Peer Community In
Evolutionary Biology

RECOMMENDATION

Disentangling the recent and ancient demographic history of European spruce species

Jason A Holliday[1]

[1] Department of Forest Resources and Environmental Conservation, Virginia Tech – Blacksburg, USA

A recommendation of

Chen J, Milesi P, Jansson G, Berlin M, Karlsson B, Aleksić JM, Vendramin GG, and Lascoux M. Genomic data provides new insights on the demographic history and the extent of recent material transfers in Norway spruce. *bioRxiv* 402016, ver 3 peer-reviewed and recommended by PCI Evol Biol (2018). DOI: 10.1101/402016

Genetic diversity in temperate and boreal forests tree species has been strongly affected by late Pleistocene climate oscillations [2, 3, 5], but also by anthropogenic forces. Particularly in Europe, where a long history of human intervention has re-distributed species and populations, it can be difficult to know if a given forest arose through natural regeneration and gene flow or through some combination of natural and human-mediated processes. This uncertainty can confound inferences of the causes and consequences of standing genetic variation, which may impact our interpretation of demographic events that shaped species before humans became dominant on the landscape. In their paper entitled "Genomic data provides new insights on the demographic history and the extent of recent material transfers in Norway spruce", Chen *et al.* [1] used a genome-wide dataset of 400k SNPs to infer the demographic history of *Picea abies* (Norway spruce), the most widespread and abundant spruce species in Europe, and to understand its evolutionary relationship with two other spruces (*Picea obovata* [Siberian spruce] and *P. omorika* [Serbian spruce]). Three major Norway spruce clusters were identified, corresponding to central Europe, Russia and the Baltics, and Scandinavia, which agrees with previous studies. The density of the SNP data in the present paper enabled inference of previously uncharacterized admixture between these groups, which corresponds to the timing of postglacial recolonization following the last glacial maximum (LGM). This suggests that multiple migration routes gave rise to the extant distribution of the species, and may explain why Chen *et al.*'s estimates of divergence times among these

major Norway spruce groups were older (15mya) than those of previous studies (5-6mya) – those previous studies may have unknowingly included admixed material [4]. Treemix analysis also revealed extensive admixture between Norway and Siberian spruce over the last 100k years, while the geographically-restricted Serbian spruce was both isolated from introgression and had a dramatically smaller effective population size (*Ne*) than either of the other two species. This small *Ne* resulted from a bottleneck associated with the onset of the iron age 3000 years ago, which suggests that anthropogenic depletion of forest resources has severely impacted this species. Finally, ancestry of Norway spruce samples collected in Sweden and Denmark suggest their recent transfer from more southern areas of the species range. This northward movement of genotypes likely occurred because the trees performed well relative to local provenances, which is a common observation when trees from the south are planted in more northern locations (although at the potential cost of frost damage due to inappropriate phenology). While not the reason for the transfer, the incorporation of southern seed sources into the Swedish breeding and reforestation program may lead to more resilient forests under climate change. Taken together, the data and analysis presented in this paper allowed inference of the intra- and interspecific demographic histories of a tree species group at a very high resolution, and suggest caveats regarding sampling and interpretation of data from areas with a long history of occupancy by humans.

References

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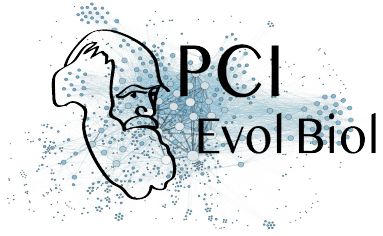
Appendix

Reviews by two anonymous reviewers, DOI: 10.24072/pci.evolbiol.100064