Disentangling adaptation from drift in bottlenecked and reintroduced populations of Alpine ibex

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Abstract

Identifying local adaptation in bottlenecked species is essential for conservation management. Selection detection methods have an important role in species management plans, assessments of adaptive capacity, and looking for responses to climate change. Yet, the allele frequency changes exploited in selection detection methods are similar to those caused by the strong neutral genetic drift expected during a bottleneck. Consequently, it is often unclear what accuracy selection detection methods have across bottlenecked populations. In this study, simulations were used to explore if signals of selection could be confidently distinguished from genetic drift across 23 bottlenecked and reintroduced populations of Alpine ibex (Capra ibex). The meticulously recorded demographic history of the Alpine ibex was used to generate comprehensive simulated SNP data. The simulated SNPs were then used to benchmark the confidence we could place in outliers identified in empirical Alpine ibex SNP data. Within the simulated dataset, the false positive rates were high for all selection detection methods but fell substantially when two or more methods were combined. True positive rates were consistently low and became negligible with increased stringency. Despite finding many outlier loci in the empirical Alpine ibex SNPs, none could be distinguished from genetic drift-driven false positives. Unfortunately, the low true positive rate also prevents the exclusion of recent local adaptation within the Alpine ibex. The baselines and stringent approach outlined here should be applied to other bottlenecked species to ensure the risk of false positive, or negative, signals of selection are accounted for in conservation management plans.

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Bottleneck Number

Gran Paradiso (remnant)

A)

Number of outlier loci detected

B)

False positive rate