

The genomes of three invasive social wasps

Peter Dearden¹, Elizabeth J. Duncan², Gregory Gimenez¹,
Monica A. M. Gruber³, Joseph Guhlin¹, Tom Harrop¹, Philip J. Lester³,
Gemma McLaughlin¹, Elizabeth Permina¹, Jessica Purcell⁴, Emily J. Remnant⁵,
Peter Stockwell¹, Oliver Quinn³, Erin E. Wilson-Rankin⁴

¹The University of Otago, Aotearoa New Zealand.

²University of Leeds, United Kingdom.

³Victoria University of Wellington, New Zealand.

⁴University of California, USA.

⁵University of Sydney, Australia.

tom.harrop@otago.ac.nz

Vespula species



*Vespula germanica*¹
German wasp

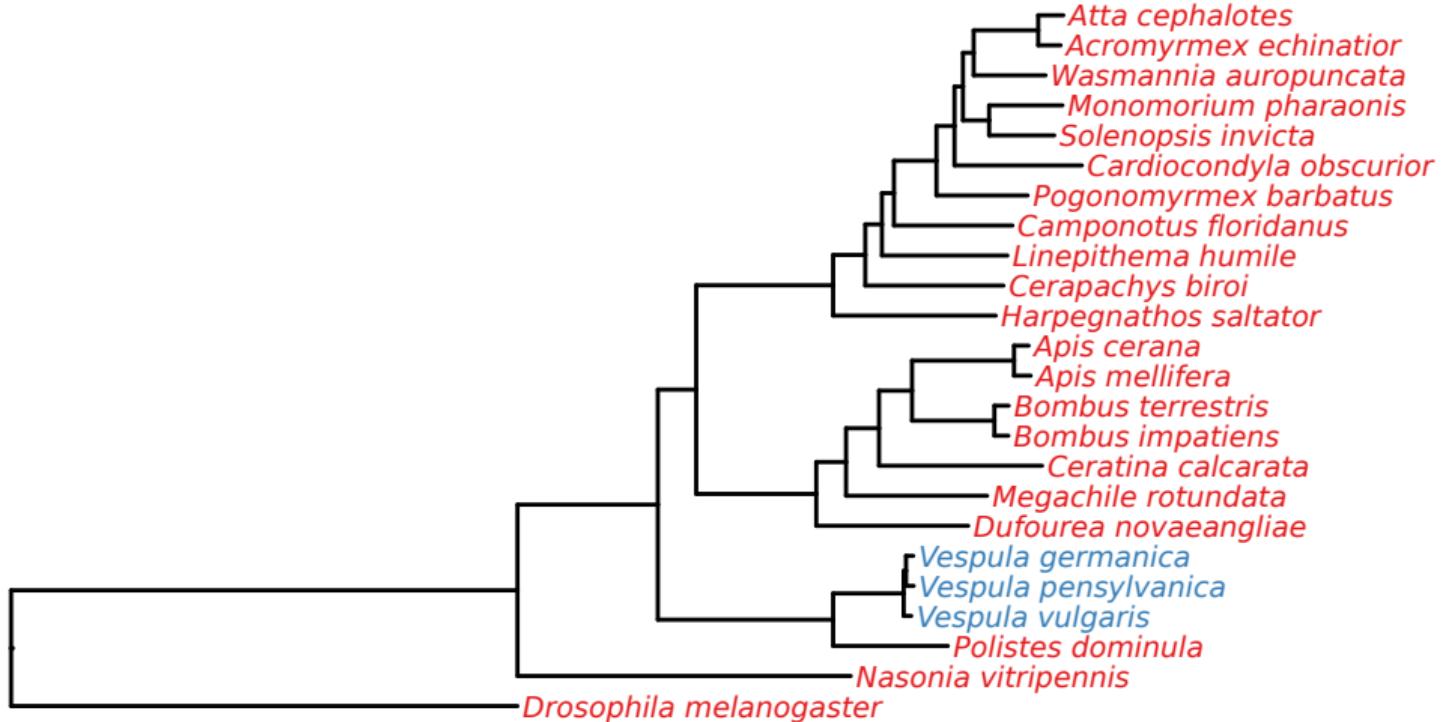


*Vespula pensylvanica*²
Western yellowjacket

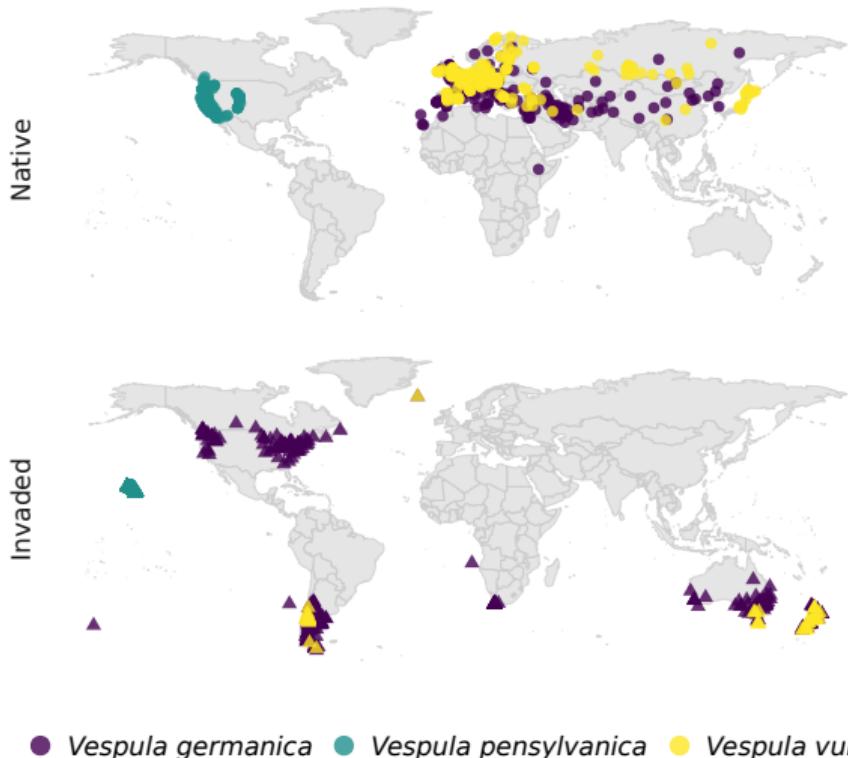


*Vespula vulgaris*³
Common wasp

Vespula species



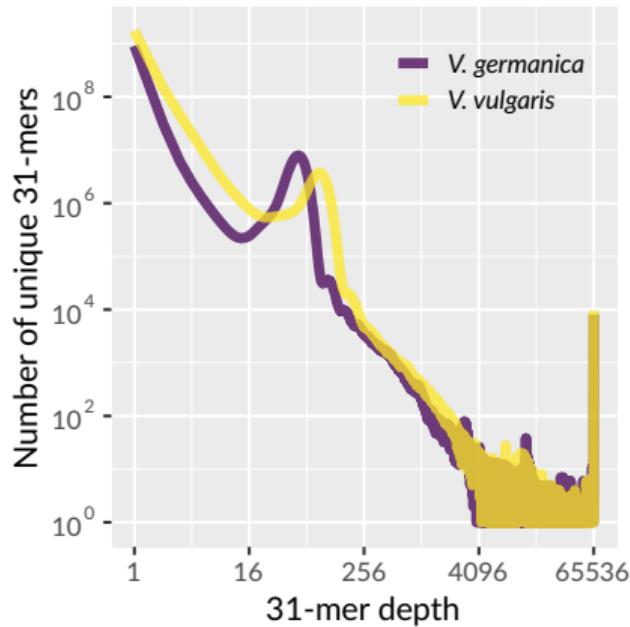
Invasive *Vespula* spp.



- Significant pest species
- Colonies > 500,000 individuals
- Potential target for genetic control strategies
- Closest genomes are two *Polistes* spp.

Location data sourced by Philip Lester

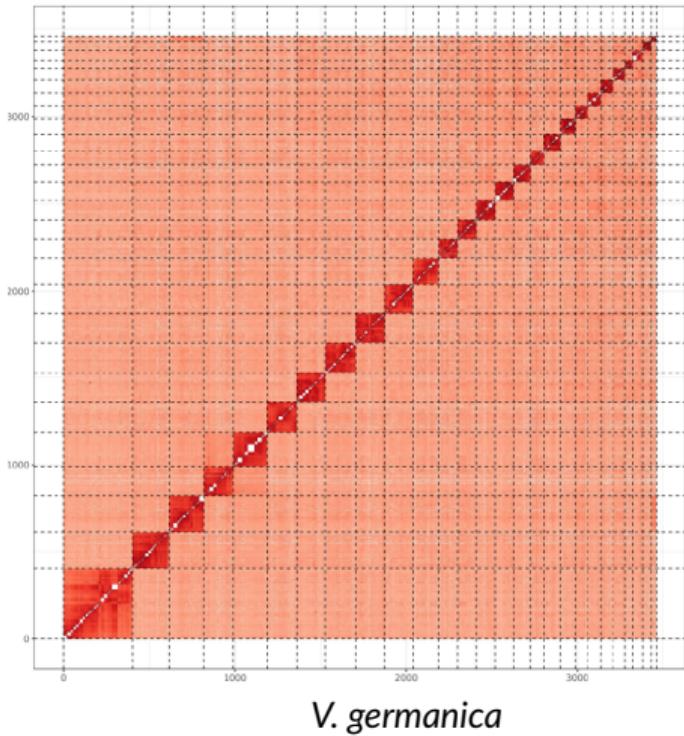
Vespula short-read assemblies



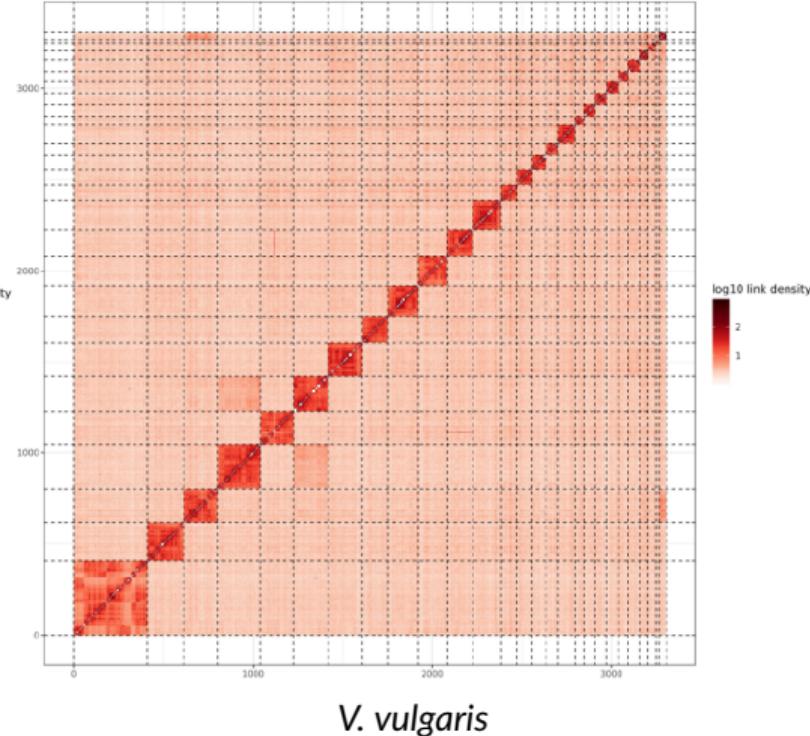
	<i>V. germanica</i>	<i>V. vulgaris</i>
Size (Mb)	178	175
Scaffolds	10,963	13,049
L_{50} (Kb)	207	37
Complete (%) ¹	93	95

¹Complete, single-copy BUSCOs

Hi-C scaffolding

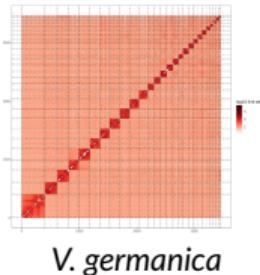


V. germanica

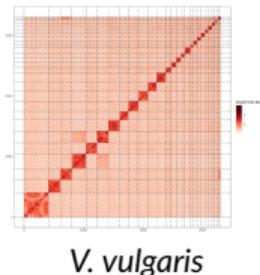


V. vulgaris

Hi-C scaffolding



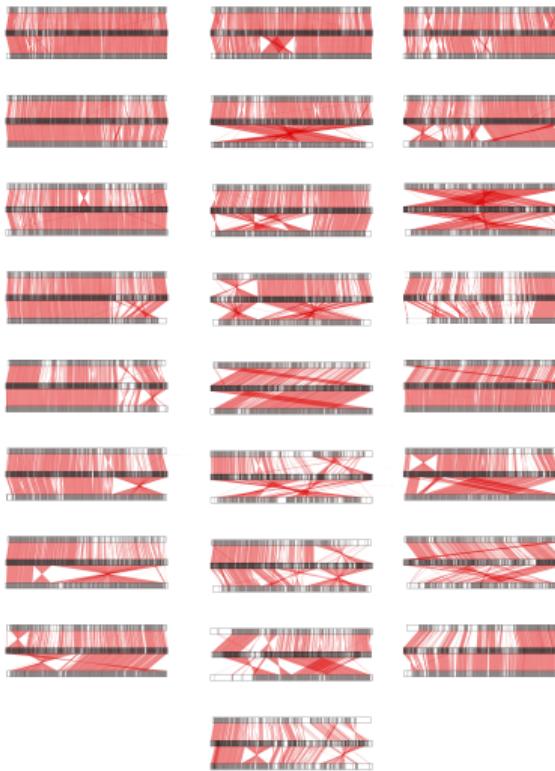
	Short read	Hi-C scaffolds
Size (Mb)	178	178
Scaffolds	10,963	133
L_{50} (Kb)	207	8,396
Complete (%) ¹	93	95



	Short read	Hi-C scaffolds
Size (Mb)	175	176
Scaffolds	13,049	35
L_{50} (Kb)	37	8,305
Complete (%) ¹	95	97

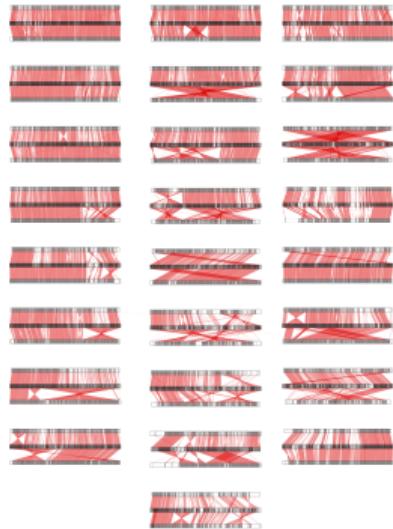
¹Complete, single-copy BUSCOs

Scaffolds oriented with D-GENIES



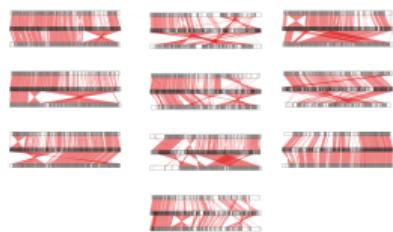
Chromosome-scale assemblies

V. germanica



	Short read	Hi-C scaffolds	Chromosomes
Size (Mb)	178	178	178
Scaffolds	10,963	133	25
L_{50} (Kb)	207	8,396	8,396
Complete (%) ¹	93	95	95

V. vulgaris

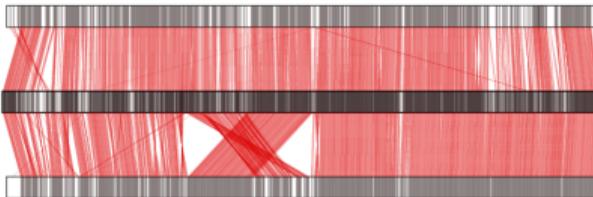


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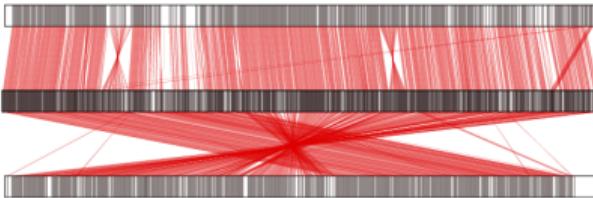
¹Complete, single-copy BUSCOs

Conservation of synteny

Chr03

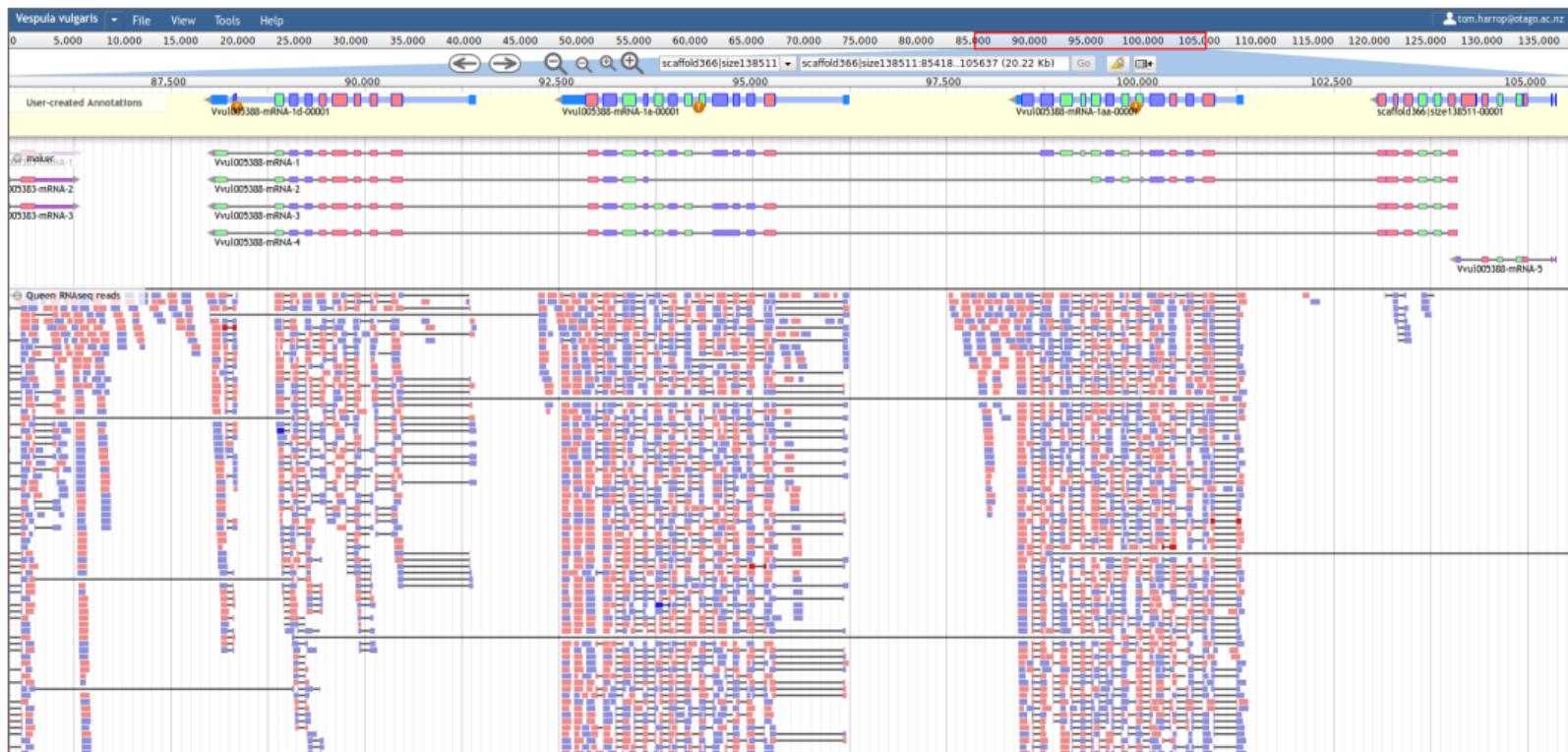


Chr05



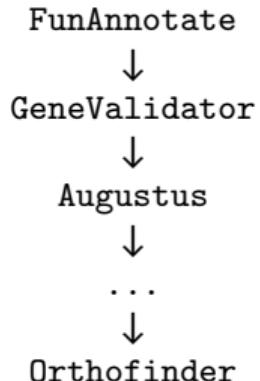
- Synteny suggests some chromosomal rearrangements between species
 - SNPs?
 - Sequence over breakpoints (Nanopore)?

Manual gene annotation



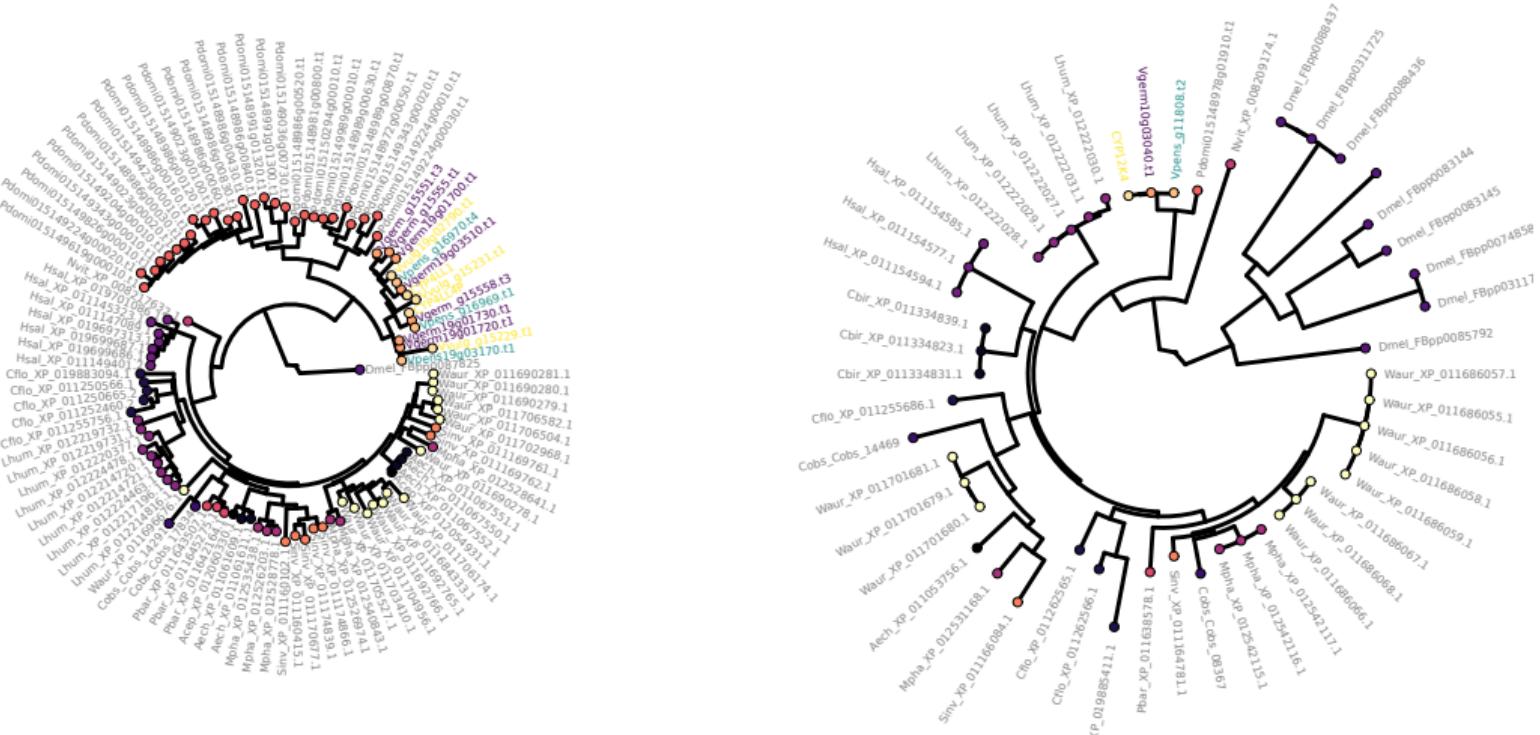
Thanks to the team of annotators!

Iterative annotation



	<i>V. germanica</i>	<i>V. pensylvanica</i>	<i>V. vulgaris</i>
Number of genes	18,710	20,220	18,065
Number of genes in orthogroups	16,429	16,655	15,862
Number of unassigned genes	2,281	3,565	2,203

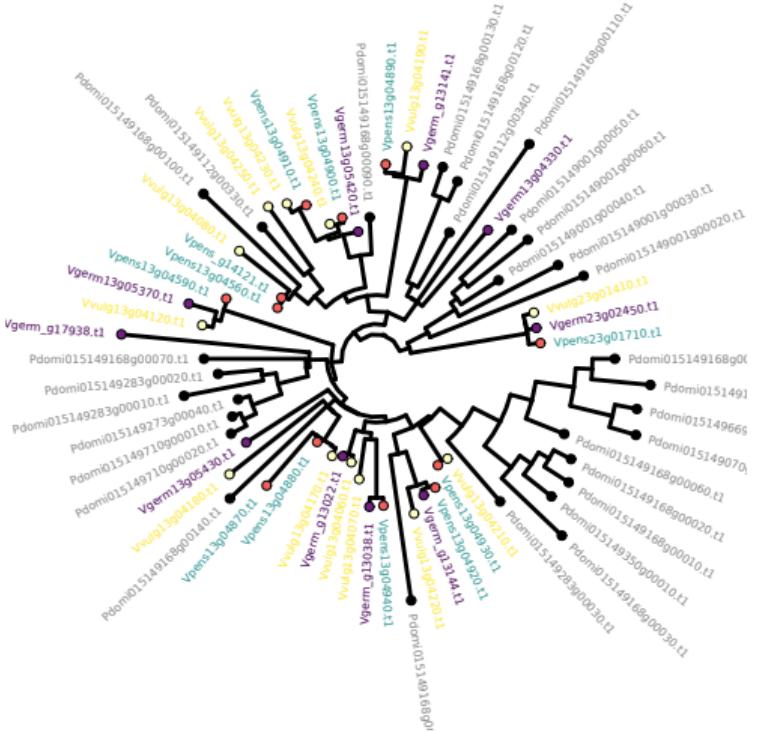
Vespula CYPomes



Cyp4 orthogroup

Mitochondrial P450 orthogroup

Summary



- Reference-quality, near-complete assemblies using short-read sequencing & Hi-C scaffolding
- Comparisons between species allowed orientation and anchoring of scaffolds
- Manual curation and iterative improvement resulted in a comprehensive annotation
- Targets for a gene drive...?

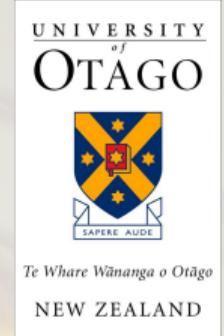
Wasp-specific OR orthogroup?

Acknowledgements

Large team that worked on the assemblies and annotations!



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Challenges

MARSDEN FUND
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genomics
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