PINE-BREED: OPTIMAL MATE SELECTION IN *PINUS TAEDA*

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Loblolly pine (*Pinus taeda*) is the most important tree crop in the US, planted over 25 million acres in the south. The Tree Improvement Program at North Carolina State University manages the genetic improvement of Loblolly pine. Loblolly pine has a high genetic load and suffers greatly from inbreeding depression. It is a challenge to balance two important but contrasting goals of capturing as much genetic gain as possible and managing short- and long- term inbreeding. While methods and algorithms for breeding of several other types of trees have been improving, an efficient algorithm suited to this species remains elusive. Developing an algorithm to design mating that optimizes genetic gain whilst putting constraints on relatedness is imperative for loblolly pine breeding. Towards this goal, we have adopted mate selection algorithms commonly used in animal breeding. Pine-breed is an optimization algorithm developed that can utilize pedigree-based relationships to create optimal mating list for breeding. Modified second-order cone programming and differential evolution algorithms have been applied to create mating lists that can be realized to give maximum return of genetic gain in future progeny while minimizing the increase in average co-ancestry in the population. The completion of this study will see the development of a suite of software that is able to not only utilize genetic relationships from pedigree but also utilize genomic relationships derived from SNP markers. The framework and methods adapted for loblolly pine breeding have relevance to breeding of other monoecies species as well.