FISHING FOR A CYTO-MOLECULAR MAP OF CHESTNUT (*CASTANEA* SPP.) USING GENETICALLY AND PHYSICALLY MAPPED BACS

Nurul Islam-Faridi[1], M.A. Majid, T. Zhebentyayev, L.L. Georgi, M.E. Staton, F.V. Hebard, P.H. Sisco, **C.D. Nelson**

[1]USDA Forest Service, Southern Research Station, Southern Institute of Forest Genetics, Forest Tree Molecular Cytogenetics Laboratory, College Station, TX

The American chestnut (*Castanea dentata*, $2n = 2x = 24$), once thriving on 200 million acres in eastern North America and known as the "King of the Forest", was eliminated as a foundation species by chestnut blight (caused by *Cryphonectria parasitica*) during the first half of the 20th century. Chinese chestnut (*C. mollissima*) is relatively resistant to chestnut blight and efforts are being made to transfer this variation into American chestnut through backcross breeding and genetic engineering. To facilitate both of these improvement approaches, the Chinese chestnut genome has been mapped and is being sequenced. In general, plant genomes contain large amounts of repetitive DNA causing difficulties in genetic mapping, gene discovery, and genome sequence assembly. Fluorescence *in situ* hybridization (FISH) is an important technique for assigning markers and/or gene sequences to specific chromosomes. To overcome some of the mapping and sequencing limitations we are using genetically and physically mapped BAC clones from all 12 linkage groups in FISH to directly locate their positions to respective chromosomes. The resulting cyto-molecular map will be valuable in assisting the assembly of the sequence contigs into scaffolds that will provide a draft genome for chestnut. For example, one results show that BAC contig 3296 on linkage group E is located distal to BAC contig 1231, not proximal as it was positioned on the integrated genetic/physical map. Details of our BAC FISH results will be presented, and discussed in the context of genome analysis and tree improvement.