Development of a high-density Affymetrix Axiom genotyping array for genomic selection in Douglas-fir

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Abstract: We designed and tested a high-density Axiom genotyping array for Douglas-fir. We designed SNP assays for 55,776 potential SNPs that were discovered from transcriptome sequencing projects described by Muller et al. (2012) and Howe et al. (2013). Because the SNPs were derived from transcriptome sequences, the array targets SNPs in the expressed genes of the Douglas-fir genome. We tested the array on ~2,300 related and unrelated Coastal Douglas-fir trees (*Pseudotsuga menziesii* var. *menziesii*) from Oregon and Washington, and found that as many as ~26K SNPs could be reliably genotyped and were polymorphic, depending on the desired call rate. We worked with Affymetrix bioinformaticists to develop protocols to 'rescue' SNPs that did not pass the default Affymetrix quality control criteria (e.g., 97% call rate). Lowering the call rate threshold from 97% to 60% using the custom R scripts increased the number of successful SNPs from 16,177 to 24,192 in one population, and from 18,932 to 25,881 in another. We used a subset of 395 unrelated trees to calculate SNP population genetic statistics. Over a range of call rate thresholds (97% to 60%), the median call rate for SNPs in Hardy-Weinberg equilibrium ranged from 99.2% to 99.8%, and the median minor allele frequency ranged from 0.198 to 0.233. Based on a small number of samples, the successful SNPs also work well on Interior Douglas-fir (*P. menziesii* var. *glauca)*. The Axiom genotyping array will serve as an excellent foundation for studying the population genomics of Douglas-fir and for implementing genomic selection. We are currently using the array to test genomic selection in a three-generation breeding program for Coastal Douglas-fir.

Further information:

Howe, G.T., Yu, J.B., Knaus, B., Cronn, R., Kolpak, S., Dolan, P., Lorenz, W.W., and Dean, J.F.D. 2013. A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation. BMC Genomics 14.

Muller, T., Ensminger, I., and Schmid, K.J. 2012. A catalogue of putative unique transcripts from Douglas-fir (*Pseudotsuga menziesii*) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. BMC Genomics 13.

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