WHITE SPRUCE IN THE SIGHTS OF RESEARCHERS

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An excellent article has just been published in the September issue of the Evolutionary Applications journal. The article demonstrates the absence of effects of genetic selection on white spruce even after intensive selection. The genotyping of the trees was done with the support of McGill University and Génome Québec Innovation Centre.

A scan involving 1134 single-nucleotide polymorphisms (SNPs) from 709 expressed genes was used to assess the potential impact of artificial selection for height growth on the genetic diversity of white spruce. Two case populations of different sizes simulating different family selection intensities ($K = 13\%$ and 5%, respectively) were delineated from the Quebec breeding program. Their genetic diversity and allele frequencies were compared with those of control populations of the same size and geographic origin to assess the effect of increasing the selection intensity. The two control populations were also compared to assess the effect of reducing the sampling size. On one hand, in all pairwise comparisons, genetic diversity parameters were comparable and no alleles were lost in the case populations compared with the control ones, except for few rare alleles in the large case population. Also, the distribution of allele frequencies did not change significantly ($P = 0.05$) between the populations compared, but ten and nine SNPs (0.8%) exhibited significant differences in frequency ($P = 0.01$) between case and control populations of large and small sizes, respectively. Results of association tests between breeding values for height at 15 years of age and these SNPs supported the hypothesis of a potential effect of selection on the genes harboring these SNPs. On the other hand, contrary to expectations, there was no evidence that selection induced an increase in linkage disequilibrium in genes potentially affected by selection. These results indicate that neither the reduction in the sampling size nor the increase in selection intensity was sufficient to induce a significant change in the genetic diversity of the selected populations. Apparently, no loci were under strong selection pressure, confirming that the genetic control of height growth in white spruce involves many genes with small effects. Hence, selection for height growth at the present intensities did not appear to compromise background genetic diversity but, as predicted by theory, effects were detected at a few gene SNPs harboring intermediate allele frequencies.

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