

## Dendrome Project and TreeGenes Database Resources

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The Dendrome project (<http://dendrome.ucdavis.edu>) and associated TreeGenes database (<http://dendrome.ucdavis.edu/treegenes>) serves the forest genetics research community through a curated and integrated web-based relational database. There are currently ten main search modules or user access points within this PostgreSQL database. These access points allow users to navigate logically through related data types. Sample Tracking contains geographic tree and DNA extraction information. The Sequencing and Primers module contains sequences from the resequencing pipelines including alignments and analysis methods. The Species module holds relevant taxonomy information and Colleagues contains information on laboratories and individuals. The Comparative Map module implements Cmap to store and view genetic maps, map relations, and molecular markers. The Literature module contains an annotated and curated set of publications related to conifer genomics. The EST module stores sequence and annotation information and ties into an automated pipeline that allows submission of trace files for full processing and Genbank submission. Recent developments have focused on increasing data content in terms of genotype and phenotype modules, functional annotations, data retrieval, and visualization tools. A new interface within TreeGenes, DiversiTree provides a desktop type environment to facilitate annotation-based searches against data generated from large-scale resequencing projects. TreeGenes was developed to provide a centralized web database with bioinformatic tools to support data storage, analysis, and exchange.

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