

TreeGenes and CartograTree

Tools for Forest Tree Genomics



dendrome.ucdavis.edu

Emily Grau
Department of Plant Sciences
University of California, Davis

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: Users

dendrome.ucdavis.edu

2,060 users from 849 organizations in 94 countries



Unique Web Visitors to TreeGenes Database per month, June 2013-June 2014

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



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TreeGenes Database: Data Sources

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User submissions

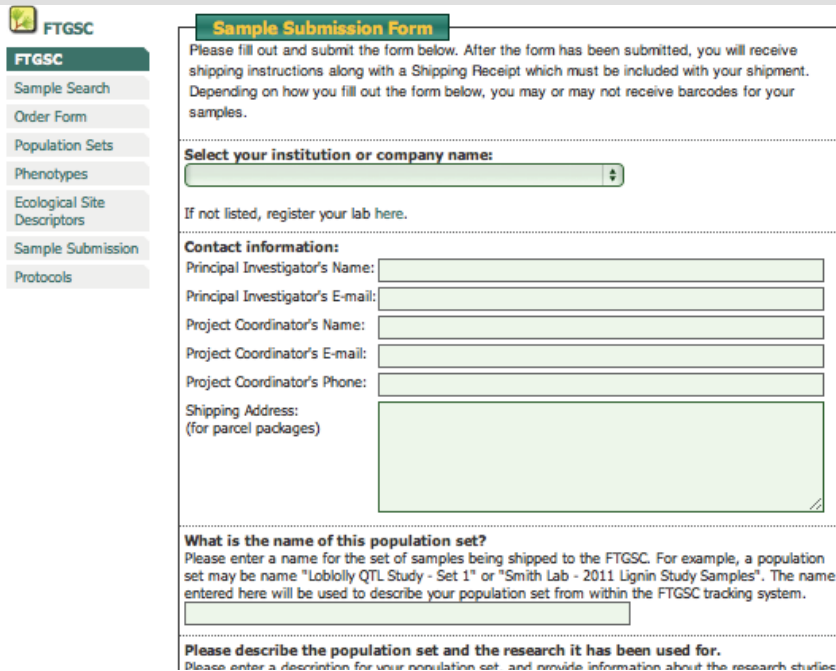
- Internal projects or collaborations (day one)
- Submissions of data post-analysis at publication time

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

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:

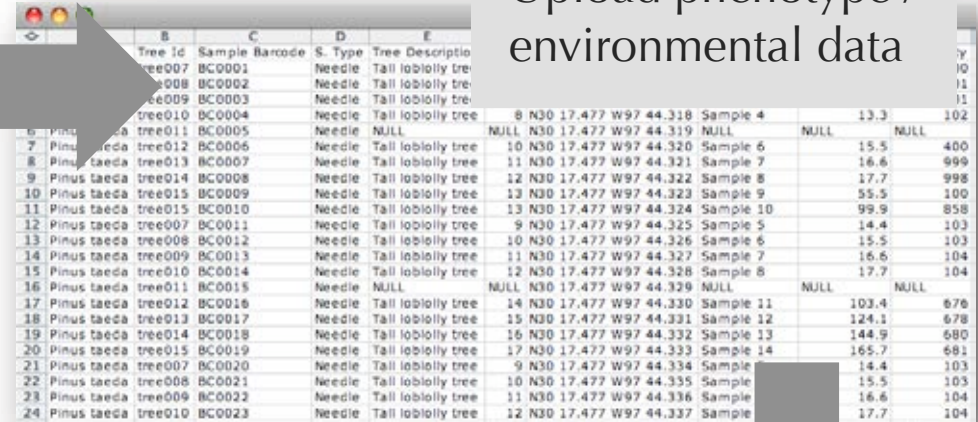
Project Coordinator's E-mail:

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	8 N30 17.477 W97 44.318	Sample 4		13.3		102
tree011	BC0005	Needle	NULL	NULL N30 17.477 W97 44.319	NULL		NULL	NULL	
tree012	BC0006	Needle	Tall loblolly tree	10 N30 17.477 W97 44.320	Sample 6		15.5		400
tree013	BC0007	Needle	Tall loblolly tree	11 N30 17.477 W97 44.321	Sample 7		16.6		999
tree014	BC0008	Needle	Tall loblolly tree	12 N30 17.477 W97 44.322	Sample 8		17.7		998
tree015	BC0009	Needle	Tall loblolly tree	13 N30 17.477 W97 44.323	Sample 9		55.5		100
tree015	BC0010	Needle	Tall loblolly tree	13 N30 17.477 W97 44.324	Sample 10		99.9		858
tree007	BC0011	Needle	Tall loblolly tree	9 N30 17.477 W97 44.325	Sample 5		14.4		103
tree008	BC0012	Needle	Tall loblolly tree	10 N30 17.477 W97 44.326	Sample 6		15.5		103
tree009	BC0013	Needle	Tall loblolly tree	11 N30 17.477 W97 44.327	Sample 7		16.6		104
tree010	BC0014	Needle	Tall loblolly tree	12 N30 17.477 W97 44.328	Sample 8		17.7		104
tree011	BC0015	Needle	NULL	NULL N30 17.477 W97 44.329	NULL		NULL	NULL	
tree012	BC0016	Needle	Tall loblolly tree	14 N30 17.477 W97 44.330	Sample 11		103.4		676
tree013	BC0017	Needle	Tall loblolly tree	15 N30 17.477 W97 44.331	Sample 12		124.1		678
tree014	BC0018	Needle	Tall loblolly tree	16 N30 17.477 W97 44.332	Sample 13		144.9		680
tree015	BC0019	Needle	Tall loblolly tree	17 N30 17.477 W97 44.333	Sample 14		165.7		681
tree007	BC0020	Needle	Tall loblolly tree	9 N30 17.477 W97 44.334	Sample		14.4		103
tree008	BC0021	Needle	Tall loblolly tree	10 N30 17.477 W97 44.335	Sample		15.5		103
tree009	BC0022	Needle	Tall loblolly tree	11 N30 17.477 W97 44.336	Sample		16.6		104
tree010	BC0023	Needle	Tall loblolly tree	12 N30 17.477 W97 44.337	Sample		17.7		104

Upload phenotype / environmental data



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!

TGG Accession Request Form

This submission process will allow you to submit genetic, phenotypic, and/or environmental data into the TreeGenes Database. Much of the information here can be generated on-line. It is important that you fill out the submission information using a TGG Accession. Results can be viewed immediately in real-time publication of the accession information.

Species
Please fill in the fields below for data submission. Please include all data for your study including multiple species, each set of species data will be collected one at a time.

Genetic Data
Does your study include Genetic Data?
 Yes No

Phenotypic Data
Does your study include Phenotypic Data?
 Yes No

Environmental Data
Does your study include Environmental Data?
 Yes No

Association Results Data
Does your study include Association Results Data?
 Yes No

TGG Accession Request Form

Please fill in the fields below for data submission. Please include all data for your study including multiple species, each set of species data will be collected one at a time.

Species
Please fill in the fields below for data submission. Please include all data for your study including multiple species, each set of species data will be collected one at a time.

Genetic Data
Does your study include Genetic Data?
 Yes No

Phenotypic Data
Does your study include Phenotypic Data?
 Yes No

Environmental Data
Does your study include Environmental Data?
 Yes No

Association Results Data
Does your study include Association Results Data?
 Yes No

Submit

Add Supplemental Data

Please enter any additional information about your accession and upload any supplemental data in either the appropriate format or upload the data to a public website and provide the URL. You can upload multiple files. You can also upload files to a public website and provide the URL. You can upload multiple files. You can also upload files to a public website and provide the URL.

Organization Info
For instructions on the acceptable formats for these fields, [click here](#).

Supplemental Data
Upload your supplemental data files here.

Genetic Map
Upload your genetic map files here.

Submit Information

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
8/3/2011	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 SNP Markers: 874 Total cpSSR Markers: 0 Total SSR Markers: 0 Total Phenotypes: 1344 Total Environmentals (per sample): 0 Total Environmentals (per site): 0	Covariate Data (Population Structure) Genotype Data (SNP) GPS Data Haplotype 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 Environmentals (per sample): 0 Total Environmentals (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 Environmentals (per sample): 0 Total Environmentals (per site): 0	Genotype Data (SSR) GPS 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:

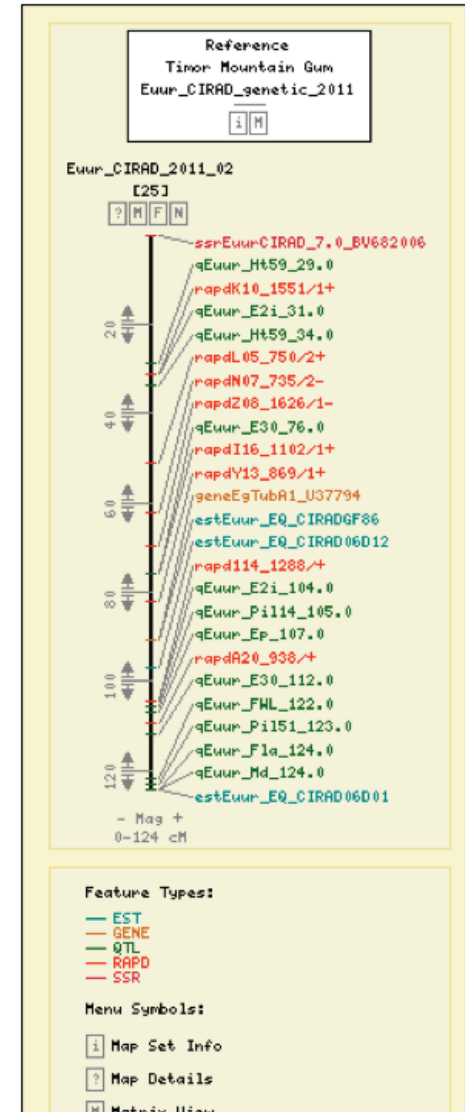
Ref. Set:

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

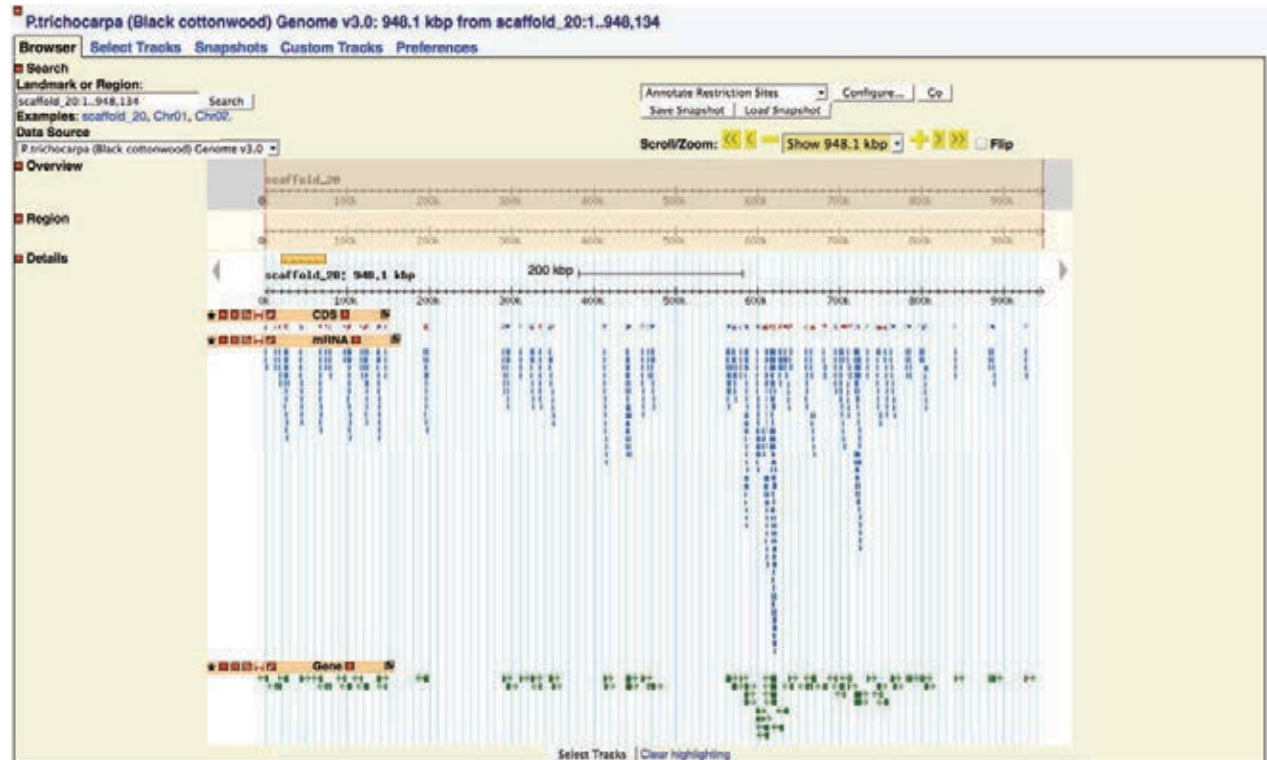


TreeGenes Database: Interfaces

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Genome browsing & annotation



TreeGenes Database: Interfaces

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– Bulk retrieval of resequencing data, genotypes, and phenotypes

A screenshot of the DiversiTree web application interface. The left sidebar contains search filters under the heading "Searches". The main content area displays the "DiversiTree" logo. The top right of the interface has navigation links: "cartogratree", "treegenes", and "dendrome plone".

Searches

- + Documentation ?
- + EST (GenBank) ?
- + Contig ?

FASTA Sequence: (Ex: CCATAG...)

Contig Name: (Ex: 0_8156)

BLAST GenBank Accession: (Ex: CBI25984)

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

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

Navigation: [cartogratree](#) [treegenes](#) [dendrome plone](#)

Logo: DiversiTree

Bottom right:

TreeGenes Database: Interfaces

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Searches

+ Documentation ?

+ EST (GenBank) ?

+ Contig ?

FASTA Sequence: (Ex: CCATAG...)

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

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
0000	0_3214	Pinus taeda (Loblolly Pine)	copper ion binding	Yes	Yes

sswap.info view selected download list

cartogratree treegenes dendrome plone

The logo for DiversiTree, featuring the text "DiversiTree" in a dark blue, serif font above a stylized dark blue graphic of three curved lines representing a tree canopy.

TreeGenes Database: Interfaces

dendrome.ucdavis.edu



Searches

+ Documentation ?

+ EST (GenBank) ?

+ Contig ?

FASTA Sequence: (Ex: CCATAG...)

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

rslt_contig_|||||copper ion binding|||Abal,Abco,Cade,Cede,Crja,Faga,Jure,Lade,Mipi,Paab,Pabw,Paen,Paee,Pama,Pial,Piar,Piam,Pi

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

sswap.info view selected download list

cartogratree treegenes dendrome plone

TreeGenes Database: Interfaces

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SSWAP: web service to connect data from website to website

The screenshot displays the sswap.info website interface. At the top, the logo "sswap.info" is shown in a blue serif font, with "beta" in a smaller font to its right. Below the logo, the text "Simple Semantic Web Architecture and Protocol" is centered. On the left, there is a "New pipeline" button with a dropdown arrow. On the right, there is a "Login / Register" link. The main content area features a light green background with a "TreeGenes Contig" icon on the left, a right-pointing arrow, a dashed blue box containing the text "Drag service icon here", and a large blue play button on the right. Below this, there is an "Input Data Set" section with a dropdown arrow. To the left of this section is the "TreeGenes Contig" logo. The section contains the following text: "Display Data: Click here to send the output data to a viewer (opens in a new window)", "Data Set URI: http://sswap.info/ipc/rrg?token=6b6979aa-07e5-4e7e-843c-ccb57275bca1", and "Produced by: http://sswap.dendrome.ucdavis.edu/resources/contigService/ContigService". At the bottom, there is a search bar with a dropdown arrow and the placeholder text "Enter a phrase or user:<login> to filter results". To the right of the search bar is a "Filter results" button. Below the search bar, it says "Showing 2 results". The first result is displayed in a light green box with the "TreeGenes Contig" logo on the left and the following text: "Name: Treegenes' Contig Service", "Description: A service that accepts a Contig ID, such as '0_10022' and returns a Contig record.", "Service URI: http://sswap.dendrome.ucdavis.edu/resources/contigService/ContigService", and "Provider: TreeGenes' Semantic Web Service Provider".

TreeGenes Database: Interfaces

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*sswap.info*_{beta}
Simple Semantic Web Architecture and Protocol

▼ New pipeline

[Login / Register](#)



▼ Input Data Set

Display Data: [Click here to send the output data to a viewer \(opens in a new window\)](#)
Data Set URI: <http://sswap.info/ipc/rrg?token=a5c81b88-29b1-442a-a239-e0bea5540321>
Produced by: <http://sswap.dendrome.ucdavis.edu/resources/contigService/ContigService>

▼ Enter a phrase or user:<login> to filter results

Filter results

Showing 1 result



Name: Treegenes' Tree Sample Service
Description: A service that accepts a Tree Sample Id, such as "Picb-1" or "LADE0725" and returns a Tree Sample record. The service also accepts Contig, Ampli
Service URI: <http://sswap.dendrome.ucdavis.edu/resources/treeSampleService/TreeSampleService>
Provider: TreeGenes' Semantic Web Service Provider

TreeGenes Database: Interfaces

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sswap.info beta

Simple Semantic Web Architecture and Protocol

▼ New pipeline - running

[Login](#) / [Register](#)



▼ Treegenes' Tree Sample Service

Name:	Treegenes' Tree Sample Service
Description:	A service that accepts a Tree Sample Id, such as "Picb-1" or "LADE0725" and returns a Tree Sample record. The service also accepts Contig, Amplicon
Service URI:	http://sswap.dendrome.ucdavis.edu/resources/treeSampleService/TreeSampleService
Provider:	TreeGenes' Semantic Web Service Provider
Time started:	N/A
Time finished:	N/A

TreeGenes Database: Interfaces

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*sswap.info*_{beta}
Simple Semantic Web Architecture and Protocol

▼ New pipeline - executed

[Login](#) / [Register](#)



▼ Output Data Set

Display Data: [Click here to send the output data to a viewer \(opens in a new window\)](#)
Data Set URI: <http://sswap.dendrome.ucdavis.edu/resources/treeSampleService/TreeSampleService/rrg?token=935da14b-34db-4e10-a004-fedfe00c393b>
Produced by: <http://sswap.dendrome.ucdavis.edu/resources/treeSampleService/TreeSampleService>

TreeGenes Database: Interfaces

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75 of 167 tree ids detected in the URL were used to populate the map

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 (16)

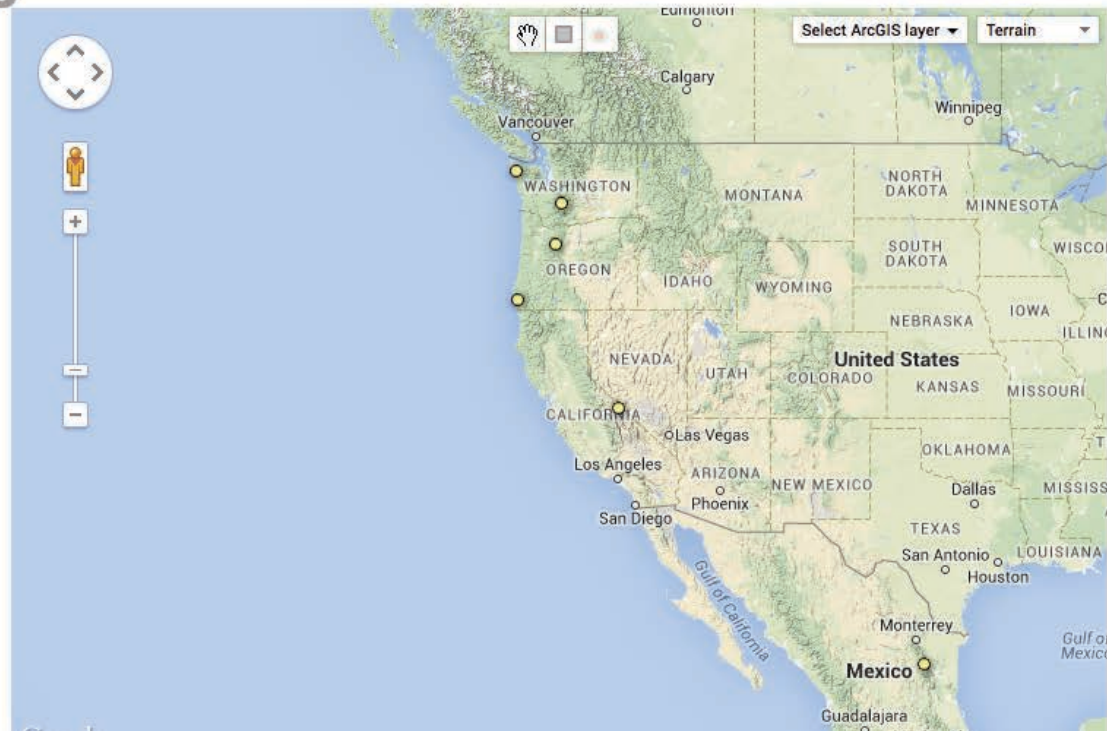
Genotyped (0)

Phenotyped (0)

GPS Resolution

Exact (0)

Approximate (16)



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

TreeGenes Database: Interfaces

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75 of 167 tree ids detected in the URL were used to populate the map

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 (16)

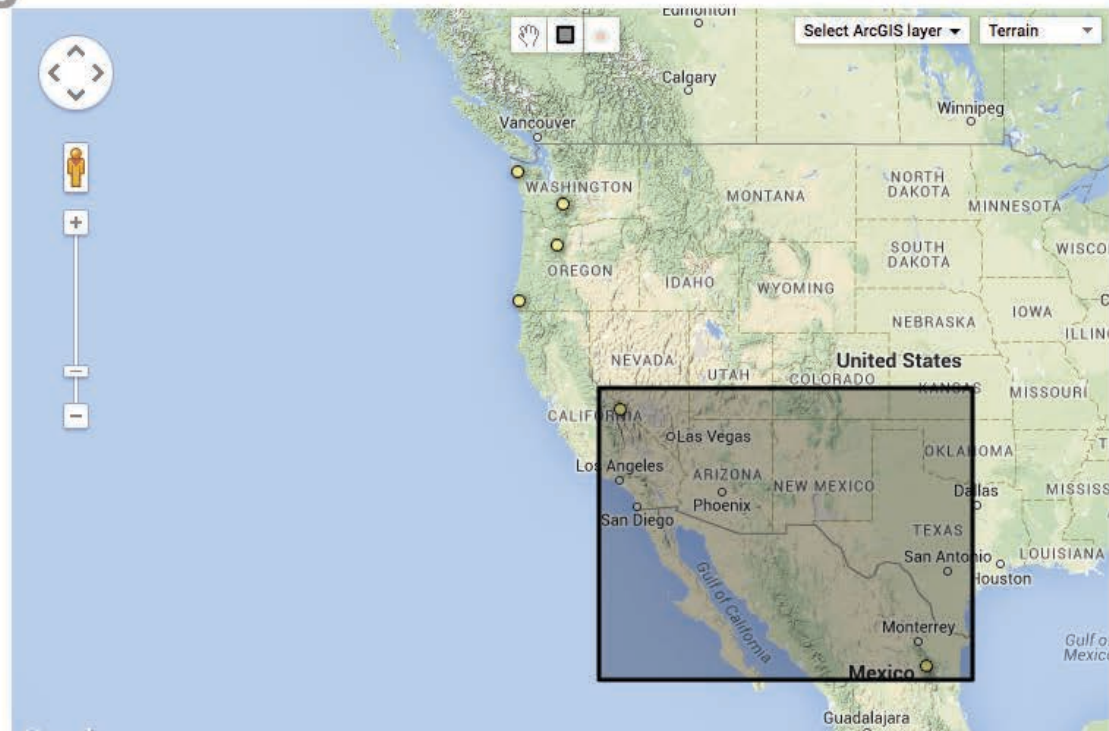
Genotyped (0)

Phenotyped (0)

GPS Resolution

Exact (0)

Approximate (16)



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

TreeGenes Database: Interfaces

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Sequenced (16)

Genotyped (0)

Phenotyped (0)

GPS Resolution

Exact (0)

Approximate (16)



Analyze the data

Map selection

Samples

TASSEL demo data

<input checked="" type="checkbox"/>	Type	ID	Latitude	Longitude	Total sequences	Total genotypes	Total phenotypes	Species
<input checked="" type="checkbox"/>		Picb-1	24.3333	-99.8333	533	0	0	Pinus cembroides
<input checked="" type="checkbox"/>		Pilo-1	37.5276	-118.1830	587	0	0	Pinus longaeva

File Edit View Tools

Find common amplicons

TASSEL at sswap

- Retrieve genotype, phenotype, environmental, and sequence data

TreeGenes Database: Interfaces

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Analyze the data

Map selection Amplicons X

File ▾ Edit ▾ View ▾ Tools ▾

<input type="checkbox"/>	ID	Amplicon ID ▾	Top Blast Description (BLAST nr)	Species-Specific BLASTs	GO Annotations	Interpro Annotations	PFAM Annotations	Discover pipelines at 5
<input type="checkbox"/>	401	UMN_6922_02	"cytochrome b6/f complex subunit IV..."	"cytochrome b6/f complex s..."	"GO:0055114 oxi..."	"IPR005798 Cytochrom..."	"PF00032 Cytochro..."	
<input type="checkbox"/>	402	UMN_6924_03	"photosystem II 47 kDa protein (chlor..."	"photosystem II 47 kDa prot..."	"GO:0055114 oxi..."	"IPR000932 Photosyste..."	"PF00421 Photosys..."	
<input type="checkbox"/>	403	UMN_915_01	"PREDICTED: U-box domain-containi..."	"PREDICTED: U-box domain..."	"GO:0044237 cell..."	"IPR011989 Armadillo-li..."	-999	
<input type="checkbox"/>	404	UMN_927_01	"PREDICTED: COBRA-like protein 7-l..."	"PREDICTED: COBRA-like p..."	-999	-999	-999	
<input checked="" type="checkbox"/>	405	UMN_CL228C...	"PREDICTED: 40S ribosomal protein ..."	"PREDICTED: 40S ribosoma..."	"GO:0005840 ribo..."	"IPR000892 Ribosomal ..."	"PF01283 Ribosoma..."	
<input type="checkbox"/>	406	UMN_CL309C...	"PREDICTED: DUF246 domain-conta..."	"PREDICTED: DUF246 dom..."	-999	-999	-999	
<input type="checkbox"/>	407	UMN_CL336C...	"Protein of unknown function DUF53..."	"Protein of unknown functio..."	-999	"IPR007493 Protein of u..."	"PF04398 Protein of..."	
<input type="checkbox"/>	408	UMN_CL415C...	"PREDICTED: LRR receptor-like serin..."	"PREDICTED: LRR receptor-..."	"GO:0006259 DN..."	"IPR013103 Reverse tra..."	"PF07727 Reverse t..."	
<input type="checkbox"/>	409	UMN_CL5Con...	"uninformative (0.15) (unspecified)"	"uninformative (0.15) (unspe..."	-999	-999	-999	

Total samples selected: 1

– Further analysis (TASSEL, MUSCLE) via SSWAP

TreeGenes Database: Interfaces

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*sswap.info*_{beta}
Simple Semantic Web Architecture and Protocol

▼ New pipeline

[Login](#) / [Register](#)



▼ Input Data Set

Display Data: [Click here to send the output data to a viewer \(opens in a new window\)](#)
Data Set URI: <http://sswap.info/ipc/rrg?token=97c82c55-b1fa-4063-bb7d-84a49a34637a>
Produced by: <http://sswap.dendrome.ucdavis.edu/resources/ampliconService/AmpliconService>

▼ Enter a phrase or user:<login> to filter results

Filter results

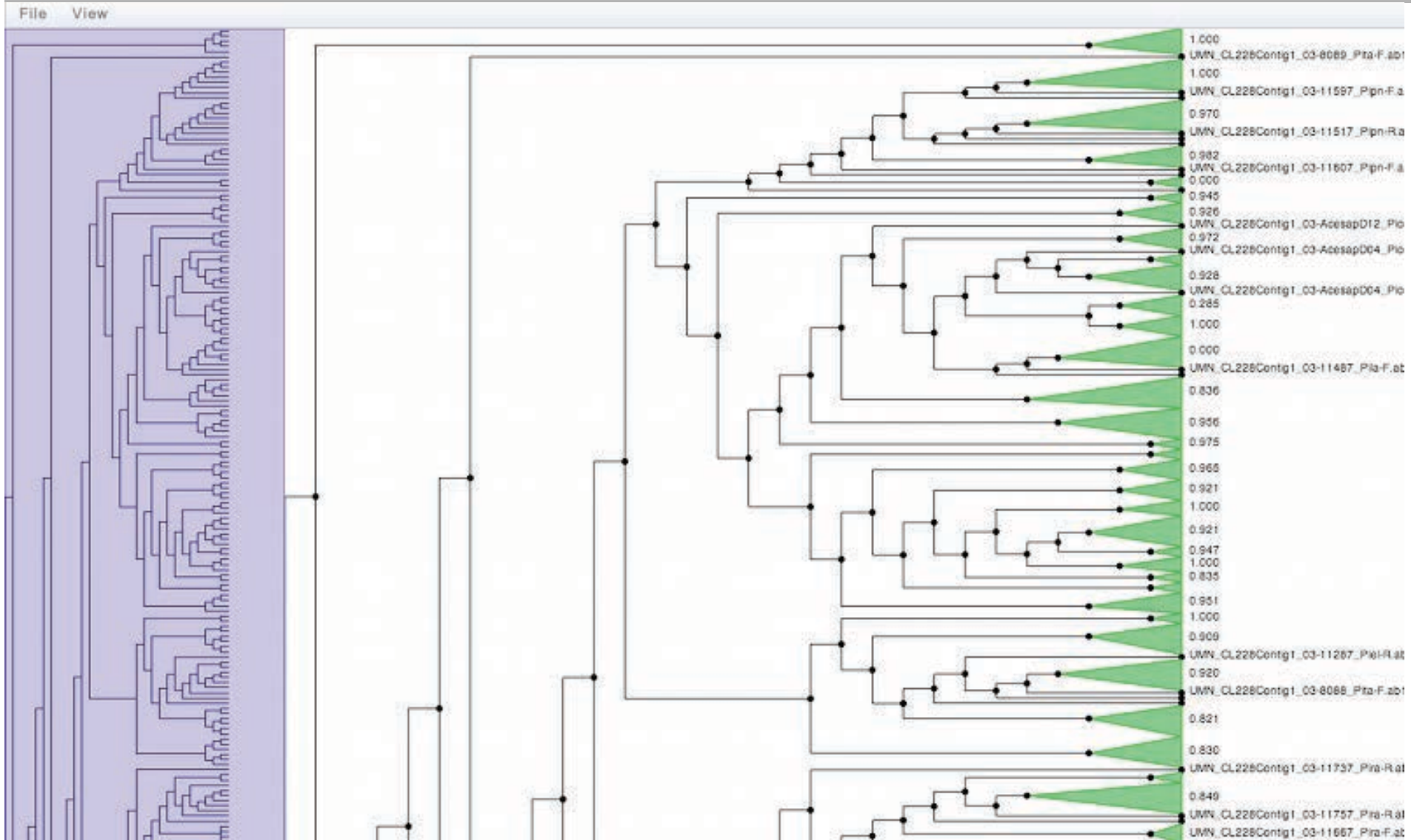
Showing 1 result



Name: Extract images from page
Description: Scans an HTML page and extracts all images from it
Service URI: <http://sswap-a.iplantcollaborative.org/sswap-pipeline-test/test/data/pipeline/extractImagesFromPage>
Provider: Test provider

TreeGenes Database: Interfaces

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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, there is a navigation menu with tabs: Project, Sequences, Files, Repeats, Masking, Genes, Consensus, Reflow, Functional, Annotate, and Publish. The 'Annotate' tab is currently selected. In the top right corner, there is a user account page link and the current project name: 'AT_120114'. Below the navigation menu, there are two tabs: 'Welcome!' and 'Project'. The 'Project' tab is active. On the left side, there is a blue arrow pointing up with the text: '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.' This is annotated with a box labeled 'C'. In the center, there is a large GenSAS logo and the text: 'Welcome to Genome Sequence Annotation Server!'. Above this, there is an orange arrow pointing up with the text: '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.' On the right side, there is a 'Job Queue' section with a table of jobs. This is annotated with a box labeled 'B'. Below the 'Job Queue' section, there is a green arrow pointing right with the text: 'Click the Job Queue to view the analysis jobs for the project. Click the Browser 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.' This is annotated with a box labeled 'A'. The 'Job Queue' table has two columns: 'Job Name' and 'Status'. The jobs listed are: Masked Consensus (Completed), RepeatMasker-at (Completed), RepeatMasker-rebase (Completed), RepeatModeler (Completed), and a section for 'Genes & Other Predictions' which includes: Augustus (Completed), BLAST (nucleotide)-gRNA (Completed), BLAST (nucleotide)-EST (Completed), BLAST (nucleotide)-refSeqPlant (Completed), BLAST (proteins)-refSeqplant (Completed), BLAST (proteins)-sprot (Completed), BLAST (proteins)-trnmpi (Completed), BLAT-cDNA (Completed), and BLAT-EST (Completed).

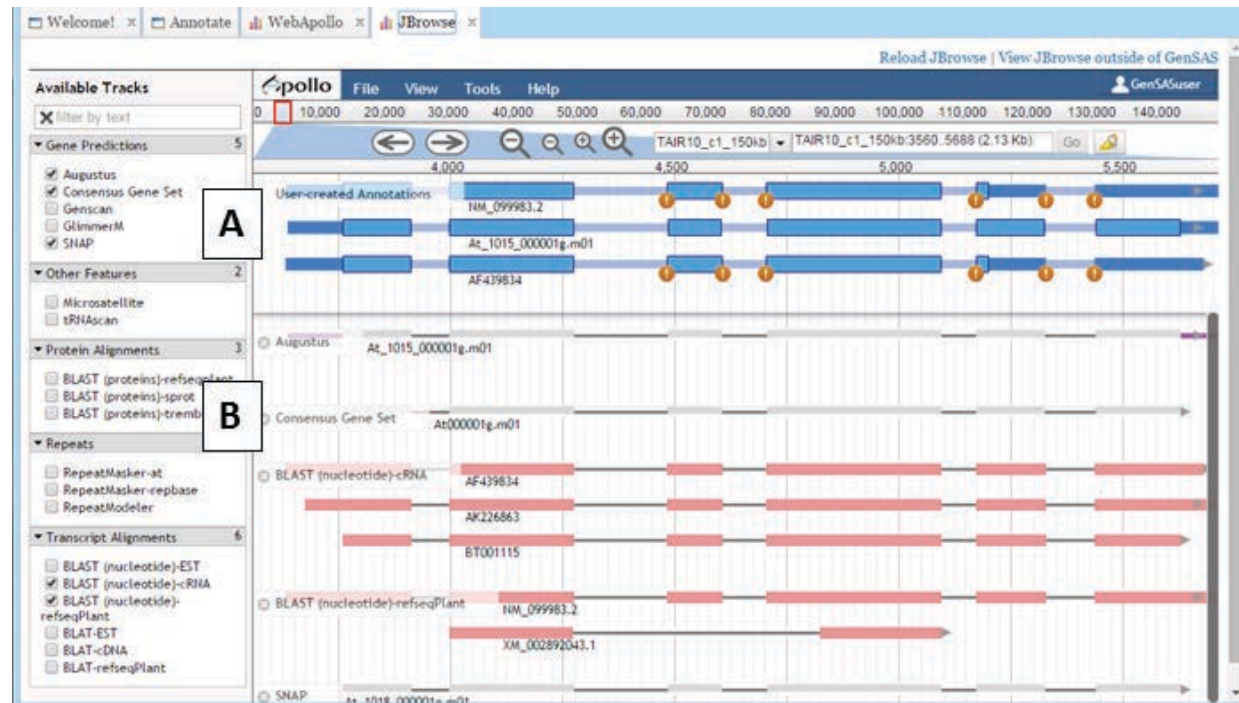
TreeGenes Database: Current Development

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– Save work, upload modifications for approval

P1153

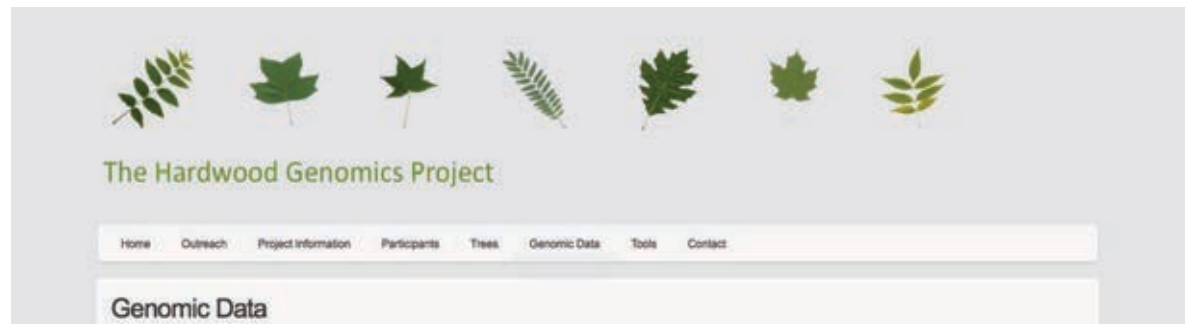


TreeGenes Database: Future Development

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Tripal Galaxy



TreeGenes Database: Future Development

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Tripal Galaxy

– Tripal

- Frontend & backend open source database solution
- Set of tools using Drupal & CHADO to allow users to easily create biological databases & web interfaces



– Galaxy

- Workflow & data analysis platform
- Build multi-step analysis pipeline



TreeGenes Database: Future Development

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Tripal Galaxy

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



TreeGenes Database: Team

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Project Leads

David Neale

Jill Wegrzyn

University of Connecticut

Lead Database

Administrator

Emily Grau

Development Team

Jacob Zieve

Hans Vasquez-Gross

Andrew Brown

Advising

Damian Gessler

Semantic Options/University of Arizona



@TreeGenes



TreeGenes Database

