# NRSP_temp321

# Database Resources for Crop Genomics, Genetics and Breeding Research

## NPGCC Meeting June 2014

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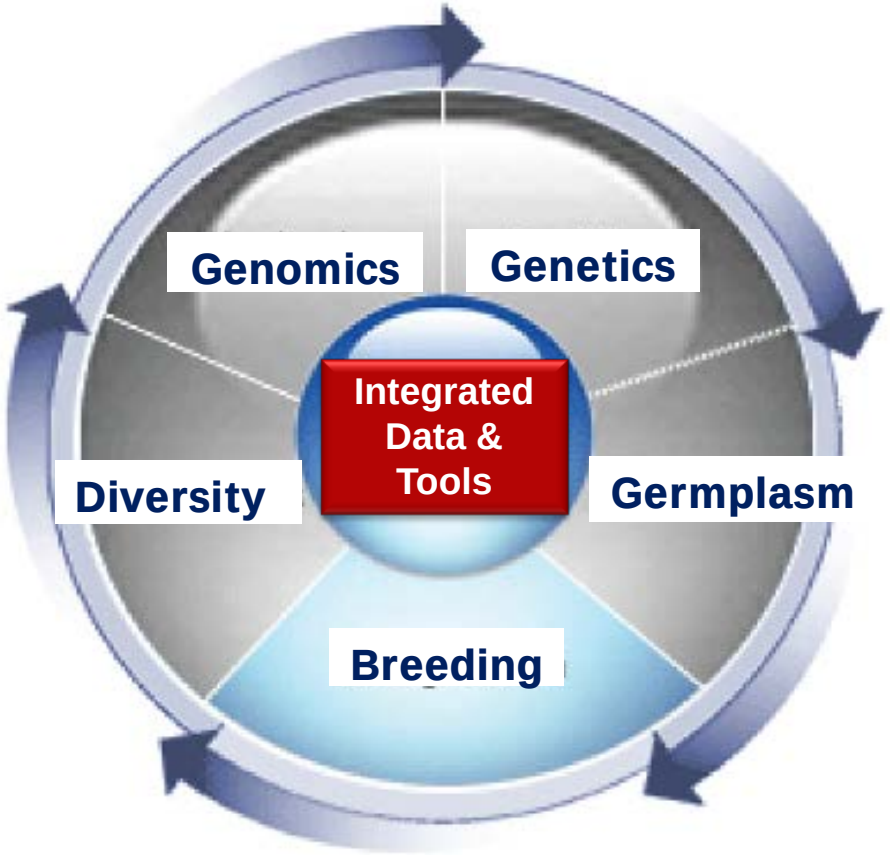
# The Challenge

- To continue to provide high-quality online community database resources for Rosaceae, Citrus, Cotton, Cool Season Food Legumes and *Vaccinium* crops – databases that are:
  - Easy to use
  - Easy to manage and update
  - Scalable and fast
  - **Resource efficient**
  - Utilize a common, interoperable platform
  - **Self-sustaining in the medium term**
  - Easy to adopt for other underserved crops

# Integrated Data Facilitates Discovery!

## Basic Science

- Structure and evolution of genomes
- Gene function
- Genetic variability
- Mechanism underlying traits

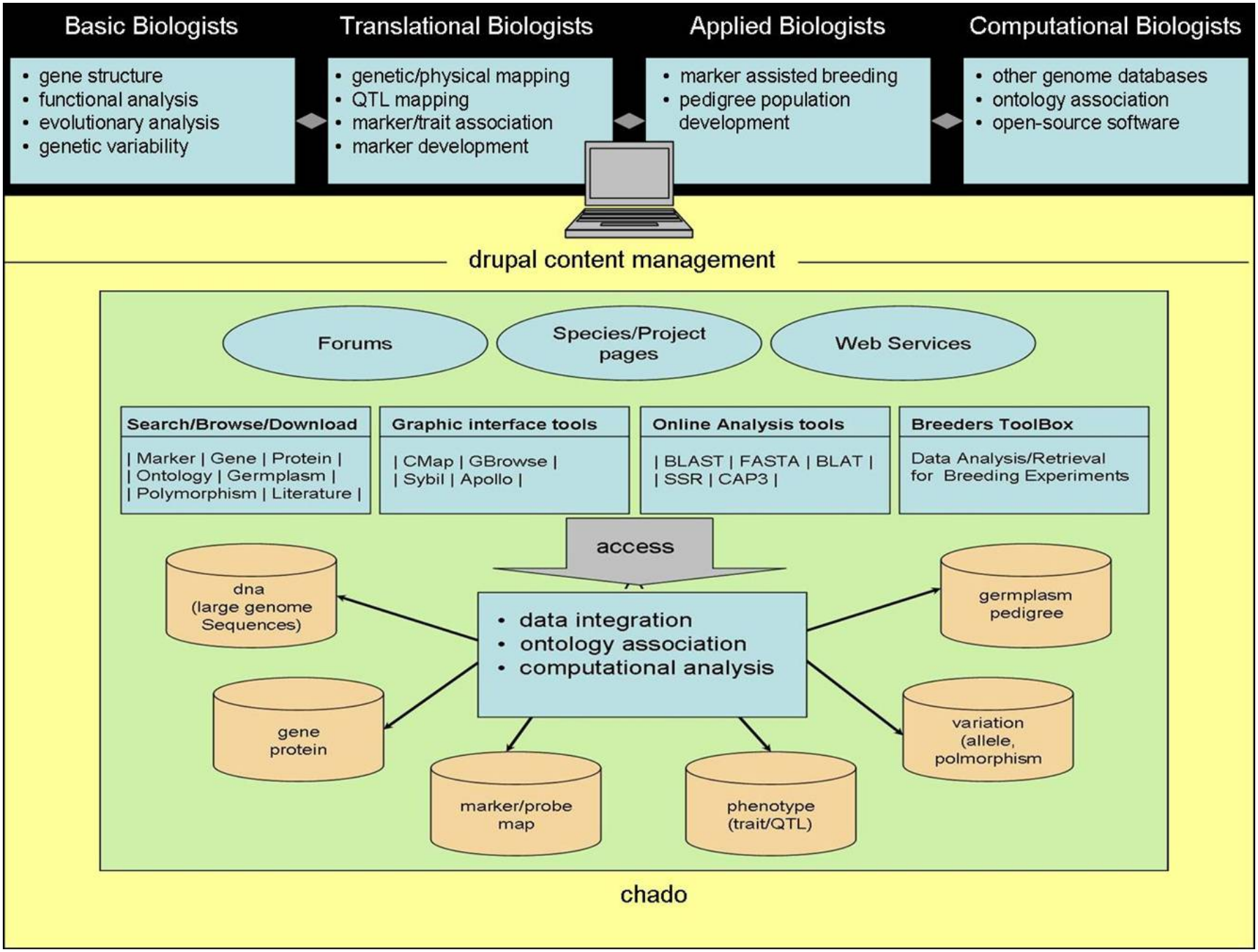



## Translational Science

- Trait discovery
- Marker development
- Genetic mapping
- Breeding values

## Applied Science

Utilization of DNA information in breeding decisions


Basic Biologists
• gene structure
• functional analysis
• evolutionary analysis
• genetic variability
Translational Biologists
• genetic/physical mapping
• QTL mapping
• marker/trait association
• marker development
Applied Biologists
• marker assisted breeding
• pedigree population development
Computational Biologists
• other genome databases
• ontology association
• open-source software
drupal content management
Forums
Species/Project pages
Web Services
Search/Browse/Download
| Marker | Gene | Protein | | Ontology | Germplasm | | Polymorphism | Literature |
Graphic interface tools
| CMap | GBrowse | | Sybil | Apollo |
Online Analysis tools
| BLAST | FASTA | BLAT | | SSR | CAP3 |
Breeders ToolBox
Data Analysis/Retrieval for Breeding Experiments
access
dna (large genome Sequences)
• data integration
• ontology association
• computational analysis
germplasm pedigree
gene protein
variation (allele, polmorphism
marker/probe map
phenotype (trait/QTL)
chado

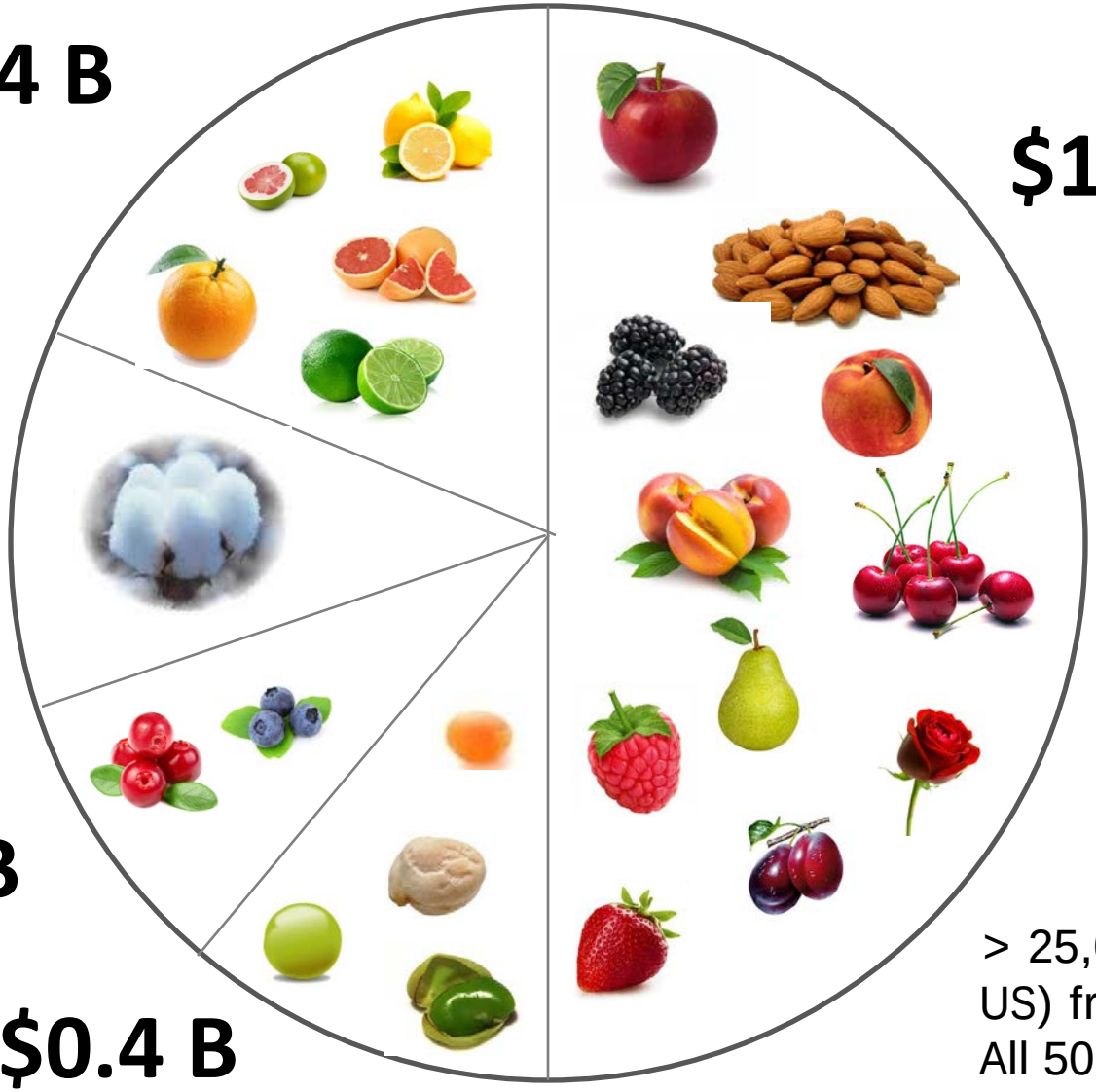
# Community Databases Even More Important!

Recent advances in sequencing, genotyping, and phenotyping technologies have led to a paradigm shift in crop science research – "Big Data" driven

**Individual scientists now routinely**

- Sequence and genotype genomes from populations, families, individuals of interest
- Pursue large-scale gene expression studies
- Create highly saturated genetic maps
- Identify genome wide loci influencing traits of interest
- Conduct large-scale standardized phenotyping.

# Why These Crops?



$3.4 B

$12.3 B

$6.0 B

$1.2 B

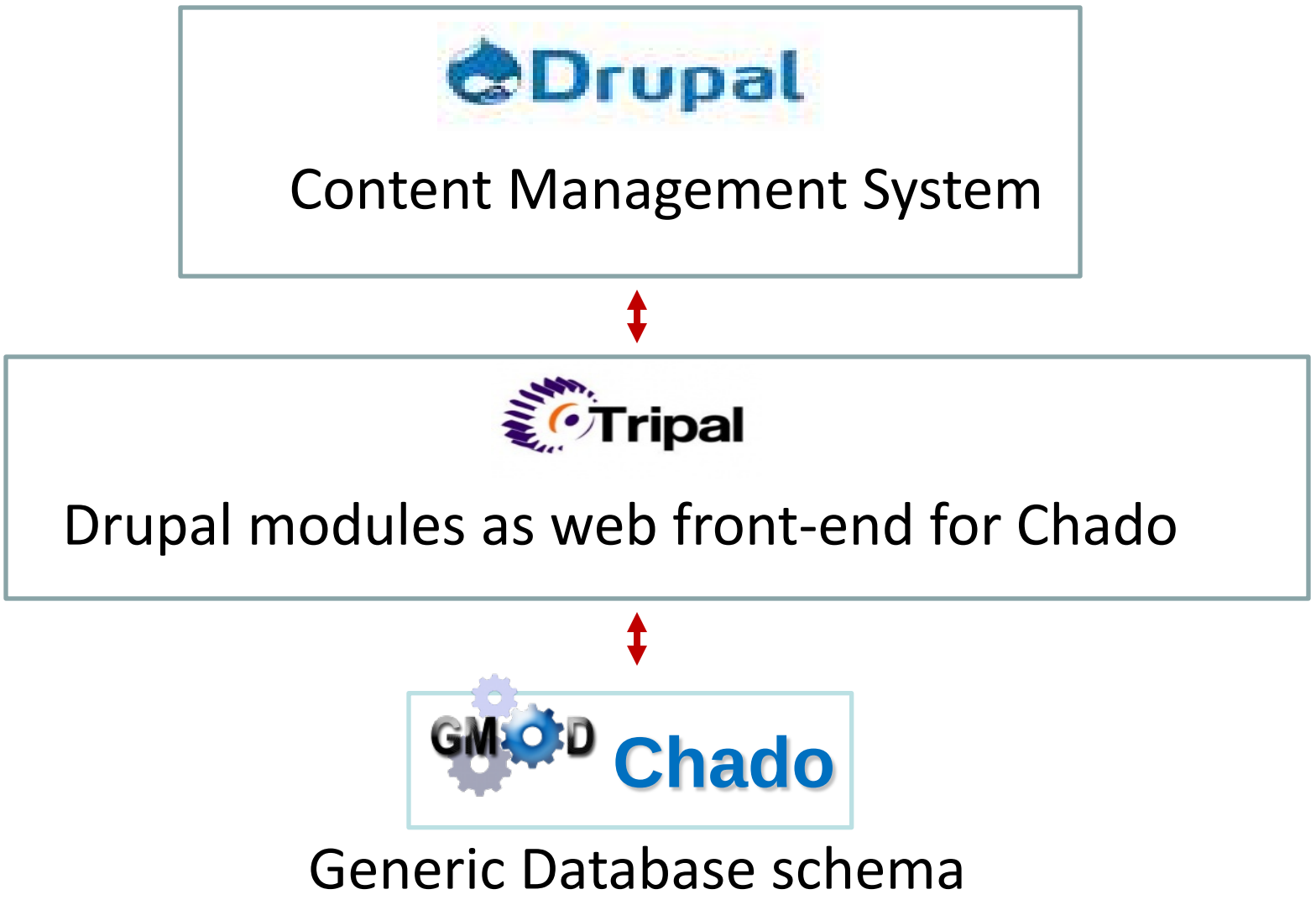
$0.4 B

> 25,000 users (60% US) from 130 countries
All 50 states

# Vision

- Enable basic, translational and applied crop research by expanding existing online databases currently housing high-quality genomics, genetics and breeding data for Rosaceae, Citrus, Cotton, Cool Season Food Legumes and Vaccinium crops – **underserved crops**
- Provide a complete open-source, flexible, database solution – **Tripal**
- Develop a model for long term sustainability of community databases – **Stakeholder driven and supported**

# Database Solution



DATABASE
The Journal of Biological Databases and Curation

*Database*, Vol. 2011, Article ID bar051, doi:10.1093/database/bar051

## Database tool

# The Chado Natural Diversity module: a new generic database schema for large-scale phenotyping and genotyping data

**Sook Jung[1,*,†], Naama Menda[2,*,†], Seth Redmond[3,‡], Robert M. Buels[2], Maren Friesen[4], Yuri Bendana[4], Lacey-Anne Sanderson[5], Hilmar Lapp[6], Taein Lee[1], Bob MacCallum[3], Kirstin E. Bett[5], Scott Cain[7], Dave Clements[6,¶], Lukas A. Mueller[2] and Dorrie Main[1]**

[1]Department of Horticulture and Landscape, Washington State University, Pullman, WA 99164, [2]Boyce Thompson Institute for Plant Research, Ithaca, NY 14853, USA, [3]Imperial College London, London SW7 2AZ, UK, [4]University of Southern California, Los Angeles, CA 90089, USA, [5]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada, [6]National Evolutionary Synthesis Center (NESCent), Durham, NC, USA and [7]Ontario Institute for Cancer Research, Toronto, Ontario, M5G 0A3, Canada

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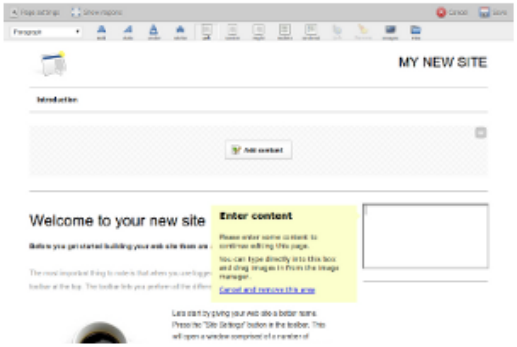
Drupal is free, flexible, robust and constantly being improved by hundreds of thousands of passionate people from all over the world. Join us!

Get Started with Drupal

## Sites Made with Drupal




Pagebuild Case Study

Drupal is used by some of the biggest sites on the Web, like The Economist, Examiner.com and The White House. Read more Drupal success stories.

## Develop with Drupal

| | | This week | |
|---|---|---|---|
| 14,121 | Modules | 3,250 | Code commits |
| 1,383 | Themes | 6,506 | Issue comments |
| 14,553 | Developers | | |

Drupal Core
Security Info
Developer Docs
API Docs

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Drupal

DATABASE
The Journal of Biological Databases and Curation

*Database*, Vol. 2013, Article ID bat075, doi:10.1093/database/bat075

# Original article

# Tripal v1.1: a standards-based toolkit for construction of online genetic and genomic databases

**Lacey-Anne Sanderson[1,†], Stephen P. Ficklin[2,†], Chun-Huai Cheng[2], Sook Jung[2], Frank A. Feltus[3], Kirstin E. Bett[1] and Dorrie Main[2,*]**

[1]Department of Plant Sciences, University of Saskatchewan. Saskatoon, SK Canada, [2]Department of Horticulture, Washington State University. Pullman, WA, USA and [3]Department of Genetics and Biochemistry, Clemson University. Clemson, SC, USA

***Correspondence author:** Tel: +1 509 335 9000; Fax: +1 509 335 8690; Email: dorrie@wsu.edu

[†]These authors contributed equally to this work.

Submitted 26 June 2013; Revised 9 September 2013; Accepted 27 September 2013

**Citation details:** Sanderson L-A., Ficklin S.P., Cheng C-H. *et al*. Tripal v1.1: a standards-based toolkit for construction of online genetic and genomic databases. *Database* (2013) Vol. 2013: article ID bat075; doi:10.1093/database/bat075.

Tripal

## QUICK LINKS

Download or Upgrade

**v2.0a Resources**
*Alpha Release for Drupal 7*
New Functionality
Installation and Tutorial

**v1.1 Resources**
*Stable Release for Drupal 6*
Installation and Tutorial
Developer's Handbook
Tripal v1.1 Demo Site

## NEWS

### Tripal v2.0a Released

The Tripal Development Team is pleased to announce an alpha release of Tripal 2.0 for Drupal 7

More

## NAVIGATION

- Feed aggregator

## USER LOGIN

Username *

Password *

Request new password

Log in

# Tripal

Tripal is a collection of open-source freely available Drupal modules and is a member of the GMOD family of tools. Tripal serves as a web interface for the GMOD Chado database and is designed to allow anyone with genomic data to quickly create an online genomic database using community supported tools. Tripal is licensed under the GNU General Public License version 2.

Sites currently using Tripal:

- Banana Genome Hub
- Cacao Genome Database
- Citrus Genome Database
- Cool Season Food Legume Genome Database
- CottonGen
- Fagaceae Genomics Web
- Genome Database for Rosaceae
- Genome Database for Vaccinium
- Hardwood Genomics Project
- KnowPulse: Pulse Crop Genomics & Breeding
- Legume Information System
- PeanutBase

Send an email to the Tripal mailing list if you would like your Tripal/Drupal/Chado site listed above!

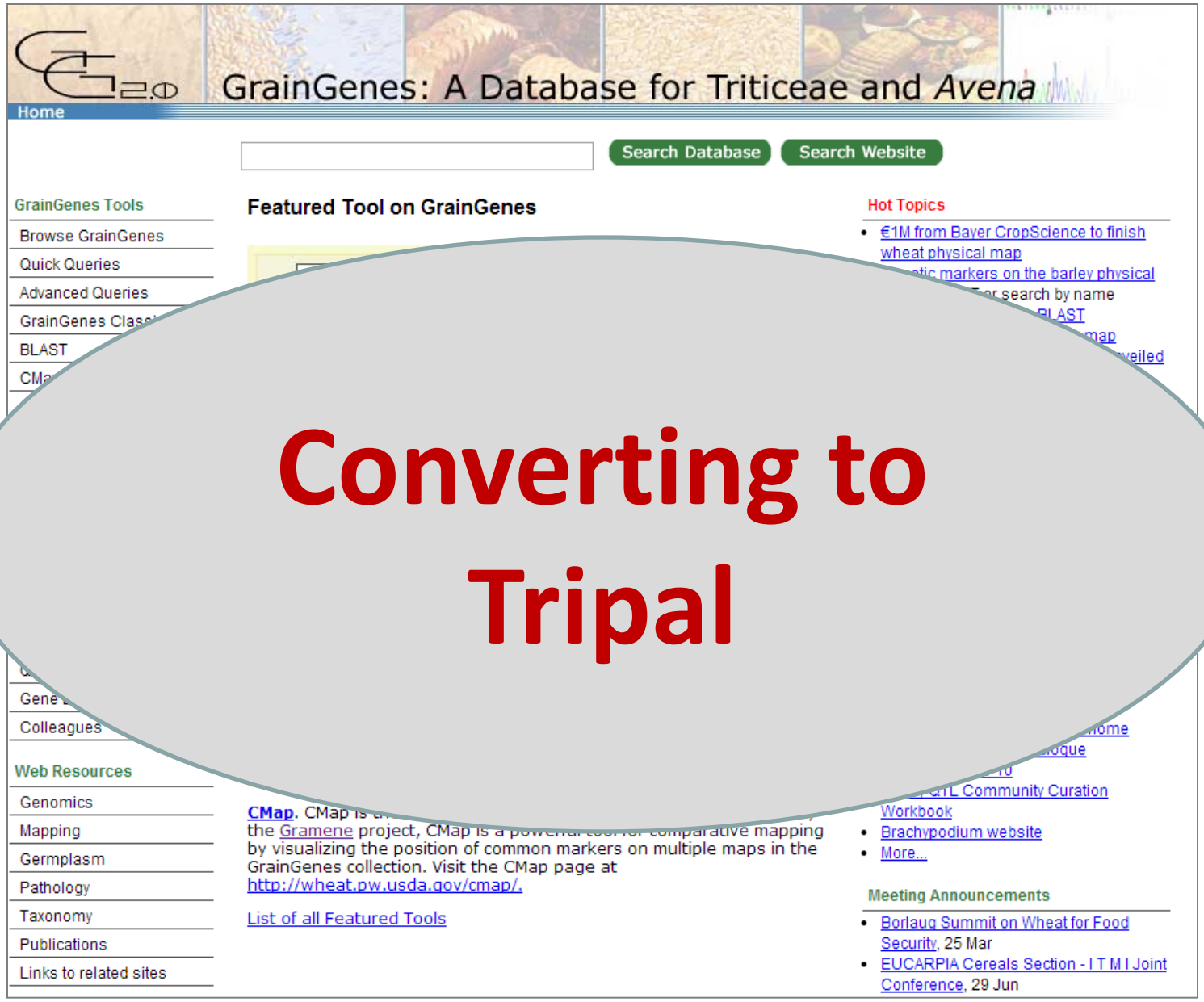
**To cite Tripal:**

Lacey-Anne Sanderson, Stephen P. Ficklin, Chun-Huai Cheng, Sook Jung, Frank A. Feltus, Kirstin E. Bett, and Dorrie Main. Tripal v1.1: a standards-based toolkit for construction of online genetic and genomic databases. *Database,* Sept 2013: bat075 doi:10.1093/database/bat075

Stephen P. Ficklin, Lacey-Anne Sanderson, Chun-Huai Cheng, Margaret Staton, Taein Lee, Il-Hyung Cho, Sook Jung, Kirstin E Bett, Dorrie Main. Tripal: a construction Toolkit for Online Genome Databases. *Database*, Sept 2011: bar044 doi:10.1093/database/bar044

**Contributing Organizations:**

Washington State University | University of Saskatchewan | CUGI | GMOD


GrainGenes: A Database for Triticeae and Avena
Home
Search Database
Search Website
GrainGenes Tools
Browse GrainGenes
Quick Queries
Advanced Queries
BLAST
Colleagues
Web Resources
Genomics
Mapping
Germplasm
Pathology
Taxonomy
Publications
Links to related sites
Featured Tool on GrainGenes
the Gramene project, CMap is a
by visualizing the position of common markers on multiple maps in the GrainGenes collection. Visit the CMap page at
http://wheat.pw.usda.gov/cmap/.
List of all Featured Tools
Hot Topics
€1M from Bayer CropScience to finish wheat physical map
Workbook
Brachypodium website
More...
Meeting Announcements
Borlaug Summit on Wheat for Food Security, 25 Mar
EUCARPIA Cereals Section - I T M I Joint Conference, 29 Jun
Converting to Tripal

# LIS

Legume Information System

Select Language

Powered by Google Translate

Home | About | News | Search | Maps | Species | Collaborators | Resources

## Entry Points

**Sequen**

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tree

**CViT Genome**

Search for sequences or ge

whole-genome views and synteny plots

legume reference genomes.

*MST* -- Open

in computational and

utionary biology

The project involves...

Read More »

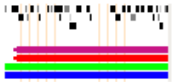
*November 11, 2013 at 16:49 MST* -- Cowpea Consortium SNP Genotyping Chip

Researchers at the University of California, Riverside,...

**Genome Browsers**

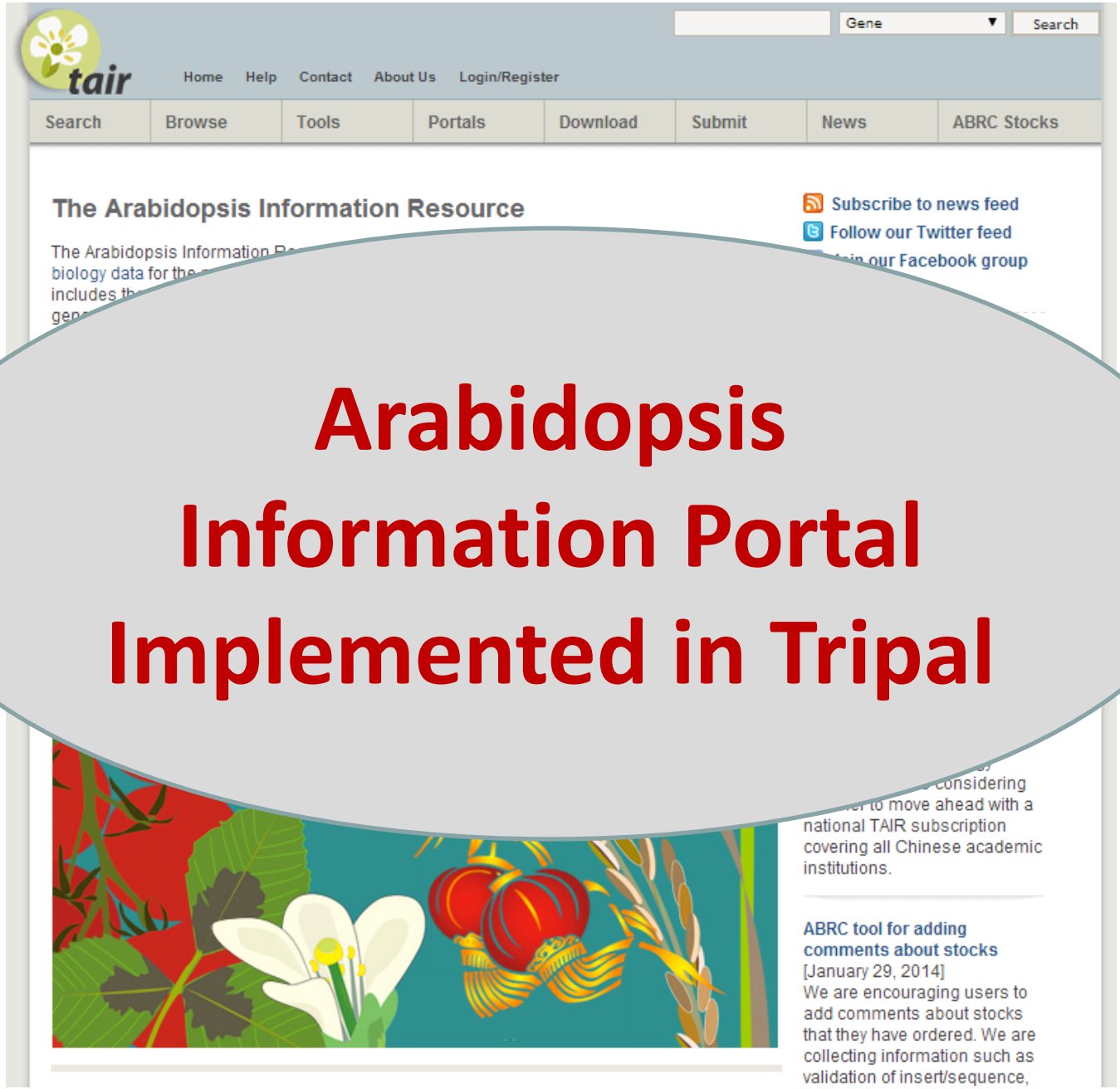
Chromosome- to gene-scale views of the *Lotus japonicus*, *Medicago truncatula*, *Cajanus cajan* (pigeonpea), and *Glycine max* (soybean) genomes

Go

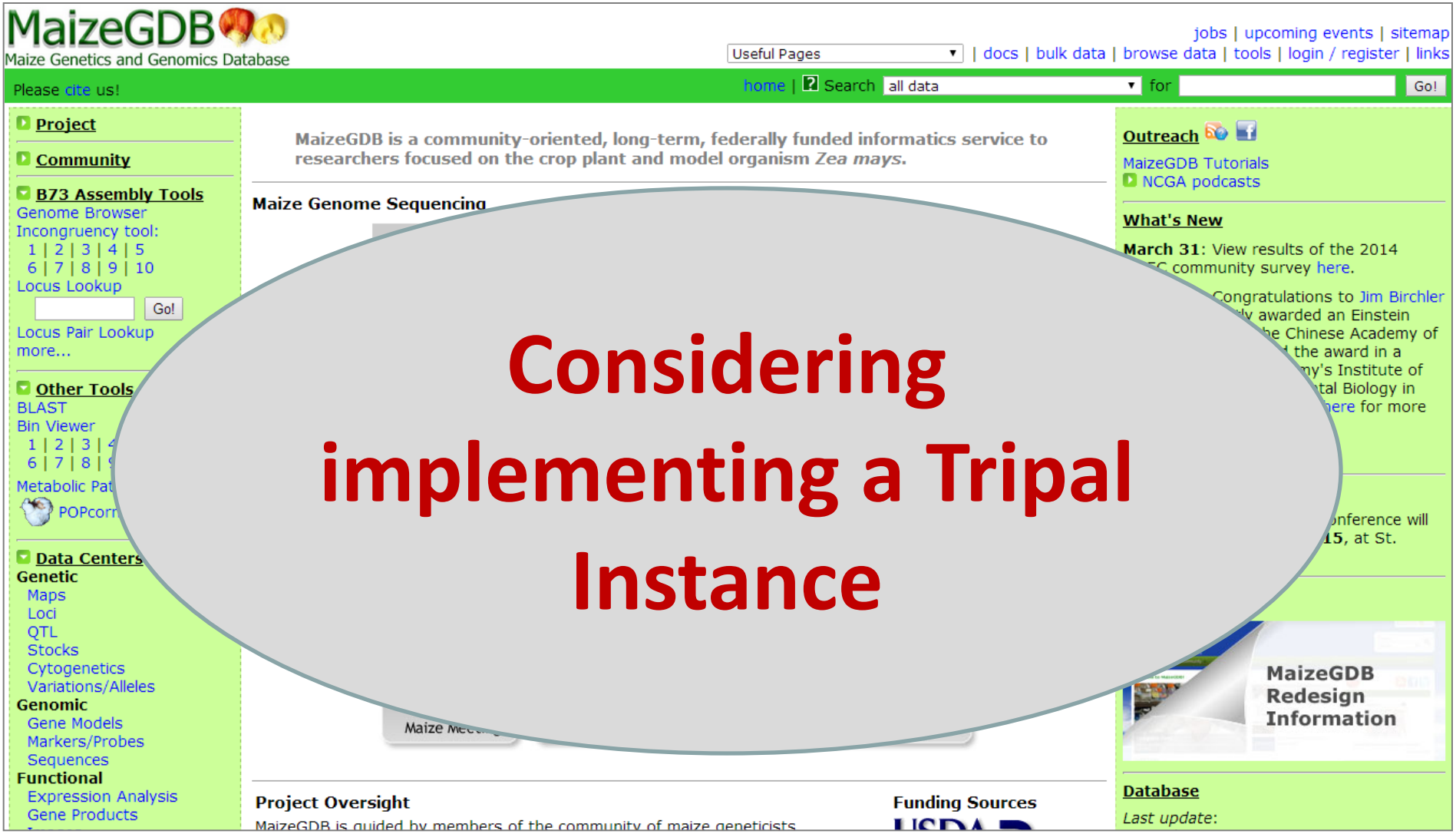


# Converting to Tripal

Home
Site Map
Site Stats
Contact Us
Dendrome
A Forest Tree Genome Database
Welcome
Research
TreeGenes
DiversiTree
FTGSC
iPlant
Resources
Events
News
Jobs
Links
Help
Downloads
Welcome to the Dendrome Proj
NATURE GENETICS
Converting to Tripal
Project Resources
AdapTree
Conifer Translational Genomics Network
TREEGENES CONNECT




# Arabidopsis Information Portal Implemented in Tripal


MaizeGDB
Maize Genetics and Genomics Database
jobs | upcoming events | sitemap
Useful Pages | docs | bulk data | browse data | tools | login / register | links
Please cite us!
home | Search all data for Go!
Project
Community
B73 Assembly Tools
Genome Browser
Incongruency tool:
1 | 2 | 3 | 4 | 5
6 | 7 | 8 | 9 | 10
Locus Lookup
Go!
Locus Pair Lookup
more...
Other Tools
BLAST
Bin Viewer
Metabolic Pat
POPcorn
Data Centers
Genetic
Maps
Loci
QTL
Stocks
Cytogenetics
Variations/Alleles
Genomic
Gene Models
Markers/Probes
Sequences
Functional
Expression Analysis
Gene Products
MaizeGDB is a community-oriented, long-term, federally funded informatics service to researchers focused on the crop plant and model organism Zea mays.
Maize Genome Sequencing
Considering implementing a Tripal Instance
Project Oversight
MaizeGDB is guided by members of the community of maize geneticists
Funding Sources
Outreach
MaizeGDB Tutorials
NCGA podcasts
What's New
March 31: View results of the 2014 community survey here.
Congratulations to Jim Birchler awarded an Einstein
the Chinese Academy of
the award in a
my's Institute of
tal Biology in
here for more
nference will
15, at St.
MaizeGDB Redesign Information
Database
Last update:

# Other Confirmed Tripal Databases

| Site | Species | Location |
|---|---|---|
| 1. Arabidopsis Information Portal | Arabidopsis | Rockville MD, USA |
| 2. Cacao Genome Database | *Cacao matina* | Ames IA, USA |
| 3. PeanutBase | *Arachis spp* | Ames IA, USA |
| 4. Legume Information System | various legumes | Ames IA, USA |
| 5. i5K Workspace @ USDA NAL | 30 insect genomes | Beltville, MD USA |
| 6. Fagaceae Genomics Web | *Fagaceae spp* | Clemson SC, USA |
| 7. MarineGenomics.org | various species | Clemson SC, USA |
| 8. GeneNet Engine | various species | Clemson SC, USA |
| 10. Banana Genome Hub | *Musa acuminata* | France |
| 11. Hardwood Genomics | various species | Knoxville TN, USA |
| 12. Fragaria x ananassa strawberry | strawberry | Malaga, Spain |
| 13. NECC Little Skate Gnome | *Leucoraja erinacea* | Newark, DE |
| 14. LiceBase | *Salmon louse* | Norway |
| 15. Wild Strawberry | *Fragaria* | OSU Orgeon, USA |
| 16. Chlamydomonas database | Chlamydomonas | Palo Alto, CA USA |
| 17. Amborella Genome | *Amborella trichopoda* | PennState PA/Athens GA, USA |
| 18. Ruditapes decusssatus db | *Ruditapes decusssatus* | Portugal |
| 19. Know Pulse | various legumes | Saskatoon SK, Canada |
| 20. Koala Genome Cosortium | *Phascolarctos cinereus* | Sydney Australia |

GDR | Genome Database for Rosaceae
Search
Login
Home | Contact
General
Help
Species
Data
Search
Tools
Breeders Toolbox
Community
Genomic, Genetic, and Breeding Resources
for Rosaceae Crop Improvement
• Crops annual production value in 2012 = $12.6 B
• Database established 2003 (NSF, USDA, Industry, University - $4 M )
• 14,237 users (from 52 US States/territories, 130 countries)
176,259 pages accessed
Washington State University
Funded by the 2009 USDA NIFA Specialty Crop Research Initiative Program
Copyright © 2002-2014. This site is designed to work with IE8, Mozilla, Safari and Opera.
Clemson University

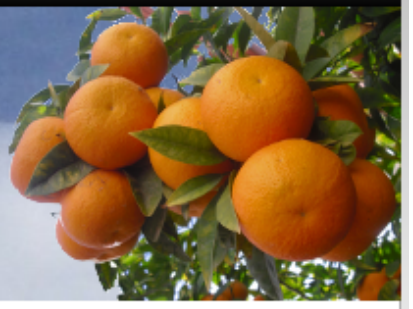
# Citrus Genome Database

Logged in as: dorrie | Log Out

Home | Species | Tools | Downloads | Community | About | Contact | Search | Administer

The Genomics, Genetics and Breeding Resource for Citrus

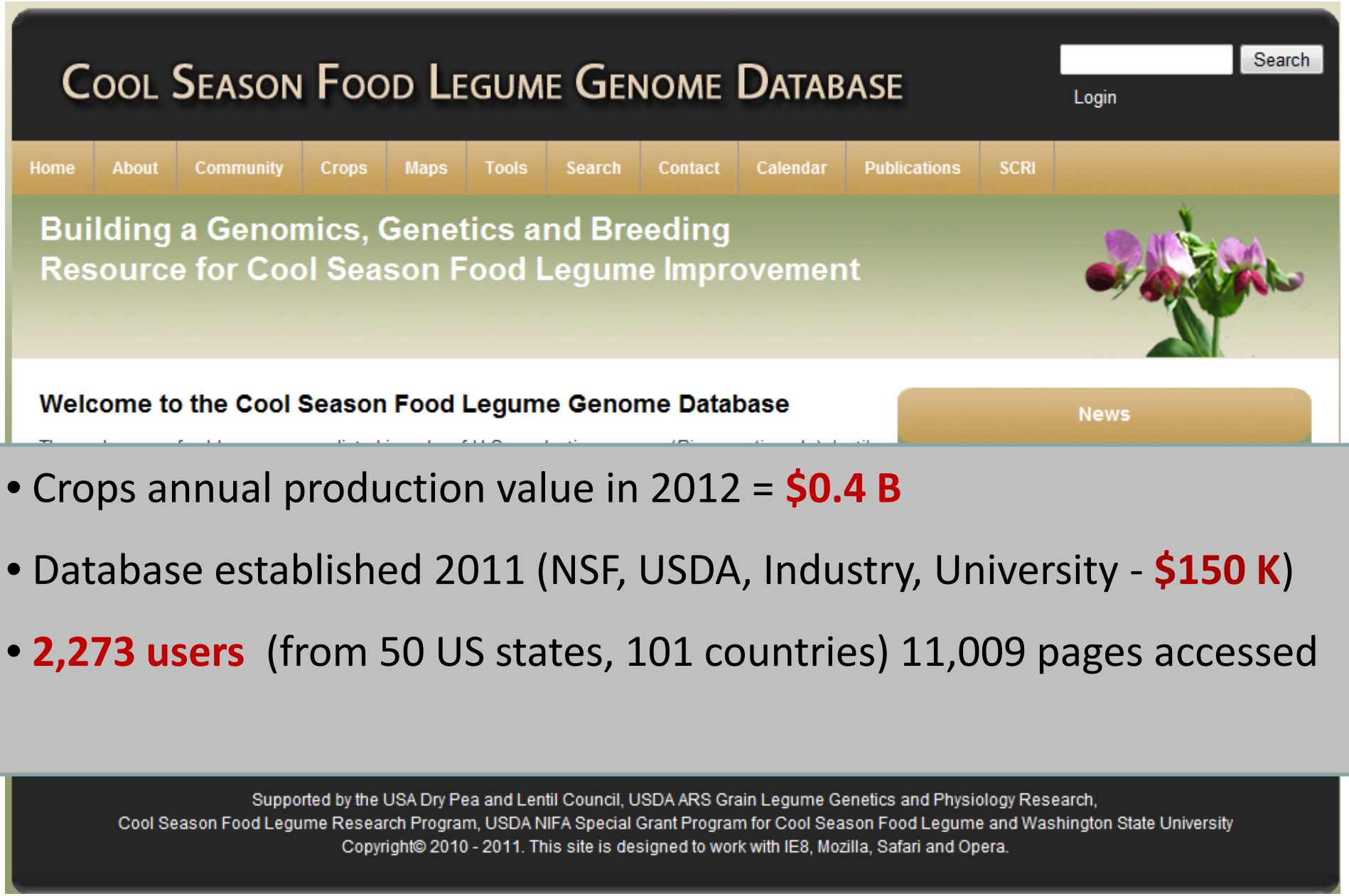
A collaboration of tree fruit breeders, genomicists, bioinformaticians, stakeholders, and extension educators



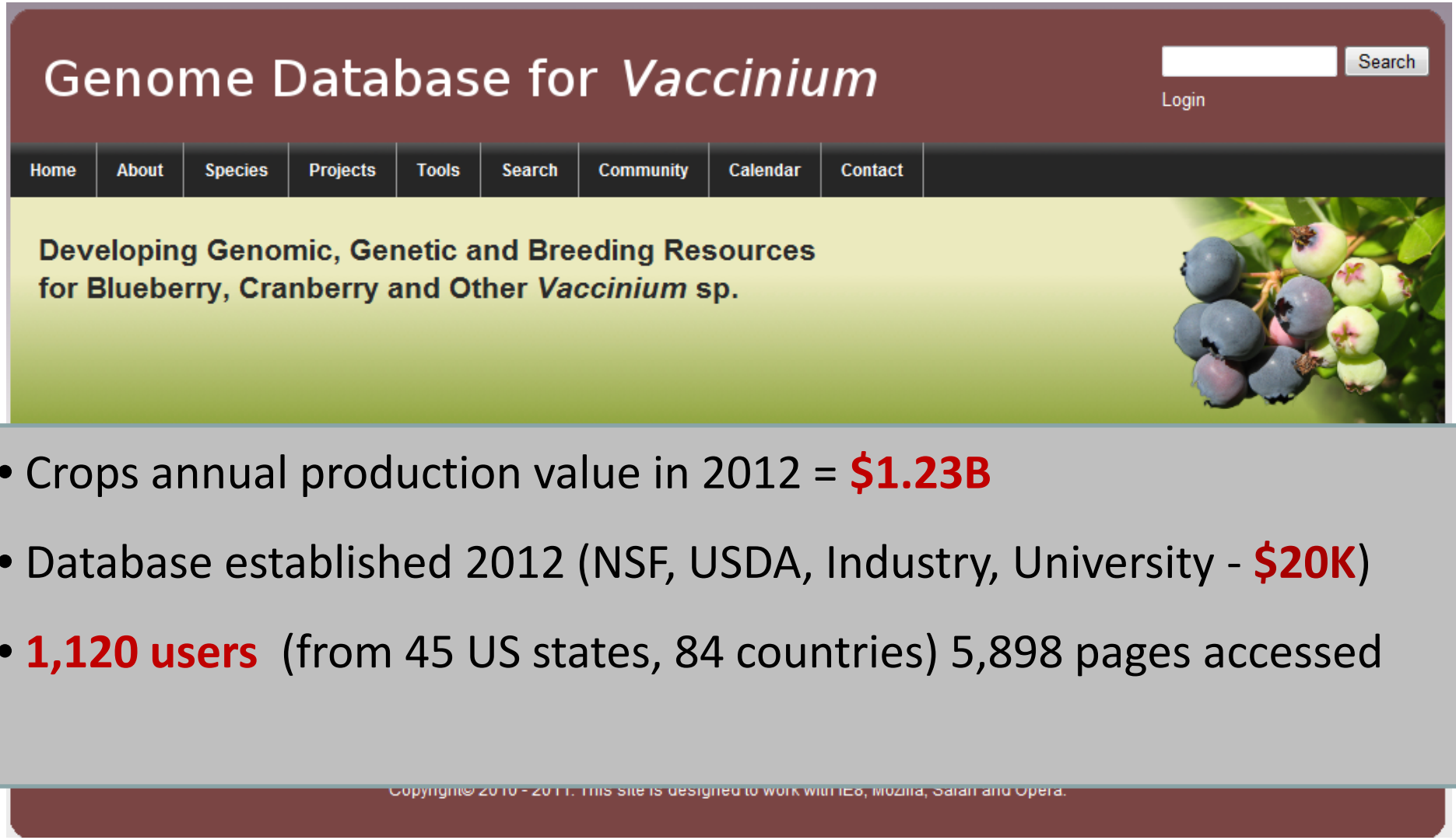
- Crops annual production value in 2012 = **$3.44 B**
- Database established 2009 (NSF, USDA, Industry, University - **$1 M**)
- **5,244 users** (from 49 US states/territories, 125 countries) 34,475 pages accessed

Funded by the 2009 USDA NIFA Specialty Crop Research Initiative Program.
Database developed and hosted at Washington State University by Mainlab Bioinformatics. Copyright 2011-2012

- Crops annual production value in 2012 = **$5.97 B**
- Database established 2011 (NSF, USDA, Industry, University - **$860 K**)
- **2,320 users** (from 43 US states, 74 countries) 46,279 pages accessed

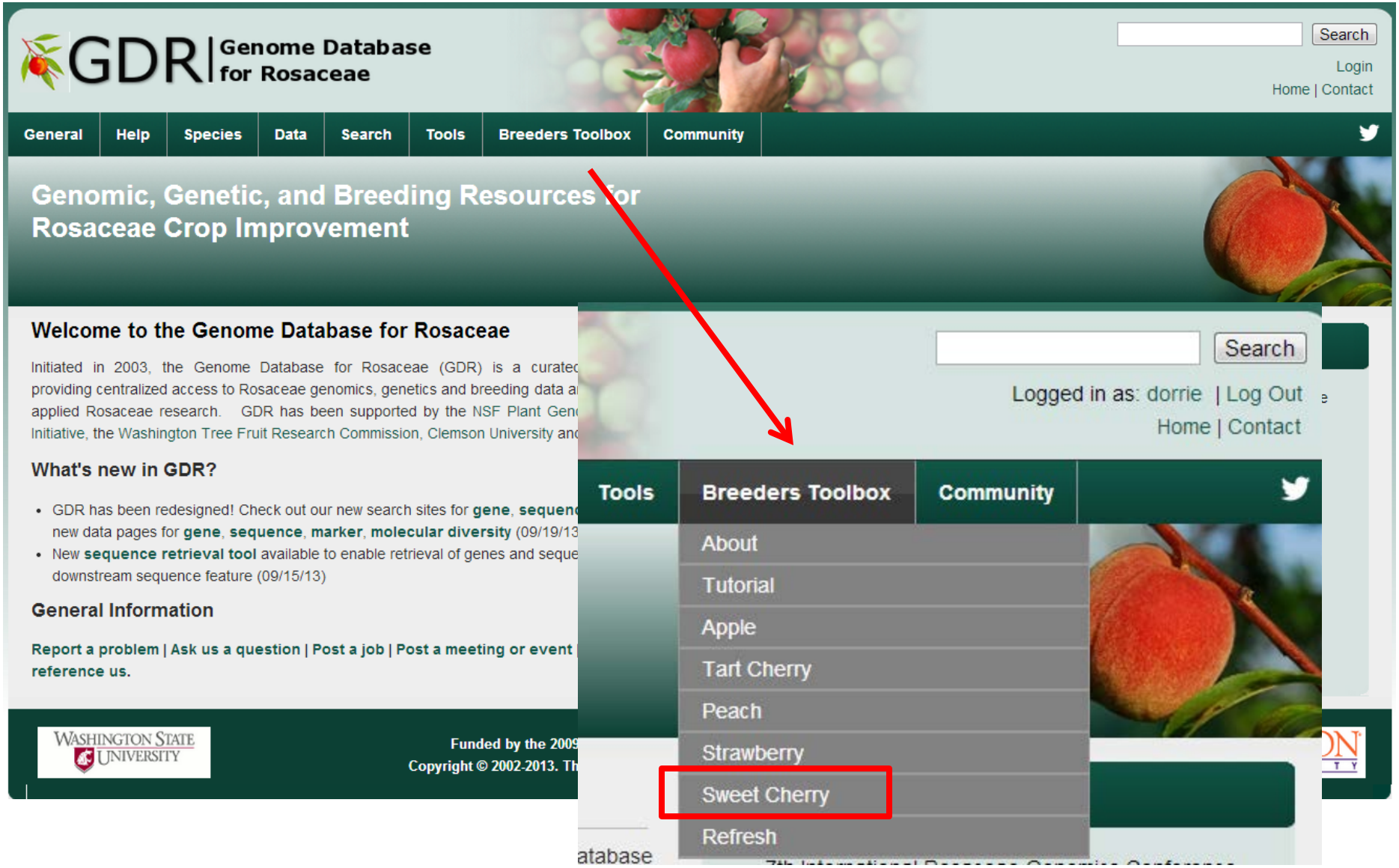



- Crops annual production value in 2012 = **$0.4 B**
- Database established 2011 (NSF, USDA, Industry, University - **$150 K**)
- **2,273 users** (from 50 US states, 101 countries) 11,009 pages accessed




- Crops annual production value in 2012 = **$1.23B**
- Database established 2012 (NSF, USDA, Industry, University - **$20K**)
- **1,120 users** (from 45 US states, 84 countries) 5,898 pages accessed

# Example of Breeding Functionality in the GDR



## Choose Crop

**Set Crop** — Sweet Cherry (RosBREED)

## Choose Breeding Group

**Set Breeding Group** — SWEET CHERRY CRS/BPS WA

## Browse Database

**Browse Varieties**

- Browse Varieties by Datasets

## Search Database

**Search Phenotyping Data**

- Search by Varieties
- Search by Traits
- Search by Parentage

**Search Genotyping Data**

- Search by Varieties
- Search by Variety/Marker
- Search by Marker/Allele

## Documentation

**Descriptors**

- View Descriptors
- Download Descriptors

**Tutorials**

- Tutorials for Public Users

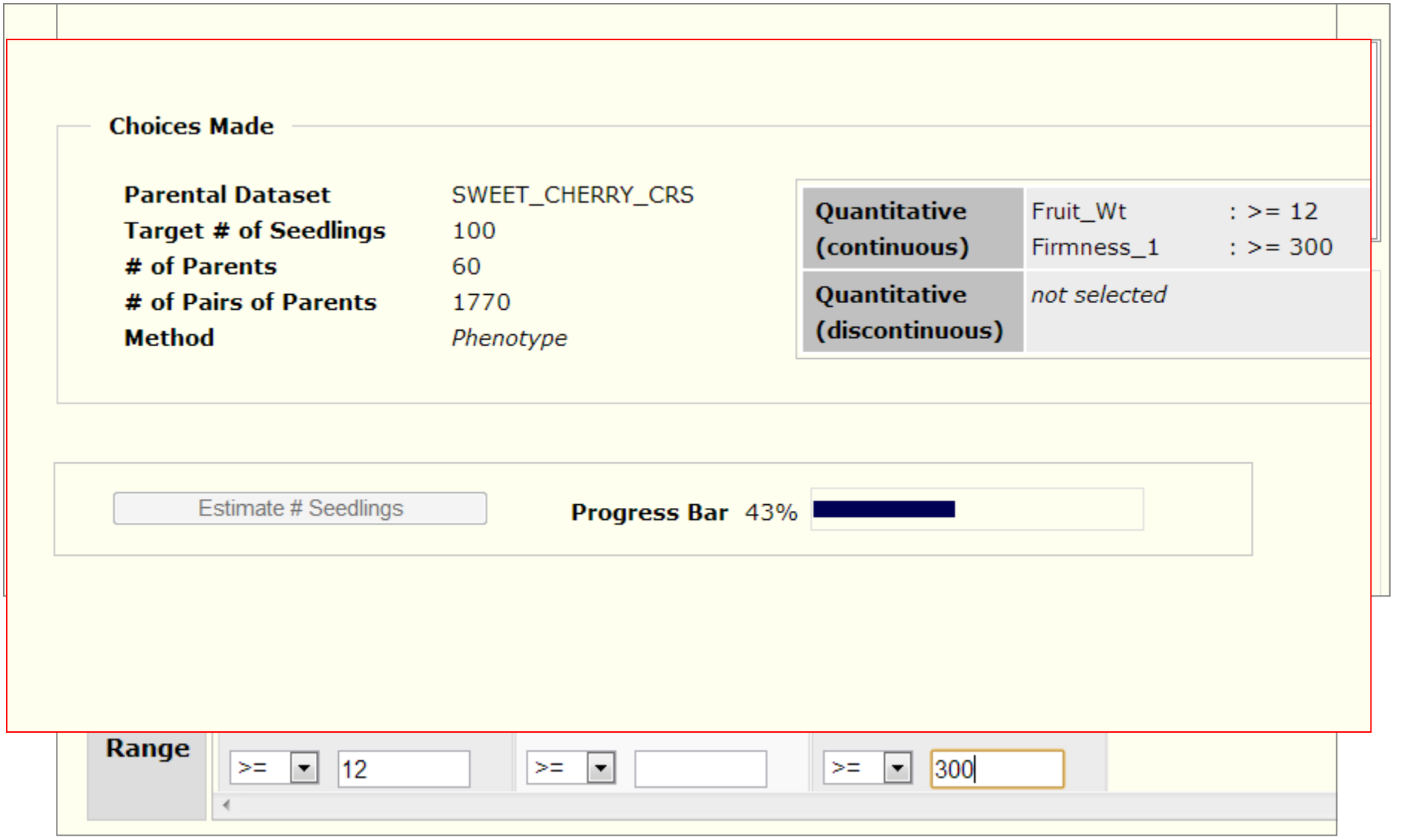
**Data Template**

- Download Data Template

## BIMS Tools (*Under Development*)

- Input File for Pedimap
- Trait Locus Warehouse
- Selection Target Identifier
- Marker Converter
- QTL Validator
- Cross Assist
- Technology Portfolio
- Seedling Select

# Cross Assist: Generates a list of parents and the number of seedlings to get progeny with desired traits



## Filter Results

**Flag** ☑ ● ☐ ●

**Number of Seedlings** < 

**Mother** cowiche

**Father**

Reset Filter | Filter Results

● Both parents have data for all selected traits
● One parent has no data for at least one trait

**Cross List**

Download Results

| | # of Seedlings Required ▲ | Mother | Father | Formula |
|---|---|---|---|---|
| ● | 187 | Cowiche | Selah | $f_x$ |
| ● | 212 | Cowiche | Lapins | $f_x$ |
| ● | 250 | Cowiche | Rainier | $f_x$ |
| ● | 283 | Cowiche | Sweetheart | $f_x$ |
| ● | 342 | Cowiche | PMR-1 | $f_x$ |
| ● | 351 | Cowiche | Ambrunes | $f_x$ |
| ● | 372 | Cowiche | Chelan | $f_x$ |
| ● | 379 | Cowiche | Glacier | $f_x$ |
| ● | 379 | Cowiche | Van | $f_x$ |
| ● | 381 | Cowiche | 9816-078 | $f_x$ |
| ● | 403 | Cowiche | JJ | $f_x$ |
| ● | 432 | Cowiche | Kiona | $f_x$ |
| ● | 462 | Cowiche | 9816-103 | $f_x$ |
| ● | 473 | Cowiche | 9816-083 | $f_x$ |

# Home Page of Kate Evans' Breeding Program

View | Edit

Page *Home Page of Kate Evans' Breeding Program* has been updated.

## Kate's Apple Breeder Group

- Create Calendar Event
- Create Group Document
- 6 members
- Manager: cho
- My membership

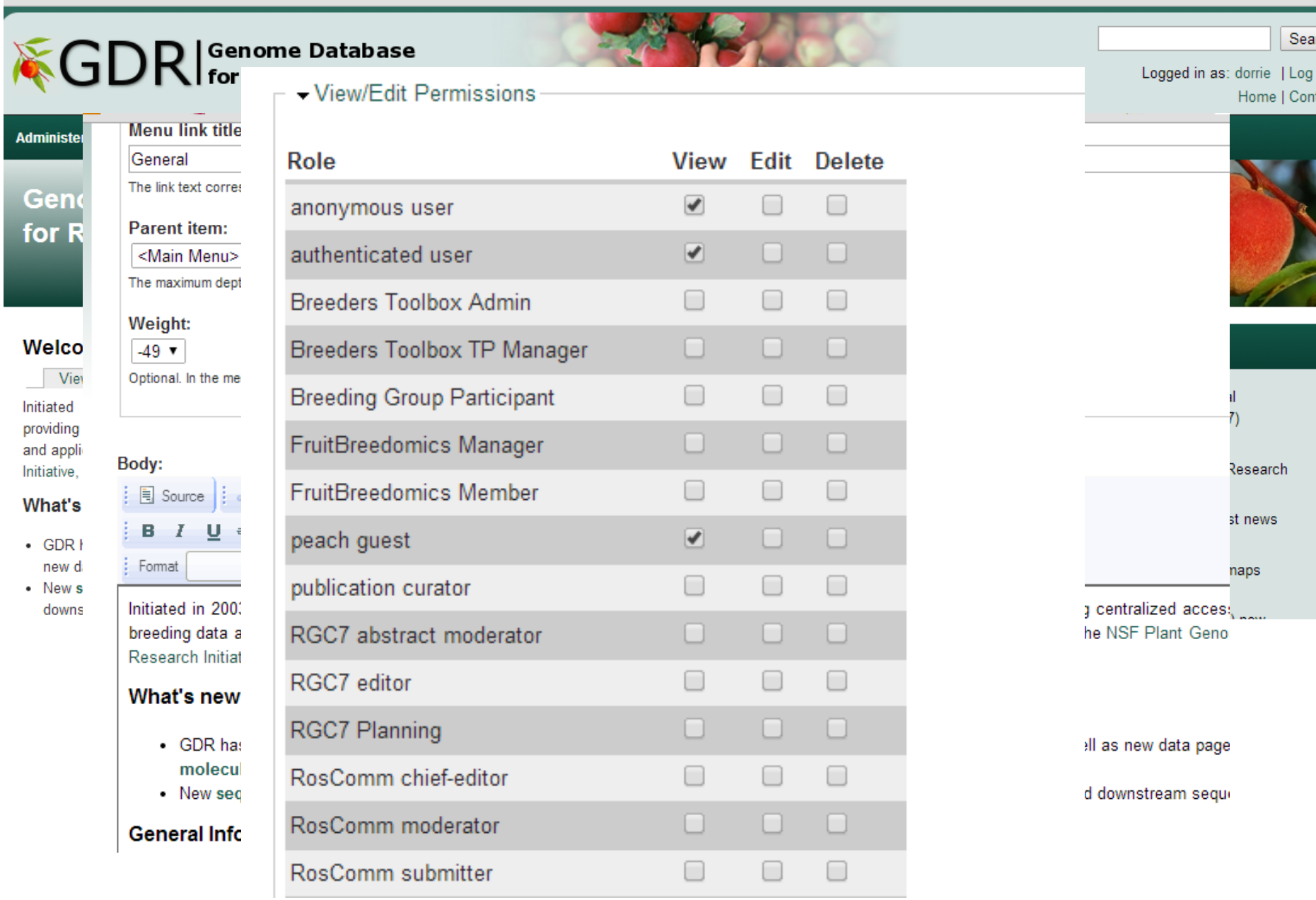
### Breeders ToolBox

Browse Germplasm
Search by Germplasm Name
Search by Evaluation Data
Search by Parentage

# Breeding Program Outline

The Washington State University apple breeding program began in 1994 to develop new varieties suitable to the unique climate of central Washington. Washington is the leading apple producing state with over 50% of U.S. production. Unfortunately, many of the new varieties developed in the world are not well adapted to growing conditions in central Washington or available to the majority of Washington growers.

The goal is to produce apples of a high eating quality with particular factors of outstanding flavor, texture and juiciness. The breeding program is a traditional breeding program, hybridizing parents with desirable traits. Promising seedlings are selected from large populations and their fruit is evaluated in the laboratory for eating quality and suitability for long-term storage. This program is one of the 12 core US breeding programs of the SCRI RosBREED project, enabling the application of marker-assisted breeding within the 4 years of the project.


GDR
Genome Database
for
Logged in as: dorrie | Log
Home | Con
Administer
Menu link title
General
The link text corres
Parent item:
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View/Edit Permissions
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Delete
anonymous user
authenticated user
Breeders Toolbox Admin
Breeders Toolbox TP Manager
Breeding Group Participant
FruitBreedomics Manager
FruitBreedomics Member
peach guest
publication curator
RGC7 abstract moderator
RGC7 editor
RGC7 Planning
RosComm chief-editor
RosComm moderator
RosComm submitter
Research
st news
naps
g centralized acces
he NSF Plant Geno
ll as new data page
d downstream sequ

Breeder without
an up to date,
comprehensive database

Button-clicking energized Breeder using an up to date database to help make breeding-decisions

# Specific Objectives

1. Expand online community databases currently housing high quality genomic, genetic and breeding data for Rosacaeae, citrus, cotton, cool season food legumes and *Vaccinium* crops
2. Develop/Implement a tablet application to collect phenotypic data from field and laboratory studies
3. Develop a Tripal Application Programming Interface for building breeding databases
4. Convert GenSAS, a community genome annotation tool, to Tripal
5. Develop Web Services to promote database interoperability

# Tripal Databases Sustainability

- Database development consists of two components
  - Core development activities
  - Data analysis and curation activities
- Database costs can be split into 4 types
  - Core development (developers, db/sys administrators)
  - Data analysis and curation (data curators)
  - Operational costs (equipment, software, space, etc.)
  - Interaction costs (investigators, travel, etc)

# Tripal Databases Sustainability Model

- Core database developer salaries funded by NRSP for 5 years, benefits funded by WSU
- Data curators salaries and benefits funded by stakeholders (commodity commissions, grants, etc) - Steering Committee Input
- Curator/analyst positions can be located anywhere
- Other orphan crops can buy into this model or implement a Tripal database themselves (and we will provide support)

# The Team

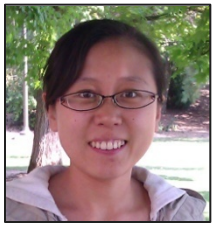
8

3

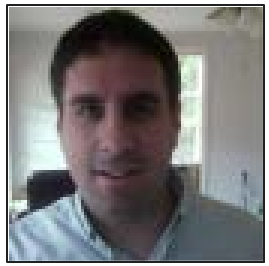
8

2

1



12



3

3

11

# **Budget Request** ($1,991,190 out of $4,158,132 )

| Description | Yr1 | Yr2 | Yr3 | Yr4 | Yr5 |
|---|---|---|---|---|---|
| Salaries | 488,154 | 596,058 | 25% NRSP core activities funded by other sources | 338,969 | 50 % NRSP core activities funded by other sources |
| | 303,631 | 315,165 | | 338,969 | |
| Fringe benefits | 170,632 | 219,097 | | 105,068 | |
| Supplies | 54,872 | 53,000 | | 35,000 | |
| | 35,000 | 35,000 | | 35,000 | |
| Travel | 25,000 | 37,000 | | 20,000 | |
| | 20,000 | 20,000 | | 20,000 | |
| Hardware | 60,000 | | | | |
| | 40,000 | | | | |
| Maintenace | 197,327 | 197,288 | | 134,759 | |
| **Project Total** | **975,985** | **1,102,443** | | **673,796** | |
| | | | | | |
| **NRSP Request** | **398631** | **370165** | | **433969** | |

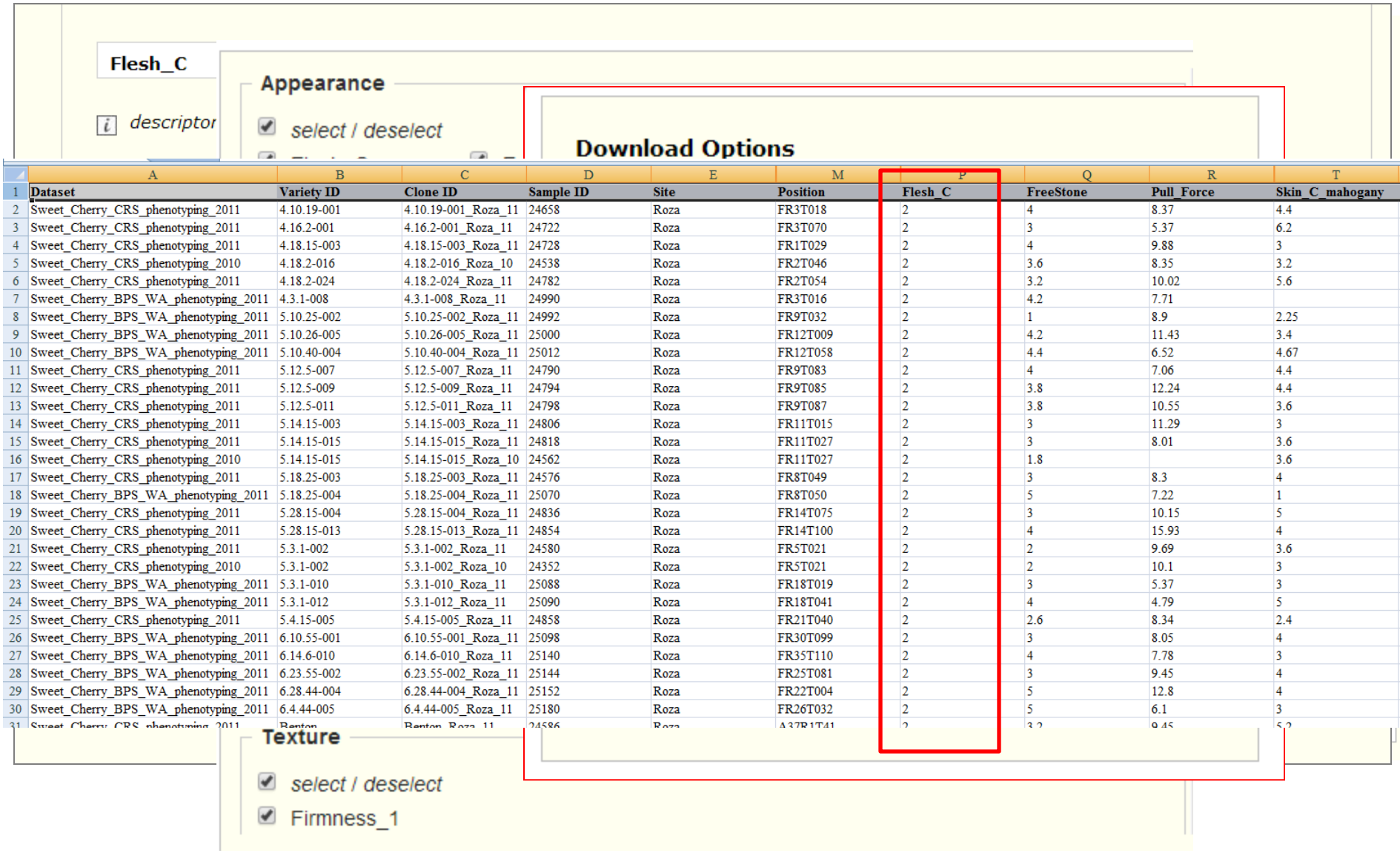
## All detailed in the Business Plan

# Acknowledgements


- Mainlab Bioinformatics Team
- Project coPIs/Pis
  - tfGDR (GDR and Citrus); Cacao Genome Database; Pine Genome Sequencing Project; Genome Database for Vaccinium; Cool Season Food Legume Database; CottonGen
- Rosaceae, Citrus, Cacao, Blueberry, Legume, Cotton and Bioinformatics Communities
- USDA NIFA SCRI, USDA DOE, 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

# Thanks for your attention

# Phenotyping Data Trait Search Example




| | A | B | C | D | E | M | P | Q | R | T |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Dataset | Variety ID | Clone ID | Sample ID | Site | Position | Flesh_C | FreeStone | Pull_Force | Skin_C_mahogany |
| 2 | Sweet_Cherry_CRS_phenotyping_2011 | 4.10.19-001 | 4.10.19-001_Roza_11 | 24658 | Roza | FR3T018 | 2 | 4 | 8.37 | 4.4 |
| 3 | Sweet_Cherry_CRS_phenotyping_2011 | 4.16.2-001 | 4.16.2-001_Roza_11 | 24722 | Roza | FR3T070 | 2 | 3 | 5.37 | 6.2 |
| 4 | Sweet_Cherry_CRS_phenotyping_2011 | 4.18.15-003 | 4.18.15-003_Roza_11 | 24728 | Roza | FR1T029 | 2 | 4 | 9.88 | 3 |
| 5 | Sweet_Cherry_CRS_phenotyping_2010 | 4.18.2-016 | 4.18.2-016_Roza_10 | 24538 | Roza | FR2T046 | 2 | 3.6 | 8.35 | 3.2 |
| 6 | Sweet_Cherry_CRS_phenotyping_2011 | 4.18.2-024 | 4.18.2-024_Roza_11 | 24782 | Roza | FR2T054 | 2 | 3.2 | 10.02 | 5.6 |
| 7 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 4.3.1-008 | 4.3.1-008_Roza_11 | 24990 | Roza | FR3T016 | 2 | 4.2 | 7.71 | |
| 8 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 5.10.25-002 | 5.10.25-002_Roza_11 | 24992 | Roza | FR9T032 | 2 | 1 | 8.9 | 2.25 |
| 9 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 5.10.26-005 | 5.10.26-005_Roza_11 | 25000 | Roza | FR12T009 | 2 | 4.2 | 11.43 | 3.4 |
| 10 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 5.10.40-004 | 5.10.40-004_Roza_11 | 25012 | Roza | FR12T058 | 2 | 4.4 | 6.52 | 4.67 |
| 11 | Sweet_Cherry_CRS_phenotyping_2011 | 5.12.5-007 | 5.12.5-007_Roza_11 | 24790 | Roza | FR9T083 | 2 | 4 | 7.06 | 4.4 |
| 12 | Sweet_Cherry_CRS_phenotyping_2011 | 5.12.5-009 | 5.12.5-009_Roza_11 | 24794 | Roza | FR9T085 | 2 | 3.8 | 12.24 | 4.4 |
| 13 | Sweet_Cherry_CRS_phenotyping_2011 | 5.12.5-011 | 5.12.5-011_Roza_11 | 24798 | Roza | FR9T087 | 2 | 3.8 | 10.55 | 3.6 |
| 14 | Sweet_Cherry_CRS_phenotyping_2011 | 5.14.15-003 | 5.14.15-003_Roza_11 | 24806 | Roza | FR11T015 | 2 | 3 | 11.29 | 3 |
| 15 | Sweet_Cherry_CRS_phenotyping_2011 | 5.14.15-015 | 5.14.15-015_Roza_11 | 24818 | Roza | FR11T027 | 2 | 3 | 8.01 | 3.6 |
| 16 | Sweet_Cherry_CRS_phenotyping_2010 | 5.14.15-015 | 5.14.15-015_Roza_10 | 24562 | Roza | FR11T027 | 2 | 1.8 | | 3.6 |
| 17 | Sweet_Cherry_CRS_phenotyping_2011 | 5.18.25-003 | 5.18.25-003_Roza_11 | 24576 | Roza | FR8T049 | 2 | 3 | 8.3 | 4 |
| 18 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 5.18.25-004 | 5.18.25-004_Roza_11 | 25070 | Roza | FR8T050 | 2 | 5 | 7.22 | 1 |
| 19 | Sweet_Cherry_CRS_phenotyping_2011 | 5.28.15-004 | 5.28.15-004_Roza_11 | 24836 | Roza | FR14T075 | 2 | 3 | 10.15 | 5 |
| 20 | Sweet_Cherry_CRS_phenotyping_2011 | 5.28.15-013 | 5.28.15-013_Roza_11 | 24854 | Roza | FR14T100 | 2 | 4 | 15.93 | 4 |
| 21 | Sweet_Cherry_CRS_phenotyping_2011 | 5.3.1-002 | 5.3.1-002_Roza_11 | 24580 | Roza | FR5T021 | 2 | 2 | 9.69 | 3.6 |
| 22 | Sweet_Cherry_CRS_phenotyping_2010 | 5.3.1-002 | 5.3.1-002_Roza_10 | 24352 | Roza | FR5T021 | 2 | 2 | 10.1 | 3 |
| 23 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 5.3.1-010 | 5.3.1-010_Roza_11 | 25088 | Roza | FR18T019 | 2 | 3 | 5.37 | 3 |
| 24 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 5.3.1-012 | 5.3.1-012_Roza_11 | 25090 | Roza | FR18T041 | 2 | 4 | 4.79 | 5 |
| 25 | Sweet_Cherry_CRS_phenotyping_2011 | 5.4.15-005 | 5.4.15-005_Roza_11 | 24858 | Roza | FR21T040 | 2 | 2.6 | 8.34 | 2.4 |
| 26 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 6.10.55-001 | 6.10.55-001_Roza_11 | 25098 | Roza | FR30T099 | 2 | 3 | 8.05 | 4 |
| 27 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 6.14.6-010 | 6.14.6-010_Roza_11 | 25140 | Roza | FR35T110 | 2 | 4 | 7.78 | 3 |
| 28 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 6.23.55-002 | 6.23.55-002_Roza_11 | 25144 | Roza | FR25T081 | 2 | 3 | 9.45 | 4 |
| 29 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 6.28.44-004 | 6.28.44-004_Roza_11 | 25152 | Roza | FR22T004 | 2 | 5 | 12.8 | 4 |
| 30 | Sweet_Cherry_BPS_WA_phenotyping_2011 | 6.4.44-005 | 6.4.44-005_Roza_11 | 25180 | Roza | FR26T032 | 2 | 5 | 6.1 | 3 |

## *Goldrush*

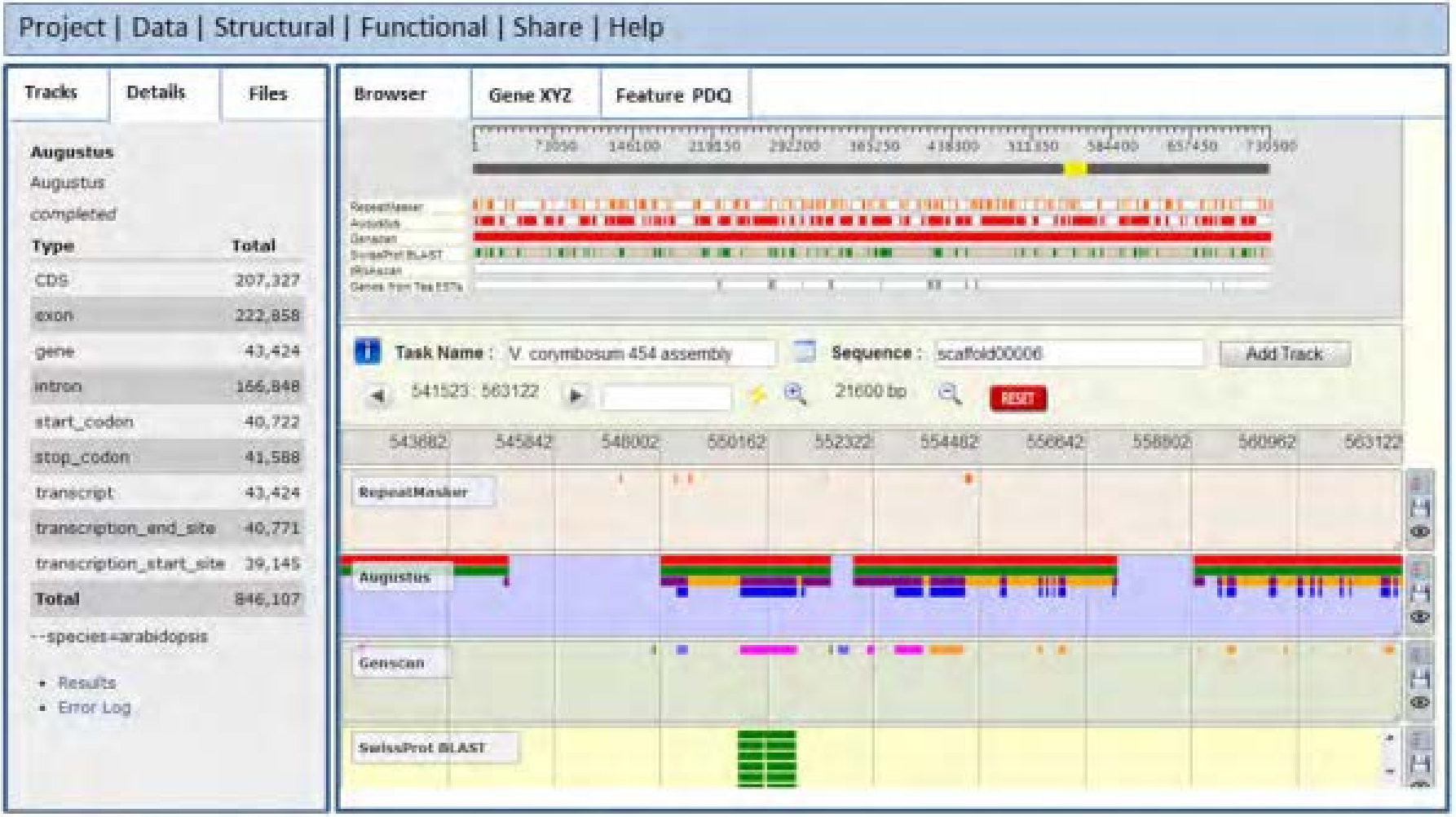
| | |
|---|---|
| **Alias** | *n/a* |
| **Mother** | **GoldenDel** |
| **Father** | **Coop17** |
| **Cross Number** | *n/a* |

***click image for larger view***

### Evaluation Data

| | |
|---|---|
| **Phenotyping Data** | **download** *phenotypic characters* |
| **Genotyping Data** | **download** |

### Associated Markers / Alleles

| | |
|---|---|
| **ACO1** | 2 |
| **CH05c06** | 116, 118 |
| **Md-Exp2** | 295 |
| **Hi04e04** | 222, 246 |
| **CH02b03** | 79, 97 |

# GenSAS: Community Annotation