

Signatures of ancient and recent selection and demographic events in spruce (*Picea*) genomes

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Abstract

DNA polymorphisms at 11 loci were studied in an average of 42 Brewer spruce (*Picea breweriana* Wats.) haplotypes sampled in four populations representative of the natural range. These data were compared with polymorphisms at corresponding loci in an average of 47 Norway spruce (*Picea abies* [L.] Karst) haplotypes sampled in seven populations representative of the natural range. The overall nucleotide variation in Brewer spruce was much lower than that in Norway spruce and is inconsistent with its relatively high isozyme diversity. Little population differentiation was observed among Brewer spruce populations and linkage disequilibrium could not be estimated due to too few polymorphic sites and short DNA sequences. In Brewer spruce, mean Tajima's D and Fay and Wu's H values across loci were both close to zero, indicating no departure from the standard neutral model. Hence, the particularly low level of nucleotide variation in Brewer spruce might simply be the consequence of a long-term limited population size. Interestingly, these results are in contrast to those obtained in Norway spruce where mean Tajima's D and Fay and Wu's H values across loci suggested the presence of a severe and ancient bottleneck. Trans-species shared polymorphisms at three orthologous nuclear gene loci among Brewer spruce and Norway spruce were detected, supporting the contention of allele coalescence preceding species divergence. The divergence data generated in this study will allow us disentangle the impact of demography and selection on genetic variation in both species and obtain new estimates of the mutation rate.

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