

GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

October 2023

Welcome to the October 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 4!

New tutorials available

Two short tutorials, "[How to go from a trait to a GWAS to a gene and to a ortholog!](#)" and "[How to use the Expression Heatmap Tool!](#)" were made available. See [the manual page](#) or our [YouTube channel](#) for more.

Database Workshop at ASHS

- We had a Database workshop at the [ASHS 2023](#) (July 31-August 4, Orlando, Florida)! The [presentations](#) for each section of workshop is available.

Upcoming Workshops

- BIC & NAPIA Breeding Tools Workshop featuring [Breeding Information Management System](#), Nov. 5, 2-5 PM
- [NRSP10 Database Workshop at PAG](#) Jan. 14, 1:30-3:40 PM

New Genome Data/Functional Analysis

- New whole genome data is available for wild peach and flowering cherry!
 - [Prunus davidiana ZXST Genome v1.0](#)
 - [Prunus campanulata Genome v1.0](#)
- GDR Functional Analysis (InterProScan, Protein Homologies, and Synteny Analysis) added to the genome:
 - [Fragaria virginiana Genome KIB CAS v1.0](#)
 - [Fragaria chiloensis Genome KIB CAS v1.0](#)
 - [Fragaria nipponica Genome KIB CAS v1.0](#)

New SNP array/assay, QTL, genotype data

[New data for 13K SNP array and KASP assay for Rubus](#) and [QTL data available for rose](#). View data in [QTL/GWAS Search](#), [Marker Search](#), and in [MapViewer](#).

New Expression Datasets available

[New expression datasets](#) from peach and strawberry available to view in [heatmap](#) and gene/mRNA page.



New Pan Genome Data available

Strawberry Pangenome constructed from six diploid Fragaria species (Qin et al. 2021) are available. Check page 2 and 3 to learn how to view the data.

- [Project page](#)
- [Pan-genome graph](#)

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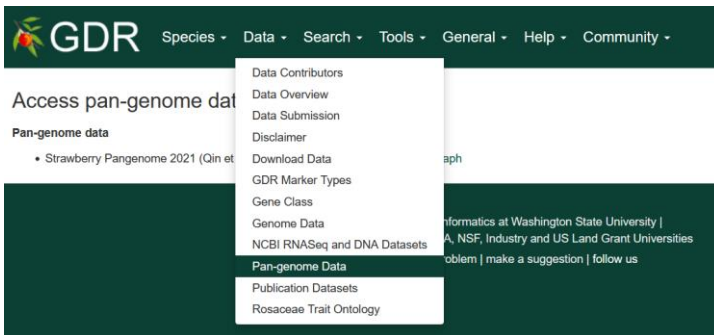
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Featured Data and Tools

How to View Pan-Genome Graph

To view available pangenome data click Pan-genome Data under Data dropdown.



Project page provide information on the pan-genome project as well as hyperlinks to the various pages and tools to access the associated data. When pan-genome graph is available for the dataset, users can access the graph using the UCSC Genome Browser. Open the link for 'Pan-genome graph'.

Links to open graph regions in UCSC Genome Browser

Other columns are links to genome information or JBrowse in GDR

	Access UCSC Genome Browser	Access Genome Page in GDR	Access JBrowse in GDR
Reconstructed Ancestral Genome*	Ancestral 0	Graphs are either by Ancestral Region or by species	
	Ancestral 1		
	Ancestral 2		
	Ancestral 3		
	Ancestral 4		
Fragaria species	<i>F. daltoniana</i>	<i>F. daltoniana</i>	<i>F. daltoniana</i>
	<i>F. iinumae</i>	<i>F. iinumae</i>	<i>F. iinumae</i>
	<i>F. mandschurica</i>	<i>F. mandschurica</i>	<i>F. mandschurica</i>
	<i>F. nilgerrensis</i>	<i>F. nilgerrensis</i>	<i>F. nilgerrensis</i>
	<i>F. vesca</i>	<i>F. vesca</i>	<i>F. vesca</i>
	<i>F. viridis</i>	<i>F. viridis</i>	<i>F. viridis</i>

*predicted reconstruction of ancestral genome at a particular node. Below is the phylogeny
 (((((vesca:1,mandschurica:1)Anc4:1,viridis:1)Anc2:1,(daltoniana:1,nilgerrensis:1)Anc3:1)Anc1:1,iinumae:1)Anc0;

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Featured Data and Tools

How to View Pan-Genome Graph

Below is a snapshot of a UCSC Genome Browser showing pan-genome graph. Learn what the colors mean and some other useful hints.

Navigation Tools

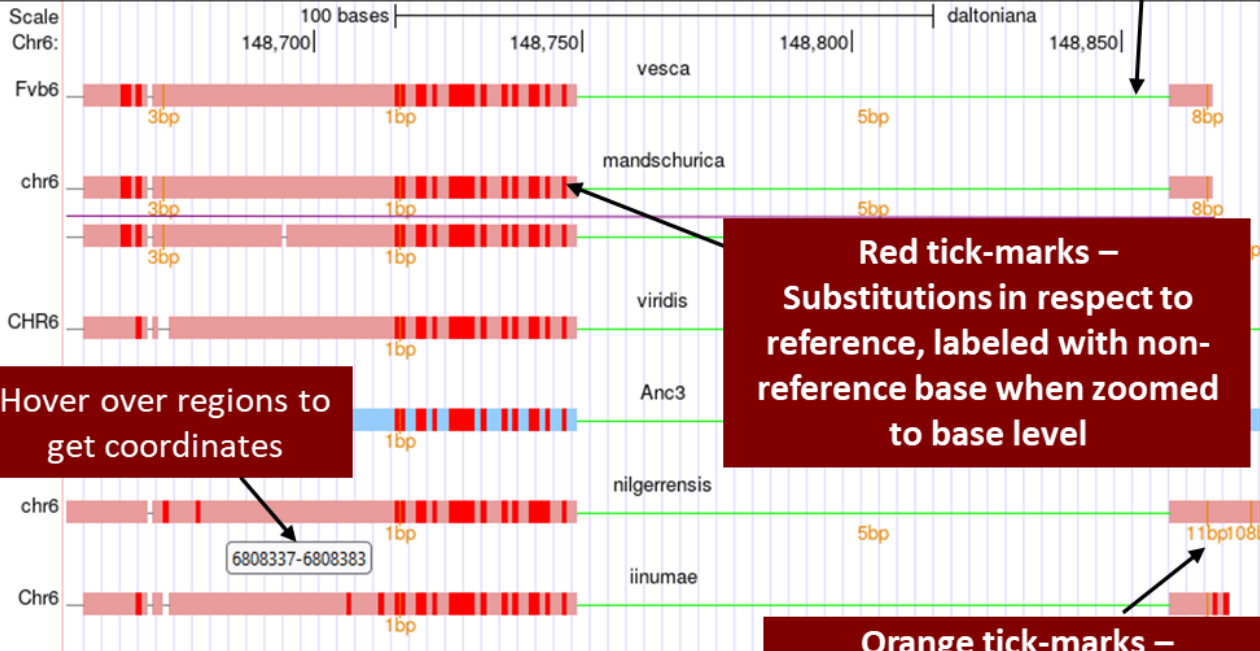
Zoom to base level

Thin lines with numbers – Insertion into reference relative to query. Length noted.

UCSC Genome Browser on *daltoniana daltoniana (daltoniana)*

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

multi-region Chr6:148,655-148,876 222 bp. chromosome range, search terms, help pages, see examples go [examples](#)



Hover over regions to get coordinates

Red tick-marks – Substitutions in respect to reference, labeled with non-reference base when zoomed to base level

Orange tick-marks – Insertions in the query relative of the reference. Length noted.

Can also click and drag to scroll left and right

RosEXEC: Rosaceae Genomics, Genetics, and Breeding Executive Committee

www.rosaceae.org/community/us_rosexec

The Q3 U.S. RosEXEC meeting took place on October 17th, 2023. Here's a quick overview!

Administrative

- Elections are coming! They will start November 1 and will end on November 17th. We expect to replace four domestic positions and 2 international liaisons. We have a strong ballot, and we are looking forward to welcoming new RosEXEC members. Stay tuned for our communication and have your GDR login handy. Your vote counts!
- Take advantage of the coming elections to learn more about RosEXEC, our mission, and member responsibilities; visit the [RosEXEC website](#) to gain more insights.
- The next RosEXEC meeting will occur during PAG XXXI, in January 2024. Stay tuned for the specific time and venue! If you have RosEXEC and/or GDR related business that you would like to have addressed, please contact standing officers.

GDR insights

- So much is going on! The [first strawberry pangenome is hosted in GDR!](#)
- Also, efforts are being focused on data curation and outreach for GDR and BIMS. Please, contact [Ksenija Gasic](#) if you want to learn more.
- Efforts are underway to increase connectivity between BIMS, Breeding Insight, and Breeder Genomics Hub. Do not lose track of the GDR announcements regarding webinars this November! Contact [Dorrie Main](#) and [Sook Jung](#) if you want to learn more.

Exciting things going on

- GDR will work on standardizing phenotyping and trait descriptors in Rosaceae! As we have specific rules for naming and annotating QTLs with Trait Ontology in GDR, well... we need something similar for trait descriptors! Starting with strawberry, standardized trait descriptors will be developed based on three pillars: trait, method, and scale. If you are interested in this effort and what can be done for stone and pome fruits, do not hesitate in contacting [Gayle Volk](#) and [Sook Jung](#). [Chris Gottschalk](#) will assist to pick the brains of breeders on this topic.
- Have your CVs ready! Driscoll's will have strawberry breeding openings for Florida and Mexico. Do not hesitate in contacting standing RosEXEC committee member [Phil Stewart](#) about these opportunities. It is also expected that soon, a pear pathology position will open in USDA-TFRL Hood River, OR, and a research leader position will open during fiscal year 2024 in Wenatchee, WA.

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

- Coordination translates to sustainability and efficacy. Thus, RosEXEC is looking for ways to improve coordination among the Rosaceae community. Some ideas have been put on the table, e.g., [NSF Research Coordination Networks](#) or Congressional Appropriation. Do not hesitate in letting us know your ideas! The long-term support for coordination meetings is fundamental to continue making progress in Rosaceae!
- Coordination and Genotyping options for Rosaceae are needed. If you know of projects or lead efforts, please, share your thoughts and experience with the RosEXEC!
- Gene expression is an immense source of knowledge just waiting to be mined. [Loren Honaas](#) is chairing a GDR Genomics Working Group to tackle the challenge of having tools in GDR to facilitate analysis of gene expression data across experiments. If you are intrigued and want to collaborate in this effort, do not hesitate to contact Loren!

Do you have interests that benefit the Rosaceae community? 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!