AgriSeq^{TM} Genotyping Panel for Quality Control in *Pinus taeda* Breeding

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The Cooperative Tree Improvement Program at North Carolina State University, in partnership with Thermo Fisher, developed an AgriSeq^{TM} targeted genotyping-by-sequencing panel for breeding in *Pinus taeda*. This panel contains 995 single nucleotide polymorphic markers selected from the Pita50K array across the genome using the linkage map (Lauer and Isik, 2021). This technology aims for a cost-efficient genotyping solution for routine applications in breeding. In this research, we present preliminary results of the AgriSeq genotyping for pedigree errors using the second-generation Atlantic Elite Population (ACE2). We first calculated genetic relationships between individuals using pedigree and AgriSeq markers. Then, for any given pair of individuals, we measured the difference between realized (G_{ij}) and expected (A_{ij}) genetic relationships, referred as the discrepancy. A significant discrepancy was defined when the standardized discrepancy exceeded three standard deviations. The frequency of the significant discrepancies among individuals were counted. Four trees displayed a noticeably high number of significant discrepancies than others in the population, which are likely caused by the errors in their pedigree. A principal components analysis (PCA) with genotypes from AgriSeq^{TM} was conducted. According to the PCs plot, trees within same full-sib family were clustered together. The same four individuals deviated away from their pedigree-based families, which showed agreement with the previous approach. We also investigated the utility of AgriSeq markers for parentage assignment with CERVUS. A reduced number of markers (50 to 500) were selected based on high minor allele frequency and high genotype call rate for parentage assignments. We compared the parental pair assignments from CERVUS with the pedigree and calculated the consistent assignment accuracy. The accuracy was lowest at 0.69 when 50 markers were used, and the accuracy reached 0.79 when 300 markers were used. In conclusion, the results are encouraging for operational breeding program and seed orchard/nursery quality control.