

Genomic variation in mountain bumblebees in Scandinavia: High levels of intraspecific diversity despite population vulnerability

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Abstract

Populations of many bumblebee species are in decline, with distributions shifting northwards to track suitable climates. Climate change is considered a major contributing factor. Arctic species are particularly vulnerable as they cannot shift further north, making assessment of their population viability important. Analysis of levels of whole-genome variation is a powerful way to analyse population declines and fragmentation. Here we use genome sequencing to analyse genetic variation in seven species of bumblebee from the Scandinavian mountains, including two classified as vulnerable. We sequenced 333 samples from across the ranges of these species in Sweden. Estimates of effective population size (NE) vary from ~55,000 for species with restricted high alpine distributions to 220,000 for more widespread species. Population fragmentation is generally very low or undetectable over large distances in the mountains, suggesting an absence of barriers to gene flow. The relatively high NE and low population structure indicate that none of the species are at immediate risk of negative genetic effects caused by high levels of genetic drift. However, reconstruction of historical fluctuations in NE indicates that the arctic specialist species *Bombus hyperboreus* has experienced population declines since the last ice age and we detected one highly inbred diploid male of this species close to the southern limit of its range, indicating elevated genetic load. Although levels of genetic variation in mountain bumblebee populations are currently relatively high, their ranges are predicted to shrink drastically due to the effects of climate change and monitoring is essential to detect future population declines.

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