GDR | *genome database for rosaceae*   **NewsLetter**
                                                    Jan 2005

Welcome to the first issue of the GDR newsletter. This newsletter will be issued quarterly 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.genome.clemson.edu/gdr/newsletter.shtml.

What's new at GDR?

1. Updates to peach physical map
2. Updates to peach transcriptome map
3. CMap, the comparative map viewer, now available
4. Updates to Rosaceae genetic map data
5. Strawberry EST data are added to GDR
6. Genbank Rosaceae and genera EST assemblies available
7. Data Overview pages are available
8. New Publication search tool is available
9. Navigation bar modified
10. New analysis tool, CAP3 Assembly Server, is available
11. GDR Tutorial is available
12. Fruit Tree Genomics Workshop summary document available
13. GDR published in BMC Bioinformatics
14. GDR presentation at PAG-XIII
15. Enhanced computational resources

1. Updates to the peach physical map

The Peach physical map now contains 1223 contigs and 16879 BACs. 134 contigs are anchored to TxE, the Prunus reference map. The current physical map data was generated from an FPC assembly done on October 13, 2004. The next updated version of the physical map will be available at the end of January, 2005. WebFPC/WebChrom displays the peach physical map.

2. Updates to the peach transcriptome map

Unique peach ESTs are being hybridized to peach BACs to map the ESTs onto the genetically anchored peach physical map. 294 peach unigenes are anchored to various Rosaceae genetic maps by direct hybridization to genetically anchored BACs. 163 unigenes are anchored to the TxE map. An additional 277 peach unigenes are anchored to genetic maps by hybridization to BACs that belong to genetically anchored BAC contigs.
The GDR map viewer displays the updated TxE map with the associated transcriptome map.

3. CMap, the comparative map viewer, now available

CMap, a web-based tool that allows users to view comparisons of maps from various species, is implemented at GDR. In this release, we present nine Rosaceae genetic maps. Thanks to all the authors who assisted GDR team for uploading their mapping data.

4. Updates to Rosaceae genetic map data

Nine Rosaceae genetic maps are available through CMap, the comparative map viewer. A total of 872 genetic markers from 11 Rosaceae genetic maps are available from the marker search page.

5. Strawberry EST data processed through GDR

Over 1800 high quality ESTs from octoploid strawberries (Fragaria x. ananassa) have been annotated and added to GDR. The annotation includes sequence assembly, homology search and SSR mining. Detailed description of the project, sequences, and the annotation results can be searched, browsed and downloaded from the data overview page and EST search site. Thanks to Dr. Kevin Folta at University of Florida for submitting his sequences for processing through the GDR. If you would like to have your sequences processed through the GDR pipeline please contact dorrie@genome.clemson.edu.

6. Genbank Rosaceae and genera EST assemblies available

All the publicly available Rosaceae ESTs have been assembled using CAP3. Assemblies were also generated for the EST sets of each genus - Malus, Prunus, Fragaria, Rosa and Pyrus. The contigs and singlets for each assembly have bee searched against the Swissprot database and the homology results are available to browse and download in the data overview page. Homology with the NCBI nr protein database and other rosaceae ESTs will be available soon.

7. Data Overview pages are available

Data Overview pages are available. For EST projects, users can browse and download the detailed project description and the annotated sequence data.

8. New Publication search tool is available

GDR introduces a publication search tool where users can perform Boolean searches by title, author, keyword and publication year. The GDR stores publications from Pubmed that satisfy the following Boolean expression: (Rosaceae OR Prunus OR Rosa OR Fragaria OR Pyrus OR Malus) AND (gene OR genome OR map OR ssr OR microsatellite OR annotation OR est OR marker OR sequence). Relevant publications from sources other than Pubmed may be included.

9. Navigation bar modified

GDR has implemented a new navigation bar on top of each page to allow organized and quick access to major features of GDR. Major headings include about us, map resources, search, tools and Rosaceae resources. Each heading has a dropdown menu for a quick access to various pages.

10. New analysis tool, CAP3 Assembly Server, is available

GDR has implemented a new analysis tool, the CAP3 assembly server, in addition to the FASTA and BLAST servers. GDR also has links to various useful remote analysis tools.

11. GDR Tutorial is available

GDR overview and mapping resources tutorials are now available. Tutorials for search tools and analysis tools will be available soon.

12. Fruit Tree Genomics Workshop summary document available

Download the summary report from the October 2004 Technology Roadmap Temperate Fruit Genomics, Genetics and Breeding Workshop at Baltimore, Maryland.

13. GDR published in BMC Bioinformatics

GDR (Genome Database for Rosaceae): integrated web resources for Rosaceae genomics and genetics research. BMC Bioinformatics. 2004; 5: 130 (Abstract|PDF)

14. GDR presentation at PAG-XIII

GDR poster presentation at PAG-XIII, January 15-19, 2005.
P830: Genome Database For Rosaceae (GDR)

15. Enhanced Computational Resources

In January 2005, Clemson University purchases a 32 node apple grid to enhance the computational infrastructure of the CUGI Bioinformatics Center. This equipment will help ensure that data analysis in GDR remains current and readily available to the Rosaceae community.

Subscription

Visit our mailing list site at GDR to be added/removed to the mailing list.
http://www.genome.clemson.edu/gdr/MailingList.shtml

Work in progress
- Processing new peach shoot ESTs and rose ESTs from vegetative apices and apices at floral transition
- New comprehensive EST search site: Search by putative function from tissue, sequence homology and anchored map position will be available in addition to current search categories.
- EST search results site with bulk download feature: Sequences in Fasta format and homology results for the EST search result sets can be downloaded.
- Tutorials for search and analysis tools.