GENOMIC CHARACTERIZATION OF GROWTH AND DROUGHT TOLERANCE IN EAST TEXAS LOBLOLLY PINE

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The loblolly pine populations of east Texas are at the species' warmest range limit. Under future climate warming scenarios the health and productivity of these populations is expected to be negatively impacted. Forestry in east Texas generates billions of dollars in annual revenue and even small negative impacts on annual productivity will have substantial short and long-term economic consequences. Therefore, our research has two primary objectives in context of the east Texas loblolly pine breeding programs. Firstly, to assess the contemporary phenotypic and genomic variation in growth and drought-related traits, and secondly, to identify productive families or trees that are also candidates for increased drought tolerance and future breeding to maintain or increase timber yields. Our approach uses the growth data of 733 trees from 50 maternal families growing in a five-year old progeny trial near Livingston, TX. From these trees we have obtained stable carbon isotope ratios ($\delta^{13}C$) and nitrogen concentrations, as traits with established relationships to water use efficiency and photosynthetic capacity. In combination with these phenotypic data we are using genotypes from the recently developed Thermo Fisher Axiom™ Pita50K loblolly pine array, and 5000 custom targeted genotype-by-sequencing (GBS) SNPs from drought-related transcripts identified in our previous research. For the GBS we are working with Tecan Genomics to develop a repeatable protocol for using their multiplexed Allegro library preparation platform that has potential to substantially reduce the cost of targeted GBS in conifers. Our preliminary results indicate there is significant variation among families for growth and $\delta^{13}C$, and that array genotyping has been highly successful, yielding ~32,000 high-quality SNPs. More detailed quantitative genetic and association genetic analyses to dissect variation among families and individuals are forthcoming.