MULTIPLE PEDIGREES ALLOW CONSTRUCTION OF A DENSELY POPULATED REFERENCE LINKAGE MAP IN LOBLOLLY PINE (*PINUS TAEDA* L.)

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A linkage map remains an indispensible tool for QTL analysis, application of marker-assisted selection (MAS), comparative mapping, and genome assembly. In loblolly pine, several high-density linkage maps are presently available (e.g. Eckert et al. 2010), including a reference map (Echt et al. 2011) and a recently released high-density linkage map (Martinez-Garcia et al. 2013). Most of these maps are based on one or two pedigrees and their map-distance resolution is limited by the size of the mapping populations. A densely-populated, high-resolution reference map, integrating as many as possible of available genetic markers in loblolly pine, is essential not only for QTL mapping but also for a better genome assembly now that a genome sequence has been released.

An integrated, framework map was constructed using about 3,000 SNP and 472 other (SSR, ESTP, RFLP) markers and the following populations: (1) two three-generation outbred pedigrees (QTL and BASE) consisting of 674 progeny-clones; (2) a pseudo-backcross family, consisting of 490 progeny-clones; and (3) a family-structured population (CCLONEs), consisting of 34 parents and 948 progeny-clones. Our goal is to define and map approximately 50 framework loci per linkage group, separated by intervals of up to 5cM. The remaining unmapped loci will be assigned to the framework map bin intervals using the multiple families in CCLONEs. Results of this work and the utility of the final map for QTL analysis of traits will be discussed.