

NRSP10 Progress Report

Database Resources for Crop Genomics, Genetics and Breeding Research

National Plant Germplasm Committee Meeting

**Cornell University
June 1, 2017**

**Jim Moyer
Washington State University**

NRSP 10 Progress by Objective

Expand online community databases currently housing high quality genomic, genetic and breeding data for Rosaceae, citrus, cotton, cool season food legumes and *Vaccinium* crops

- Four of the five databases redesigned and implemented in Tripal 2.1 with improved access to data, tools and tutorials - easy upgrade path to Tripal 3
- Presentations at over 50 conferences, workshops, and meetings
- Widespread use of the databases (Oct 1, 2014 – May 30, 2017)

Database	# Visitors	# Visits	# Pages Served	# Countries
Rosaceae	50,458	131,742	605,960	171
Cotton	25,262	60,331	349,731	163
Citrus	12,169	18,756	83,045	146
Legumes	8,027	13,218	60,606	144
Vaccinium	4,049	5,527	18,934	94
Total	99,965	229,574	1,118,276	



CSFL

Crops ▾ Data ▾ Search ▾ Tools ▾ General ▾ Help ▾

Login



COOL SEASON FOOD LEGUME CROP DATABASE RESOURCES

Genomic, Genetic and Breeding Resources for Pea, Lentil, Chickpea and
Faba Bean Crop Improvement

News and Events

- PathwayCyc for *C. reticulatum* PI489777 added (2/1/17)
- New CSFL Video Tutorials (1/7/17)
- CSFL poster at PAG, January 14-18, 2017
- New CSFL User Manual (11/21/16)

[more...](#)

Crops Quick Start



lentil



pea



chickpea



faba bean

Tools Quick Start

genomics

- View Genomes
- Find Sequences
- Search Genes
- BLAST Sequences

genetics

- Browse Maps
- Search Markers
- Find QTLs
- Compare Maps

breeding

- Manage Breeding
- Manage Data
- Analyze Data
- Decision Tool

general

- Submit Data
- Presentations
- Work in Progress
- Contact Us

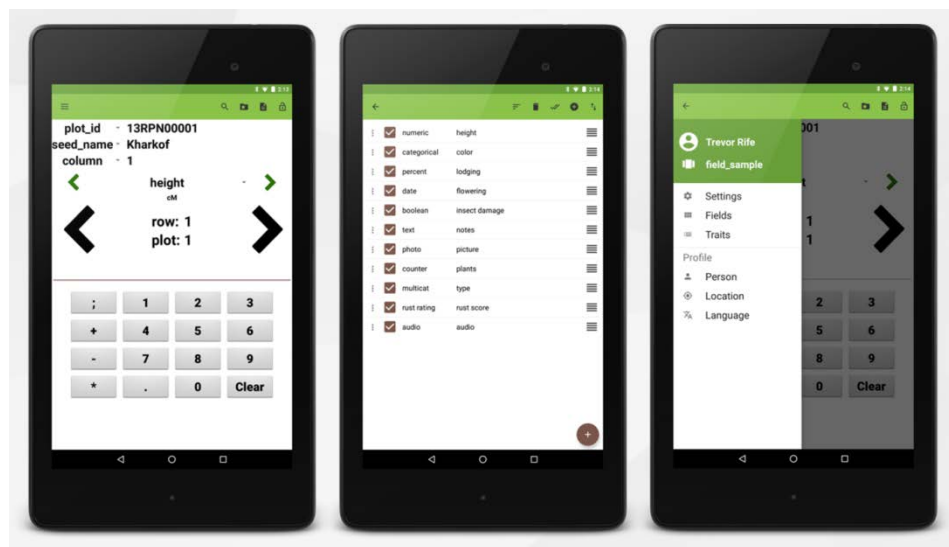


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NRSP 10 Progress by Objective

Develop/Implement a tablet application to improve efficiency and accuracy of phenotypic data collection and ease of upload to private breeding program databases

- Collaborating with Jesse Poland to further develop the widely used FieldBook App for the needs of NRSP10 crops – NRSP10 provides funds for 1/2 developer position
- Provided Samsung tablets with FieldBook to over 50 NRSP10 breeders and scientists – feedback fueling new feature development
- Provide webinars, hands-on training and support with frequent presentations at conferences and meetings – encouraging adoption



3090 installs by users from 137 countries

NRSP 10 Progress by Objective


Develop a Tripal Application Programming Interface for building breeding databases to connect private breeding databases with public genomics, genetics and breeding data

- Many input sessions held with NRSP10 breeders to identify specific needs for a Tripal Breeding Information Management System (Tripal BIMS)
- Beta testing of development by focus group of 4 NRSP10 breeders
- Presentations at conferences/workshops by NRSP10 breeders Ksenija Gasic (Clemson University Peach Breeding) and Todd Campbell (USDA-ARS, Cotton Breeding) to provide more feedback and advertise for breeding program planning (e.g. start using FieldBook)
- Status: design for V1.0 completed, data loaders in place for breeders to upload their own data, data uploaded for 3 programs, breeders testing and providing feedback. Full release of V1.0 in early 2018.

Example: Todd Campbells BIMS in CottonGen

Todd Campbell Breeding Program

Program

 Hello dorrie | [Site Home](#) | [Log out](#)

Archive

Manage Breeding

- Trait
- Location
- Cross
- Germplasm
- Trial
 - Trial Tree
 - Breeding Line Tree

Data Import

Data Edit

Search

Download

Field Book App Management

Data Analysis

Manage Cross

Instructions

Cross Admin Menu

Cross	Cross Details										
PDCR090001	<table><tr><td>Cross Number</td><td>PDCR090001</td></tr><tr><td>Dataset Name</td><td>Campbell_Cotton_Cross</td></tr><tr><td>Paternal Parent</td><td>PD03026</td></tr><tr><td>Maternal Parent</td><td>MD25</td></tr><tr><td>Progeny</td><td>PDCR090001</td></tr></table>	Cross Number	PDCR090001	Dataset Name	Campbell_Cotton_Cross	Paternal Parent	PD03026	Maternal Parent	MD25	Progeny	PDCR090001
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PDCR090016											
PDCR090025											
PDCR090038											
PDCR090040											
PDCR090049											
PDCR090057											
PDCR090071											
PDCR090072											

View information on existing crosses

NRSP 10 Progress by Objective

Convert GenSAS, a comprehensive online community genome annotation and curation tool, to Tripal

- A single online portal that combines numerous genome annotation tools into a single platform
- Easy-to-use interfaces, with integrated instructions allowing researchers at all skill levels to annotate genome sequences
- User accounts keep data private and secure as well as allow users to share data for collaborative annotation
- Initially funded by the 2011-2015 USDA NIFA PineRefSeq Project
- Since v3.0 release it has been accessed by 2,129 visitors from 82 countries, with 5,701 sessions and 24,419 pages viewed

NRSP 10 Progress by Objective

Convert GenSAS, a comprehensive online community genome annotation and curation tool, to Tripal

Why is it GenSAS needed?

Driven by the volume of genome sequences being generated by individual labs, most without access or skills to run and reformat the output of gene prediction programs, perform manual and format the results into files needed for publication.

- V5.0 released January 2017, V5.1 in June
- More functionality and improved performance
- Linked with Tripal but not fully integrated yet (GenSAS and GenSASLite)
- Being used now by many communities to do community curation of genomes
- We are exploring commercialization opportunities for the standalone software (largely due to the processor power needed to support the demand for this software and the resources needed to run big jobs)
- Manuscript in preparation for submission in July

Welcome to GenSAS

The Genome Sequence Annotation Server (GenSAS) is an online tool that provides a pipeline for whole genome structural and functional annotation. Users can upload genome sequences and select from a variety of tools for repeat masking, prediction of gene models and other structural features as well as functional annotation tools. GenSAS integrates with [JBrowse](#) and [Apollo](#) to provide visualization and editing. Please see our video tutorial under the "Help" tab.

User login

Username *

Password *

- [Create new account](#)
- [Request new password](#)

Log in


NRSP 10 Progress by Objective

[Home](#) [Download](#) [Support](#) [Extensions](#) [API](#) [About](#) [Demo Site](#) [Log In](#)

Quick Links

- v2.x User's Guide
 - Quick Docker install
 - Download and install
 - Upgrade instructions
 - Developer's handbook
- Other documentation
- Tripal @ [gitHub.com](#)
- Tripal @ [drupal.org](#)

Tweets by @TripalProject

 **The Tripal Project**
@TripalProject

Tripal provides an out-of-the-box setup for a genomics website easily put a new genome assemblies & annotations online
#PAGXXV

 **The Tripal Project**
@TripalProject

Tripal provides an integration with the @gmodproject Chado database schema and Drupal, a popular Content Management Systems
#PAGXXV



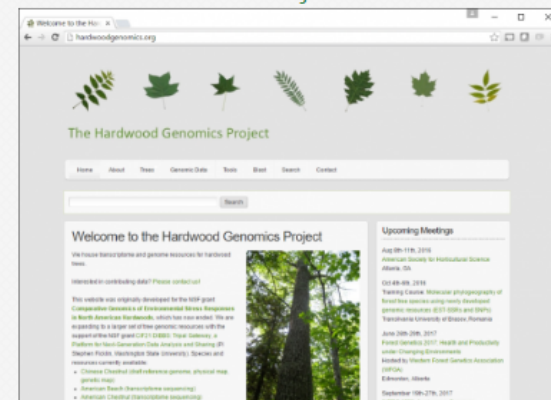
Tripal is a toolkit for construction of online biological (genetics, genomics, breeding, etc), community database, and is a member of the [GMOD](#) family of tools. Tripal provides by default integration with the [GMOD Chado database schema](#) and [Drupal](#), a popular Content Management Systems (CMS). Tripal is licensed under the [GNU General Public License version 2](#).

Objectives

- Provide a framework for those with genomic, genetic and breeding data for creation of an online site for display, search and visualization.
- To use community-derived standards and ontologies to facility continuity between sites which in turn fosters collaboration and sharing
- Provide an out-of-the-box setup for a genomics site for those who simply want to put new genome assemblies and annotations online.
- Provide Application Programming Interfaces (APIs) for complete customization such that more advanced

Sites Using Tripal

Hardwood Genomics Project



[\[View more\]](#)

News

TRIPAL: Meeting & Hackathon

01/03/2017 - 23:42

Where: Plant & Animal Genome, San Diego, CA

Town & Country in Royal Palm Salon 4

When: Thursday, January 12 and Friday, January 13 from 8am - 5pm

Support

- Highly engaged and supportive user communities 😊
- Leveraged funding
 - Further Development of CottonGEN: A Genomics, Genetics and Breeding Database for Cotton Improvement (PI Main). Cotton Incorporated and USDA-ARS, Jan 1, 2017- Dec 31, 2020, **\$741,889**.
 - Standards and CyberInfrastructure that Enable Big-Data Driven Discovery for Tree Crop Research (PI Main) NSF Plant Genome Research Program, July 15 2016 - July 14 2019, **\$2,983,307**.
 - Genome Database for Rosaceae: Empowering Specialty Crop Research through Big-Data Driven Discovery and Application in Breeding (PI Main) USDA NIFA Specialty Crop Research Initiative, Sept 1 2014 – Aug 31 2019, **\$2,700,000**.
 - CIF21 DIBBS: Tripal Gateway, a platform for next-generation data analysis and sharing” (PI Ficklin, CoPI Main) NSF CIF21 Program, Jan 2015 – Dec 31 2017, **\$1,498,066**
 - US Land Grant Universities – participating scientist salaries
- Community of developers working on Tripal Database modules

AgBioData Outreach

- AgBioData consortium workshop (funded by NSP to PI Main)



- Funded by NSF award to PI Main
- 43 scientists participated representing over 20 databases
- Whitepaper on Agricultural Biological Databases by August
- Opinion papers following the whitepaper

- Monthly conference calls for the last 2 years
- In person yearly meeting at PAG
- AgBioData communication website developed

NRSP10 Workshop at ASHS

- An NRSP10 Workshop has been organized for September, 2017 at annual ASHS meeting
- Focuses on presentations by users of NRSP10 resources
- Discussion on users needs and future of NRSP10

[\(id=25937\) What Is NRSP10 and What Can It Do for Specialty Crop Research](#) . **D. Main**

[\(id=25935\) NRSP10 Resources for Translational Tree Fruit Research](#) . **C. P. Peace**

[\(id=25936\) Using Tripal As a Project Database](#) . **M. Staton**

[\(id=25900\) NRSP10 Resources for Small Fruit Research](#) . **N. Bassil**

[\(id=25901\) Using Gensas for Specialty Crop Community Genome Annotation](#) . **J. Humann**

[\(id=25899\) Using Fieldbook and Other Free Apps for Specialty Crop Field and Lab Data Collection](#) . **T. Rife**

[\(id=25898\) A Breeders Perspective on Using the Breeding Information Management System for Fruit Breeding](#) . **K. Gasic**

[\(id=25939\) Open Discussion on Direction of NRSP10](#) . **M. Kahn**

NRSP 10 Future

- We are investigating further avenues for sustainability of the NRSP10 resource - **Stakeholder driven and supported, including the possibility of commercialization (e.g. GenSAS)**
- **However** given (1) the uncertainty of current US funding and (2) the fact that our major grants all end in July-Oct 2019, we would like to explore the possibility of renewing NRSP10 for another 5 years from 2018 instead of 2019 – **will allow us retain some of our highly skilled core team**

and years working in the Mainlab

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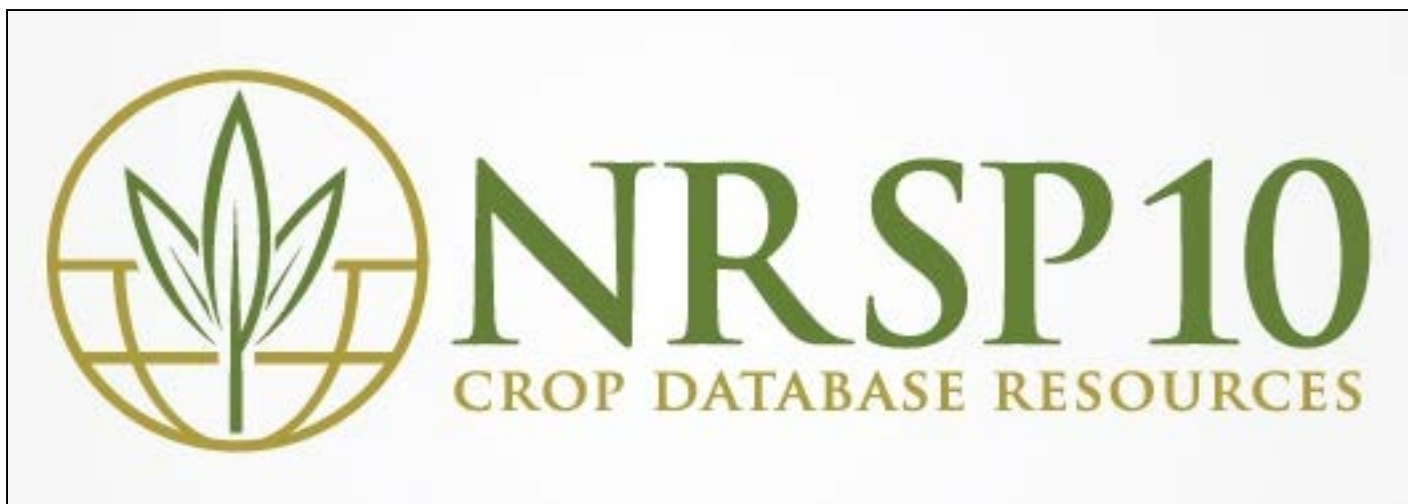
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Thanks for your attention
and support



Acknowledged with Thanks

- Mainlab Bioinformatics Team
- Project coPIs and associated project Pis/CoPIs
- Rosaceae, Citrus, Cacao, Blueberry, Legume, Cotton and Bioinformatics Communities
- USDA NIFA SCRI, NSF Plant Genome Program, USDA-ARS, SAAEDS, Mars Inc, Washington Tree Fruit Research Commission, Cotton Incorporated, USA Dry Pea and Lentil Commission, Northern Pulse Growers
- US Land Grant University researchers and extension agents