

Pulling the wings off wasps: determining the likely Eurasian origin of New Zealand populations of *Vespula vulgaris*

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Eligible for student prize

The development of biological control options for invasive species requires knowledge of their native range. Here, we estimate the native range of New Zealand populations of the invasive common wasp *Vespula vulgaris*, which is one of our most serious biodiversity and conservation threats. We collected these wasps from New Zealand and from 23 countries across their native Eurasian range. We used mitochondrial DNA markers (cytochrome oxidase c subunit 1, and cytochrome b) to assess genetic variation among 100 wasp samples. No variation existed in sequences from New Zealand population, which were most genetically similar to samples from the UK and Belgium. In addition, we assayed the samples for the presence of *Nosema* spp., which are a genus of microsporidian pathogens associated with population regulation in other social insects. We observed *Nosema* infection in New Zealand at a similar rate to those in Europe. Our work has identified the likely origin of *V. vulgaris* and is an important first step in the examination of this native range for potential biological control agents. These population regulators could include microbial pathogens, which can have a major influence on social insect population dynamics. Given their effects on other social insects, pathogens such as *Nosema* spp. are good candidates for further study.

