

Project Report: The effect of social parasitism on genome evolution in social wasps

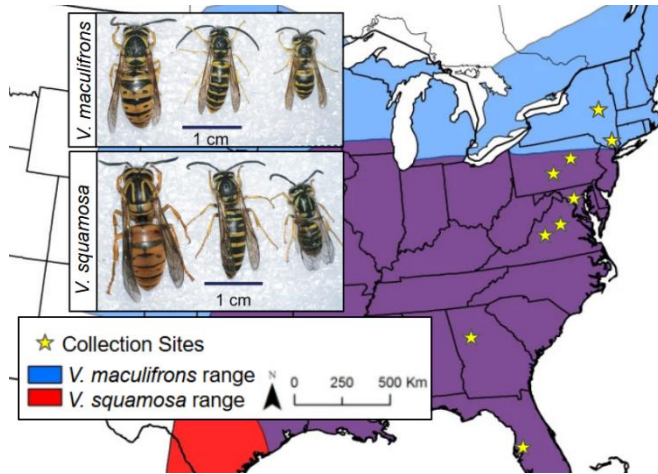


Figure 1. Range of *Vespula maculifrons* and *V. squamosa* in the United States, with collection sites highlighted by yellow stars.

Social parasites hijack the colonies of other social insects to jumpstart their own life cycle. The social wasp *Vespula squamosa* is a facultative social parasite of *V. maculifrons*. These two species overlap for much of their range, but also exist separately on the edges of their respective ranges (figure 1). Thus, these species provide a great opportunity to test hypotheses on the genome evolution of social parasites and hosts.

This study investigates the effects of social parasitism on genome evolution by studying the population genomics of *V. squamosa* and *V. maculifrons* across their

ranges. The first goal of this study is to assess the selective pressures operating on genes in the parasite and host. The second goal is to evaluate effective population size and gene flow and determine how these factors impact selection.

We are making great progress on this project. We have collected 25 *V. maculifrons* samples ranging from Georgia to New York, and 19 *V. squamosa* samples ranging from Florida to Pennsylvania. Additionally, our sampling of the eastern United States also uncovered 4 *V. germanica*, 5 *V. flavopilosa*, 3 *V. alascensis*, 1 *V. vidua*, and 1 *Dolichovespula arenaria*.

I sequenced the cytochrome B gene of the samples to confirm species identity and construct a phylogeny of the taxa. Our results suggest some population structuring (figure 2). We are proceeding with genome sequencing for the *V. maculifrons* and *V. squamosa* samples. I have extracted their genomic DNA, and performed quality control on these samples by measuring concentration and purity. These samples have been sent out for genome sequencing

Our next steps include genome assembly and analysis. Low quality reads will be trimmed, and sequences will be mapped to existing genomes. We will look for geographic clustering and population structure within species, assess gene flow, estimate effective population size, and calculate linkage disequilibrium. Finally, we will assess selective signatures, and compare these signatures within and outside overlapping regions. Ultimately, our research will provide insight into how social parasitism shapes the evolution of both parasite and host.

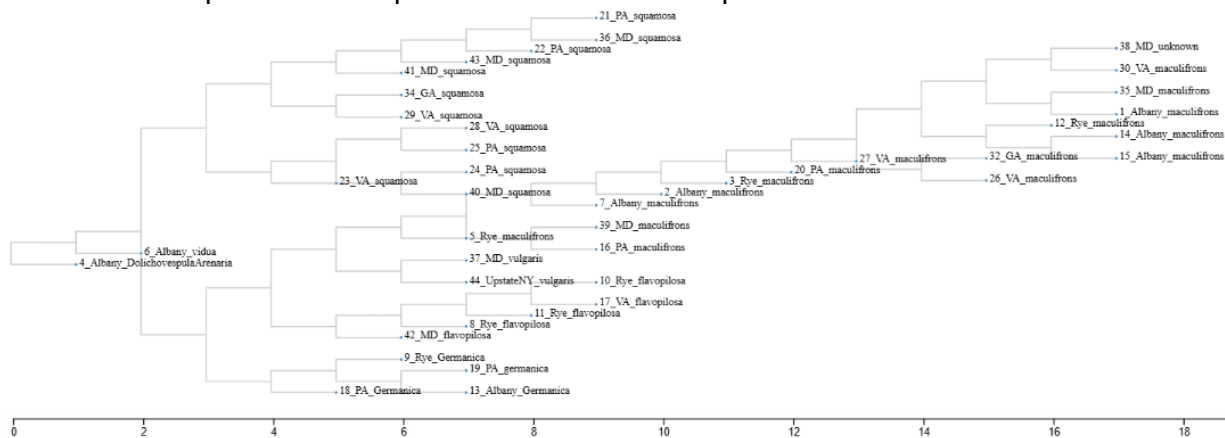


Figure 2. Phylogenetic tree showing cytochrome B sequences from all collected *Vespula* and *Dolichovespula* samples. Constructed with PHYLIP NJ