

Selection despite low genetic diversity and high gene flow in a rapid island invasion of the bumblebee, *Bombus terrestris*

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Abstract

Invasive species are predicted to adjust their morphological, physiological, and life-history traits to adapt to their non-native environments. Although a loss of genetic variation during invasion may restrict local adaptation, introduced species often thrive in novel environments. Despite being founded by just a few individuals, the bumblebee *Bombus terrestris* (Hymenoptera: Apidae) has successfully spread across the island of Tasmania (Australia) in less than 30 years, becoming abundant and competitive with native pollinators. We use RADseq to investigate the neutral and adaptive genetic processes associated with environmental and morphological variation following the invasion of *B. terrestris* in Tasmania. Across 15 sites, we found high gene flow with low genetic diversity, significant isolation-by-distance, and spatial variation in effective migration rates. A longitudinal band of restricted migration was evident across the mid-central region of Tasmania, corresponding to sites with high elevation, pastoral land, low wind speeds and low precipitation seasonality. Tajima's D indicated a recent population expansion for central sites extending from the south to the north of the island. Significant selection signatures were found for loci in relation to precipitation, wind speed, and wing loading. Candidate loci were annotated to genes with functions related to cuticle water retention, and insect flight muscle stability. Understanding how a genetically impoverished invasive bumblebee has rapidly adapted to a novel island environment provides further understanding about the evolutionary processes that determine successful insect invasions, and the potential for invasive hymenopteran pollinators to spread globally.

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