

RCG8 GDR Workshop: Introduction

8th Rosaceae Genomics Conference, Angers, France, 2016

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Genomic, Genetic, and Breeding Resources for Rosaceae Crop Improvement



Welcome to the Genome Database for Rosaceae

Initiated in 2003, the Genome Database for Rosaceae (GDR) is a curated and integrated web-based relational database providing centralized access to Rosaceae genomics, genetics and breeding data and analysis tools to facilitate basic, translational and applied Rosaceae research. GDR is supported by grants from the NSF Plant Genome Program (2003-2008), USDA NIFA Specialty Crop Research Program (2009-2019), USDA NIFA National Research Support Project 10 (2014-2019), and the Washington Tree Fruit Research Commission (2008-2016), Clemson University, University of Florida and Washington State University.

What's new in GDR?

- Genome assembly and annotation of Black raspberry (*Rubus occidentalis* L.) available (04/01/16)
- New QTL, markers and genetic map data available (3/31/16)
- 480K SNP array data for *Malus x domestica* (Bianco et al. 2016) available (3/31/16)
- Species summary information contributed by community members available (3/31/16)
- Genome Assembly of *F. x ananassa* and four wild species v1.0 available (9/10/15)

General Information

Report a problem | Ask us a question | Post a job | Post a meeting or event | Used GDR data or tools in your research - how to reference us.

News

- Mapping between *M. x domestica* genome MDP genes and NCBI genes available (6/1/16)
- Genome assemblies of *F. x ananassa* and four wild species are available in JBrowse (5/27/16)
- GDR Cyc databases updated with MetaCyc v19.5 (4/14/16)
- GDR Newsletter April 2016 available (04/13/16)
- NCBI SRA RNASeq and GBS data summary pages available (04/12/16)
- Black raspberry genome sequence and annotation available (04/01/16)
- 8th International Rosaceae Genomics Conference (RGC8) on June 21-24, 2016 in Angers, France
- Announcements archive

Major Work in Progress

- Converting GDR from Tripal 1 to Tripal 2 with major redesign – **August 2016**
- Designing and implementing a comprehensive breeding information management system (TripalBIMS) – **Sook Jung talk**
- Evaluating the FieldBook App for collection of phenotype data – **Ksenija Gasic talk**
- Adding more GGB data and working on data standards and ontologies
- Integration of GenSAS for community curation of annotated Rosaceae genomes



Quick links to work completed and work in progress



The image shows a screenshot of the GDR (Genome Database for Rosaceae) website. The header features the GDR logo, which includes a stylized orange fruit on a branch, followed by the text "GDR | Genome Database for Rosaceae". Below the header is a navigation bar with tabs for "General", "Help", "Species", "Data", "Search", "Tools", and "Breeding". A dropdown menu is open under the "General" tab, listing several options: "About", "Archives", "Data Overview", "Newsletters", "Steering Committee", "Usage", "Work Completed", "Work in Progress", "GDR People", and "Presentations". The "Work Completed" option is highlighted with a red rectangular box. In the background, a banner for "Genome Database for Rosaceae and Breeding Research Improvement" is visible, along with a brief description of the database's purpose and funding sources.

GDR | Genome Database for Rosaceae

General | Help | Species | Data | Search | Tools | Breeding

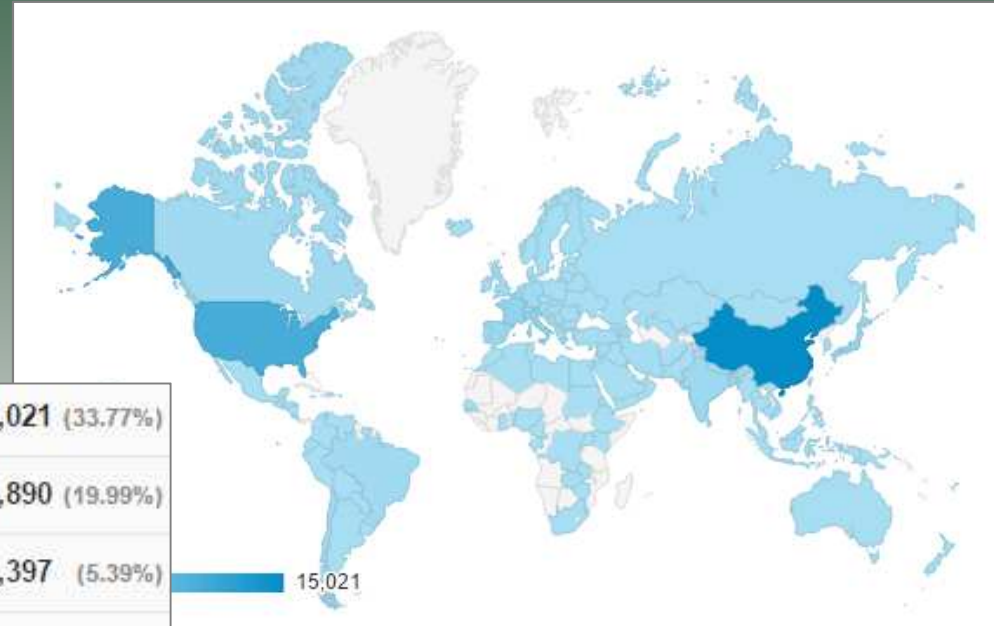
- About
- Archives
- Data Overview
- Newsletters
- Steering Committee
- Usage
- Work Completed**
- Work in Progress
- GDR People
- Presentations

Genome Database for Rosaceae and Breeding Research Improvement

Genome Database for Rosaceae (GDR) is a comprehensive resource for the genomes, genetics and breeding of Rosaceae species. GDR is supported by grants from the National Science Foundation (2009-2019), USDA NIFA National Specialty Crop Research Program (2009-2019), USDA NIFA National Washington Tree Fruit Research Commission (2008-2016), Clemso

Usage of GDR in 2015

- 18,244 visitors
- 44,479 visits
- 199,936 pages
- 144 countries



1.	 China	15,021 (33.77%)
2.	 United States	8,890 (19.99%)
3.	 Italy	2,397 (5.39%)
4.	 France	2,152 (4.84%)
5.	 Japan	1,803 (4.05%)
6.	 Spain	1,552 (3.49%)
7.	 India	1,065 (2.39%)
8.	 Germany	914 (2.05%)
9.	 Brazil	827 (1.86%)
10.	 Canada	735 (1.65%)

New Data in GDR in 2015

Data Type	01- 2015	01-2016	Increase
Genes	233,191	330,235	97,044
Genomes	6	11	5
Genetic maps	123	160	37
Genotypes	28,298	15,513,927	15,485,631
Germplasm	13,500	16,345	2,845
Markers	2,193,827	2,311,771	117,944
Phenotypes	734,343	783,639	49,296
Publications	6,319	6,703	384
QTLs	2255	2318	63

New Species Pages

Malus x domestica

Overview

Genus	Malus
Species	<i>x domestica</i>
Abbreviation	M. x domestica
Scientific Name	Malus x domestica
Common Name	Apple
Geographic Origin	cultivated
Haploid Chromosome Number	17
Ploidy	2x, 3x
Growth Habit	tree
Propagation Method	grafting for clones
Usage	fruit
Resistance to biotic stress	Dessert, cider varieties
Germplasm	[view all 5445]
Sequence	[view all 3703185]

Resources

Data

- Overview
- Publications
- Genetic Maps
- Genes
- Markers
- Sequences
- Trait Loci
- Whole Genomes
- SNP arrays
- Germplasm

Tools

- GBrowse
- JBrowse
- GBrowse_Syn
- CMap
- AppleCyc
- NCBI Blast
- Batch Blast
- Sequence Retrieval Tool
- GO Viewer
- KEGG Pathway Viewer

Gene Naming Guideline Page

Gene Naming Guideline

[View](#)[Moderate](#)[Edit](#)[Devel](#)[Open Access Publication](#) | [Detailed Guideline](#) | [Gene Class Symbol](#) | [Species Prefix](#)

Gene Naming Guidelines

Genes in GDR are composed of two types:

1. Genes with gene symbol, assigned by individual investigators, usually with known or predicted function or phenotype.
 - These genes with gene symbols in GDR are obtained by parsing the NCBI nr database and submission from individual investigators.
 - Prior to naming your genes, please refer to the list of [gene class symbols in Rosaceae](#) and gene naming guidelines below and **submit the gene/gene class data**.
2. Genes predicted from the whole genome assembly

1. Naming Guideline for Genes with known or predicted function or phenotype

(for gene data submission and gene nomenclature in manuscript)

The guideline has been put together by [Rosaceae Gene Name Standardization Subcommittee of RosEXEC/RosIGI](#).

Gene Symbol is composed of:

[species prefix][3-letter code class symbol].[numeric suffix for a gene][-][numeric suffix for an allele or a splice variant]

Where

- [species prefix]: *publication purposes* - three letter prefix for major species and 5 letter prefix for others

The Team



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

Some Requests (Please)

- Cite us (Jing et al., 2014 – on website)
- Join our mailing list to receive biannual newsletters and community communication
- Please tell us if you find a problem with the site, have new functionality you would like