

The genetic underpinning of eusociality in the socially polymorphic sweat bee *Halictus rubicundus*

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Eusociality is a major evolutionary innovation that has independently arisen multiple times in insects and led to the ecological dominance of the ants, eusocial bees and wasps. Our overall aim is to identify candidate genes that underpin this trait. Socially polymorphic species exhibiting both solitary and eusocial behaviour provide a powerful means by which to identify those genes. As study organism we use the socially polymorphic sweat bee *Halictus rubicundus*, chosen because of phylogeographic evidence for genetic differences between solitary versus eusocial phenotypes in North America. Our biological starting material comprises the transcriptomes of individuals from one US solitary population and two US eusocial populations of *H. rubicundus* as well as the transcriptomes of individuals from European solitary and eusocial populations. In this study we have developed a modular software pipeline for performing (i) de-novo transcriptome assembly, (ii) gene prediction and annotation, (iii) SNP calling, and (iv) population genetic analyses. Using this pipeline, we have assembled a draft transcriptome of *H. rubicundus*, annotated approximately 14,343 unigenes, and identified common SNPs in the North American and European populations differentiating the two phenotypes on both continents. Here, we focus on the software pipeline that we developed, and present putative candidates of 'sociality' genes underpinning the eusocial transition in *H. rubicundus* in both North America and Europe.