

Genomic and gene regulatory basis of cuticular hydrocarbon diversification in aculeate Hymenoptera

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Evolutionary innovation can result from various mechanisms from genomic to regulatory changes. Evolutionary innovation is particularly interesting to study complex phenotypic traits that are vital for the organism, yet evolve rapidly. Cuticular hydrocarbon (CHC) profiles represent such a multifunctional trait in insects. CHCs cover the body of all terrestrial insects, protecting against water loss and carrying communicating information. CHC profiles can differ drastically between closely related species, conspecific sexes, and — in social species — between castes, suggesting a versatile underlying genetic machinery. Despite a generally good understanding of CHC biosynthesis, we still know little about the molecular mechanisms behind intra- and interspecific CHC variation and novel phenotypes. Our project aims to identify the genomic, transcriptomic, and epigenetic underpinnings of CHC diversification. We study 13 pairs of closely related yet chemically distinct species that cover the major lineages of aculeate Hymenoptera (stinging wasps, ants, and bees), and also consider sex and caste differences in some of these species. We are sequencing the genomes of 13 species, and exploit available genomes where possible. Applying a cross-species comparative genomic approach, we will assess the relative importance of gene copy number variation, non-synonymous changes in coding sequences, alternative mRNA splicing, and other regulatory changes for fostering diversification of this multifunctional trait.