GDR | genome database for rosaceae

NewsLetter
Apr 2005

Welcome to the second issue of the GDR newsletter. This newsletter is 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.mainlab.clemson.edu/gdr/newsletter.shtml.

Community News

1. View the projects funded through the 2004 USDA CSREES National Research Initiative.
2. Announcing 3rd International Rosaceae Genomics Conference in Napier, New Zealand, March 19-23, 2006
3. Rosaceae workshop to be held at the ASHS Annual Meeting in Las Vegas, NV, July 18-21, 2005
4. Download the notes from the 2005 Fruit and Nut Workshop at the Plant and Animal Genome Conference

What's new at GDR?

1. Updates to peach physical map
2. Updates to CMap
3. Updates to Genbank Rosaceae EST data
4. Advanced EST search page available
5. Download/view transcriptome data
6. New feature in EST data page
7. Community page available
8. New online analysis tool, SSR server, is available
9. GDR Message Board available
10. GDR web address is changed

1. Updates to the peach physical map
The latest peach physical map contains 16895 BACs 1388 contigs. A total of 152 contigs are anchored to the TxE map, the Prunus reference map. The current physical map data was generated from an FPC assembly done on January 6, 2004. WebFPC/WebChrom displays the peach physical map.

2. Updates to CMap
19 Rosaceae genetic maps are available through CMap, the comparative map viewer. Recent addition includes seven apple maps and two cherry maps archived from RoseDB by Anjela Baldo at USDA, ARS PGRU and peach PMP2 map.

3. Updates to GenBank Rosaceae EST data
GenBank Rosaceae EST data have been annotated by sequence homology analyses against SwissProt database in addition to GenBank nr protein database.

4. Advanced EST search page available
A new comprehensive EST search page is available for the EST datasets. Users can search ESTs in any combination of clone name, organism (genus, species), tissue type, putative

function or species of the homologs, and anchored map position where relevant. The search results site has an option for downloading the sequences in fasta format.

5. Download/view transcriptome data
The peach transcriptome page provides the current status of the peach transcriptome map and links to an Excel spreadsheet with transcriptome map data detail and other relevant resources.

6. New feature in EST data page
A new option, "Printable Data" is available in the EST data page to present all the EST data in one page. View an example page.

7. Community page available
Visit our community page for conference news, information on our outreach program and other community resources such as a list of the thirteen projects funded through the 2004 USDA CSREES National Research Initiative: Plant Genome, Bioinformatics, and Genetic Resources.

8. New online analysis tool, SSR server, is available
GDR has implemented a new analysis tool, the SSR server. Using this online tool users can upload a batch file of sequences and have summary, individual and fasta formatted library file of the SSR containing sequences returned. The SSR server joins the growing list of online GDR tools such as the CAP3 assembly, FASTA and BLAST servers.

9. Searchable archives of GDR Message Board available
Users can view the searchable archives from the gdr mailing list. If you are a registered gdr user you can use the GDR email mailing list gdr-list@genome.clemson.edu to send out community based information or requests from your own computer. These emails will automatically be archived onto the message board where they can be searched by subject, thread, author or date.

10. GDR web address is changed.
GDR web address is now http://www.mainlab.clemson.edu/gdr/. The old address will be automatically redirected to the new address.

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
1. Processing new peach shoot ESTs and rose ESTs from vegetative apices and apices at floral transition
2. EST search by uploading a list of clone names/accession numbers
3. EST search results site with bulk download feature: Excel files with sequence homology data for the EST search result sets can be downloaded.
4. Development of an online sequence processing tool where users can upload their sequence files (trace or seq and qual files) and have the high quality sequences returned. These in turn can be assembled using the existing CAP3 assembly tool, mined for SSRs using the SSR server and then searched against known plant proteins or rosaceae ESTs using the FASTA and BLAST servers.
5. Tutorials for search and analysis tools
6. Addition of more mapping data.