Estimation of Population Structure in the Coastal Douglas-fir Association Mapping Study

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The population structure has been thoroughly studied in a range-wide sample of ~1300 coastal Douglas-fir trees from Washington and Oregon that are used for association mapping between cold-hardiness and phenology related phenotypes and SNPs in the adaptive trait related candidate genes. All trees have been genotyped for 25 isozyme and 6 SSR markers using individual megagametophytes. Population structure analysis has been done separately for isozyme and SSR markers, as well as for both data sets combined using the standardized measure of population differentiation that takes high levels of within population variation for SSR markers into account. Results based on isozyme and SSR data sets have been compared and discussed. The relatively low level of population differentiation has been found for both markers, which should help to avoid false associations between phenotypes and genotypes for pooled samples in association mapping due to the demographic or population structure. However, clinal variation has been observed for several loci that could be explained by ecogeographic adaptation and possibly by influx of genes from interior Douglas-fir.