

Genetic diversity and biocontrol in Argentine stem weevils

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@tharrop_



Biological control



Bidgee, CC BY

Biological control



Beatrix Moisset, CC BY-SA

Modified ecosystems have low biotic resistance



Argentine stem weevil, *Listronotus bonariensis*



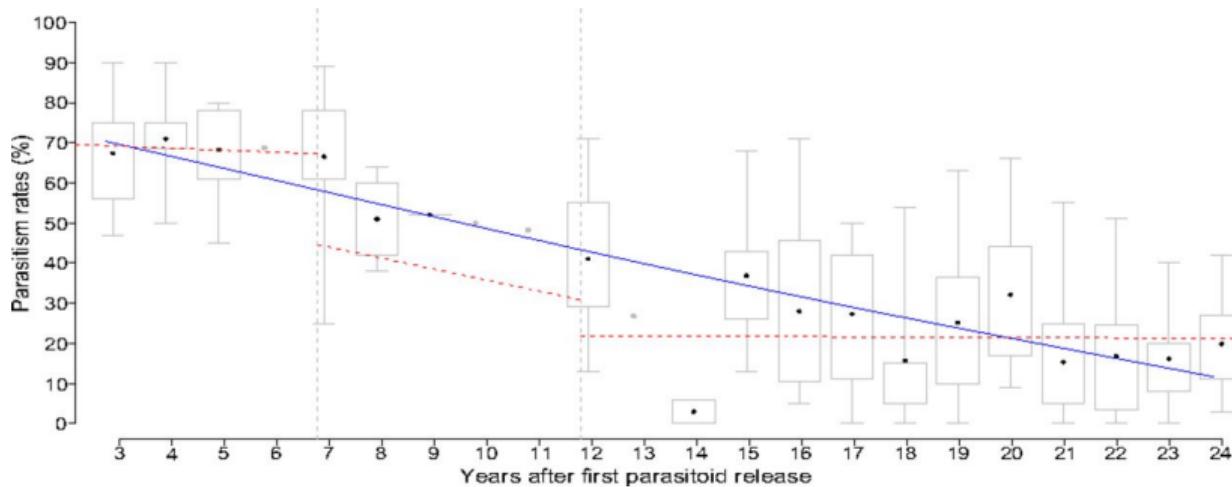
Microctonus hyperodae



UGA1295012

Mark McNeill, CC-BY-3.0.

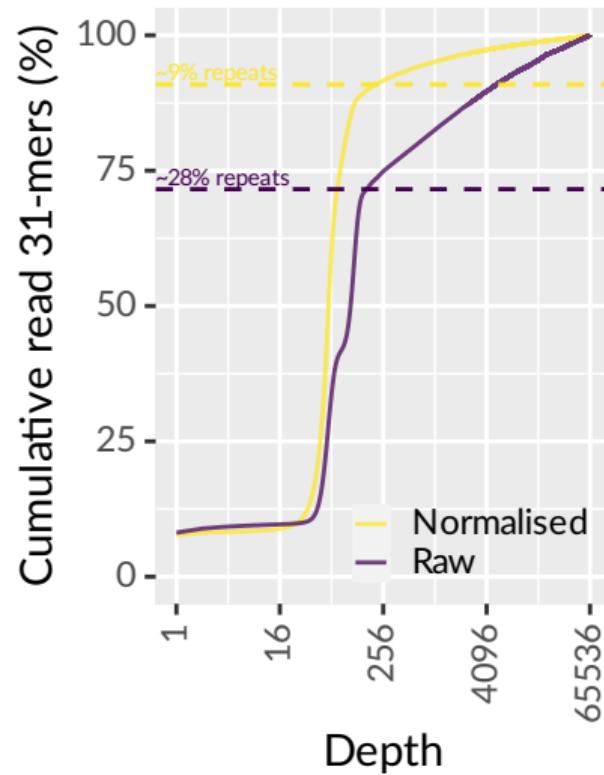
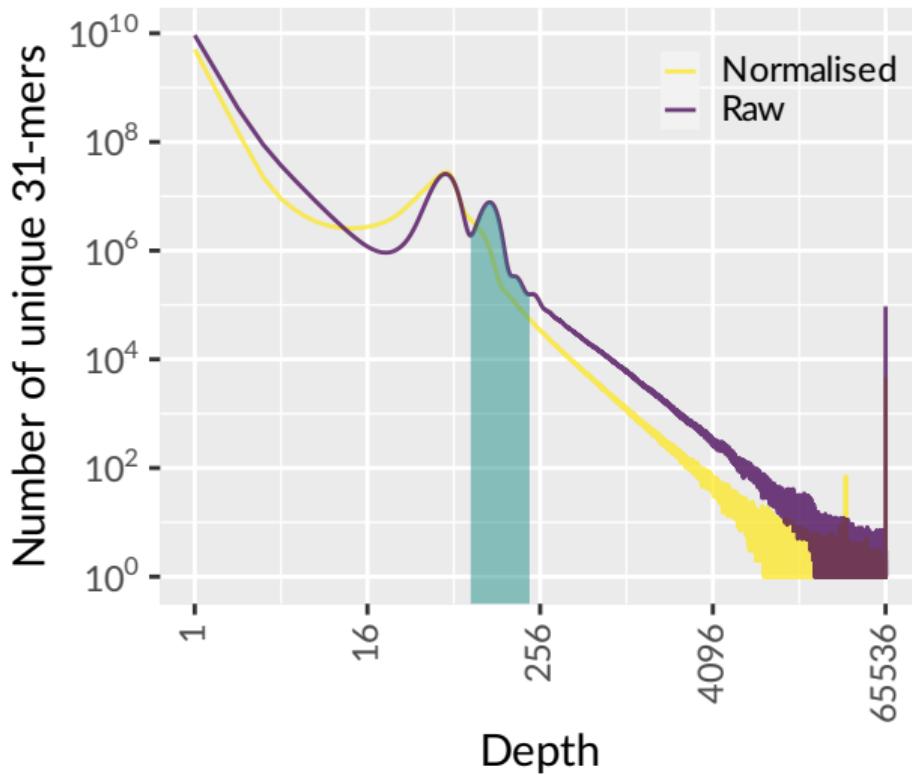
Decline in effectiveness



Check out these genomes 🌱



Short-read genome assembly



We started a genome project by mistake



Iterative improvements to the genome

	Short read	Single indiv. long read	Pooled long read	Comb. long read	Final draft
Assembly length (Gb)	1.3	1.2	1.2	1.7	1.1
N_{50} length (kb)	7.1	74.4	112.6	86.4	122.3
Complete	32.7	72.2	71	69.2	78.8
BUSCOs (%)					
Multiple-copy BUSCOs (%)	17.2	7.5	5.9	17.4	5.1
Min. repeat content (%)	n.d.	71	71.4	71.4	71.3

Nanopore genome

Listronotus bonariensis (Argentine stem weevil)
Representative genome: [Listronotus bonariensis \(assembly ASM1417023v1\)](#)

Download sequences in FASTA format for [genome](#)
Download genome annotation in [GenBank](#) format
BLAST against Listronotus bonariensis [genome](#)

NEW Try [NCBI Datasets](#) - a new way to download genome sequence and annotation we're testing in NCBI Labs

Display Settings: [Overview](#) Send to: [▼](#)

Organism Overview ID: 9381

Listronotus bonariensis (Argentine stem weevil)

Lineage: Eukaryota[5786]; Metazoa[2316]; Ecdysozoa[764]; Arthropoda[631]; Hexapoda[539]; Insecta[520]; Pterygota[519]; Neoptera[513]; Holometabola[435]; Coleoptera[39]; Polyphaga[37]; Cucujiformia[21]; Curculionidae[5]; Cyclomiminae[1]; Listroderini[1]; Listronotus[1]; Listronotus bonariensis[1]

[Summary](#)

Assembly level: Scaffold
Assembly: GCA_014170235.1 ASM1417023v1 scaffolds: 22,156 contigs: 22,298 N50: 120,328 L50: 2,727
BioProjects: PRJNA640511
Whole Genome Shotgun (WGS): INSDC: JACEGR000000000.1
Statistics: total length (Mb): 1112.44
GC%: 31.3

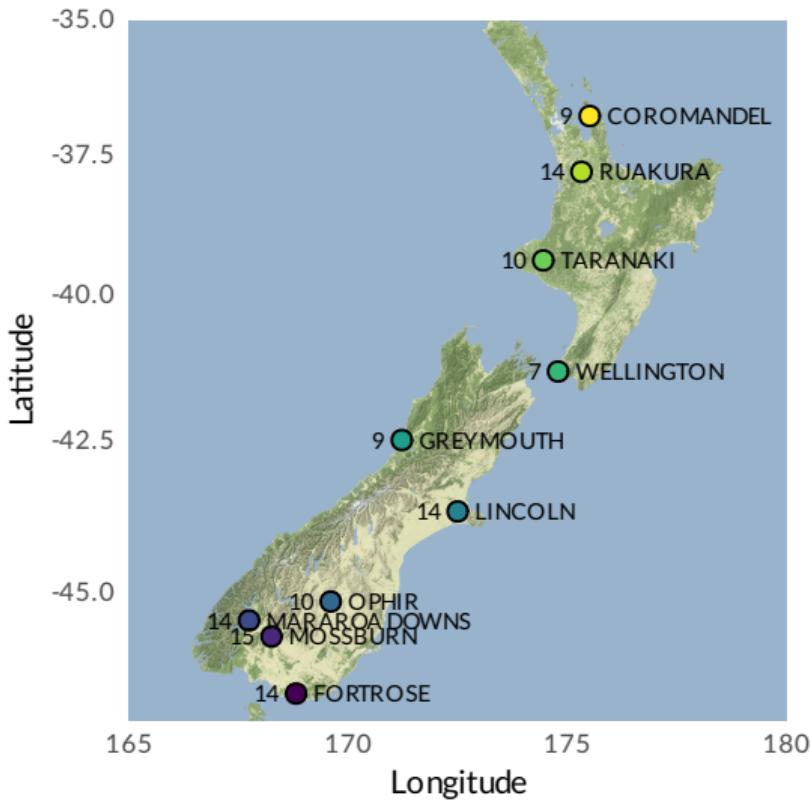
[Publications \(limited to 20 most recent records\)](#)

1. Genetic Diversity in Invasive Populations of Argentine Stem Weevil Associated with Adaptation to Biocontrol. Harrop TWR, et al. Insects 2020 Jul 14

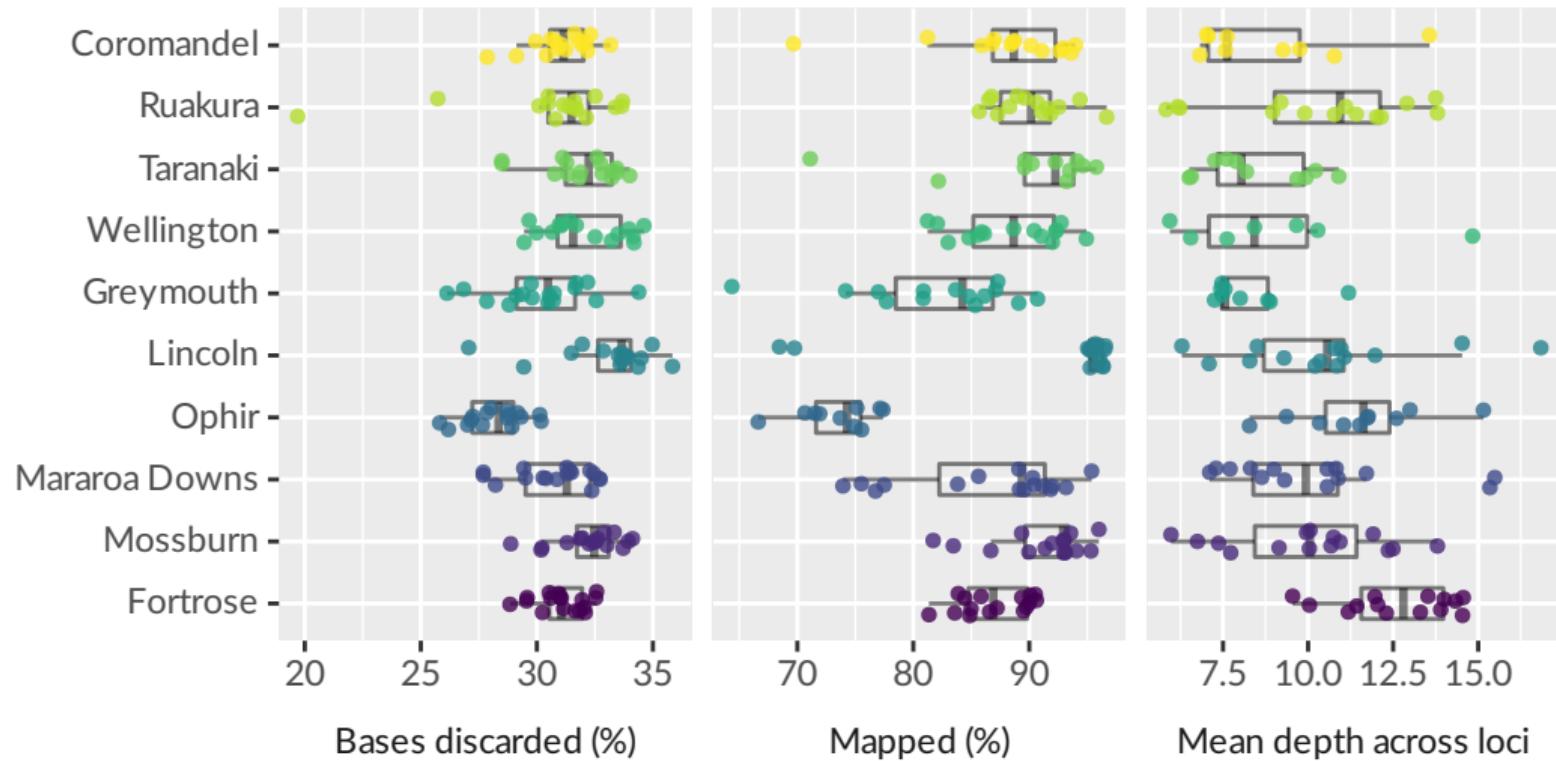
[Genome Assembly Annotation](#)

Loc	Type	Name	RefSeq	INSDC	Size (Mb)	GC%
		master WGS	-	JACEGR000000000.1	1,112.44	31.3

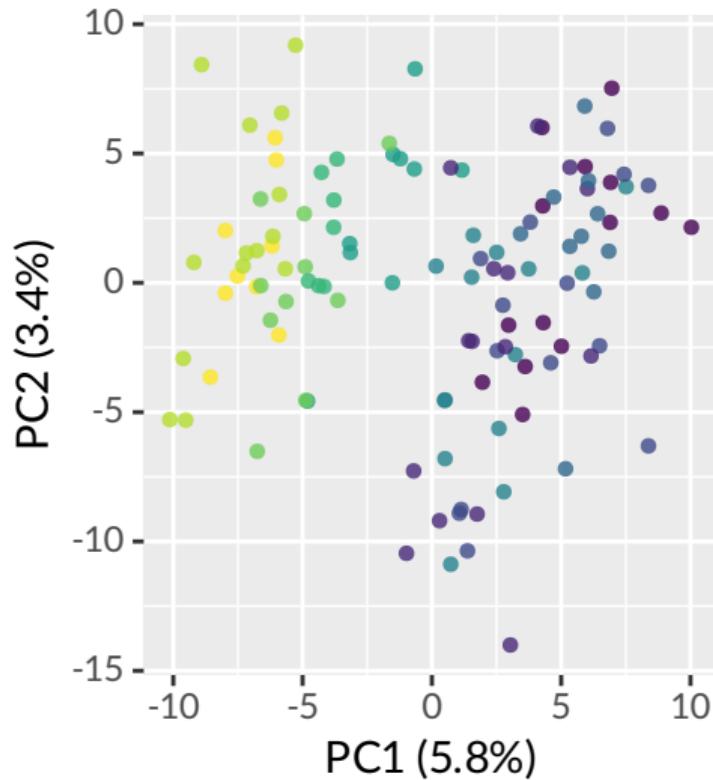
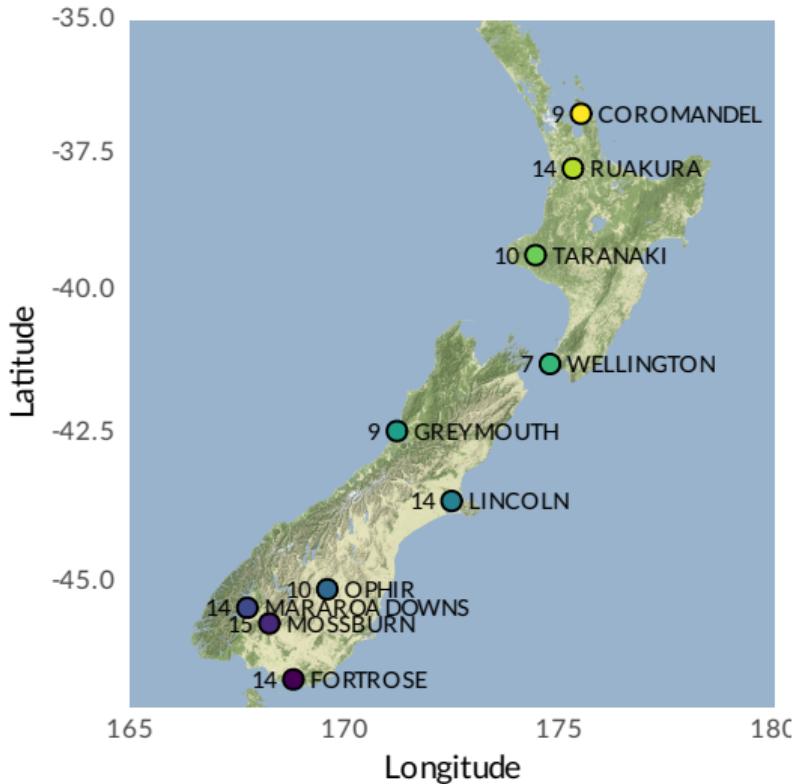
Survey of ASW diversity in NZ



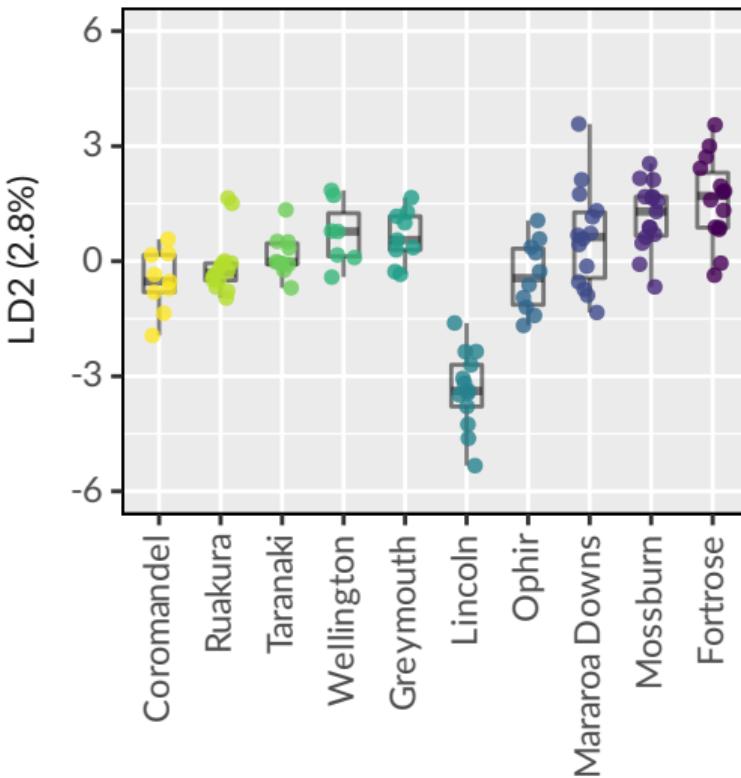
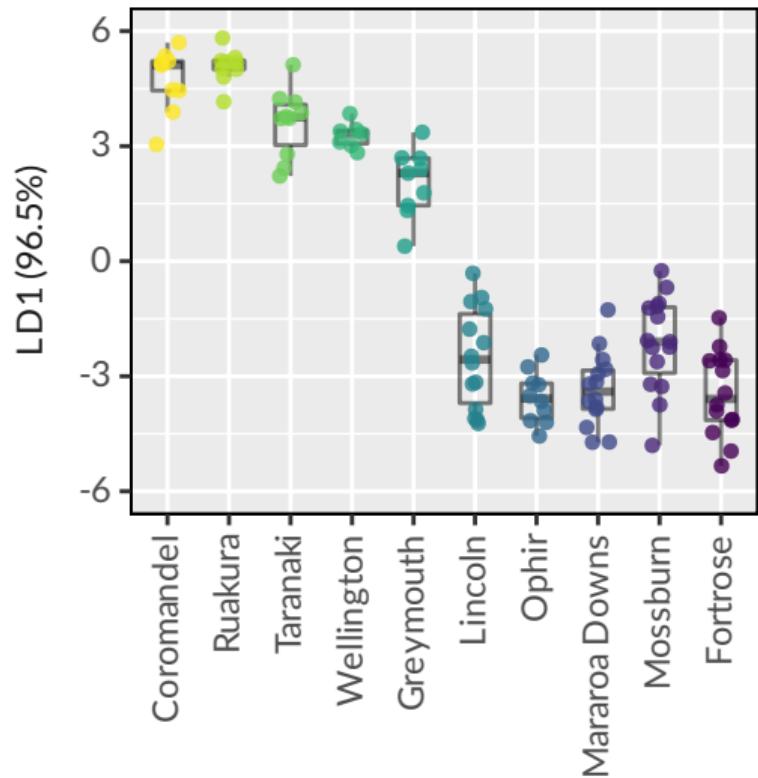
18,715 SNPs after processing, calling and filtering



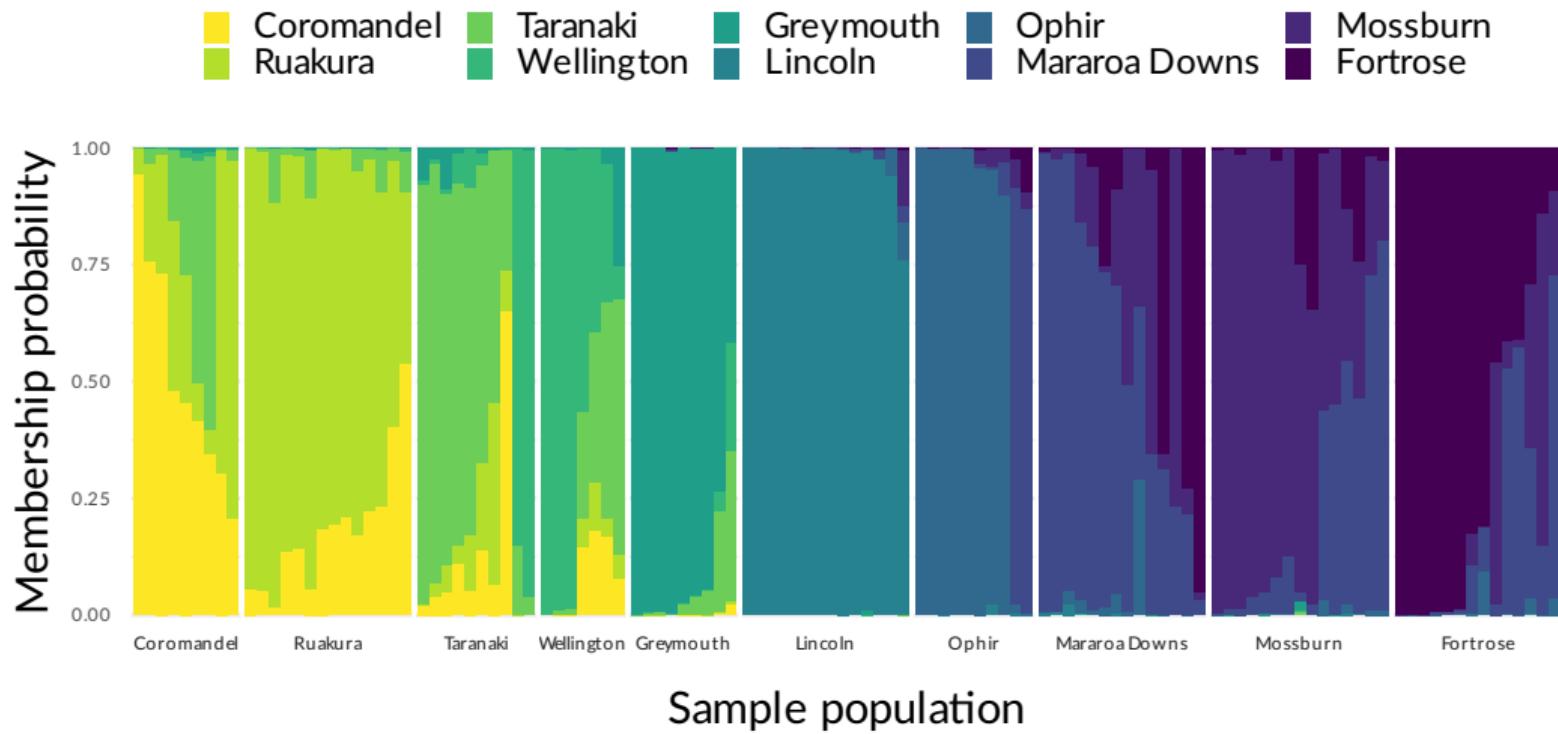
116 individuals genotyped at 18,715 SNPs



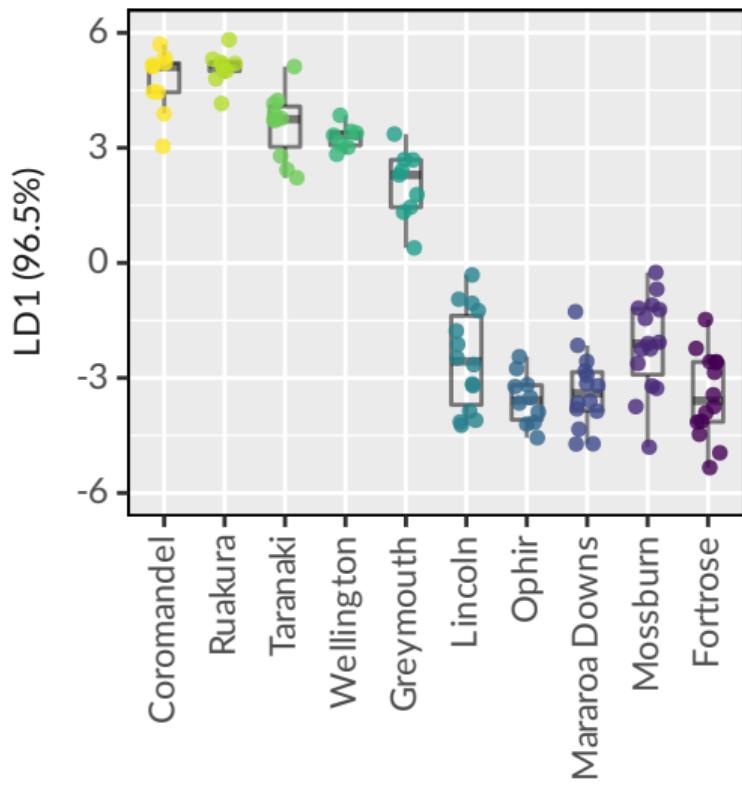
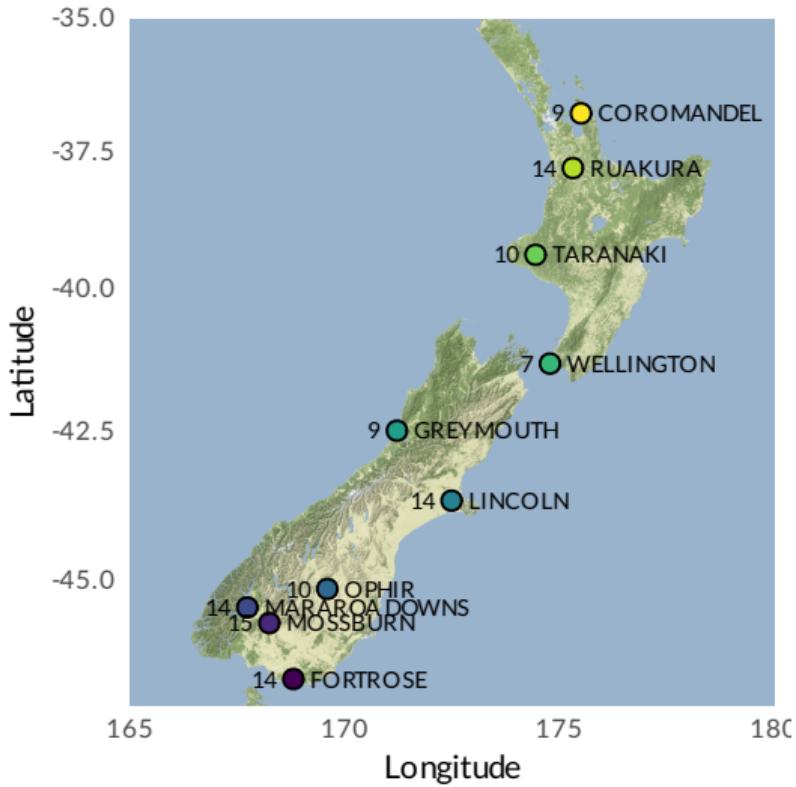
DAPC of PCs 1--16



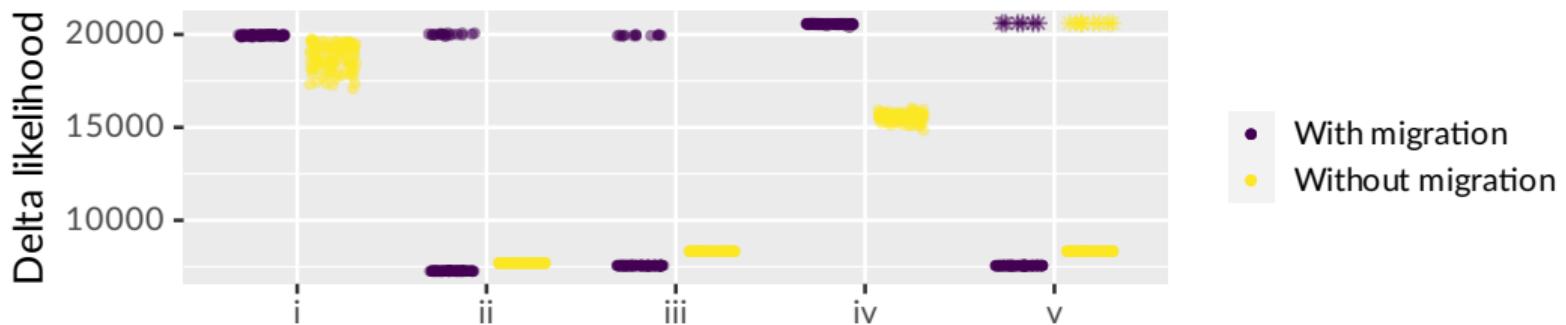
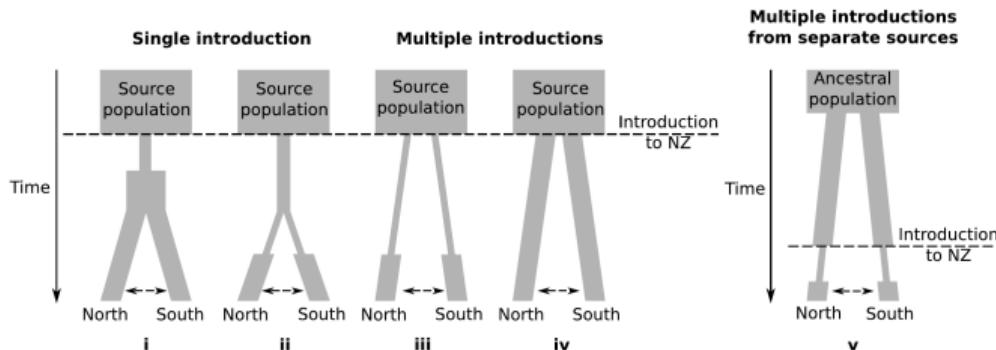
Group memberships



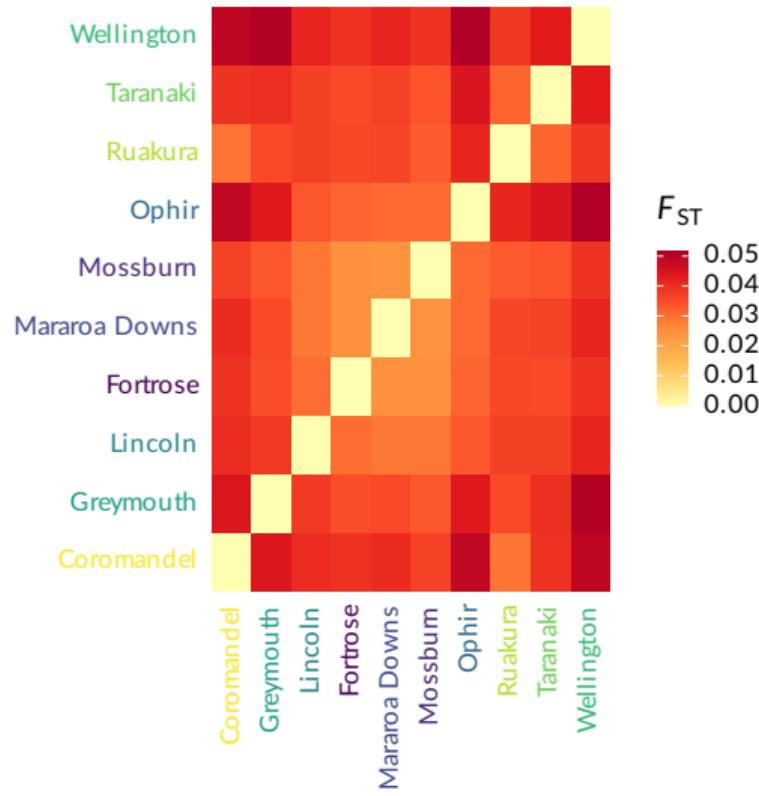
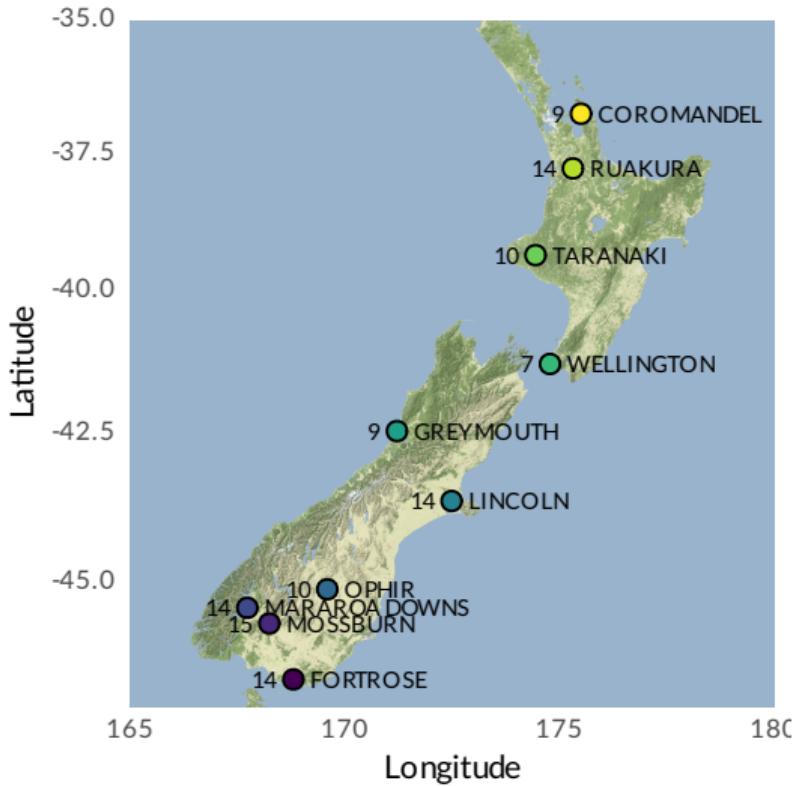
Main divide separates ASW populations



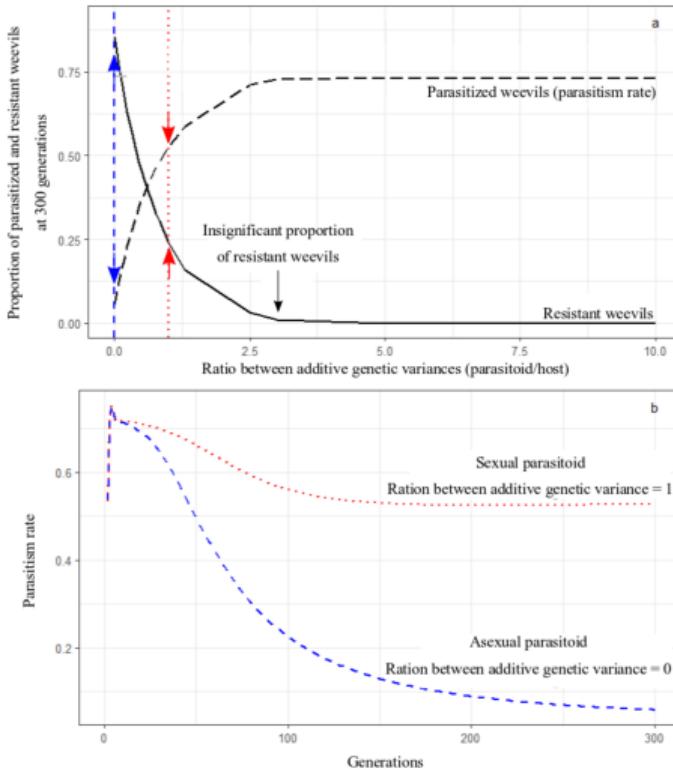
Demographic modelling



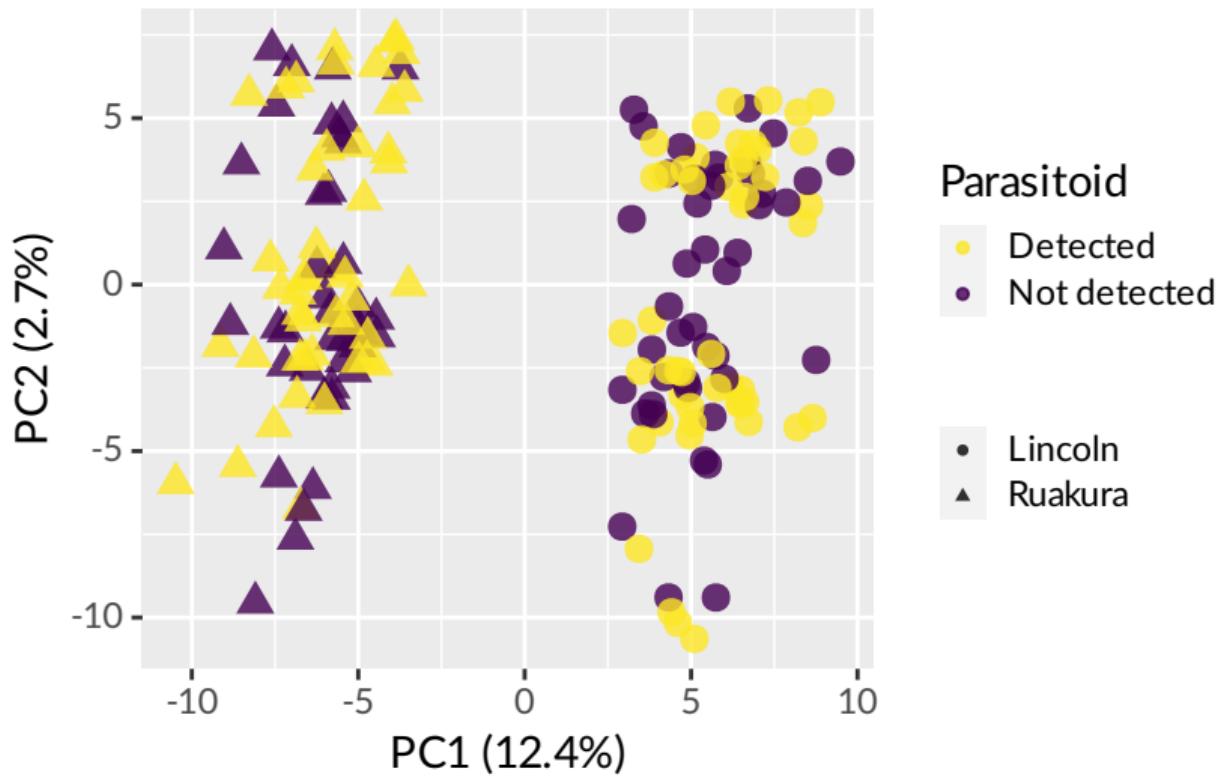
High heterozygosity (0.18--0.20), low structure



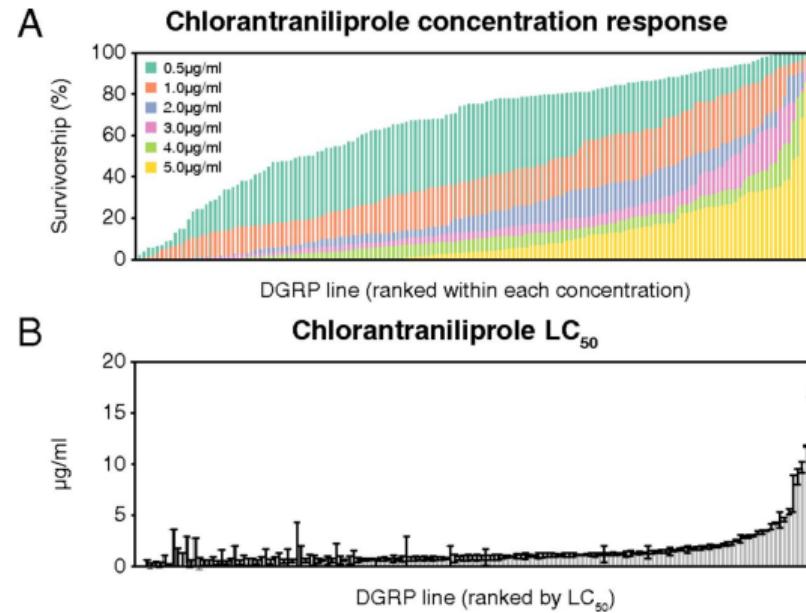
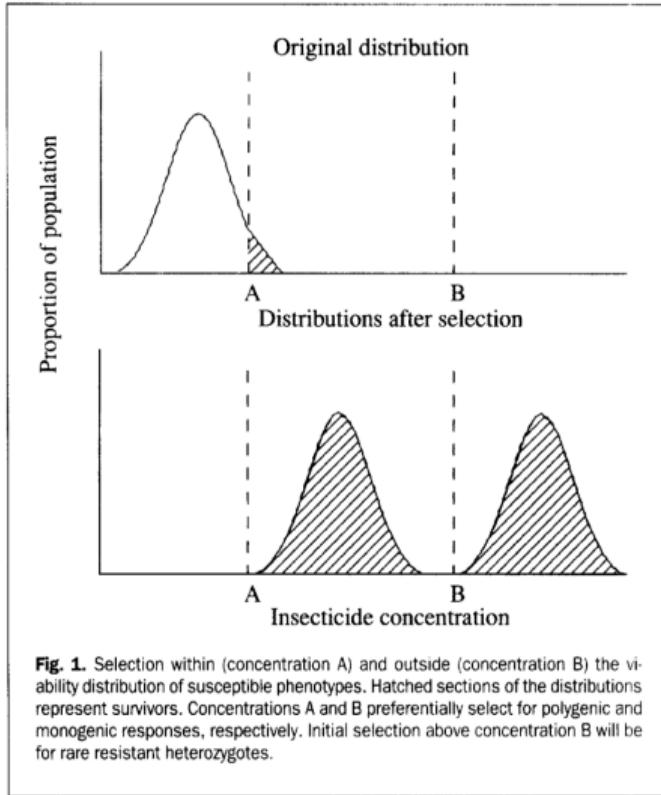
Unequal arms race



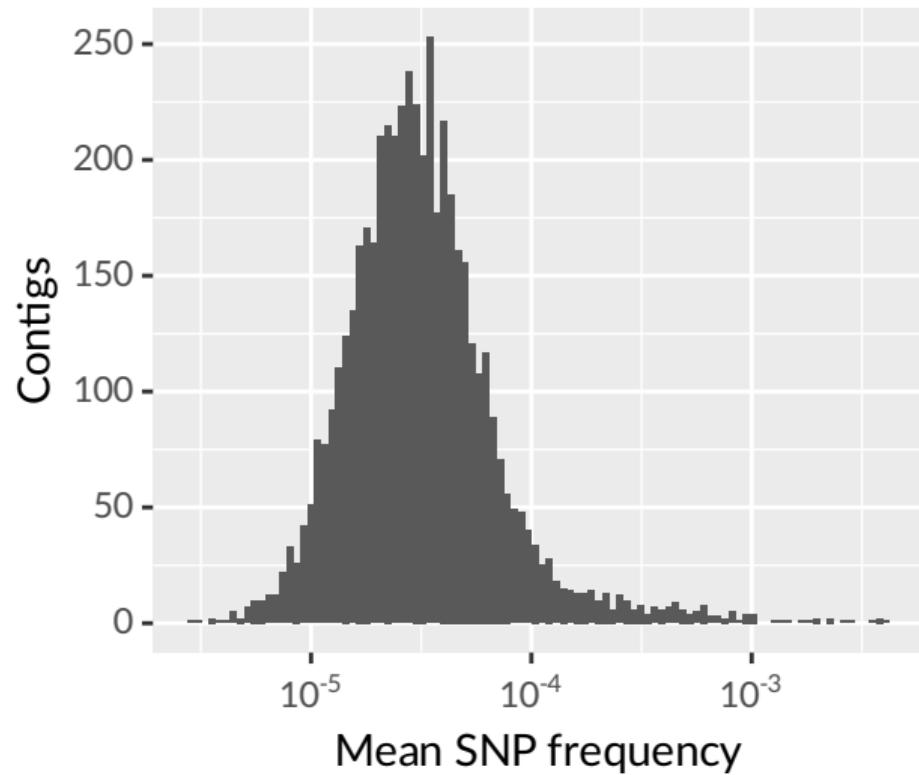
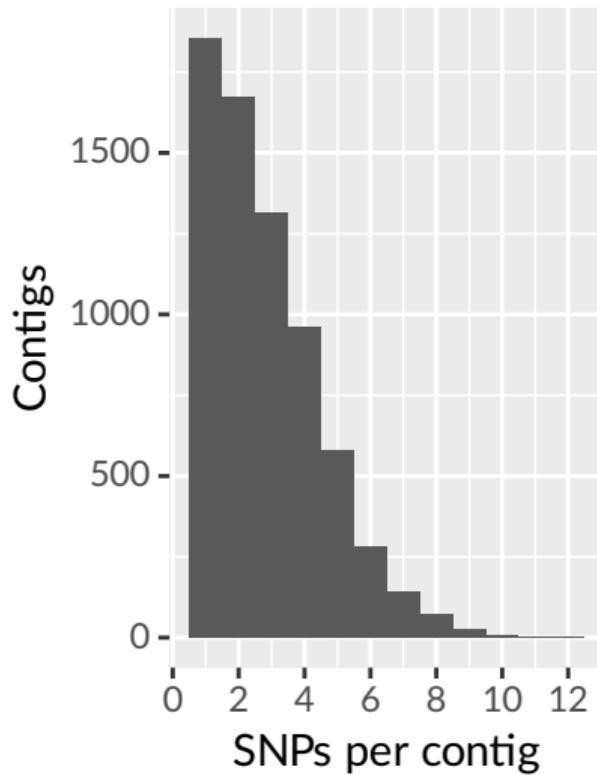
No genetic variation associated with parasitoid detection



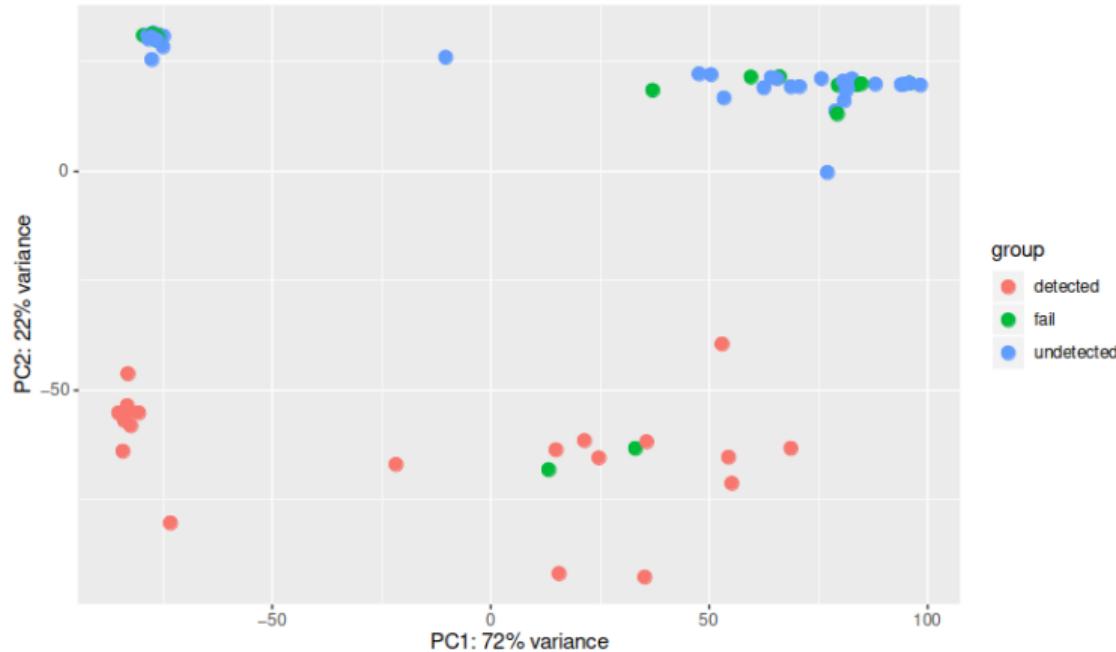
What sort of variation do we expect biocontrol to act on?



One SNP every 38,263 bp

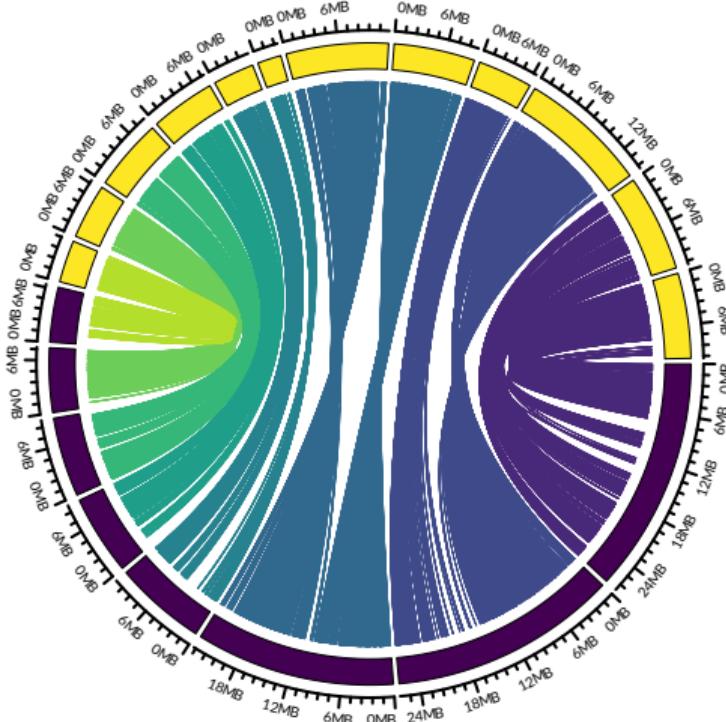


What is the resistance mechanism?



Parasitoid genomes

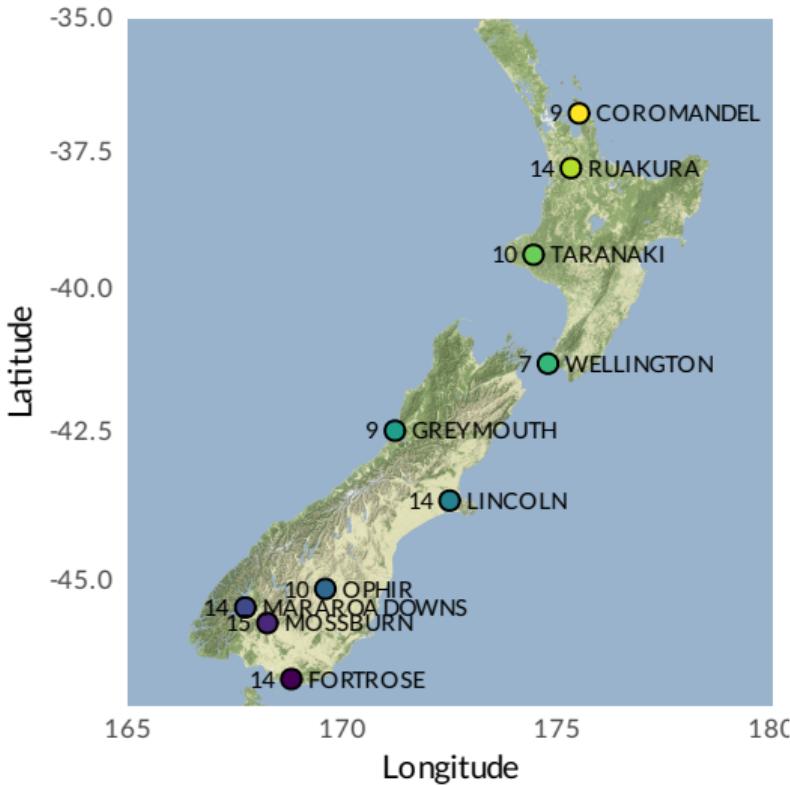
M. hyperodae



M. aethiopoides

John Skelly

Genetic diversity in the parasitoid?



- Geographical survey of NZ populations of *M. hyperodae*
- Historical specimens from 7 ecotypes that were collected from South America

Acknowledgements

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