

TreeGenes

A Comprehensive Resource for Forest Tree Genomics



dendrome.ucdavis.edu

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TreeGenes Database: History

dendrome.ucdavis.edu

- Began as the Dendrome project (USDA funded initiative) in 1993 to hold forest tree genetic maps and associated markers



TreeGenes Database: History

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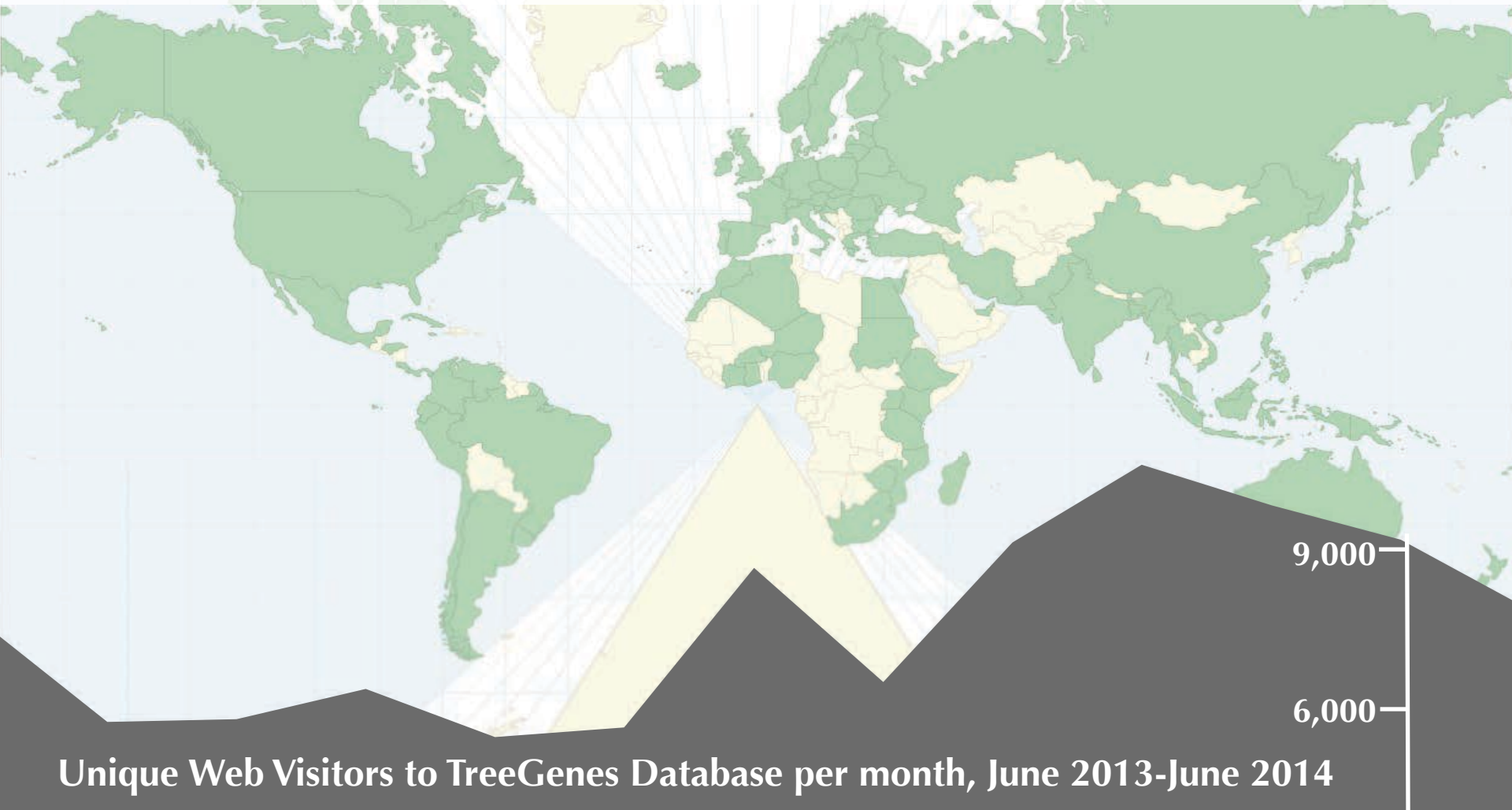
- Began as the Dendrome project (USDA funded initiative) in 1993 to hold forest tree genetic maps and associated markers
- Expanded to other data types
 - Sequence
 - Resequencing, Large-Scale Genotyping, Transcriptomics/Expression
 - Full Genome Sequences
 - Analysis and Visualization Tools
 - Ability for users to mine the data
 - Resources for the user community
 - Literature, Colleagues



TreeGenes Database: Users

dendrome.ucdavis.edu

2,060 users from 849 organizations in 94 countries



TreeGenes Database: Species

dendrome.ucdavis.edu



- 1,290 species from 101 genera
 - At least one genetic artifact from each species
 - Conifers but is also inclusive of all forest trees
- Full genome sequence: 13 species
- Transcriptome/Expression resources:
3,920,817 sequences from 263 species
- 106 genetic maps from 35 species

TreeGenes Database: Data Sources

dendrome.ucdavis.edu

Automated

User submissions

TreeGenes Database: Data Sources

dendrome.ucdavis.edu

Automated

- NCBI (primary repositories)
 - Protein, EST, cDNA, TSA, Unigene databases
 - Introduced to TreeGenes with added value
 - Information should be sent to primary dbs first
- Literature
 - Web of Science, PubMed



TreeGenes Database: Data Sources

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User submissions

- Internal projects or collaborations (day one)
- Submissions of data post-analysis at publication time

TreeGenes Database: Data Sources

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User submissions (Software with full front-end and back-end support)

Laboratory Information Management System

Sequence, Genotype, Phenotype, Environmental Information

Track barcoded samples from collection through sequencing



FTGSC

- FTGSC
- Sample Search
- Order Form
- Population Sets
- Phenotypes
- Ecological Site Descriptors
- Sample Submission
- Protocols

Sample Submission Form

Please fill out and submit the form below. After the form has been submitted, you will receive shipping instructions along with a Shipping Receipt which must be included with your shipment. Depending on how you fill out the form below, you may or may not receive barcodes for your samples.

Select your institution or company name:

If not listed, register your lab here.

Contact information:

Principal Investigator's Name:

Principal Investigator's E-mail:

Project Coordinator's Name:

Project Coordinator's E-mail:

Project Coordinator's Phone:

Shipping Address:
(for parcel packages)

What is the name of this population set?

Please enter a name for the set of samples being shipped to the FTGSC. For example, a population set may be name "Loblolly QTL Study - Set 1" or "Smith Lab - 2011 Lignin Study Samples". The name entered here will be used to describe your population set from within the FTGSC tracking system.

Please describe the population set and the research it has been used for.

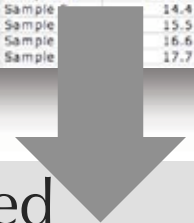
Please enter a description for your population set and provide information about the research studies



Tree ID	Sample Barcode	S. Type	Tree Description
tree007	BC0001	Needle	Tall loblolly tree
tree008	BC0002	Needle	Tall loblolly tree
tree009	BC0003	Needle	Tall loblolly tree
tree010	BC0004	Needle	Tall loblolly tree
tree011	BC0005	Needle	NULL
tree012	BC0006	Needle	Tall loblolly tree
tree013	BC0007	Needle	Tall loblolly tree
tree014	BC0008	Needle	Tall loblolly tree
tree015	BC0009	Needle	Tall loblolly tree
tree016	BC0010	Needle	Tall loblolly tree
tree017	BC0011	Needle	Tall loblolly tree
tree018	BC0012	Needle	Tall loblolly tree
tree019	BC0013	Needle	Tall loblolly tree
tree020	BC0014	Needle	Tall loblolly tree
tree021	BC0015	Needle	NULL
tree022	BC0016	Needle	Tall loblolly tree
tree023	BC0017	Needle	Tall loblolly tree
tree024	BC0018	Needle	Tall loblolly tree
tree025	BC0019	Needle	Tall loblolly tree
tree026	BC0020	Needle	Tall loblolly tree
tree027	BC0021	Needle	Tall loblolly tree
tree028	BC0022	Needle	Tall loblolly tree
tree029	BC0023	Needle	Tall loblolly tree

Upload phenotype / environmental data

8	N30	17.477	W97	44.318	Sample 4		13.3	102
9	N30	17.477	W97	44.319	Sample 5	NULL	NULL	102
10	N30	17.477	W97	44.320	Sample 6		15.5	400
11	N30	17.477	W97	44.321	Sample 7		16.6	999
12	N30	17.477	W97	44.322	Sample 8		17.7	998
13	N30	17.477	W97	44.323	Sample 9		55.5	100
14	N30	17.477	W97	44.324	Sample 10		99.9	858
15	N30	17.477	W97	44.325	Sample 11		14.4	103
16	N30	17.477	W97	44.326	Sample 12		15.5	103
17	N30	17.477	W97	44.327	Sample 13		16.6	104
18	N30	17.477	W97	44.328	Sample 14		17.7	104
19	N30	17.477	W97	44.329	Sample 15	NULL	NULL	676
20	N30	17.477	W97	44.330	Sample 16		103.4	676
21	N30	17.477	W97	44.331	Sample 17		124.1	678
22	N30	17.477	W97	44.332	Sample 18		144.9	680
23	N30	17.477	W97	44.333	Sample 19		165.7	681
24	N30	17.477	W97	44.334	Sample 20		14.4	103
25	N30	17.477	W97	44.335	Sample 21		15.5	103
26	N30	17.477	W97	44.336	Sample 22		16.6	104
27	N30	17.477	W97	44.337	Sample 23		17.7	104



Data can be integrated into TreeGenes in real time or at project end

TreeGenes Database: Data Sources

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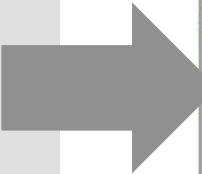
User submissions: external
Most submissions from TGG

Submit genetic maps or population
study data

Obtain TGDR accession number!

This screenshot shows the 'Add New Genetic Map' section of the TreeGenes Data Repository submission form. It includes fields for 'Genetic Data' (a dropdown menu), 'Phenotype Data' (a dropdown menu), and 'Environmental Data' (a dropdown menu). There are also checkboxes for 'Add New Genetic Map' and 'Add New Phenotype Data'. The form is titled 'TreeGenes Data Repository' and 'Add New Genetic Map'.

This screenshot shows the 'Add Supplemental Data' section of the TreeGenes Data Repository submission form. It includes fields for 'Supplemental Data' (a dropdown menu), 'Genetic Map' (a dropdown menu), and 'Phenotype Data' (a dropdown menu). There are also checkboxes for 'Add New Supplemental Data', 'Add New Genetic Map', and 'Add New Phenotype Data'. The form is titled 'TreeGenes Data Repository' and 'Add Supplemental Data'.



TreeGenes Data Repository					
A listing of data submissions is displayed below. To submit data to TreeGenes, click here.					
Date	Accession	Paper Title	Species	Data Statistics	Data Files
8/5/2011	TGDR001	Association genetics of traits controlling lignin and cellulose biosynthesis in black cottonwood (<i>Populus trichocarpa</i> , Salicaceae) secondary xylem.	<i>Populus trichocarpa</i>	Total Sites: 1 Total Samples: 480 Total Genotypes: 419520 Total AFLP Markers: 0 Total RAPD Markers: 0 Total cpSSR Markers: 0 Total SSR Markers: 0 Total Phenotypes: 1344 Total Environmental (per sample): 0 Total Environmental (per site): 0	Covariate Data (Population Structure) Genotype Data (SNP) GPS Data Haplotype Data Phenotype Data Phenotype Definitions
9/25/2012	TGDR002	Astonishingly low genetic variation in <i>Quercus acutissima</i> , an important tree species in Satoyama, a traditional Japanese rural forest and agricultural landscape, revealed by chloroplast microsatellite markers	<i>Quercus acutissima</i>	Total Sites: 59 Total Samples: 2152 Total Genotypes: 12912 Total AFLP Markers: 0 Total RAPD Markers: 0 Total SNP Markers: 6 Total cpSSR Markers: 0 Total SSR Markers: 0 Total Phenotypes: 0 Total Environmental (per sample): 0 Total Environmental (per site): 0	Genotype Data (cpSSR) GPS Data Haplotype Data Supplemental Data
11/5/2012	TGDR003	Extensive selfing in an endangered population of <i>Pinus parviflora</i> var. <i>parviflora</i> (Pinaceae) in the Boso Hills, Japan	<i>Pinus parviflora</i>	Total Sites: 2 Total Samples: 116 Total Genotypes: 464 Total AFLP Markers: 0 Total RAPD Markers: 0 Total SNP Markers: 0 Total cpSSR Markers: 0 Total SSR Markers: 4 Total Phenotypes: 0 Total Environmental (per sample): 0 Total Environmental (per site): 0	Genotype Data (SSR) GPS Data Supplemental Data Supplemental Data Supplemental Data Supplemental Data
11/14/2012	TGDR004	Pollen dispersal and fine-scale spatial genetic structure of <i>Dryobalanops lanceolata</i> in a Bornean rain forest	<i>Dryobalanops lanceolata</i>	Total Sites: 1 Total Samples: 858 Total Genotypes: 13728 Total AFLP Markers: 0 Total RAPD Markers: 0 Total SNP Markers: 0 Total cpSSR Markers: 0	Environmental Metric Data Environmental Metric Definitions Genotype Data (SSR)

TreeGenes Database: Data Access

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Interfaces

- Existing viewers
- Custom development

TreeGenes Database: Interfaces

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Comparative mapping



Feature Search

Search On:

Search For:

Separate multiple names with commas or whitespace. Use "" or "%" for wildcards. To find features with spaces in the name, surround the name in double quotes, e.g., "abc 123."

Restrict species:
Acacia mangium
Castanea sativa mill
Corylus avellana
Cryptomeria japonica

Restrict feature types:
AFLP
CAPS
Centromere
Clone

Map Search

Published:

Ref. Species:

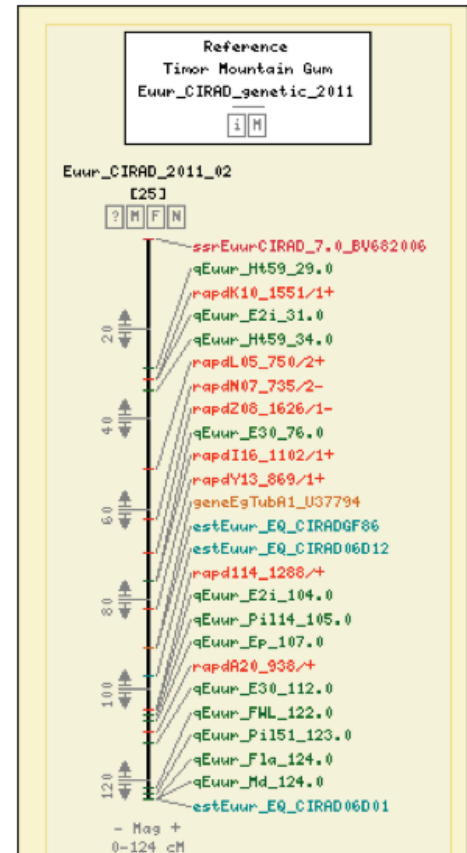
Ref. Set:

Name (optional):

Min # of Related Maps:

Items 1 to 11 of 11.

Map Name	Related Maps	Related Maps per unit	Correspondences	Correspondences per unit	Start	Stop	SSR	
							total	per unit
Euca_UFV_2014_1 (spider)	0	0/unit	0	0/unit	0.00	165.80	12	72.38/K
Euca_UFV_2014_10 (spider)	0	0/unit	0	0/unit	0.00	159.50	8	50.16/K
Euca_UFV_2014_11 (spider)	0	0/unit	0	0/unit	0.00	64.60	6	92.88/K
Euca_UFV_2014_2 (spider)	0	0/unit	0	0/unit	0.00	65.00	9	0.14/unit
Euca_UFV_2014_3 (spider)	0	0/unit	0	0/unit	0.00	14.80	3	0.20/unit
Euca_UFV_2014_4 (spider)	0	0/unit	0	0/unit	0.00	70.30	8	0.11/unit
Euca_UFV_2014_5 (spider)	0	0/unit	0	0/unit	0.00	53.20	3	56.39/K
Euca_UFV_2014_6 (spider)	0	0/unit	0	0/unit	0.00	144.90	8	55.21/K
Euca_UFV_2014_7 (spider)	0	0/unit	0	0/unit	0.00	185.60	5	26.94/K
Euca_UFV_2014_8 (spider)	0	0/unit	0	0/unit	0.00	67.20	8	0.12/unit
Euca_UFV_2014_9 (spider)	0	0/unit	0	0/unit	0.00	53.70	5	93.11/K



Feature Types:

— EST
— GENE
— QTL
— RAPD
— SSR

Menu Symbols:

[i] Map Set Info

[?] Map Details

[M] Matrix View

TreeGenes Database: Interfaces

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Genome browsing & annotation



TreeGenes Database: Interfaces

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- Bulk retrieval of resequencing data, genotypes, and phenotypes

Searches

+ Documentation ?

+ EST (GenBank) ?

+ Contig ?

+ Amplicon ?

Amplicon Name:
(Ex: 0_2576_02)

BLAST GenBank
Accession:
(Ex: XP_002285663)

BLAST GenBank
GI:
(Ex: 225459069)

BLAST Hit:
(Ex: ATPase)

GO Term:
(Ex: Heat shock)

InterPro Term:
(Ex: Lipid)

Enzyme:
(Ex: ATP)

Results: 86

+ Tree / Phenotypes ?

+ Sequence Alignments ?

+ SNP ?

rs1t_amplicon_|||||lipid

ID	Amplicon Name	EST Contig Name	InterPro Term	Has Alignments	Has SNPs
3080	0_14784_01	C2 calcium/lipid-binding domain, CaLB	0_14784	Yes	Yes
5737	0_2632_01	Plastid lipid-associated protein/fibrillin conserved domain	0_2632	Yes	Yes
6820	0_4936_01	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor	0_4936	Yes	Yes
6820	0_4936_01	Plant lipid transfer protein/hydrophobic protein, helical domain	0_4936	Yes	Yes
12903	2_9857_02	Plant lipid transfer protein/hydrophobic protein, helical domain	2_9857	Yes	Yes

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[cartogratree](#) [treegenes](#) [dendrome phone](#)



TreeGenes Database: Interfaces

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DiversiTree Download results



Searches

+ Documentation ?

+ EST (GenBank) ?

+ Contig ?

FASTA Sequence: (Ex: GCATAG...)

Contig Name: (Ex: 0_8156)

BLAST GenBank Accession: (Ex: CB125984)

BLAST GenBank GI: (Ex: 270238748)

BLAST Hit: (Ex: p-type ATPase)

GO Term: copper ion binding (Ex: Heat shock)

InterPro Term: (Ex: Lipid)

Enzyme: (Ex: ATP)

Mark all species of interest:
Select: ALL | NONE

ID	Contig Name	Species	GO Term	Has Alignments	Has SNPs
1697	0_11582	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
8140	0_17607	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
8866	0_1829	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
9909	0_2414	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
10957	0_3937	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
11256	0_4342	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
13739	0_7878	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
14065	0_8291	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
14200	0_8419	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
14320	0_8531	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
15122	0_9288	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
15266	0_9423	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
22822	2_1343	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
30763	2_8946	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg47012	CL1367Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg48716	CL2662Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg49217	CL3147Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg50235	CL4447Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg50336	CL4575Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg50472	CL4726Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes
cg50688	CL569Contig1	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes

sswap.info view selected download list

Select	Species
<input checked="" type="checkbox"/>	Abies alba
<input checked="" type="checkbox"/>	Abies concolor
<input checked="" type="checkbox"/>	Calocedrus decurrens
<input checked="" type="checkbox"/>	Cedrus deodara
<input checked="" type="checkbox"/>	Cryptomeria japonica

cartogratree treegenes dendrome phone



TreeGenes Database: Interfaces

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Download results or pipe to CartograTree via SSWAP
(Simple Semantic Web Architecture Protocol)

Searches

+ Documentation ?

+ EST (GenBank) ?

+ Contig ?

FASTA Sequence:

(Ex: GCATAG...)

Contig Name:

(Ex: 0_8156)

BLAST GenBank Accession:

(Ex: CB125984)

BLAST GenBank GI:

(Ex: 270238748)

BLAST Hit:

(Ex: p-type ATPase)

GO Term:

(Ex: Heat shock)

InterPro Term:

(Ex: Lipid)

Enzyme:

(Ex: ATP)

Mark all species of interest:
Select: ALL | NONE

☒ Abies alba

☒ Abies concolor

☒ Calocedrus decurrens

☒ Cedrus deodara

☒ Cryptomeria japonica

rsst_contig_||||copper ion binding|||Abal,Abco,Cade,Cede,Crja,Faga,Jur

ID	Contig_Name	Species
1697	0_11582	Pinus taeda (Loblolly Pine)
8140	0_17607	Pinus taeda (Loblolly Pine)
8866	0_1829	Pinus taeda (Loblolly Pine)
9909	0_2414	Pinus taeda (Loblolly Pine)
10957	0_3937	Pinus taeda (Loblolly Pine)
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30763	2_8946	Pinus taeda (Loblolly Pine)
cg47012	CL1367Contig1	Pinus taeda (Loblolly Pine)
cg48716	CL2662Contig1	Pinus taeda (Loblolly Pine)
cg49217	CL3147Contig1	Pinus taeda (Loblolly Pine)
cg50235	CL4447Contig1	Pinus taeda (Loblolly Pine)
cg50336	CL4575Contig1	Pinus taeda (Loblolly Pine)
cg50472	CL4726Contig1	Pinus taeda (Loblolly Pine)
cg50688	CL569Contig1	Pinus taeda (Loblolly Pine)

sswap.info

cartogratree treegenes dendrome phone

http://sswap.info/pc/4d43d44-60b1-4c65-8ba0-a84d69b55a07

sswap.info beta

Simple Semantic Web Architecture and Protocol

New pipeline

Input Data Set

Display Data: <http://sswap.info/pc/ctg?token=4ce1fc5a-128e-48fa-9693-4dc7ea771869>

Data Set URI: <http://sswap.dendrome.ucdavis.edu/resources/contigService/ContigService>

Produced by:

	Yes	Yes
copper ion binding	Yes	Yes
copper ion binding	Yes	Yes
copper ion binding	Yes	Yes
copper ion binding	Yes	Yes

sswap.info view selected download list

TreeGenes Database: Interfaces

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Map Display

Ctrl+Click or Cmd+Click for multiple selections

All

▶ Published Studies

▶ Taxa

▶ Environmental

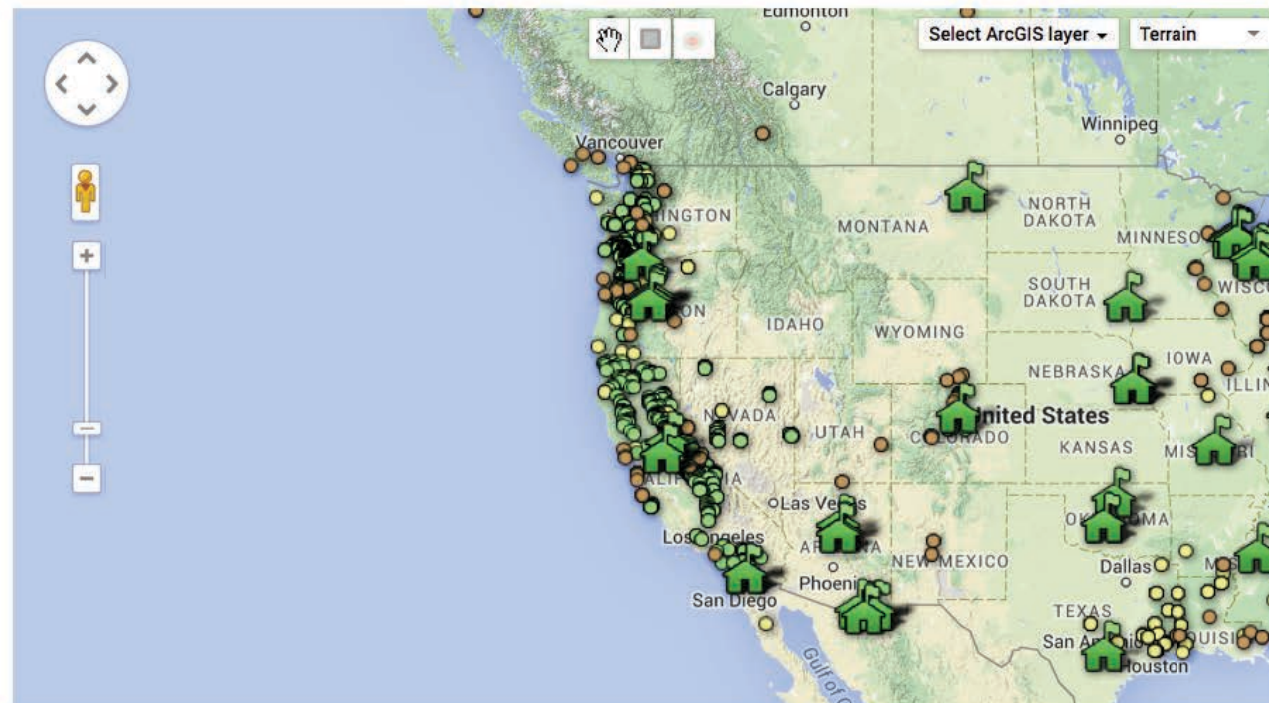
▶ Phenotypes

Filter Map Display

☐ Sequenced (83)

☐ Genotyped (2940)

☐ Phenotyped (9385)



- Providing context to geo-referenced data
- Originated from Tree Biology Working Group through iPlant

TreeGenes Database: Interfaces

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Map Display

Search for a tree id

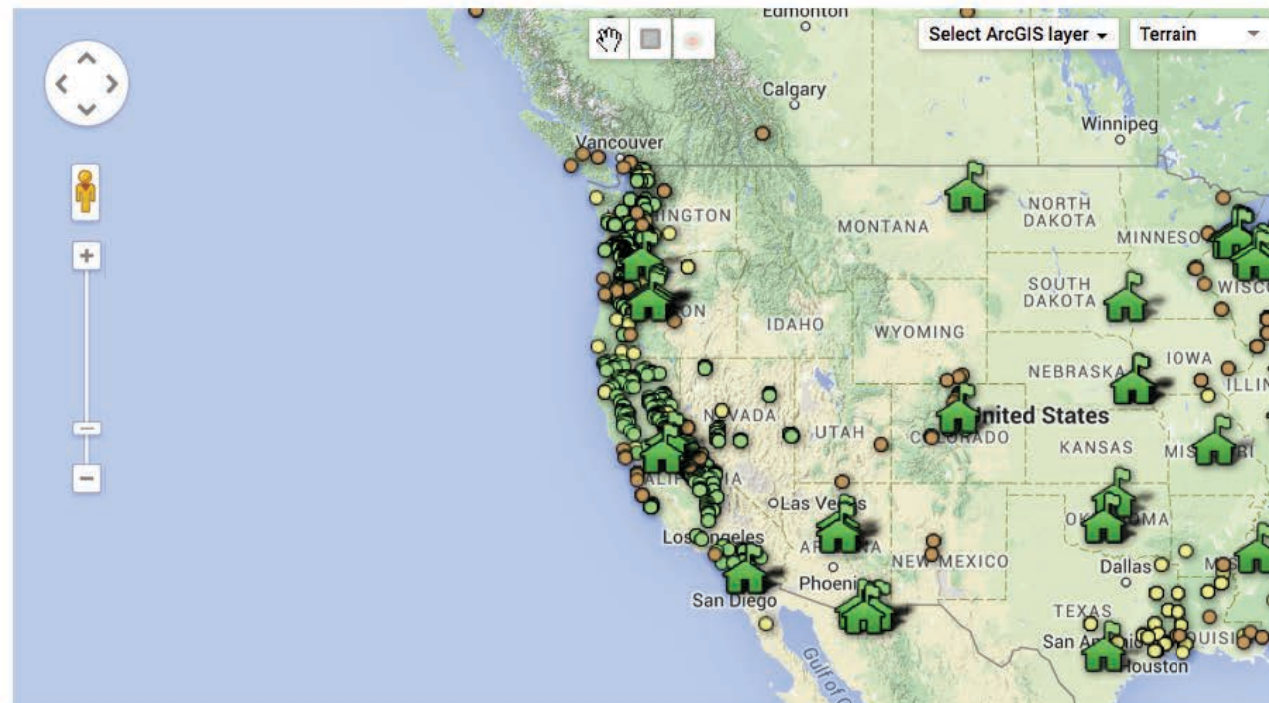
Ctrl+Click or Cmd+Click for multiple selections

All

- Published Studies
- Taxa
- Environmental
- Phenotypes

Filter Map Display

- ☐ Sequenced (83)
- ☐ Genotyped (2940)
- ☐ Phenotyped (9385)



- Data from TreeGenes, WorldClim, Ameriflux, TRY-db
- Google fusion tables & Google maps

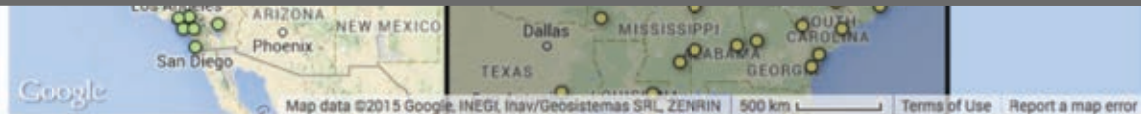
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☐ Exact (15)
☐ Approximate (68)



Analyze the data

Map selection

Amplicons



File

Edit

View

Tools

Discover pipelines at SSWAP

<input checked="" type="checkbox"/>	ID	Amplicon ID	Top Blast Description (BLAST nr)	Species-Specific BLASTs	GO Annotations	Interpro Annotations	PFAM Annotations
<input checked="" type="checkbox"/>	1	0_10054_01	"NAC domain protein: IPR003441 [Po...	"NAC domain protein: IPR00...	"GO:0003676 nucl...-999		-999
<input checked="" type="checkbox"/>	2	0_10706_01	"uninformative (1.90E-27) (unspecified)"	"uninformative (1.90E-27) (u...	"GO:0009536 plas...-999		-999
<input checked="" type="checkbox"/>	3	0_11090_01	"PREDICTED: protein OBERON 4-like...	"PREDICTED: protein OBER...	-999	"IPR004082 Protein of u...-999	
<input checked="" type="checkbox"/>	4	0_11270_01	"PREDICTED: probably inactive leuci...	"PREDICTED: probably inact...	"GO:0016740 tran...-999		-999
<input checked="" type="checkbox"/>	5	0_11389_01	"PREDICTED: protein phosphatase 2...	"PREDICTED: protein phosp...	"GO:0001932 reg...-999		-999
<input checked="" type="checkbox"/>	6	0_11411_01	"PREDICTED: galactose oxidase-like	"PREDICTED: galactose oxi...	-999	"IPR013783 Immunop...	"PF09118 Domain o...

- Retrieve genotype, phenotype, environmental, and sequence data
- Further analysis (TASSEL, MUSCLE) via SSWAP

TreeGenes Database: Current Development

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Genome Sequence Annotation Server

– Can handle large, complex genomes



The screenshot shows the GenSAS web interface. At the top is a navigation bar with tabs: Project, Sequences, Files, Repeats, Masking, Genes, Consensus, Reflow, Functional, Annotate, and Publish. The 'Annotate' tab is currently selected. On the right, the user is logged in as 'Hello GenSASuser' with an account page link, site home link, and a log out button. The current project is 'AT_120114'.

Annotations on the interface:

- A**: Points to the 'Project' button in the top navigation bar.
- B**: Points to the 'Job Queue' section on the right, which contains two tables: 'Repeats & Masking' and 'Genes & Other Predictions'.
- C**: Points to the 'Welcome' tab in the left sidebar.

Instructions on the interface:

- Blue arrow: Tabs will appear here to provide the content needed for each stage. Some tabs can be closed and re-opened later but others will always remain. The tabs will provide instructions for each workflow stage.
- Orange arrow: Click the buttons above to move through the annotation workflow. As you complete a stage the next button becomes available. Click the **Project** button to begin.
- Green arrow: Click the **Job Queue** to view the analysis jobs for the project. Click the **Browsers** tab to view the predicted features aligned to the genomic sequence. Click the **Sharing** tab to share the project with other GenSAS users. Click the **Manage Sequences** tab to manage the uploaded sequences.

GenSAS logo and text: "Welcome to Genome Sequence Annotation Server !"

Job Name	Status
Masked Consensus	Completed
RepeatMasker-at	Completed
RepeatMasker-rebase	Completed
RepeatModeler	Completed

Job Name	Status
Augustus	Completed
BLAST (nucleotide)-cRNA	Completed
BLAST (nucleotide)-EST	Completed
BLAST (nucleotide)-refseqPlant	Completed
BLAST (proteins)-refseqplant	Completed
BLAST (proteins)-spmot	Completed
BLAST (proteins)-trsmbl	Completed
BLAT-cDNA	Completed
BLAT-EST	Completed

Bottom navigation: Browsers, Sharing, Manage Sequences

TreeGenes Database: Current Development

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– Save work, upload modifications for approval

P1153

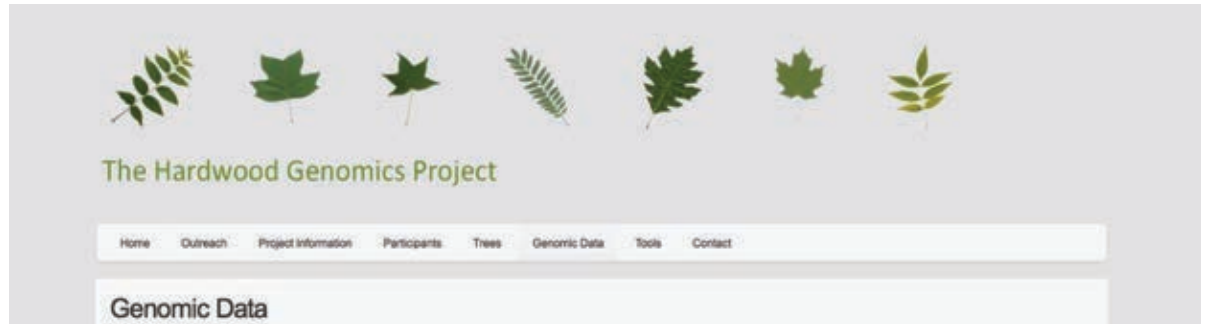


TreeGenes Database: Future Development

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Tripal Galaxy



TreeGenes Database: Future Development

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Tripal Galaxy

– Tripal

- Frontend & backend open source database solution
- CHADO: database schema from GMOD
- Drupal: open source web development platform
- TreeGenes will transition into using Tripal to ease data transfer

TreeGenes Database: Future Development

dendrome.ucdavis.edu



Tripal Galaxy

– Galaxy

- Workflow & data analysis platform
- Build multi-step analysis pipeline
- Tripal Galaxy will develop modules for analysis with Galaxy



TreeGenes Database: Future Development

dendrome.ucdavis.edu



Tripal Galaxy

- Work with other databases
- Improve data integration, data transfer
- Pull datasets easily from other datasets & sources on the web for analysis

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TreeGenes Database

