

## GENOMIC RESOURCE DEVELOPMENT FROM LOW COVERAGE WHOLE GENOME SEQUENCING OF TEN HARDWOOD TREE SPECIES

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Low coverage whole genome sequencing is a viable and inexpensive technique to produce an initial set of genomic resources for under-researched species. For this project ten hardwood tree species were sequenced on a single lane of Illumina HiSeq: black cherry (*Prunus serotina*), black gum (*Nyssa sylvatica*), black walnut (*Juglans nigra*), green ash (*Fraxinus pennsylvanica*), honeylocust (*Gleditsia triacanthos*), red bay (*Persea borbonia*), sugar maple (*Acer saccharinum*), sweetgum (*Liquidambar styraciflua*), white ash (*Fraxinus americana*), and white oak (*Quercus alba*). The species chosen have little or no previous genomic data, are under biotic and abiotic stress, and/or have significant economic impact in the United States. The amount of sequence recovered for each species was variable, and genome coverage ranged from .4X to 4.7X. Unique microsatellite loci were identified for all ten species and primers designed to enable mapping and diversity studies. A set of 96 SSR primer pairs for eight of the ten species were tested for amplification in a minimum of 6 individuals with varying levels of success. The genomic sequence data has been further analyzed to characterize the conserved and novel repeat sequences in each genome as well as overall sequence similarity to reference plant genomes. All sequence data and analysis will be made publicly available on the Hardwoods Genomics Website ([hardwoodgenomics.org](http://hardwoodgenomics.org)).