Evaluating genomic offset predictions in a forest tree with high population genetic structure

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Résumé

Predicting how tree populations will respond to climate change is an urgent societal concern. An increasingly popular way to make such predictions is the genomic offset (GO) approach, which aims to use genomic and climate data to identify populations that may experience climate maladaptation in the near future. More precisely, GO tries to represent the change in allele frequencies required to maintain the current gene-climate relationships under climate change. However, the GO approach has major limitations and, despite promising validation of its predictions using height data from common gardens, it still lacks broad empirical testing. In the present study, we evaluated the consistency and empirical validity of GO predictions in maritime pine (Pinus pinaster Ait.), a tree species from southwestern Europe and North Africa with a marked population genetic structure. First, gene-climate relationships were estimated using 9,817 SNPs genotyped in 454 trees from 34 populations; and candidate SNPs potentially involved in climate adaptation were identified. Second, GO was predicted using four methods, namely Gradient Forest (GF), Redundancy Analysis (RDA), latent factor mixed model (LFMM) and Generalised Dissimilarity Modeling (GDM), two sets of SNPs (candidate and control SNPs) and five climate general circulation models (GCMs) to account for uncertainty in future climate predictions. Last, the empirical validity of GO predictions was evaluated within a Bayesian framework by estimating the associations between GO predictions and two independent data sources: mortality data from National Forest Inventories (NFI), and mortality and height data from five common gardens in contrasting environments. We found high variability in GO predictions across methods, SNP sets and GCMs. Regarding validation, GO predictions with GDM and GF (and to a lesser extent RDA) based on the candidate SNPs showed the strongest and most consistent associations with mortality rates in common gardens and NFI plots. We found almost no association between GO predictions and tree height in common gardens, most likely due to the overwhelming effect of population genetic structure on tree height in this species. Our study demonstrates the imperative to validate GO predictions with a range of independent data sources before they can be used as informative and reliable metrics in conservation or management strategies.

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Mots-Clés: genomic offset, forest trees, adaptation to climate, climate change, population genetic structure