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Population genomic approaches for studying the evolution of sociality

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Why and how did sociality evolve? There are several adaptive explanations for the evolution of sociality, yet we know little about the prevalence of natural selection acting on the genomes of solitary, primitive and advanced eusocial insects. The emerging field of population genomics holds great promise for answering important questions in the field. Sequencing the genomes of many individuals per species allows researchers to quantify the strength of selection on protein-coding and regulatory loci in an unbiased manner. Population genomic data can thus be used to identify loci with signatures of kin-selection. Additionally, this data can be used to study the fitness effects of mutations in queen-biased and worker-biased loci, and to understand how pleiotropy influences the molecular evolution of loci that affect both queen and worker traits. Ultimately, population genomics will provide the needed link between theory and functional studies, which will allow us to develop and test mechanistically explicit theories for the evolution of social behaviour. I will illustrate the utility of population genomics using two bee datasets.