

Welcome to the second issue of the GDR newsletter in 2015. 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 [www.rosaceae.org/contact](http://www.rosaceae.org/contact). The online version can be found at [www.rosaceae.org/GDR\\_newsletter](http://www.rosaceae.org/GDR_newsletter).

### What's new at GDR?

1. GDR usage statistics
2. New genome sequences
3. New map, marker and QTL data
4. New SNP array data
5. New interface to access SNP data
6. Evaluation of the FieldBook App to collect phenotypic data
7. Reorganization of species pages
8. Effort toward gene naming standardization
9. Work in progress
10. Employment opportunities
11. Sign up for our newsletter
12. Upcoming events

#### 1. GDR Usage Statistics

Between April 1 and September 30, 2015 GDR was accessed by 9,383 users from 129 countries with 91,426 pages viewed. The top ten users by country were China, USA, Italy, France, Japan, Spain, India, Brazil, Germany and Chile. Of the users, 46% were female and 54% male.

#### 2. New *Fragaria* Genome Sequences

Several genome assemblies of *Fragaria* ([Hirakawa et al., 2014](#)) submitted by Dr. Sachiko Isobe from the Kazusa DNA Research Institute, Japan have been released on GDR. They include the genome assembly of *Fragaria x ananassa* and four wild species v1.0.

Users can access these new genome assembly data from the [Fragaria Genome Page](#) and the [GDR NCBI Blast Server](#) and the [GDR BATCH Blast server](#).

- *Fragaria x ananassa* Genome v1.0 (FAN\_r1.1)

- *Fragaria x ananassa* Reference Genome v1.0 (FANhybrid\_r1.2)
- *Fragaria iinumae* Genome v1.0 (FII\_r1.1)
- *Fragaria nipponica* Genome v1.0 (FNI\_r1.1)
- *Fragaria nubicola* Genome v1.0 (FNU\_r1.1)
- *Fragaria orientalis* Genome v1.0 (FOR\_r1.1)

### 3. New Map, Marker and QTL Data

New markers and data for quantitative trait loci (QTL) are continuously being added either by direct submission from research groups or extracted from publications by GDR curators.

New information from 8 publications are now available on GDR. These include 2 from *Malus*, 2 from *Prunus*, 2 from *Fragaria*, 1 from *Pyrus* and 1 from *Rosa*. A list of these publications can be found in [GDR News items 9/7/15](#). Access 2,322 traits from the [MTL/QTL search site](#).

Search QTLs and/or MTLs (Mendelian Trait Loci) by any combination of species, trait category, trait name, published symbol or label. ([Help](#))

Type  MTL QTL

Species  *Fragaria x ananassa* *Malus fusca* *Malus robusta*

Trait Category  anatomy and morphology trait biochemical trait growth and development trait

Trait Name   (e.g. self-incompatibility, chilling requirement or fruit weight)

Published Symbol   (e.g. Pm1, Ls1, PPV-D or Skc)

QTL/MTL Label   (e.g. qFS.DE-chD10-2, qLN.FD-chF7 or qLS.DE-chE15-9)

### 4. New Apple, Rose and Strawberry SNP Array Data

- 90K SNP array for the cultivated strawberry *Fragaria x ananassa* ([Bassil et al. 2015](#))
- 20K SNP Array for *Malus x domestica* ([Bianco et al. 2014](#))
- 68K SNP array for Rose ([Koning-Boucoiran et al. 2015](#))

### 5. New Interface to Access SNP Data

New SNP array pages are available to access SNP data and SNP project details. They can be accessed through the header bar from the 'Species' menu > specific species > 'SNP array' pages.

General	Help	Species	Data	Search	Tools	Breeders Toolbox	Community
20K SNP Arra		Rosaceae family (all species)					
Download		Fragaria (all species)					
Download SNP		Fragaria x ananassa (strawberry)					
File Descriptio		Fragaria vesca (Woodland strawberry)					
Full-sib families		Malus (all species)	Overview				
List of the 18,0		Malus x domestica (apple)	Whole Genomes				
VCF file for the		Prunus (all species)	Transcripts				
		Prunus armeniaca (apricot)	SNP array				
		Prunus dulcis (almond)	Maps				
		Prunus serotina (black cherry)	AppleCyc				

## 6. Evaluation of the FieldBook App to Collect Phenotypic Data



Field Book is an application developed by Trevor Rife as part of the Kansas State University Wheat Genetics and Germplasm Improvement Program run by Dr. Jesse Poland. It is designed to collect phenotypic data for field research plots. We are working with Rosaceae crop breeders, Dr. Ksenija Gasic (Clemson University, GDR Co-PI, peach breeder), Dr. Kate Evans (Washington State University, GDR Co-PI, pome fruit breeder), Dr. Amy Iezzoni (Michigan State University, RosBREED PI, cherry breeder,) and Dr. Gina Fernandez (North Carolina State University, strawberry and caneberry breeder), as well as several other breeders from the [NRSP10](#) project to evaluate this commonly used commodity crop app.

Currently we are working with the developers to improve and modify the app for collecting electronic tree and small fruit phenotypic data. In the future, this phenotypic data could be uploaded into GDR to improve breeding tools such as the Breeders' Toolbox. At this time, it is only available for Android devices at the Google Play Store:

<https://play.google.com/store/apps/details?id=com.fieldbook.tracker>.

## 7. Species Pages Reorganized

The species pages have been reorganized to enable clear, one-stop access to all the data and tools available for each genus and species. The example below highlights the Overview page for *Malus x domestica*.

Example: Malus x domestica page Overview Page

Overview	
Genus	Malus
Species	<i>x domestica</i>
Abbreviation	M. x domestica
Scientific Name	Malus x domestica
Common Name	Apple
Geographic Origin	cultivated
Haploid Chromosome Number	17
Ploidy	2x, 3x
Growth Habit	tree
Propagation Method	grafting for clones
Usage	fruit
Resistance to biotic stress	Dessert, cider varieties
Germplasm	[view all 5428]
Sequence	[view all 3694436]

### Resources

*Data*


- Overview
- Publications
- Genetic Maps
- Genes
- Markers
- Sequences
- Trait Loci
- Whole Genomes
- SNP arrays
- Germplasm

*Tools*

- GBrowse
- JBrowse
- GBrowse\_Syn
- CMap
- AppleCyc
- NCBI Blast
- Batch Blast
- Sequence Retrieval Tool
- GO Viewer
- KEGG Pathway Viewer

## 8. Effort Toward Gene Naming Standardization for our Community

Tree Genetics & Genomes (2015) 11: 108  
DOI 10.1007/s11295-015-0931-5



OPINION PAPER

### A standard nomenclature for gene designation in the Rosaceae

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'A standard nomenclature for gene designation in the Rosaceae' has been published as an open-access manuscript in Tree Genetics and Genomes (October 2015; 11:108). This publication is a result of several months' worth of work with the U.S. RosEXEC group, which is comprised of scientists, industry and outreach members of the Rosaceae community. We have contacted the

top 22 journals where genes are published for Rosaceae to facilitate gene name submission to GDR during the publication process. Standardization will help research groups to ensure that there is “uniformity and clarity” as new information is being described from recently published genomes.

## 9. 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 an up-to-date database
- Upgrading GDR to Drupal 7 and implementing a new theme for GDR that will display a streamlined version of the site when viewed on mobile devices
- Converting the current breeders toolbox to Tripal and adding more functionality
- Working with breeders on design of a new breeders toolbox to provide better interfaces and functionality
- Modifying further terms for Trait Ontology to describe Rosaceae traits
- Modifying the data dictionary and templates for marker and QTL data that can be shared with other plant databases
- Surveying public and agriculture teacher audiences about genetic literacy.
- Developing a survey of GDR users to ask for your feedback and recommendations

## 10. Employment Opportunities

We are currently looking to recruit a postdoctoral data curator/sequence analyst 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](#).

## 11. 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 [contact us](#).

## 12. Upcoming Events

- The Crop Science Society of America Annual Meeting, Nov 15-18, 2015, Minneapolis. MN, USA. GDR will be presented at the Crop Breeding Database Symposium on Tuesday Nov 17 at 1.45 PM.
- The International Plant and Animal Genome XXIV Conference, Jan 9-13, 2016, San Diego, CA, USA. Some Rosaceae and GDR activities include (1) The Tree and Fruit Workshop on Sat Jan 9, 8AM-12PM (2) The RosEXEC and RosIGI Annual Meeting on Sun Jan 10, 8 AM-

12 PM (3) GDR Computer Demonstration (4) Tripal Workshop and the (5) Plant Database Booth. More details will be posted soon on the [GDR conferences page](#)

- The 8<sup>th</sup> International Rosaceae Genomics Conference, June 22-24, 2016, Angiers, France. More details will be posted in the [GDR conferences page](#) as they become available.