CONIFER TRANSLATIONAL GENOMICS NETWORK: BRINGING GENOMICS-BASED BREEDING TO APPLICATION

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The Conifer Translational Genomics Network (CTGN) consists of researchers from six institutions representing tree improvement cooperatives, genomics laboratories, and USDA Forest Service research projects responsible for developing most of the conifers planted in the United States. The goal of the CTGN project is to provide tree breeders with the genomic based tools to make tree breeding both more effective and efficient. The four-year project, funded by the USDA National Institute for Food and Agriculture (formerly CSREES) and the USDA Forest Service, seeks to leverage more than 50 years of population development conducted by the tree improvement cooperatives with the genomic and population genetics skills provided by researchers at those same institutions and UC Davis. Additional activities supported by the project include comprehensive education and outreach programs and the development of a genetic stock center for both southern pine and Douglas fir. While each institution has its own research emphasis, all are based on the use of genotyping large numbers of single nucleotide polymorphisms (SNPs) for substantial numbers of individuals. These data are being used to characterize genetic variation in managed populations, seek signatures of natural and artificial selection, and improve selection efficiency through marker-trait association and development of better analytical tools. Just as the CTGN was built on previous research, one of its chief accomplishments has been to provide impetus and tools for future projects, most notably the recently announced Pine Reference Sequence Project and the Southern Pine Climate Change Mitigation and Adaptation Project. A brief overview of significant progress emerging from the CTGN will be presented.