

Characterisation of the core and community microbiome of *Vespula vulgaris*

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The insect microbiome has a critical impact on host fitness, and may be particularly important for invasive species. The intertwined relationships within the microbiome can have a positive or negative impact on the host, causing a shift in microbial balance. Thus, microbial influences acting on the individual host or at the colony level, can potentially drive the ecological success of a population. For the first time, we investigate the microbiota of the invasive wasp *V. vulgaris* in the native Europe and introduced New Zealand range. This wasp can have detrimental effects on recipient communities, causing ecological changes through overwhelming predation of native invertebrates as well as competing with native species for resources. Here we test for microbiota differences in three distinct life stages across the two ranges. Using next generation sequencing techniques, we compared bacterial, microbial eukaryote and viral communities in larvae, workers and queens. Our results demonstrate a change in community composition between life stages. Larvae had greater bacterial, microbial eukaryote and viral diversity compared with that of workers and queens. Remarkably, queens were largely free of microbial eukaryotes and completely free of known RNA viruses. We also highlight evidence of a microbial shift that may have occurred in the invaded New Zealand range that potentially increases fitness of this invasive wasp. Our results support the hypothesis that the microbiome varies between distinct life stages and provides preliminary data proposing differences between the native and invaded ranges.

