Title: Linking landscape genomics with viromics to assess evolutionary trade-offs in native and invasive bumblebees

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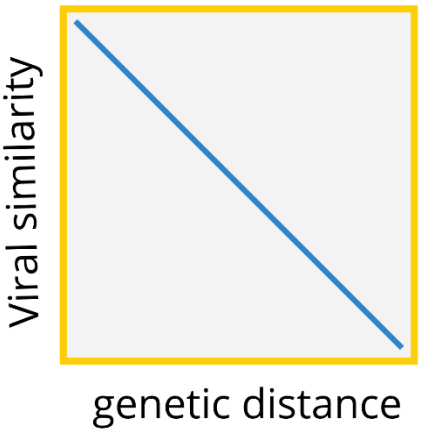
Background: Native to Europe, *Bombus terrestris* invaded many parts of the world, causing disturbance to native plant-pollinator ecosystems, and in turn has had to adapt to variable landscapes, climatic conditions and pathogen pressures. This pathogen pressure is increased by a variety of bee viruses transmitted to honeybees by the parasitic mite, *Varroa destructor*, and then transmitted via pathogen spillover to bumblebees.

Aims: I aim to: 1) Compare how climate and land use variables affect genetic connectivity and test for a role of landscape genetic connectivity in predicting site-level viral diversity and composition, and 2) Investigate the presence of trade-offs between being locally adapted to environmental conditions and persisting under pathogen selection pressures

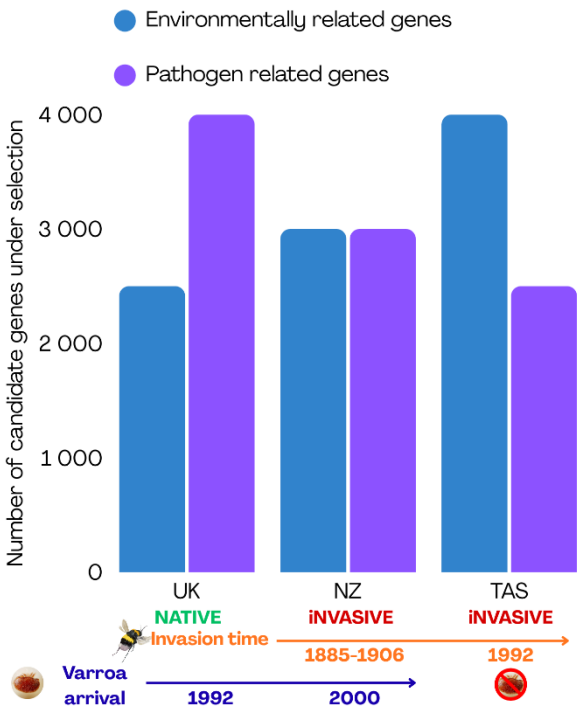
Method: Whole genome sequencing and total RNA sequencing of *B. terrestris* female workers collected in the UK, New Zealand and Tasmania (see **figure 1**). Genomic and viral results obtained from the three focal regions will be compared considering their differences in historical colonisation times (UK – native range vs New Zealand and the more recently invaded Tasmania) as well as their differences in exposure timelines to *Varroa,* which is present in the UK and New Zealand but remains absent from Tasmania.

Expected results (hypothesis):

Hypothesis Aim 1 – neutral landscape genetics



Hypothesis Aim 2 – adaptive landscape genetics



Discussions/conclusions: This study will provide insight into how pathogens interact with hosts during invasion and help understand how insects adapt in novel environments. This study is also novel in its combination of landscape genomic data analysis together with viromics (RNAseq) to investigate the presence of pathogen-related selection trade-offs.

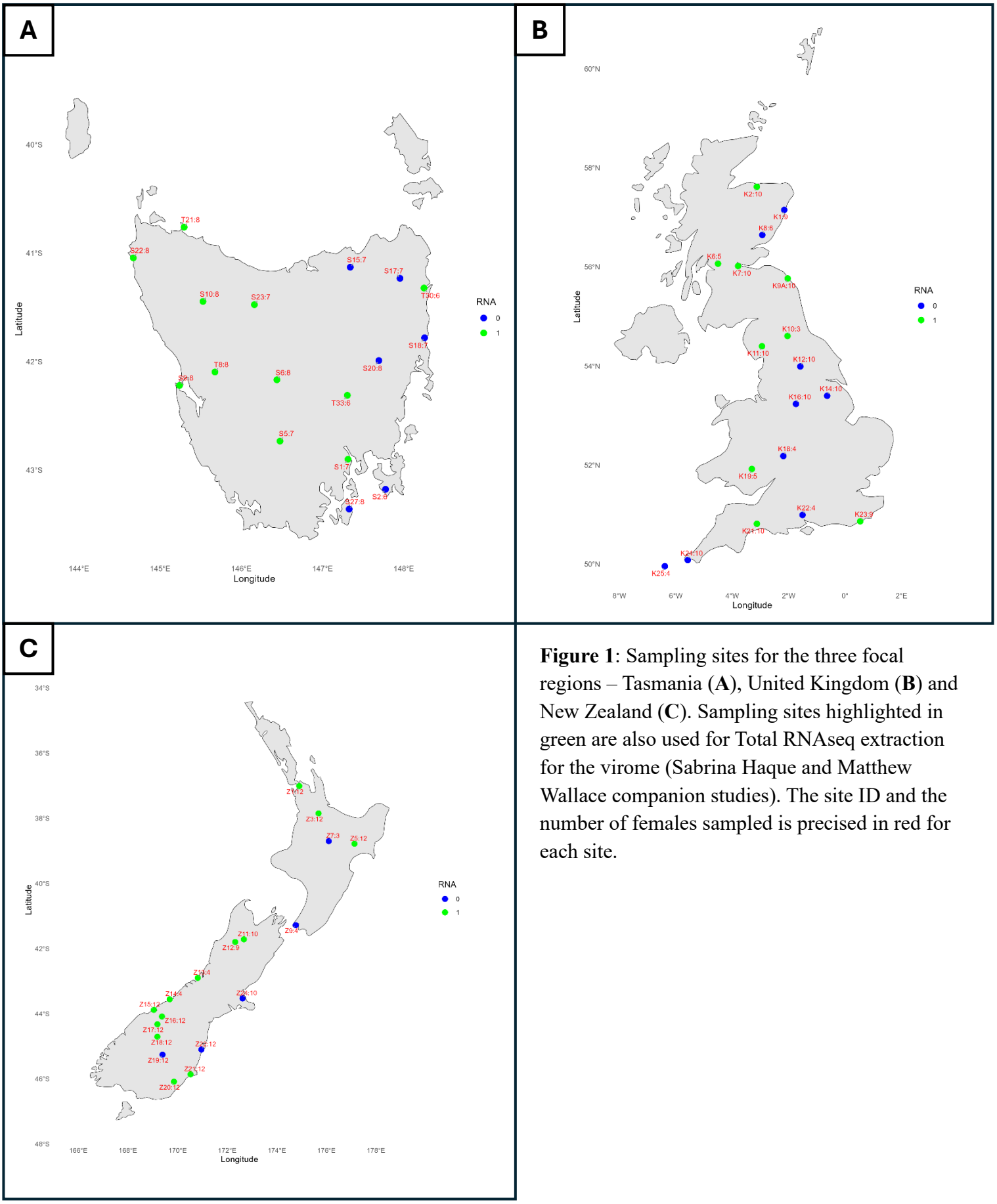


Figure 1: Sampling sites for the three focal regions – Tasmania (**A**), United Kingdom (**B**) and New Zealand (**C**). Sampling sites highlighted in green are also used for Total RNAseq extraction for the virome (Sabrina Haque and Matthew Wallace companion studies). The site ID and the number of females sampled is precised in red for each site.