SEARCHING, DOWNLOADING AND ANALYZING TREE GENETIC AND GENOMIC DATA WITH THE HARDWOOD GENOMICS WEBSITE

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The Hardwood Genomics Website (HWG) provides access to genetic and genomic data from woody plant species, including many ecologically important and threatened forest trees such as American chestnut, green ash, black walnut, and American beech. The site has tree genomes and transcriptomes that are not housed elsewhere or lack publicly available annotation. It provides searchable annotation for all genes and transcripts, including BLAST results to curated plant protein databases, protein domains, and gene ontology terms. To further characterize gene sequences, HWG houses expression values from high throughput RNASeq studies. We identify simple sequence repeats (SSRs) and flanking primers from genome and gene sequences and make these available on HWG for use as genetic markers. Where available, HWG also provides access to published microsatellite markers. To facilitate access to these datasets, we have a number of tools for researchers, including a powerful keyword search, JBrowse, and BLAST. Most recently we have added access to bioinformatics analysis workflows powered by Galaxy software. Users can select from a number of common analysis types, including mapping DNA or RNA reads, performing differential gene expression analysis, calling genetic variants from reads, etc. A user can upload their own data for analysis, select HWG site data, or use both as input to a workflow. To meet the growing need for forest tree breeding programs and genetic research, we are beginning a new effort to add additional genetic markers, genetic maps including association and QTL studies, and high throughput genotyping and phenotyping data. The site will also be adding descriptions of physical collections such as germplasm or mapping populations with contact information for the maintainer. The HWG is a growing resource for tree scientists, and we welcome feedback, data submissions, or new partnerships to continue site development. HWG is supported by the National Science Foundation (NSF) awards numbers 1443040 and 1444573.

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