

Sequencing and community annotation of the *Vespula vulgaris* genome

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The *Vespula vulgaris* invasion of New Zealand has affected vulnerable native invertebrate populations as well as agriculture, tourism and human health, and effective control is a critical issue. Current strategies are limited to pesticides and other chemicals, but these are not effective against high-density wasp populations or in large areas. Gene silencing or RNA interference (RNAi) is a promising 'next generation' pest control method that can be used to specifically interrupt the function of essential genes. This technique requires high-quality genomic sequence for target design. We have prepared a draft assembly of the *V. vulgaris* genome, consisting of 175 million base pairs on 684 scaffolds. Using *ab initio* and evidence-based gene detection algorithms we have annotated 11,556 putative protein-coding genes. Computational gene prediction algorithms perform well, but manual curation of the resulting gene models improves the accuracy of downstream applications including RNAi, for example by correcting annotations of potential targets such as developmental genes. We are now in the community curation phase of annotation, where researchers can add their expertise to computationally predicted models of their favourite genes. We are hosting the *V. vulgaris* community curation on the Web Apollo annotation editing platform at the University of Otago. I will give a short introduction to the curation process and encourage community participation in the project.

