

GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

January 2023

Welcome to the January 2023 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 meetings!

Our newsletter now provides a summary from the quarterly RosEXEC meetings! Check page 3!

GDR Workshop at RGC11!

Join us for the GDR workshop at [RGC11](#) (13-16 March 2023, Nelson, NZ). Check page 4 for details!

New tutorial videos available

[Overlaying Omics Data in PathwayCyc](#) short tutorials were made available this past quarter. See [the manual page](#) or our [YouTube channel](#).

New Genome Assemblies

Data from 5 whole genome assemblies of *Fragaria*, *Prunus*, *Eriobotrya*, and *Potentilla* have been added to GDR this past quarter. Access data from [Gene Search](#), [MegaSearch](#), [Synteny Viewer](#), [JBrowse](#), [BLAST](#) as well as the individual genome pages linked below.

- [Prunus cerasus cv. 'Montmorency'](#)
- [Prunus fruticosa 27e12\(2\)](#)
- [Fragaria x ananassa Yanli](#)
- [Potentilla anserina](#)
- [Eriobotrya japonica](#)

New Cyc available

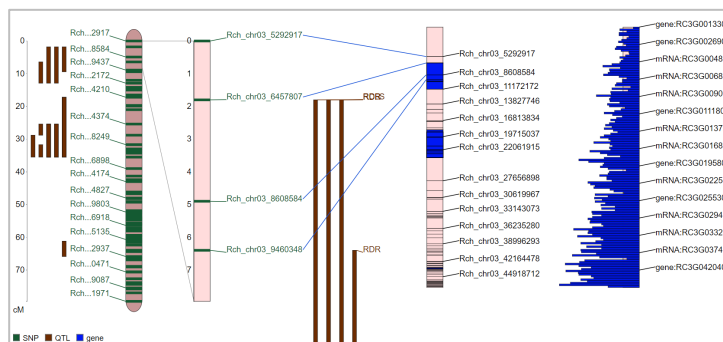
[New GDR Cyc db](#) constructed using the gene models from *Malus x domestica* Genome v1.0 NCBI annotation

Hyperlink to Fruit and Nut DB

[Some GDR cultivars](#) now have hyperlinks to [Fruit and Nut Cultivars Database](#)

New GWAS, QTL, map, marker, genotype Data

[New GWAS, QTL, map, marker, and SNP/Indel genotype data](#) are available for peach, pear and rose. View data in [QTL/GWAS Search](#), [Genotype Search](#), [Marker Search](#), and in [MapViewer](#).



Chr03 of a rose map TX2WOB with *Rosa chinensis* genome

Access GWAS data in MegaSearch/MapViewer

We just started building GWAS database and tools. Search both QTLs and GWAS data in [QTL/GWAS MegaSearch](#). More data and interface functionality to come! Check page 2 for details!

Methylation tracks in JBrowse

[Methylation tracks for strawberry mutants](#) with reduced organ size (Zheng et al. 2022) available in JBrowse. Please [contact us](#) with your methylation or other omics data to display in JBrowse!

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Featured Data and Tools

Search and View GWAS Data

Did you know?

We just started building GWAS database and tools. Search both QTLs and GWAS data in QTL/GWAS MegaSearch. More data and interface functionality to come!

Search QTL/GWAS

Triplal MegaSearch is a tool for downloading biological data. (Current limit per download: 1,000,000 records, 200,000 FASTA sequences.)
 Video tutorial: 2020 presentation | 2021 tutorial (Gene/Transcript) | 2022 tutorial (QTL) | 2022 tutorial (Map)

Select a data type to start building your own query and download data in bulk:

Data Type:

6,812 QTL/GWAS. Note: actual rows in downloaded file depend on the selected fields.

Query

Type:

Organism:
 Fragaia vesca
 Fragaia virginiana
 Fragaia x amarantha

Trait:
 Trait Category:
 Trait Name:
 1-decanol content
 1-hexanol content
 1-methylbutyl butanoate content
 1-methylhexyl acetate content

Downloadable Fields

- All Fields
- QTL/GWAS Label
- Trait Name
- GWAS Marker
- Gene
- Organism
- Type
- Dataset
- Published Symbol
- P value
- LOD
- R²

GWAS result table

Query, select fields, view and/or download dataset. From the result table, you can go to pages like GWAS, marker, gene, trait, and dataset.

#	QTL/GWAS Label	Trait Name	GWAS Marker	Gene	Dataset	Published Symbol	P value	Location
1	<input type="checkbox"/> GWAS00000001	flesh adhesion	snp_6_13059650	Prupe.GG151100_v2.0.a1	Peach-fruit_quality-GWAS-Linge-2021	ADH_2012	1.5240527537973E-5	Pp06:13073956..13073956
2	<input type="checkbox"/> GWAS00000002	flesh adhesion	snp_6_13059650	Prupe.GG151100_v2.0.a1	Peach-fruit_quality-GWAS-Linge-2021	ADH_2012	2.289812912108E-8	Pp06:13073956..13073956
3	<input type="checkbox"/> GWAS00000003	flesh adhesion	snp_6_13059650	Prupe.GG151100_v2.0.a1	Peach-fruit_quality-GWAS-Linge-2021	ADH_2012	1.7934942968627E-8	Pp06:13073956..13073956
4	<input type="checkbox"/> GWAS00000004	flesh adhesion	snp_6_13059650	Prupe.GG151100_v2.0.a1	Peach-fruit_quality-GWAS-Linge-2021	ADH_2012	3.7289241475247E-10	Pp06:13073956..13073956
5	<input type="checkbox"/> GWAS00000005	flesh adhesion	SNP_IGA_107819	Prupe.1G403500_v2.0.a1	Peach-fruit_quality-GWAS-Linge-2021	ADH_2011	1.6432362237028E-6	Pp01:35529762..35529762

GWAS marker related Gene page

Gene Overview

Alignments

Analyses

Cross References

Relationships

Sequences

Gene Overview

Name	Prupe.GG151100
Unique Name	Prupe.GG151100_v2.0.a1
Type	gene
Organism	Prunus persica (Peach)
Sequence length	910

GWAS Marker page

Marker Overview

Alignments

Analyses

Annotated Terms

Contact

Libraries

Map Positions

Publications

Relationships

Sequence

Marker Overview

Name	snp_6_13059650
dbSNP ID	N/A
SNP Array ID	IRSC 9K SNP array for peach: snp_6_13059650 IRSC 19K SNP array for peach: snp_6_13059650 3K SeqSNP for peach: snp_6_13059650
Type	SNP
SNP Alleles	[T/C]
Species	Prunus persica
Source Type	WGS
Primer 1	snp_6_13059650_LEFT_primer_0: ACCACTCTCCAAATGATGCT
Primer 2	snp_6_13059650_RIGHT_primer_0: TCATCTCTGTCATCTCAATCCG

GWAS page

Get all the details of the GWAS data and go to JBrowse or MapViewer to view chromosomes and other associated data as well as other associated pages.

GWAS Overview

Annotated Terms

Genome Location

Germplasm

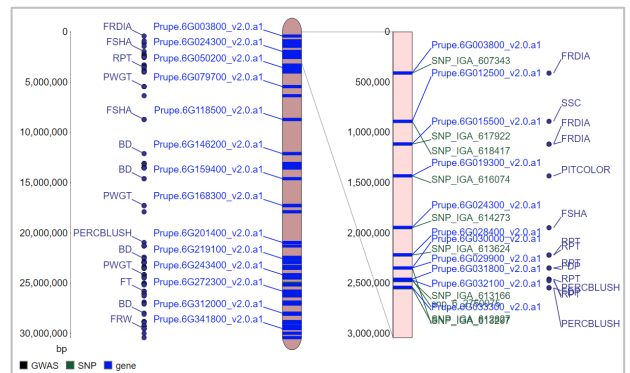
Publications

Relationships

GWAS Overview

GWAS Label	GWAS0000001 [MapViewer]
Published Symbol	ADH_2012
Trait Name	flesh adhesion
Trait Alias	N/A
GWAS Marker	snp_6_13059650
GWAS Study	Peach-fruit_quality-GWAS-Linge-2021
Genome Assembly	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (v2.0.a1)
Statistical Method	pLArMEB
Experimental Model	N/A

GWAS in MapViewer



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

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The most recent U.S. RosEXEC meeting occurred at PAG 30! It was great to have attendance options for both in-person and remote participation. Here's a quick overview!

Administrative

- RosEXEC will hold an election in Fall 2023. So, prepare your nominations. RosEXEC members serve for 3 years, and international representatives serve for 2 years. Do not hesitate to contact standing officers: [Gayle](#), [Jonathan](#), [Per](#), if you have any questions!
- RosEXEC seeks to facilitate communication and coordination in the US Rosaceae genomics, genetics and breeding community. RosIGI (Rosaceae International Genomics Initiative) helps coordinate international efforts for comparative, structural and functional genomics of Rosaceae. RosIGI has been inactive since about 2013, but now the community has spoken and wants to re-energize RosIGI! To move that forward, a meeting will be planned during the March [RGC11 in Nelson, New Zealand](#).
- At RosEXEC we aim to have more interaction with the community, thus, we hope to facilitate some interactive sessions at events such as RGC and ASHS for both in-person and virtual community participation. Stay tuned!

GDR insights

- GDR has made amazing progress on several aspects and adding nice features, such as [MegaSearch](#), educational resources as a [tutorial on PathwayCyc](#). As well as great datasets including [methylation tracks for strawberry mutants](#), and [Cyc for the apple genome](#). Powerful tools for a powerful community!
- GDR has reached the mark of 109 genomes! How many more will we get in 2023? With any great power a great responsibility comes, so, please do not hesitate in letting [Sook Jung](#) & know about new data that your groups has released, or exiting datasets that you are planning to publish soon, in GDR, your data has a home!
- Give a look to the [GDR Newsletter](#), a ton of nice stuff and details are being deployed and in the works at [Rosaceae.org](#).

Future plans

- Taskforces for GBS/genomics ([Loren Honaas](#)), and interoperability of GDR with GRIN-Global ([Nahla Bassil](#)), collaboration between BIMS and Breeding Insight ([Dorrie Main/Sook Jung](#)), as well as the sharing of standardized protocols for data collection ([Gayle Volk](#)) are underway and your input is welcome. Please, do not hesitate to communicate with the leaders!

Engagement with the Rosaceae community (What you can do? / How to get involved?)

- If you are a user of the 20K, 8K and 6K SNP arrays for apple, peach and cherry, respectively, you might already know that they are no longer available. [David Chagné](#) is proposing to use a cost-effective multi-species array—please contact him if you'd like more information. FEM is also developing a multi-species SNP array.
- Do you have ideas or interests that benefit the Rosaceae community? Do not hesitate to get involved with RosEXEC and GDR and form a task force. You can contact [Gayle Volk](#), current Chair of RosEXEC, [Jonathan Fresnedo Ramirez](#), current vice-chair, or [Per McCord](#), current secretary. We are looking forward to hearing from you!

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Announcing the GDR Training Workshop at RGC11

Workshop Synopsis:

The Genome Database for Rosaceae (GDR) is the longstanding community database of the Rosaceae Genomics, Genetics and Breeding Community. In this workshop we will demonstrate how to use the integrated data and tools in GDR to gather information for research. Use case examples will be chosen based on input from the Rosaceae community. Training on how to use BIMS to manage your private breeding data will be included as well.

When: Monday, March 13: 9 AM - Noon

Organizers and Trainers: Sook Jung and Dorrie Main

- 9:00 Workshop Introduction
- 9:10 Introduction to GDR
- 9:20 New data and tools in GDR
- 9:40 GDR Use Case demonstrations 1
- 10:20 Beverage break
- 10:40 GDR Use Case demonstrations 2
- 11:20 Community discussion on future functionality and data
- 11:35 Community brainstorming on how to make GDR sustainable
- 11:50 Summary and wrap up
- 12:00 Lunch

Email us with your use case questions at www.rosaceae.org/contact