

# TreeGenes & Tripal



[treegenesdb.org](http://treegenesdb.org)

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# TreeGenes Database: History

treegenesdb.org

- Began as the Dendrome project (USDA funded initiative) in 1993 to hold forest tree genetic maps and associated markers
- One of the 1<sup>st</sup> USDA funded databases on the internet
- Schema has been changing and evolving ever since



# TreeGenes Database: History

treegenesdb.org

- Began 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

treegenesdb.org

2,086 users from 862 organizations in 94 countries



Unique Web Visitors to TreeGenes Database per month, January-December 2015

# TreeGenes Database: Species

treegenesdb.org



- 1,774 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

treegenesdb.org

## **Automated scripts**

- Primary databases such as NCBI
- Appropriate data should be submitted to primary databases **first**

## **User submissions**

- For data and metadata not captured well by primary databases

# TreeGenes Database: Data Sources

treegenesdb.org

## Automated scripts

### – NCBI

- Transcripts, Protein, Unigene Databases
- Linked to literature records, etc.
- Incorporated into visualization tools

### – Literature

- Web of Science, PubMed



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    </AbstractText>
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      Pollination drops were sampled from eight gymnosperm
      species. Leaves were sampled from 100 trees of each species.
    </AbstractText>
  </Abstract>
</Article>
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```

# TreeGenes Database: Data Sources

treegenesdb.org

## **User submissions**

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



# TreeGenes Database: Data Sources

treegenesdb.org

## User submissions

Submit genetic maps, association or population study data

Most submissions from journal requirement: Tree Genetics and Genomes

**TGAO Accession Request Form**

This submission process will allow you to upload genetic, phenotypic, and/or environmental data into the TreeGenes database. Results of the association tests will be accessible on the P-Value and all files will be collectively available using a TGAO accession. Results can be released immediately or held until publication of the associated manuscript.

**Species**

Please fill in the fields below for data pertaining to **Primate** taxa samples only. If your study includes multiple species, each set of species data will be collected one at a time.

**Genetic Data**

Does your study include Genetic data?  Yes  No

**Phenotype Data**

Does your study include Phenotype?  Yes  No

**Environmental Data**

Does your study include Environmental data?  Yes  No

**TGAO Accession Request Form**

Please fill in the fields below for data pertaining to **Primate** taxa samples only. If your study includes multiple species, each set of species data will be collected one at a time.

**GPS Data**

Select the statement that describes how GPS coordinate data was used in your study.

GPS coordinates were not collected in this study.

**Phenotype Data**

Select the statement that describes how Phenotype data was used in your study.

Defined Phenotype measurements were performed on each genotype.

**Environmental Data**

Select the statement that describes how Environmental data was used in your study.

Environmental measurements were performed on each genotype indiv.

**Association Results Data**

Select the statement that best describes your Association results data.

Single Marker.

**Upload TreeGenes Accession Number**

This system is for the submission of genetic map files and will provide the user with a TreeGenes accession number for each submission. The user will be able to view the accession number and the location of the files in the TreeGenes database. The location of the files will be provided with a TreeGenes accession number. The location of the files will be provided with a TreeGenes accession number.

Please enter your TreeGenes accession number and upload your genetic map file to the TreeGenes database. Contact the TreeGenes team for more information and the location of the files in the TreeGenes database.

Following a successful submission, you will receive a TreeGenes accession number for the new data and a new TreeGenes accession number will be added to our database to begin the submission process.

Please reference the TreeGenes database and the reference number information in the manuscript for the associated accession data.

For more information, please visit our website: [treegenesdb.org](http://treegenesdb.org)

**Metadata**

Species:   
 Accession:

**Add Supplemental Data**

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

**Organization info**

Author:   
 Paper:   
 Supplement:   
Type:

**Genetic Map**

File:   
 Organization:

# TreeGenes Database: Data Sources

treegenesdb.org

## User submissions

Genetic maps, association or population studies

**TGAD Accession Request Form**

The submission process will allow you to upload genetic, phenotypic, and/or environmental data into the TreeGenes database. Results of the association tests will be accessible on the P-Value and all files will be collectively available using a TGAD accession. Results can be released immediately or held until publication of the associated manuscript.

**Species**  
Please fill in the fields below for data pertaining to *Pinus* needle samples only. If your study includes multiple species, each set of species data will be collected.

**Genetic Data**  
Does your study include Genetic data?  
Yes

**Phenotype Data**  
Does your study include Phenotype?  
Yes

**Environmental Data**  
Does your study include Environmental data?  
Yes

**TGAD Accession Request Form**

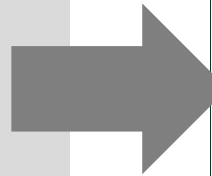
Please fill in the fields below for data pertaining to *Pinus* needle samples only. If your study includes multiple species, each set of species data will be collected one at a time.

**GPS Data**  
Select the statement that describes how GPS coordinate data was used in your study.  
GPS coordinates were not collected in this study.

**Phenotype Data**  
Select the statement that describes how Phenotype data was used in your study.  
Detailed Phenotype measurements were performed on each genotype.

**Environmental Data**  
Select the statement that describes how Environmental data was used in your study.  
Environmental measurements were performed on each genotype only.

**Association Results Data**  
Select the statement that best describes your Association results data.  
Single Marker



**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 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 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: 0 Total cpSSR Markers: 6 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 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)

**Upload TreeGenes Accession Number**

The system is set up for the submission of genetic map files and will provide the number and a TreeGenes accession number for each submission that is in the TreeGenes database. The number is needed for maps associated with a manuscript that will be submitted to a peer-reviewed journal.

I have read and I understand if my submission for a manuscript that has already been published, please follow the steps.

Please enter gene/protein translation, nucleotide sequence and upload your genetic map to use in our image gallery. Contact the authors on the instructions page for the format of the files you can upload.

Following a successful submission, you will receive a TreeGenes accession number for the new accessions and a new TreeGenes accession number for all data in our database to be used to begin the submission process.

Please reference the TreeGenes database and the accession number instructions in the manuscript associated with the submission.

For more information, please visit our website: [http://treegenesdb.org](#)

**Add Supplemental Data**

For instructions on the acceptable formats for these fields, click here.

**Organization Info**

Author: [Select] Robert Andron  
Paper: [Select] Patterns of population structure and associations to broad scale events  
Supplement: [Select] Genetic Map  
Type: [Select]

**Genetic Map**

File: [Select] jggenes\_map\_v01s  
Organization: [Select] University of California at Davis

Submit Information

# TreeGenes Database: Data Sources

treegenesdb.org

## User submissions

Genetic maps, association or population studies

Obtain TGDR accession number!

**TGDR Accession Request Form**

The submission process will allow you to upload genetic, phenotypic, and/or environmental data into the TreeGenes database. Results of the association tests will be accessible on the WebSite and all files will be collectively available using a TGDR accession. Results can be released immediately or held until publication of the associated manuscript.

**Species**  
Please fill in the fields below for data pertaining to *Pinus taeda* samples only. If your study includes multiple species, each set of species data will be collected.

**Genetic Data**  
Does your study include Genetic data?  
Yes

**Phenotype Data**  
Does your study include Phenotype?  
Yes

**Environmental Data**  
Does your study include Environmental data?  
Yes

**TGDR Accession Request Form**

Please fill in the fields below for data pertaining to *Pinus taeda* samples only. If your study includes multiple species, each set of species data will be collected one at a time.

**GPS Data**  
Select the statement that describes how GPS coordinate data was used in your study.  
GPS coordinates were not collected in this study.

**Phenotype Data**  
Select the statement that describes how Phenotype data was used in your study.  
Detailed Phenotype measurements were performed on each genotype.

**Environmental Data**  
Select the statement that describes how Environmental data was used in your study.  
Environmental measurements were performed on each genotype only.

**Association Results Data**  
Select the statement that best describes your Association results data.  
Single Marker



**TreeGenes Data Repository**

A listing of data submissions is displayed below.  
To submit data to TreeGenes, click here.

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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 Supplemental Data
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**Obtain TreeGenes Accession Number**

The system is set up for the submission of genetic map files and will provide the accession and a TreeGenes accession number for each submission. The accession number is provided for maps associated with a manuscript that will be submitted to a peer-reviewed journal.

Please enter your email address (you will receive a TreeGenes accession number on the new access and a new TreeGenes accession number on the new access) and click on the "Obtain Accession Number" button to obtain your accession number.

Please provide the TreeGenes accession and the reference number (accession number) in the manuscript (if available) for the submission.

For more information, please click on the "More Info" link.

**Add Supplemental Data**

For instructions on the acceptable formats for these fields, click here.

**Organization Info**

The TreeGenes population structure and association analysis was performed by:  
Author: E. J. Anderson  
Paper: Patterns of population structure and associations to broad scale events  
Supplement: Genetic Map  
Type: Genetic Map

**Genetic Map**

File: [jlgeneas\_map\_v01n1] Browse...  
Organization: University of California at Davis

Submit Information

# TreeGenes Database: Data Sources

treegenesdb.org

## User submissions

Genetic maps, association or population studies

Will be converted to Tripal module and made available to the community

**TGAD Accession Request Form**

This submission process will allow you to upload genetic, phenotypic, and/or environmental data to the TreeGenes database. Results of the association tests will be accessible as the First author collectively available using a TGAD accession. Results can be released immediately upon publication of the associated manuscript.

**Species**

Please fill in the fields below for data pertaining to Pinus taeda samples only. If your study includes multiple species, each set of species data will be collected separately.

**Genetic Data**

Does your study include Genetic data?  Yes  No

**Phenotype Data**

Does your study include Phenotypic?  Yes  No

**Environmental Data**

Does your study include Environmental data?  Yes  No

**Upload TreeGenes Accession Number**

This system is for the submission of genetic maps and will provide the user with a TreeGenes accession number for association studies in the TreeGenes database. The number of records for maps associated with a TreeGenes accession will be limited to a maximum of 1000.

I have read and I agree with the conditions for a manuscript that has already been published, please leave this box.

Please enter previously submitted accession numbers and upload your genetic map to use for image group. Create new accessions or the accession and the corresponding File for your map.

Following a successful submission, you will receive a TreeGenes accession number for the new accessions and a new TreeGenes accession number for all data in our database available through the submission process.

Please reference the TreeGenes Database and the reference number associated with the manuscript throughout your publications.

For more information, please visit our website: [http://treegenesdb.org](#)

**Accession**

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

**Organization info**

**Genetic Map**

		Data Files	
		Covariate Data (Population Structure) Genotype Data (SNP) GPS Data Haplotype Data Phenotype Data Phenotype Definitions	
		Genotype Data (cpSSR) GPS Data Haplotype Data Supplemental Data	
		Genotype Data (SSR) GPS Data Supplemental Data Supplemental Data Supplemental Data Supplemental Data	
		Environmental Metric Data Environmental Metric Definitions Genotype Data (SSR)	

		markers			
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 Supplemental Data
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# TreeGenes Database: Data Access

treegenesdb.org

## **Tools**

- Existing viewers
- Custom development

# TreeGenes Database: Interfaces

treegenesdb.org



Reference  
Timor Mountain Gum  
Euur\_CIRAD\_genetic\_2011

Euur\_CIRAD\_2011\_02  
[25]

Feature Types:  
EST  
GENE  
QTL  
RAPD  
SSR

Menu Symbols:  
[i] Map Set Info  
[?] Map Details  
[M] Matrix View

**P.trichocarpa (Black cottonwood) Genome v3.0: 948.1 kbp from scaffold\_20:1..948,134**

Browser | Select Tracks | Snapshots | Custom Tracks | Preferences

Search  
Landmark or Region: scaffold\_20:1..948,134 Search  
Examples: scaffold\_20, Chr01, Chr02

Annotate Restriction Sites | Configure... | Go  
Save Snapshot | Load Snapshot

Data Source  
P.trichocarpa (Black cottonwood) Genome v3.0

Scroll/Zoom: << < Show 948.1 kbp > >> Flip

Overview  
Region  
Details

Select Tracks | Clear highlighting



# TreeGenes Database: Interfaces

treegenesdb.org



– Bulk retrieval of resequencing data, genotypes, and phenotypes

Searches
cartogratree treegenes dendrome plone

**+ 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

- Abies alba
- Abies concolor
- Calocedrus decurrens
- Cedrus deodara
- Cryptomeria japonica

rslt\_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)
11256	0_4342	Pinus taeda (Loblolly Pine)
13739	0_7878	Pinus taeda (Loblolly Pine)
14065	0_8291	Pinus taeda (Loblolly Pine)
14200	0_8419	Pinus taeda (Loblolly Pine)
14320	0_8531	Pinus taeda (Loblolly Pine)
15122	0_9288	Pinus taeda (Loblolly Pine)
15266	0_9423	Pinus taeda (Loblolly Pine)
22822	2_1343	Pinus taeda (Loblolly Pine)
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)

Contig	Gene	Yes	Yes
cg47012	copper ion binding	Yes	Yes
cg48716	copper ion binding	Yes	Yes
cg49217	copper ion binding	Yes	Yes
cg50235	copper ion binding	Yes	Yes
cg50336	copper ion binding	Yes	Yes
cg50472	copper ion binding	Yes	Yes
cg50688	copper ion binding	Yes	Yes

sswap.info beta

Simple Semantic Architecture and Protocol

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

Drag service icon here

**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/rng?token=4ce1fc5a-128e-48fa-9b93-4dc7ea771869>

Produced by: <http://sswap.dendrome.ucdavis.edu/resources/contigService/ContigService>

[sswap.info](#) [view selected](#) [download list](#)



# TreeGenes Database: Interfaces

treegenesdb.org



[About](#) [TreeGenes](#) [DiversiTree](#) [Example](#) [Contact](#) [Credits](#)

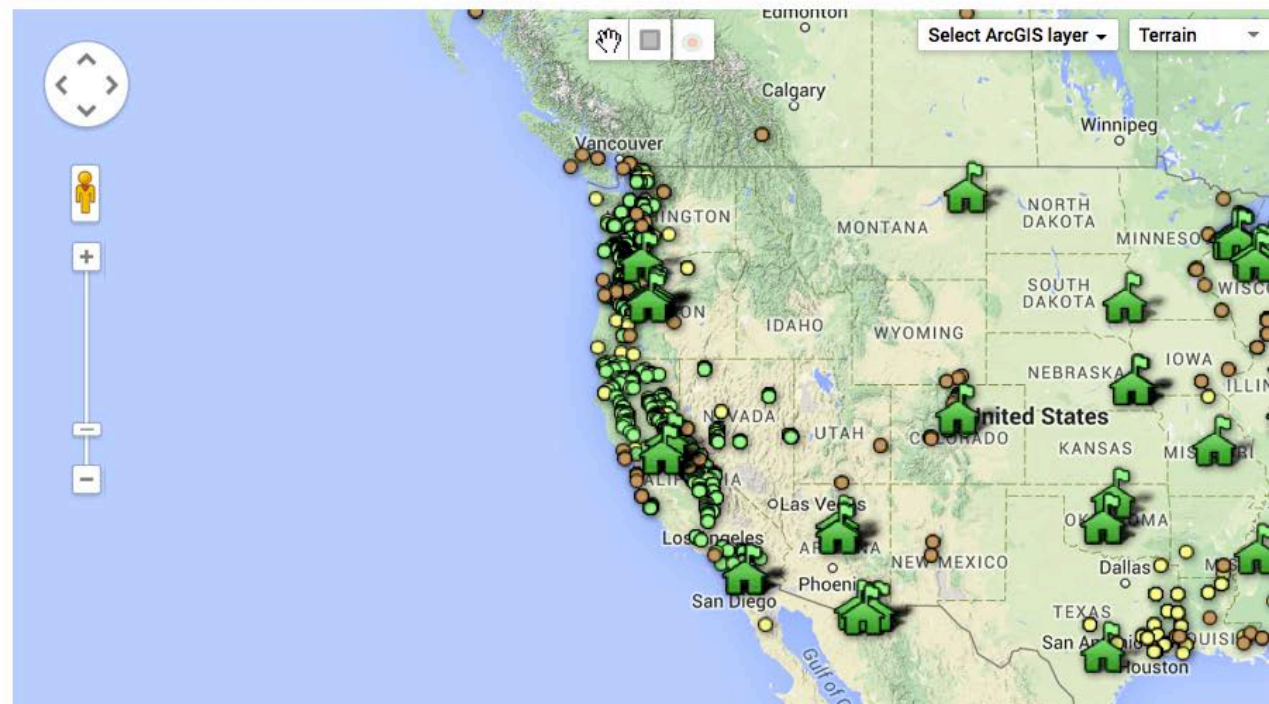
### Map Display

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
- Data from TreeGenes, WorldClim, Ameriflux, TRY-db



# TreeGenes Database: Transition to Tripal

treegenesdb.org

## **Transition to Tripal and Chado**

### Challenges

- Ontologies
- Standardizing for the first time
  - 25 years of custom schemas!

# TreeGenes Database: Transition to Tripal

treegenesdb.org

## Transition to Tripal and Chado

### Advantages

- Ontologies
- Save time!
- Connect data with other databases (Tripal Gateway)
- Improve analytical capabilities (Tripal Gateway)
  - **Our contribution: analytical workflows**
- Review & clean up database

# TreeGenes Database: Transition to Tripal

treegenesdb.org

## Outcomes

- Expanded datasets: access Hardwood Genomics, GDR, TreeGenes from one location
- Expanded analytical, HPC resources
  - Improve CartograTree capabilities
- New Tripal module: user submission

# TreeGenes Database: Team

[treegenesdb.org](http://treegenesdb.org)

[tg-help@ucdavis.edu](mailto:tg-help@ucdavis.edu)

## Project Leads

Jill Wegrzyn

*University of Connecticut*

David Neale

## Lead Database

Administrator

Emily Grau **P0322**

## Development Team

Steven A Demurjian Jr **P0383**

Hans Vasquez-Gross

## Advising

Damian Gessler

*Semantic Options*



@TreeGenes



TreeGenes  
Database

