GDR | genome database for rosaceae

Newsletter

May 2006

Welcome to the fifth issue of the GDR newsletter. 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 either directly by email or via our online form. The online version can be found at http://www.mainlab.clemson.edu/gdr/newsletter.shtml as are previous editions.

Community News

White Paper

The US National Rosaceae Genomic, Genetics and Breeding Executive Committee have completed the US white paper on Rosaceae Genomics. It can be downloaded from GDR and any comments can be addressed to the executive committee chair, Dr Amy Iezonni.

Funding

1. A US based proposal, supported by strong international collaboration, is being submitted to the NSF Plant Genome Comparative Sequencing program in June. We are proposing to sequence the peach genome as a reference for Rosaceae, with skim sequencing of strawberry and apple, and targeted deep coverage of selected loci across multiple species. For more information contact Bryon Sosinski of NC State.

2. A US based proposal is being submitted to the NSF Networking program in June to fund a "Rosaceae Informatics Network" where international bioinformatics researchers will meet regularly and develop a collaborative bioinformatics infrastructure for the community database. For more information contact Dorrie Main or Bert Abbott.

Conferences

The 3rd International Rosaceae Genomics Conference was held March 19-22, 2006, in Napier, New Zealand. Download the conference outcomes and the abstracts from this meeting. The 4th International Rosaceae Genomics Conference is scheduled to be held in Pućon, Chile in March 2008. More details will be posted in the GDR conferences page as they become available.

Employment

A faculty position in plant breeding is available at the Pontificia Universidas Catolica de Chile.

What's new at GDR?

1. SNPs (Single Nucleotide Polymorphisms)
2. Updates to the peach physical map
3. Updates to the Comparative Mapping Viewer CMap
4. Marker/Map data template available
5. Rosaceae Genomics White papers
6. Species page/Project page
7. New header bar
8. Community pages and mailing lists
9. New publication from GDR
10. Additions to the publication database

1. SNPs (Single Nucleotide Polymorphisms)
The new Fragaria, Malus, Prunus, Pyrus, and Rosa unigenes have been searched for SNPs using the software package AutoSNP. A total of 14,801 SNPs are available to be viewed and searched, including 10426 SNPs from Malus, 3776 from Prunus, 316 from Rosa, and 283 from Fragaria.

2. Updates to the peach physical map
The latest peach physical map contains 18387 BACs and 1367 contigs. Physical length of the contigs is appoximately 210-230Mb and that of the anchored contigs is 33Mb. WebFPC / WebChrom displays the peach physical map. Anchored peach BAC contigs can be accessed directly from the prunus reference TxE map from the GDR map viewer.

3. Updates to the Comparative Mapping Viewer CMap
Four new maps (Apricot GxV F1 2002, Apricot LxL F2 2003, Peach AxJ 2005 and 815x903BC diploid Fragaria 2006) have been added to the genetic maps available through CMap. This now makes a total of 24 Rosaceae CMaps are available through CMap at GDR.

These include:
- Prunus: Prunus bin map 2005, TxE almond x peach F2 2004, Myrobalan Plum x Almond- Peach hybrid 2004, GxN almond x peach F2 2001
- Peach: Peach AxJ 2005, Peach PMP2 2005, Peach peach x P. ferganensis BC1 PxF 2001, Peach JxF 2004, Peach Sc x B 1998
- Apricot: Apricot GxV F1 2002, Apricot LxL F2 2003
- Almond: Almond FxT 2000, Almond FxB F1 1998
- Sour Cherry: PcerasusEB, PcerasusRS
- Strawberry: FVxFN diploid Fragaria reference map, 815x903BC diploid Fragaria 2006
- Apple: MNY75441-58, MNY75441-67, MWijcik McIntosh, MRomeBeauty, MRomeBeauty 2, MWhiteAngel, MWhiteAngel 2

If you have mapping data that we can add, please contact us and we will work with you to make your data available via GDR.

4. Marker/Map data template available
Efforts are underway to curate more extensive genetics data to GDR, and data templates for map/marker/trait/polymorphism/gene/QTL/Diversity are available.

5. Rosaceae Genomics White papers
The US National Rosaceae Genomic, Genetics and Breeding Executive Committee have completed the US white paper on Rosaceae Genomics. They can be downloaded from GDR and any comments can be submitted to the executive committee chair, Dr Amy Iezonni.

6. Species page/Project page
GDR has been reorganized to enhance navigation in the website. We have created specific species pages, under each genus where you can access all the information related to that species in GDR. Go to apple, prunus, almond, apricot, cherry, peach, rose, strawberry pages for all GDR structural genomics, functional genomics and funded project information.

7. New header bar
Dropdown and left side navigation bars remodeled to enhance ease of access to GDR data.

8. Community pages and mailing lists
The community page at GDR has been modified to make it easier to access the community pages of interest. In addition new International and US communication pages have been added, with

new mailing lists to join (via a web form). We encourage you to join the appropriate mailing lists and use them to communicate to the community using these tools.

9. New publication from GDR

Synteny conservation between the Prunus genome and both the present and ancestral Arabidopsis genomes. Sook Jung, Dorrie Main, Margaret Staton, Ilhyung Cho, Tatyana Zhebentyayeva, Pere Arus and Albert Abbott. BMC Genomics 2006, 7:81

10. Additions to the publication database

The publication database on GDR now contains publication data from Agricola, the catalog of articles maintained by the National Agricultural Library. 564 relevant publications are online and can be searched by title, authors, keywords, and date published.

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.
The GDR mailing list.
The International Rosaceae Genomics Community mailing list.
The USA Rosaceae Genomics Community mailing list.

Work in progress

1. Efforts to integrate more extensive map/marker data
We are updating our map/marker database structure to integrate the details of molecular marker data such as primer sequences, source BAC/ESTs, produce size and much more.
2. Creation of other databases within GDR
We are also creating new database modules such as gene, trait loci, QTL, polymorphism/allele, germplasm, and diversity data.