GENOME DATABASE FOR ROSACEAE

Resources for Rosaceae Research Discovery and Crop Improvement

January 2024

Welcome to the January 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.**

RosEXEC in the first week of February!

The first RosEXEC meeting of 2024, usually held at PAG, had to be rescheduled. It will be open to any Rosaceae community researchers. Sign up for the GDR mailing list to get the meeting info.

New tutorials available

Two short tutorials, "**Learn how to view correspondences between genomes and genetic maps**!" were made available. See **the manual page or our YouTube channel for more.**

Database Workshop at PAG

- We had a Database workshop and other presentations at PAG 31 (January 12-17, 2024, San Diego, CA)! The presentations are posted on GDR.

New Genome Data/Functional Analysis

- New whole genome data are available for Fragaria, Prunus, Pyrus, and Malus species!
    - *Fragaria moupinensis haplotype Genome v1.0*
    - *Fragaria x ananassa Benihoppe Genome v1.0*
    - *Prunus avium Regina Genome v1.0*
    - *Malus x domestica Antonovka 172670-B Genome v1.0*
    - *Malus angustifolia Genome v1.0*
    - *Pyrus communis d'Anjou Genome v2.3.a1*
    - *Malus x domestica Golden Delicious Genome NCBI annotation*
- GDR Functional Analysis (InterProScan, Protein Homologies, and Synteny Analysis) added to the genome:
    - *Prunus campanulata* Genome v1.0

New SNP array/assay, QTL, genotype data

New GWAS, QTL, and genotype data are available for Rubus, Fragaria, Mauls, and Prunus. View data in QTL/GWAS Search, Marker Search, Genotype Search, Trait Evaluation Search, and in MapViewer.

- Montanari S, et al. A multiplexed plant-animal SNP array for selective breeding and species conservation applications. *G3 (Bethesda, Md.).* 2023 Aug 11.
- Clare, S. J., et al. Development of KASP fingerprinting panel for clonal identification in red raspberry (Rubus idaeus L.). *Plant Breeding.*
- Montanari S, et al. Development of a highly efficient Axiom™ 70 K SNP array for Pyrus and evaluation for high-density mapping and germplasm characterization. *BMC genomics.* 2019 May 02; 20(1):331. (reloaded with the GRIN PI names)
- Holušová K, et al. High-resolution genome-wide association study of a large Czech collection of sweet cherry (Prunus avium L.) on fruit maturity and quality traits. *Horticulture research.* 2023; 10(1):uhac233.
- Kumar S, et al. GWAS provides new insights into the genetic mechanisms of phytochemicals production and red skin colour in apple. *Horticulture research.* 2022; 9:uhac218.
- Branchereau C, et al. Genotype-by-environment and QTL-by-environment interactions in sweet cherry (Prunus avium L.) for flowering date. *Frontiers in plant science.* 2023; 14:1142974.

Image Management in BIMS

Breeders who are using BIMS to manage their private data can load their image data now (either through Field Book App or the BIMS template/files)!

GDR by the Numbers!

The database has seen major growth in the number of data, citations, pages accessed, and users over the last decade. Let's look at the numbers! First, let's look at usage. The number of users has grown as has the number of times they visit the site (Session) and the number of pages they view (Pageviews).

GDR Usage over the last 10 Years

Year	Sessions	Pageviews	Users	Countries
2023	97,580	1,396,008	28,190	153
2022	105,683	1,093,215	37,027	149
2021	100,576	1,318,554	37,674	165
2020	87,859	1,138,573	31,150	155
2019	92,436	784,576	39,388	165
2018	69,841	657,087	27,108	159
2017	59,216	392,245	21,845	157
2016	51,870	245,787	19,821	149
2015	44,479	199,936	18,244	144
2014	42,707	192,330	16,992	152
Total	**752,247**	**7,418,311**	**277,439**	**1,548**

Last, let's look at the amount of data that has been added over the last 10 years. The amount of genetic data (markers, maps, QTL) has grown steadily. This year we started adding GWAS data and more Expression data. We are adding data as it is published and feature newly curated data in the News section of the homepage. Genome data has also steadily grown. 23 more genomes was added to GDR in 2023 to bring us up to 130 genome, with associated annotation data such as gene, putative gene function, and orthologs. Be on the look out for the new additions!

The number of **peer-reviewed manuscripts** that cite GDR continues to grow as more data, analyses, and tools are added. Primary citations refer to manuscripts that cite GDR directly. Secondary citations are the number of times the primary citations were cited. Since its inception in 2003, GDR has been cited in **2170** publications, with **82,296** secondary citations. Go GDR and her community of users. We would like to thank our users for citing GDR! Your paper that cited GDR, and papers that cited yours can be accessed here!

GDR Citations over the last 12 years

Year	Primary Citations	Secondary Citations
2023	238	251
2022	330	1788
2021	257	5359
2020	173	4340
2019	172	6887
2018	156	5655
2017	152	6929
2016	142	6730
2015	135	6471
2014	111	6926

Growth in major GDR Data types since 2013 and the last Year

Year	Genomes	Genes	mRNA	Maps	Markers	QTL	GWAS
2023	130	5,654 897	6,167,084	392	4,467,319	4,627	1403
2022	107	4,021,994	4,477,278	389	4,251,449	4406	0
2013	5	236,191	0	84	2,229,311	1247	0

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