



Investigating Patterns of Selection in Immune-Responsive Genes across Anthophila

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Social insect societies can contain between tens to millions of genetically similar individuals packed into a dense, interconnected community, which makes them ideal parasite breeding grounds. Counterintuitively, social bee species have been found to have a restricted immune gene repertoire in comparison to model species, a phenomenon that was assumed to perhaps be a result of these taxa developing specialised social immunity behaviours. However, recent research has found that this depauperate immune repertoire is present in solitary bee species too, suggesting that it predates sociality in bees, rather than being a consequence of it. However, it is likely that the drastically different lifestyles across Anthophila would have led to a variety of different selection pressures in the evolution of each lineage's immunity. Using a number of bioinformatics tools, this project has begun to tease out the interaction between sociality and immunity by identifying signatures of site-specific positive selection across the whole transcriptomes of 11 bee species, focusing on where these signatures occur in immunity-associated genes and then comparing these patterns across different social lifestyles, from solitary to subsocial and up to advanced eusocial. Also included were non-canonical genes, identified as putative immune-related players thanks to post-challenge transcriptomic analyses, allowing for the first steps in identifying Hymenoptera-specific immune responsive candidates.