

Hymenopterans are an important order of insects consisting of bees (Apoidea), wasps (various families) and ants (Formicidae) significantly contributing to ecosystem function. Many important pollinators in this group are declining worldwide. Can sociality and disease be a driver of these declines? We documented spatial and socially influenced distributions hymenopterans inhabiting the Big Horn Basin using point-of-collection software (Anecdata.org). We investigated the microbiome of these samples collecting more this year. We extracted DNA from whole-body homogenates, amplifying both 16S ribosomal DNA (V4/V5 region) and 18S COI regions following Earth Microbiome Project. We characterized metabarcoding data via the QIIME2 pipeline comparing patterns of microbial diversity across space and bee/ant/wasp taxa. From highest occurrence to lowest, these bacteria were most well-represented: Bacilli, Gammaproteobacteria, Nucleomycetes, Bacteroidetes, and Mollicutes. We found the common insect parasite, *Wolbachia* sp., in only one sample, an overwintering European paper wasp (*Polistes dominula*) queen. Can this non-native species be spreading bacterial disease among native community members. Furthermore, we will test whether degree of sociality can predict disease occurrence and microbial diversity for we hypothesize that asocial (solitary) hymenopterans may individually harbor less species (OTU) richness but increased  $\beta$  diversity compared to more social and eusocial members of the order.