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From Forest Nursery Notes, Summer 2007

51. © Within and among family variation of orchard and wild-stand progeny of interior spruce in British Columbia. Stoehr, M., O'Neill, G., Hollefreund, C., and Yanchuk, A. Tree Genetics and Genomes 1:64-68. 2005.

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Within and among family variation of orchard and wild-stand progeny of interior spruce in British Columbia

Received: 24 January 2005 / Revised: 6 May 2005 / Accepted: 30 June 2005 / Published online: 17 August 2005
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Abstract A common garden study was conducted with seedlings of the interior spruce complex [*Picea glauca* (Monch) Voss and *Picea engelmannii* Parry and their hybrids], comparing seedling height growth using open-pollinated orchard families and wild-stand (WS) families from the same breeding zone. Phenotypic variances of three bulked orchard seedlots and three WS seedlots did not differ. Orchard seedlots had generally higher within-family variance components than WS families. To examine year-to-year variation in orchard seedlots, three seedlots, composed of the same 18 orchard families collected in three different years, were evaluated in the same common garden study. Family mean heights within the three crop years were statistically not different; however, large rank changes in family mean heights and family variances were observed. This study shows that orchard seed derived from breeding programs does not reduce phenotypic variability in commercial plantations. In spite of the moderate to high selection intensities applied to the selection of orchard parents, large amounts of phenotypic variation are maintained because of the lack of coancestry in the orchard pollen cloud and large temporal variation in mating success and fecundity of the various parents contributing to the crop.

Introduction

In British Columbia, over 200 million conifer seedlings are planted every year, comprising more than ten different species, and one half of these are now derived from orchard seed. The maintenance of genetic diversity in such a large reforestation effort is a concern, as genetic diversity is important for the future sustainability of managed forests (El-Kassaby and Namkoong 1995). There are several isozyme studies that address this question by evaluating the levels of isozyme variation between seed orchard parents and wild-stand (WS) populations (Knowles 1985; Bergman and Ruetz 1991; El-Kassaby and Ritland 1996; Stoehr and El-Kassaby 1997). These studies show that selection does not reduce isozyme variation relative to WSs. This lack of divergence is not surprising, as isozymes are neutral markers (Bongarten et al. 1985), and as such, are supposedly not affected by direct selection. Data on variation levels in metric or quantitative traits in seed orchard progeny and progeny from WSs are not readily available.

Temporal variation in the performance of seedlings from bulked seed orchard seedlots is expected, as there is high clonal variation in fecundity (O'Reilly et al. 1982; Kjær and Wellendorf 1997), year-to-year differences in gamete contribution among orchard clones (Kang 2000; Askew 1988), and most importantly, year×clone interactions for male and female flowering (Schmidting 1983). These factors, coupled with annual variation in the potential for pollen contamination (Pakkanen and Pulkkinen 1991; Caron and Leblanc 1992), could conceivably lead to drastically different genetic make-up among orchard seedlots of the same orchard. However, in literature, there are no reports quantifying this variation.

The objectives of this study are twofold: first, to test for differences in phenotypic variation in progeny from orchard crops with those of WSs, and second, to evaluate temporal variation in progeny performance from a number of seed orchard families (i.e., within and among seedlots produced in different years). To achieve these objectives, a common garden study was carried out using interior spruce

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