of thelytokous reproduction in honeybees

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Large scale sequencing approaches facilitated our understanding of evolutionary processes within social insects in general, and have helped to unravel the genetic architectures underlying phenotypic novelties in particular. However, broad (population) sampling and variable genetic backgrounds often result in added complexity, covariation and lower power to resolve a precise genetic mechanism. On the other hand, the application of controlled genetic crosses/mapping approaches in combination with genomics offers powerful possibilities, but are often challenging due to experimental accessibility of the particular species or the required large sample sizes. However, ever dropping sequencing costs increasingly make such approaches feasible and clear experimental frameworks combined with sufficient sequencing resolution can be extremely beneficial to resolve long standing questions about precise genetic architectures of phenotypic traits for good. Here, we use phenotyped offspring of a naturally (multiple) mated Cape honeybee queen to study the mendelian trait of thelytokous reproduction, which is characteristic for this subspecies exclusively. Employing high depth whole genome sequencing on >70 individuals we find strong signatures of genetic differentiation between arrhenotokous offspring and thelytokous offspring at a novel single locus with an unexpected genetic architecture. Our results show that a single gene, unusually shaped by both, a strong selective sweep, as well as a partial increase in heterozygosity, and a specific single nucleotide variant is putatively underlying the thelytoky phenotype. We corroborate our results using RNAseq data and propose a model by which both reproductive modi are maintained in the population.