Welcome to the first issue of the GDR newsletter in 2021. This newsletter is issued to inform users about **new or updated data and tools in GDR**. In addition to new and updated data, each issue will provide more information on data or tools on **the featured tool/data** section.

New Genome Assemblies

Data from **20 whole genome assemblies** have been added to GDR. It includes data from **diploid strawberry** (*Fragaria vesca* CFRA 2339), **apple** (*Malus x domestica* Gala haploid and diploid, *Malus sieversii* haploid and diploid, and *Malus sylvestris* haploid and diploid), **apricot** (*Prunus armeniaca* Marouch n14, *Prunus armeniaca* Stella, *Prunus mandshurica* CH264_4, *Prunus sibirica* CH320_5, *Prunus armeniaca* Sungold, *Prunus armeniaca* Longwangmao, and *Prunus sibirica* F106), **peach** (*Prunus persica* Chinese Cling), **plum** (*Prunus salicina* Sanyueli FAAS), **pear** (*Pyrus pyrifolia*), **rose** (*Rosa rugosa*), and **other Rosaceae species** used for medicinal purposes (*Rubus chingii* Hu, and *Gillenia trifoliata*). Access data from Gene Search, MegaSearch, Synteny Viewer, JBrowse, BLAST as well as the individual genome pages linked above.

GDR Gene Database Updated

This update included additional 43,692 genes and 35,284 mRNAs in NCBI Rosaceae gene and mRNA sequences in GDR and 42,231 genes in GDR Gene Database. NCBI Rosaceae gene and mRNA is gene-coding sequence data from NCBI nr database excluding predicted genes from the whole genome assembly. Distinct gene symbols for each species are stored as GDR Gene Database and linked to multiple gene/mRNA sequences from NCBI nr. Predicted genes from whole genome assemblies are also linked when users submit those data. See an example page of Malus x domestica ABP gene page with associated mRNA from nr and predicted genes from whole genome assemblies. Please submit your gene data!

New QTL, SNP array, Genotype, and Haplotype data

New apple 50K SNP array data as well as haplotype and QTL data from Rymenants et al. (2021) are available. View SNP, QTL, and haplotype block in Mapviewer, search haplotype block, and SNP data.
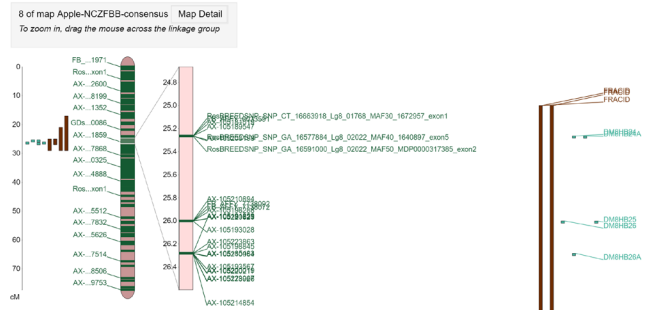
MapViewer with SNPs, haplotype blocks and QTLs.

New data also includes QTL and haplotype data for peach from Rawandoozi et al. (2020 and 2021), apple SNP genotype data (Howard et al. 2021), and apple SSR genotype data (National Laboratory for Genetic Resources Preservation, USDA). IRSC 1K SNP array for pear, part of 9K apple/pear SNP array, is searchable separately from apple SNPs.

Haplotype block search result page

GENOME DATABASE FOR ROSACEAE

Resources for Rosaceae Research Discovery and Crop Improvement

September 2021

BIMS is made BrAPI compliant

The Breeding Information Management System (BIMS) in GDR is made BrAPI compliant. BrAPI is a web service API specification for communicating plant breeding data. With this new functionality, BIMS users can import data in Field Book app to BIMS just by clicking buttons!
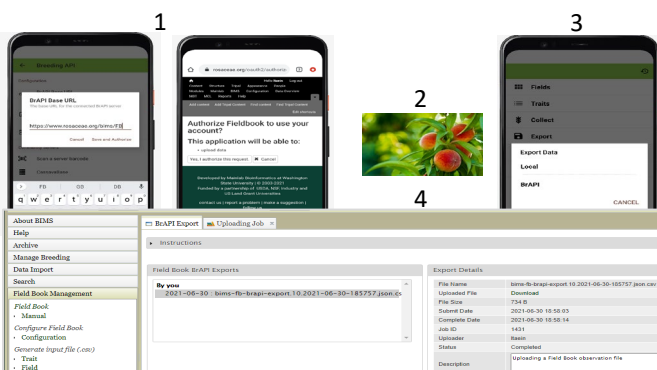
1. Connect to BIMS from FieldBook App and receive an input file through BrAPI 2. Collect phenotype data. 3. Export phenotype data to BIMS. 4. View data in BIMS!

A manuscript on BIMS has been published (Jung et al. 2021). Visit BIMS website breedwithbims.org, join the BIMS Mailing List and follow us on Twitter for more information!

More..

- **Updated DNA Testing Handbook for Strawberry** available
- **Dynamic Rosaceae Trait Ontology page** available
- Genes in Prunus persica v1.0 linked to gene family tree data in **PhyloGenes**. Check out an **example gene page.**
- Video tutorials from GDR workshop at RGC10 available. Go to **the manual page** or our **YouTube channel**.

Retrieve Sequences around SNPs and Genes

Sequence retrieval with user-defined length of upstream and downstream available in Marker Search and Gene Search! Users can filter the list of genes and markers or load a file with gene names or marker names before retrieving sequences around them.
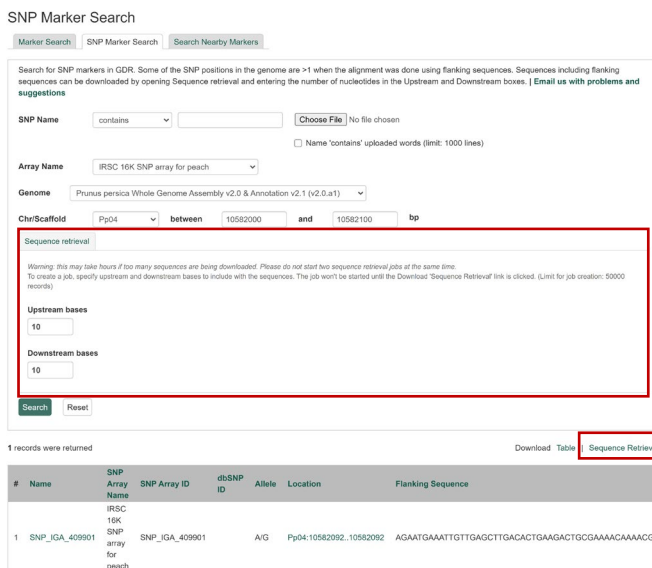

SNP search page with sequence retrieval option
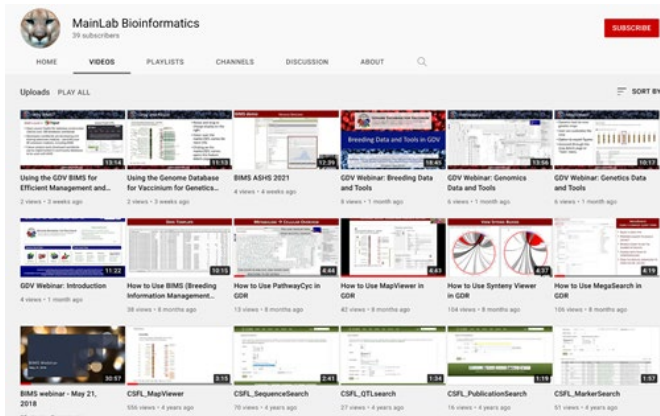
YouTube channel with video tutorials

Genome Synteny Viewer

One of the additional analyses that GDR does with provided genome data is a synteny (gene order) comparison between the genomes. The analysis is conducted with MCScanX and displayed using the Tripal Syntenic Viewer module.

Using the simple web interface, select the first genome and a chromosome or scaffold, and then select one or more genomes to compare against. The pairwise comparison data is displayed in a circus plot and syntenic blocks can be selected and viewed in a more detailed, linear side-by-side view.

In the detailed view, there is also an accompanying table that lists the corresponding mRNAs and has hyperlinks to the corresponding mRNA feature page on GDR. Each mRNA feature page has the associated sequences and details about homology to the Swiss-Prot protein and InterPro protein family databases.
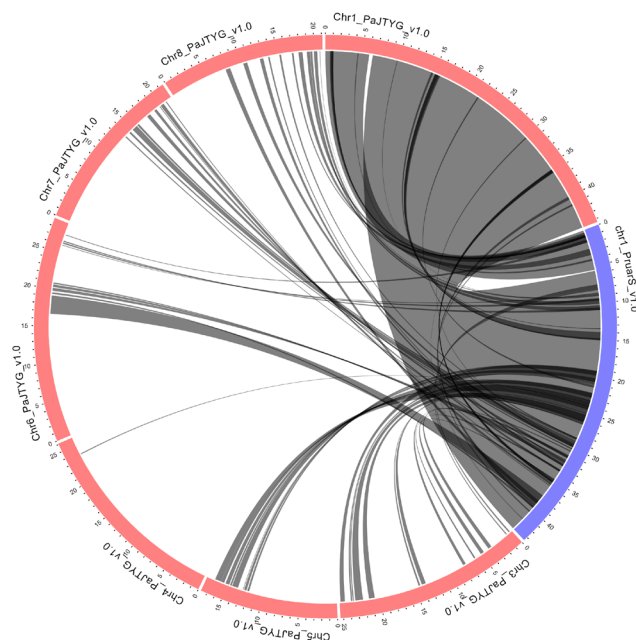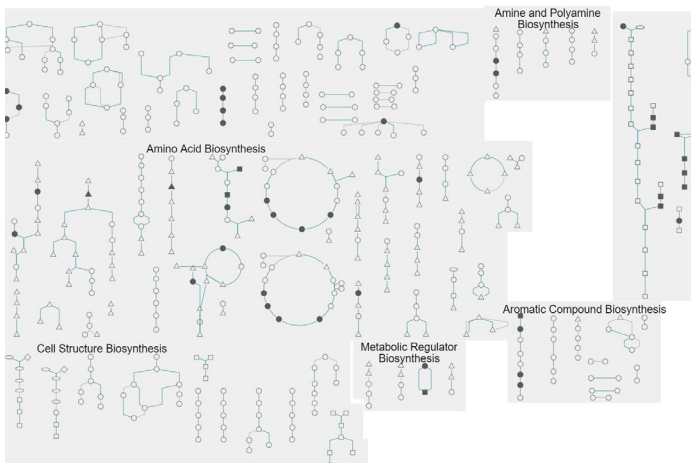

Synteny plot of Chromosome 1 from *Prunus armeniaca* cv.Stella compared to the *Prunus armeniaca Sungold* genome.

Section of the Cellular Overview diagram from the *Fragaria x ananassa* genome.

PathwayCyc

Genomes added to GDR are also analyzed with Pathway Tools to identify metabolic pathways. The data is then displayed with an embedded instance of the software on GDR under the PathwayCyc tool.

Users can also overlay data from transcriptomics or metabolomics experiments onto the cellular overview graphic. The pathways that have corresponding data are color coded to show over- or under-expression.

PathwayCyc accounts can also be requested to allow users to upload, sort, and save data using the SmartTables feature. For more details on how to use the PathwayCyc tool, watch the video on the MainLab Bioinformatics YouTube channel.

Join the **GDR Mailing List** and follow us on **Twitter**