

GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

April 2024

Welcome to the April 2024 issue of the GDR newsletter. This newsletter is issued to inform users about new or updated data and tools in GDR and provide a summary from the quarterly Rosaceae Executive Committee (RosEXEC) meetings.

Summary of RosEXEC meeting!

The summary of the second RosEXEC meeting of 2024 is available on page 3! Make sure to check it out to learn new things happening in Rosaceae Community!

New tutorials available

Two short tutorials, "[Finding a marker associated with a trait](#)" and "[Downloading markers from a map region](#)" were made available. See [the manual page](#) or our [YouTube channel](#) for more tutorials.

New Genome Data/Functional Analysis

- New whole genome data are available for Prunus and Malus species!
 - [Malus x domestica WA 38 v1.0](#)
 - [Malus x domestica Fuji v1.0.a2](#)
 - [Malus x domestica M9 v1.0.a2](#)
 - [Malus x domestica MM106 v1.0.a2](#)
 - [Prunus cerasus Montmorency v1.0.a2](#)
 - [Prunus armeniaca Yinxiangbai v1.0](#)
- GDR Functional Analysis (InterProScan, Protein Homologies, and Synteny Analysis) added for the following genomes:
 - [Fragaria moupinensis haplotype v1.0](#)
 - [Fragaria x ananassa Benihoppe v1.0](#)
 - [Pyrus communis d'Anjou v2.3.a1](#)
 - [Prunus campanulata v1.0](#)

New Cyc available for two apple genomes

- [Malus x domestica HFTH1 Whole Genome v1.0](#)
- [Malus x domestica Honeycrisp v1.0 genome](#)

New SNP array/assay, QTL, genotype data

New GWAS, QTL, phenotype, and genotype data from 20 publications are available. View data in [QTL/GWAS Search](#), [Marker Search](#), [Genotype Search](#), [Trait Evaluation Search](#), and in [MapViewer](#). Check next page for all the new publications that have been curated!

Recommendation for Genome and Gene Nomenclature

[Genome/gene naming guideline](#) updated following [AgBioData](#) recommendation. Please refer to the guidelines for the new whole genome assembly project!

Standardized Rosaceae Trait Terms Updated

Standardized Rosaceae Trait Terms, Rosaceae Trait Ontology, have been updated to be more general for Rosaceae crops, have better descriptions, and include more aliases. These Trait terms are associated with similar QTLs and GWAS. Search/view in [Search Trait Names](#).

GDR has made an effort to standardize the trait names and the abbreviations for all the trait data entered in the database such as QTLs and descriptors used in phenotyping studies. Each of these trait terms is either an existing term or a child term of the existing term of the Plant Trait Ontology. One trait term can belong to multiple trait categories.

Category:

Keyword:

5 records were returned

[Download Table](#)

#	Category	Abbreviation	Trait	Alias	Definition
1	quality trait	ANTHERCOL	anther color		color of anther
2	quality trait	FLCOL	flower color	inflorescence color / petal color	color of flower
3	quality trait	FRFLCOL			

Trait Overview
Descriptors
QTLs/MTLs
Dataset
Publications

Trait Overview

Trait	anther color
Trait Category	plant morphology trait; quality trait
Abbreviation	ANTHERCOL
Definition	color of anther
Descriptors	[view all 2]
QTLs	[view all 2]

New data added during first quarter of 2024 by curation!

We are making good progress on curating publications to add new data. We have focused on Prunus crops, and will continue with other crops. Below are publications that we have curated to add data to GDR this quarter! View data in [QTL/GWAS Search](#), [Marker Search](#), [Genotype Search](#), [Trait Evaluation Search](#), and in [MapViewer](#).

Peach (*Prunus persica*):

1. [Cao et al. Genome-wide association study of 12 agronomic traits in peach.](#)
2. [da Silva Linge et al. Ppe.RPT/SSC-1: from QTL mapping to a predictive KASP test for ripening time and soluble solids concentration in peach.](#)
3. [Fu et al. Genome-Wide Association Study of Brown Rot \(*Monilinia* spp.\) Tolerance in Peach.](#)
4. [Mas-Gómez et al. Genetic Diversity and Genome-Wide Association Study of Morphological and Quality Traits in Peach Using Two Spanish Peach Germplasm Collections.](#)
5. [Liu et al. Genome-wide association study and transcriptome of olecranon-type traits in peach \(*Prunus persica* L.\) germplasm.](#)
6. [Cao et al. Discovery of a key gene associated with fruit maturity date and analysis of its regulatory pathway in peach.](#)
7. [Li et al. Multiple-statistical genome-wide association analysis and genomic prediction of fruit aroma and agronomic traits in peaches.](#)
8. [Huang Z et al. Preliminary Identification of Key Genes Controlling Peach Pollen Fertility Using Genome-Wide Association Study.](#)
9. [Font I Forcada C et al. Association Mapping Analysis for Fruit Quality Traits in *Prunus persica* Using SNP Markers.](#)
10. [Martínez-García PJ, Mas-Gómez J, Prudencio AS, Barriuso JJ, Cantín CM. Genome-wide association analysis of *Monilinia fructicola* lesion in a collection of Spanish peach landraces.](#)

Sweet Cherry (*Prunus avium*):

1. [Crump et al. Detection of Breeding-Relevant Fruit Cracking and Fruit Firmness Quantitative Trait Loci in Sweet Cherry via Pedigree-Based and Genome-Wide Association Approaches.](#)
2. [Donkpegan et al. Genome-wide association mapping in a sweet cherry germplasm collection \(*Prunus avium* L.\) reveals candidate genes for fruit quality traits.](#)

Almond (*Prunus dulcis*):

1. [Pavan et al. Almond diversity and homozygosity define structure, kinship, inbreeding, and linkage disequilibrium in cultivated germplasm, and reveal genomic associations with nut and seed weight.](#)
2. [Sideli et al. Genome-wide association analysis and validation with KASP markers for nut and shell traits in almond \(*Prunus dulcis* \[Mill.\] D.A.Webb\).](#)
3. [Pérez de los Cobos et al. Almond population genomics and non-additive GWAS reveal new insights into almond dissemination history and candidate genes for nut traits and blooming time.](#)

Apricot (*Prunus armeniaca*):

1. [Zhang et al. Re-sequencing and morphological data revealed the genetics of stone shell and kernel traits in apricot.](#)
2. [Omrani et al. Genome-wide association multi-locus and multi-variate linear mixed models reveal two linked loci with major effects on partial resistance of apricot to bacterial canker.](#)

Strawberry (*Fragaria*):

1. [Feldmann et al. Accelerating genetic gains for quantitative resistance to verticillium wilt through predictive breeding in strawberry.](#)
2. [Zurn et al. Assessing Cultivated Strawberries and the *Fragaria* Supercore for Resistance to Soilborne Pathogens.](#)
3. [Zurn et al. Exploring the diversity and genetic structure of the U.S. National Cultivated Strawberry Collection.](#)

Join the [GDR Mailing List](#)
Follow us on [Twitter](#)

Funded by: USDA SCRI, NIFA NRSP10, WSU
and other U.S. Land Grant Universities

Hello! The second 2024 quarterly meeting of RosEXEC (Rosaceae Genomics Genetics and Breeding Executive Committee) took place virtually on Monday, April 15th. Here's what happened:

GDR Updates

More genomes! Five new genomes were added to GDR in the first quarter of 2024: 1 *Fragaria*, 3 *Malus*, and 1 *Prunus*. In addition, haplotype data were added for the *Fragaria* × *ananassa* 'Yanli' genome, as well as a lot of new GWAS, QTL, phenotype and genotype data. Trait names based on plant ontology have been standardized, which is used to standardize the data within GDR. There is now a new protocol for genome/gene naming and annotation nomenclature recommended by AgBioData. This tool (available in the GDR Help tab) does NOT alter the original molecule or gene names but is recommended for the community to adopt for their new genome assemblies. There have been continued updates to BIMS on the management of permission levels and image data. The GDR team attended PAG 31 in San Diego in January where they held a workshop and gave four other presentations on a range of GDR topics, including BIMS and BrAPI. More GDR presentations are planned for the upcoming ASHS meeting in September (see Upcoming Events/Activities).

GDR – Coming Soon

The GDR team are hard at work on a range of annotation and data functionality activities. The ability to map marker primers to genomes is in the works, as are updates to search interfaces and tools in Tripal 4 and upgrading BIMS to accept and display data related to multiple measurements and increase the speed of SNP data query. Developing Strawberry Crop Ontology is another area of focus.

RosEXEC Taskforces

RosEXEC has several taskforces organized around themes that make data generated by the Rosaceae community more accessible and useful. The Transcriptomics task force (led by Loren Honaas) has some exploratory analysis tools ready for use in analyzing data across gene expression experiments via a standardized expression matrix and are ready to test the tools on some solid datasets. Stay tuned for more information. In addition, Loren is spearheading an effort to set criteria for quality determination of reference genomes. He will work with crop experts in the various Rosaceae species (including our international partners) to identify which reference genomes are already in use by their respective communities and characterize them according to quality criteria. The goal is for a solid reference list to be ready by the next RosEXEC meeting.

Upcoming Events/Activities

The next RosEXEC meeting will be held in mid-July (exact date to be determined). Also in July is the National Association of Plant Breeders (NAPB) meeting in St. Louis, MO (21-25 July) – Look out for GDR BIMS training. The American Society for Horticultural Science (ASHS) conference will be held in Honolulu, HI, 23-27 September. Also, the next Rosaceae Genomics Conference (RGC) will be held near Barcelona, Spain (6-9 May 2025). RosEXEC is working to get financial support for travel to RGC for early-career scientists and those from economically disadvantaged locations.

Officer Contact Information:

Jonathan Fresnedo Ramirez (Chair): fresnedoramirez1@osu.edu; Per McCord (Vice-chair): pmmcord@wsu.edu; Chris Gottschalk (Secretary)