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Bacteria diversity and virus detection in the invasive Argentine ant

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Argentine ant (*Linepithema humile*), originally from South America, can now be found worldwide in Mediterranean like environments, threatening native fauna and flora. One key of the Argentine ant's invasive success is the high density colonies reach in their new environments like it is the case in New Zealand. However unexplained colony collapses have been reported in well-known invaded sites in New Zealand. As some pathogens and viruses have previously been shown to have dramatic effects on populations, the role of infections in the population decline of Argentine ant in New Zealand was investigated. For the first step of this study, samples were collected in two cities with a high density of ants and two cities with a low density in 2011 and 2012. Using universal 16S primers and 454 sequencing, bacteria diversity was shown to be dominated by beneficial and non-pathogenic bacteria from the phylum Proteobacteria - including the endosymbion *Rickettsia*-, and the phylum Firmicutes - mostly gut bacteria such as the acid lactic bacteria *Lactobacillus* and *Pediococcus*. Bacteria diversity did not differ between cities or years. Preliminary results from Illumina sequencing indicated the presence of *Solenopsis invicta* virus -2 (SINV-2), bee Kashmir virus and Israeli acute paralysis bee virus, three viruses known for their involvement in ant and bee population drastic decline. Further sampling and specific targeting of those viruses will confirm their presence throughout New Zealand which might explain at length the observed population collapse in Argentine ant. The second step of this study will later involve the infection with chosen bacteria / virus and treatment with antibiotics of colonies in the laboratory to characterize the evolution of the colony fitness throughout time. Characterizing the bacteria diversity and access the presence of viruses in Argentine ant might lead to a better understanding of invasive ants' population fluctuations.