

# GDR OBJECTIVES

- Develop a genomic, genetic and breeding web database for Rosaceae Crop Improvement
- Integrate information on maps, markers, sequences, genes, QTL, genotype, phenotype, germplasm and publications to facilitate interdisciplinary collaboration
- Develop /Use ontologies in collaboration with consortia to facilitate data sharing through usage of ontologies
- Develop bioinformatics community resources to facilitate sharing of tools



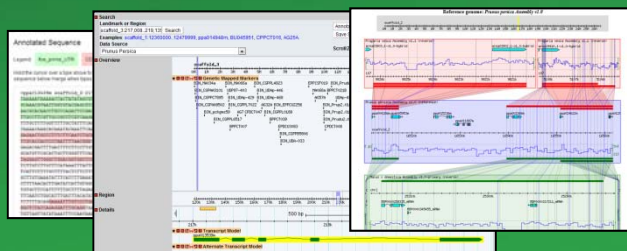
## CURRENT SPECIES, DATA AND TOOLS

- Almond, Apple, Apricot, Blackberry, Cherry, Peach, Pear, Raspberry, Rose, Strawberry
- Annotated peach, strawberry, pear, apple and black raspberry genome sequences
- Apple-peach-strawberry-pear synteny available through GBrowse\_Syn
- Annotated Rosaceae NCBI sequences
- Published RNASeq data assembled and annotated
- Pathway data (PeachCyc, FragariaCyc and AppleCyc)
- SNP array data for apple (9K, 20K, 480K), peach (9K), cherry (6K), strawberry (90K) and rose (68K)
- Genetic maps, gene, transcript, marker, trait, QTL, polymorphism, publications search
- Genotypic, phenotypic and breeding data for search and download
- BLAST, Sequence Retrieval online tools
- Short audio-visual and text tutorials

# AIDING TRANSLATIONAL RESEARCH

Worldwide, Rosaceae scientists have contributed to the data housed in GDR. Genetic and Phenotypic data collected over multiple seasons helps breeders and scientists to make sound and efficient decisions for breeding Rosaceae cultivars. Genotypic data is added regularly, representing up-to-date information for the Rosaceae family.

## GENE/GENOME BROWSER/SYNTENY BROWSER

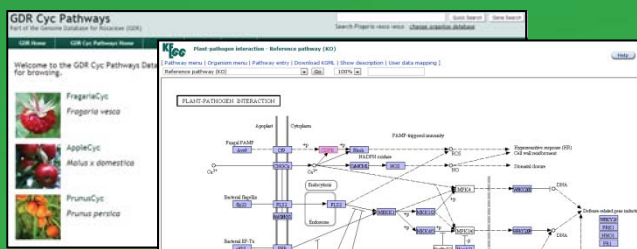


Search/Browse genes, genomes with anchored features, syntenic regions among related genomes

## DATA SETS IN GDR

16 Genomes	242,182 Genes	180 Genetic Maps
2,900,263 Markers	2,695 QTLs and MTLs	18,641 Germplasm
10,511,195 Genotypes	876,885 Phenotypes	6,888 Publications

## PATHWAY: GDR Cyc AND KEGG ANALYSIS



Search and browse genes in metabolic pathways of apple, peach and strawberry annotated by MetaCyc

## COMMUNITY RESOURCES

Connect with the Rosaceae community!

Post a job, join a mailing list to network with other scientists around the world, or participate in community governance.

- GDR video and text tutorials and FAQs - <http://www.rosaceae.org/help>
- Job Postings for Rosaceae Community
- Mailing lists
  - RosEXEC (U.S. Rosaceae Community)
  - Genomic Database for Rosaceae (GDR)
  - International Rosaceae Genomics Community
  - U.S. Rosaceae Genomics Community
- Conference Announcements/Current Events
- Community links/projects

## MARKERS, QTL, MAPS

**BPCT002 (genetic\_marker) Prunus persica**

#	Map Name	Linkage Group	Bin	Position	Locale	CMap
1	Sweet Cherry_EFAY1-F1-2005	10Y2	NA	63.32	BPCT002	View
2	Sweet Cherry_EFAY1-F1-2005	EF2	NA	41.43	BPCT002	View
3	Peach-PF-051-2005	02	NA	11.40	BPCT002	View
4	Peach-DS-F1-2005	02	NA	20.70	BPCT002	View
5	Almond-H-F1-2016	02	NA	21.30	BPCT002	View
6	Peach-TE-F2	02	NA	20.90	BPCT002	View

Map Positions: Total 6 map positions

Map 1: Sweet Cherry\_EFAY1-F1-2005

Map 2: Sweet Cherry\_EFAY1-F1-2005

Map 3: Peach-PF-051-2005

Map 4: Peach-DS-F1-2005

Map 5: Almond-H-F1-2016

Map 6: Peach-TE-F2

QTL/MTL Search Criteria

Search QTLs and/or MTLs (Mendelian Trait Loci)

Type:  QTL  MTL

Species:  Any  Fragaria ananassa  Malus x domestica  Prunus americana

Trait Category:  Any  anatomy and morphology trait  biochemical trait  growth and development trait

Trait Name:  Contains  (e.g. self-incompatibility, chilling requirement or fruit weight)

Published Symbol:  Contains  (e.g. Pm1.Ls1, PPV-D or Skc)

QTL/MTL Label:  Contains  (e.g. qFS-DE-cH10-2, qN-FD-cH7 or qLS-DE-cH15-9)

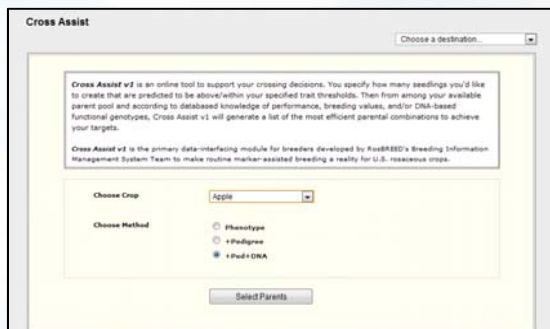
## RNASeq REFERENCE TRANSCRIPTOMES

Reference transcriptomes (RefTrans v1.0) assembled, functionally annotated and aligned to genomes from published RNASeq data. Available for peach and rubus species. May be searched by function keyword, GO Term, KEGG, genome location or name.



## ENHANCING BREEDING EFFICIENCY

### BREEDERS' TOOL BOX (DECISION TOOLS)



Identify ideal parents for crosses to obtain progeny with certain traits (Cross Assist) or estimate seedling selection costs in various marker-assisted seedling selection schemes (Seedling Select).

### PROVIDING PHENOTYPIC, GENOMIC, GENETIC, AND QTL DATA TO ENHANCE PUBLIC RESOURCES FOR ROSACEAE CROPS RESEARCH AND IMPROVEMENT

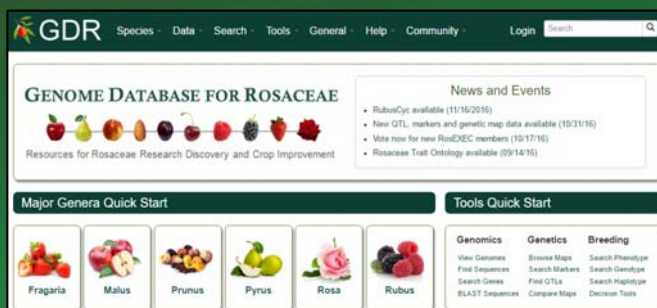
## PROJECT SUPPORT



[WWW.ROSACEAE.ORG](http://WWW.ROSACEAE.ORG)

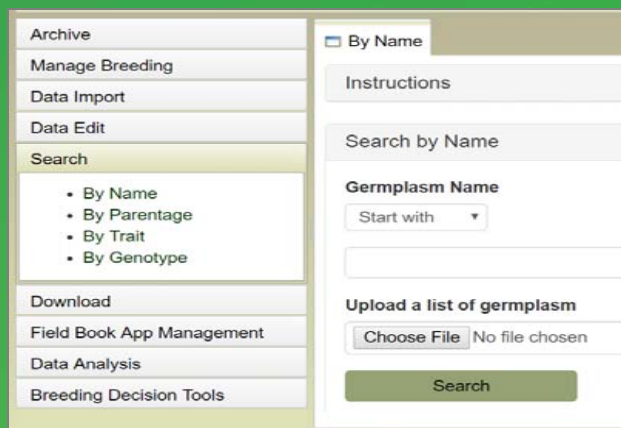
## NEW AND ENHANCED WEB DESIGN

Providing more intuitive data and tool access by crop group



### Work in Progress

- Adding more genetic and genomic data.
- Developing a site-wide search and Bio-mart type search/download tool
- Developing an integrated comparative map viewer in Tripal
- Developing BIMS (Breeding Information Management System) in Tripal
- Breeders able to upload, manage, compare and analyze their own private data, integrated with public data. V0.9 being tested using the Clemson University Peach Breeding Program Data



## A GENOMICS, GENETICS AND BREEDING RESOURCE FOR ROSACEAE

# GENOME DATABASE FOR ROSACEAE



[WWW.ROSACEAE.ORG](http://WWW.ROSACEAE.ORG)

For more information contact:

Dorrie Main (dorrie@wsu.edu)

Sook Jung (sook\_jung@wsu.edu)

@GDR\_news