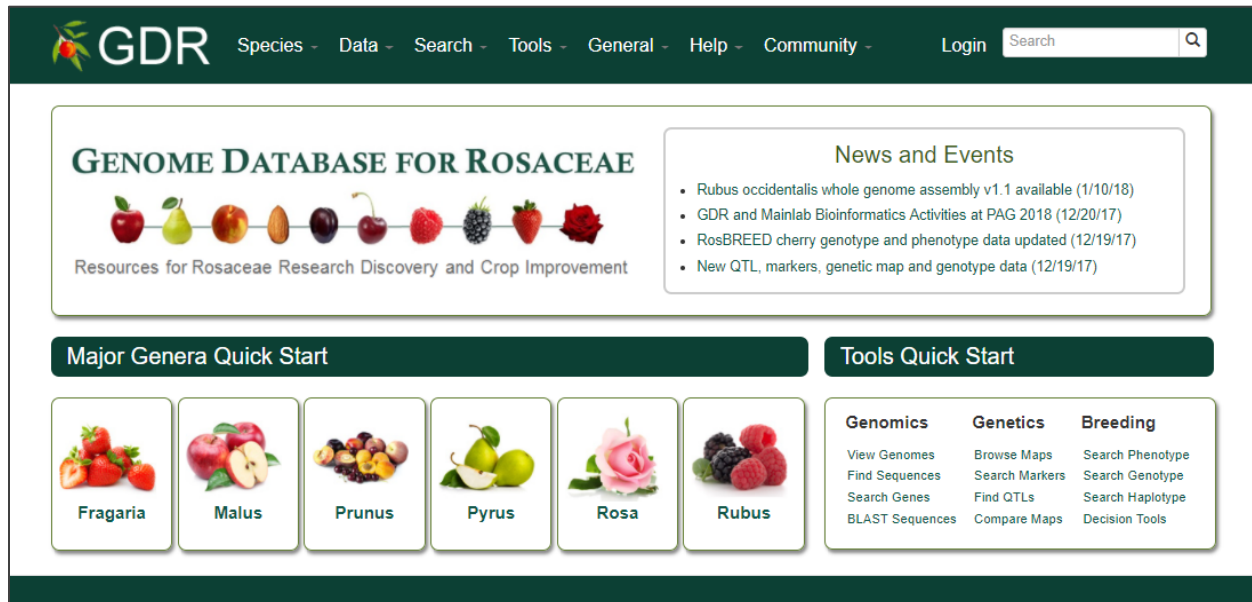


Welcome to the first issue of the GDR newsletter in 2018. This newsletter is issued to inform users about new or updated data and features in GDR and community related news. Please feel free to provide feedback and news via <https://www.rosaceae.org/contact>. The online version can be found at [https://www.rosaceae.org/GDR\\_newsletter](https://www.rosaceae.org/GDR_newsletter). We acknowledge with thanks funding for GDR from USDA, NSF, US Land Grant Universities and Industry.



The screenshot shows the GDR website homepage. At the top, there is a navigation bar with the GDR logo and menu items: Species, Data, Search, Tools, General, Help, and Community. A search box is also present. Below the navigation bar, the main content area features a large banner for the 'GENOME DATABASE FOR ROSACEAE' with a row of fruit icons and the text 'Resources for Rosaceae Research Discovery and Crop Improvement'. To the right of the banner is a 'News and Events' section listing recent updates. Below the banner are two 'Quick Start' sections: 'Major Genera Quick Start' with icons for Fragaria, Malus, Prunus, Pyrus, Rosa, and Rubus; and 'Tools Quick Start' with sub-sections for Genomics, Genetics, and Breeding, each containing a list of available tools.

## What's new at GDR?

1. New whole genome assembly and annotation data available: *Prunus avium* v1.0.a1 and *Malus x domestica* GDDH13 v1.1
2. New genome assembly data, *Rubus occidentalis* v1.1, and new genome annotation data, *Fragaria vesca* v2.0.a2, available
3. Reference Transcriptomes for *Malus x domestica*, *Prunus avium* and *Prunus persica* assembled, mapped and annotated
4. Mapping between NCBI annotated gene and genes from the original genome assembly available
5. New map, marker and QTL data
6. RubusCyc database available
7. Search by trait available in Marker Search
8. SNP Marker Search page available
9. SNP genotype search page available
10. Trait evaluation search page available

11. New MapViewer available
12. New enhanced BLAST interface available
13. Pathway Inspector from FEM available
14. Work in Progress
15. Employment opportunities
16. Subscription
17. Upcoming Conferences

**1. New whole genome assembly and annotation data available:**

[Prunus avium v1.0.a1](#) and [Malus x domestica GDDH13 v1.1](#)

**2. New genome assembly data and new genome annotation data available**

New genome assembly data, [Rubus occidentalis v1.1](#) and new genome annotation data, [Fragaria vesca v2.0.a2](#)

**3. Reference Transcriptome for Malus x domestica, Prunus avium and Prunus persica built and made available**

RefTrans for [Malus x domestica](#), [Prunus avium](#), and [Prunus persica](#) combines published RNA-Seq and EST data sets to create a reference transcriptome (RefTrans) for the species and provides putative gene function identified by homology to known proteins. RefTrans are mapped to genomes and available in JBrowse

**4. Mapping between NCBI annotated gene and genes from the original genome assembly available**

[Mapping between NCBI annotated gene and genes from the original genome assembly](#) available for F. vesca v1.0, M. x domestica v1.0 and GDDH13 v1.1 and P. persica v1.0

**5. New map, marker and QTL data**

New QTL, markers, genetic map and genotype data have been added to GDR. It includes data from 34 publications: 22 from Prunus, 8 from Malus, 1 from Fragaria, 1 from Rosa, 1 from Rubus and 1 from Pyrus. A list of these publications can be found at the GDR News items [04/14/17](#), [09/29/17](#), and [12/19/17](#).

**6. GDRcyc RubusCyc database available**

Explore pathway data in [RubusCyc](#) in MetaCyc v19.5.

**7. Search by trait available in marker search**

Search markers that are associated with QTL for certain traits in [marker search page](#).

**8. SNP marker search available**

[New SNP marker search page](#) (Figure 2) lets users search SNP by name, SNP array name, and genome positions. Users can see or download the result table with name, array name, aliases, alleles, genome location and flanking sequences.

The screenshot shows a search form with the following fields and controls:

- SNP Name:** A dropdown menu set to "contains" followed by an empty text input box. To the right is a "Choose File" button and the text "No file chosen".
- Array Name:** A dropdown menu set to "Any".
- Genome:** A wide dropdown menu set to "Any".
- Chr/Scaffold:** A dropdown menu set to "Any", followed by the text "between", an empty text input box, the text "and", another empty text input box, and the text "bp".
- Buttons:** A green "Search" button and a white "Reset" button.

Figure 2

### 9. SNP genotype search page available

[SNP genotype search page](#) (Figure 3) lets users search for the SNP genotype dataset based on the germplasm and SNP markers in the dataset. Users can filter by genome positions of the SNPs. Users can view or download the result table shows dataset name, germplasm, SNP and their genotype.

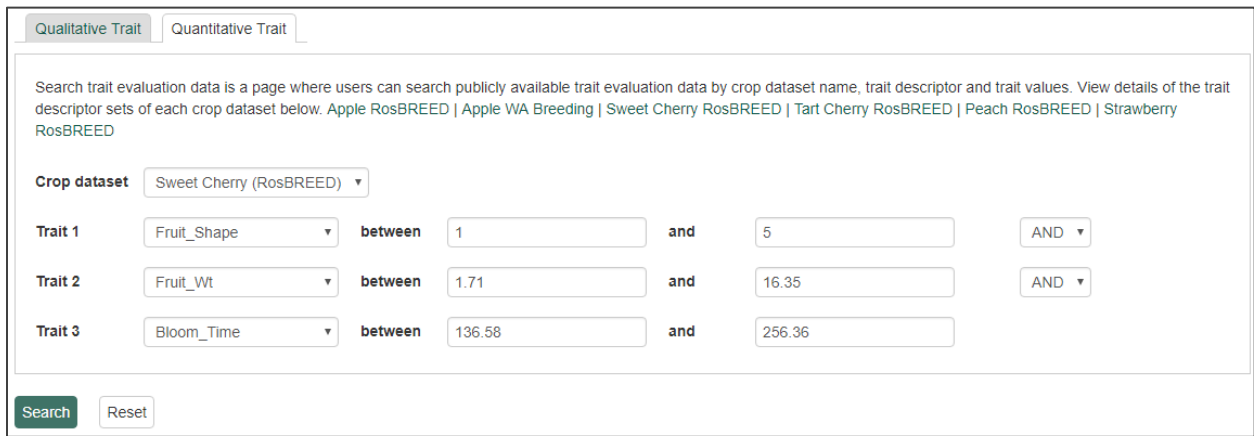
The screenshot shows a search form with the following fields and controls:

- Dataset:** A dropdown menu set to "Any".
- Species:** A dropdown menu with a list of options: "Any", "Fragaria x ananassa", "Malus x domestica", and "Prunus avium".
- Germplasm Name:** A dropdown menu set to "Any". To the right is a "Choose File" button and the text "No file chosen".
- SNP:** A dropdown menu set to "contains" followed by an empty text input box.
- Genome:** A wide dropdown menu set to "Any".
- Chr/Scaffold:** A dropdown menu set to "Any", followed by the text "between", an empty text input box, the text "and", another empty text input box, and the text "bp".
- Buttons:** A green "Search" button and a white "Reset" button.

Figure 3

## 10. Trait evaluation search page available

[Trait evaluation search page](#) (Figure 4) let users search for the publicly available trait evaluation data by trait values.



The screenshot shows a web interface for searching trait evaluation data. At the top, there are two tabs: "Qualitative Trait" and "Quantitative Trait". Below the tabs is a search bar with the text: "Search trait evaluation data is a page where users can search publicly available trait evaluation data by crop dataset name, trait descriptor and trait values. View details of the trait descriptor sets of each crop dataset below. Apple RosBREED | Apple WA Breeding | Sweet Cherry RosBREED | Tart Cherry RosBREED | Peach RosBREED | Strawberry RosBREED".

The "Crop dataset" is set to "Sweet Cherry (RosBREED)". There are three trait search criteria:

- Trait 1: Fruit\_Shape, between 1 and 5, AND
- Trait 2: Fruit\_Wt, between 1.71 and 16.35, AND
- Trait 3: Bloom\_Time, between 136.58 and 256.36, AND

At the bottom, there are "Search" and "Reset" buttons.

Figure 4

## 11. New MapViewer available

New Tripal [MapViewer](#) (Figure 1) available for dynamic visualization of genetic maps.

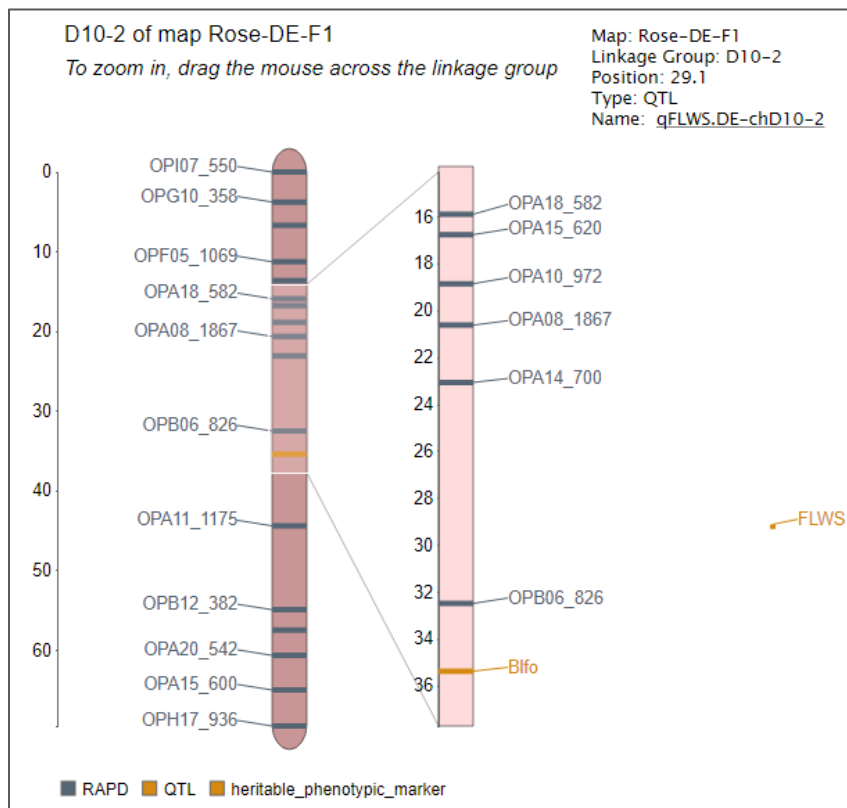


Figure 1

## 12. New enhanced Tripal BLAST interface available

[New enhanced BLAST](#) with graphic results and hyperlinks to the JBrowse or gene page available (Figure 5)

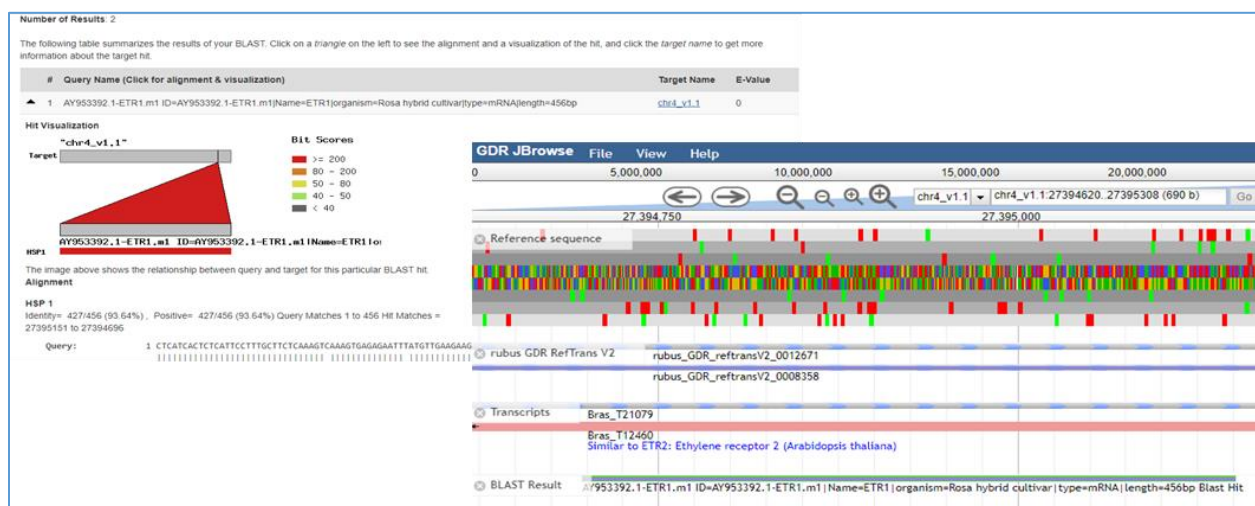


Figure 5

## 13. Pathway Inspector from FEM available

[Pathway Inspector](#) (PI) from FEM Research and Innovation Center, a web tool designed to identify enriched pathways and differentially expressed genes from RNA-Seq data, is available in GDR.

## 14. Work in Progress

- Addition of more map, marker and QTL data: We are continuously adding more map, marker and QTL data from publications to keep GDR up to date.
- Adding genome data as it becomes available
- Developing more functionality in BIMS (Breeders Information Management System). V1.0 now being tested by core breeders and will be made available to all Rosaceae breeders in 2018.
- Developing further terms for Trait Ontology to describe Rosaceae traits.
- Adding more functionality in MapViewer.

## 15. Employment opportunities

We are currently looking to recruit a postdoc for GDR and related work. A very competitive compensation package is available for the right candidate. If you know of any candidates for this job, please have them contact [Dorrie Main](#).

## 16. Subscription

Visit our mailing lists be added/removed to the available [GDR mailing lists](#). Once you have registered you may use the mailing lists to send out relevant information the community and it will be stored in searchable web archives. More information is available on each page on how to use them. If you have any difficulties please use the [contact us form](#).

## 17. Conferences 2018

- [XXVI Plant and Animal Genome Conference \(PAG\): January 13-17, 2018, San Diego, USA  
GDR and associated Mainlab activities at PAG 2018](#)
- [The 9<sup>th</sup> Rosaceae Genomics Conference \(RGC9\): June 26-30, 2018, Nanjing, China](#)
- [American Society of Horticultural Science Annual Conference \(ASHS2018\): July 30-Aug 3, Washington DC, USA](#)
- [National Association of Plant Breeders Annual Meeting: August 7-10, Guelph, Canada](#)
- [XXX International Horticultural Congress \(IHC2018\): August 12-16, Istanbul, Turkey](#)