

Welcome to the fourth 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> as are previous editions.

Community News

1. [Fruit and Nut Workshop](#), Saturday January 14, 8 am-12 pm. Plant and Animal Genome Conference XIV, San Diego, January 14-18, 2006. Conference organizer: [Dr Amy lezzoni](#). A Rosaceae genomics roundtable meeting will be held on Sunday January 15th, 8-10 am and the Rosaceae executive committee will meet on Sunday January 15th, 10am-12pm.
2. [3rd International Rosaceae Genomics Conference](#) will be held in Napier, New Zealand, March 19-23, 2006.
3. [The International Fruit Tree Association Annual Conference](#) will be held in Hershey, Pennsylvania, USA, February 26-March 1, 2006

What's new at GDR?

1. Proposal to renew funding for GDR submitted to the NSF Plant Genome Program.
2. New EST libraries are available.
3. Rosaceae Unigene v2 with enhanced annotation available.
4. Prunus bin map data is available in CMap and marker search engine.
5. Enhanced SSR server now available with primer generating option.
6. More databases are available for blast/fasta sequence similarity search.
7. Data available for the three peach BACs that are completely sequenced.
8. New Roseaceae Genomics Executive Committee web page.
9. The GDR publications database now contains 242 papers relevant to Rosaceae genetics/genomics.

1. GDR Renewal Proposal Submitted to NSF Plant Genome Program

In November 2005, a multi-institution proposal was submitted to the [National Science Foundation Plant Genome Program](#) to renew funding support for GDR through August 2009. The proposal if funded will significantly enhance the functionality and usefulness of GDR for the rosaceae community. If you'd like more information on this proposal please contact Dorrie Main.

2. New EST libraries are available.

The diploid strawberry species, *Fragaria vesca*, a putative genome donor to the octoploid, cultivated species (*Fragaria x ananassa*) is being developed as a model system for genetic and genomic research in strawberry. Tom Davis at the University of New Hampshire, USA, has provided 2717 ESTs from the unopened flower buds of diploid strawberries. A full analysis results of his library can be viewed/downloaded from [the project page](#) and the ESTs can be queried at [the EST search site](#).

Peach (*Prunus persica*) represents a model species for prunus and a reference species for Rosaceae. To develop an extensive Prunus EST database for identification and cloning of genes important to fruit and tree development, Bert Abbott at Clemson University, USA, generated 8832 high-quality expressed sequence tags (ESTs) from a peach cDNA library of shoot tissue. After assembly and annotation, a putative peach unigene set consisting of 5381 ESTs was defined. Full

analysis results of his library can be viewed/downloaded from [the project page](#) and the ESTs can be queried at [the EST search site](#).

3. Rosaceae Unigene v2 with enhanced annotation available.

A second version of the Rosaceae family unigene is now available. A new assembly process is being utilized; the ESTs are assembled using CAP3 within each genera (Fragaria, Malus, Prunus, Pyrus, and Rosa), and these assemblies are compiled and re-assembled together to produce the family-wide unigene. The new Rosaceae Unigene contains 72114 unigenes. Putative function has been assigned using the arabidopsis protein database and will be further expanded using the swissprot and NCBI nr protein databases. The unigenes have been analyzed for microsatellites and the results including suggested primers can be downloaded. Please see each project page ([Fragaria](#), [Malus](#), [Prunus](#), [Rosa](#) and [Rosaceae](#)) to view/download all the GDR unigene data.

4. Prunus bin map is available in CMap and marker search engine.

A Prunus bin map ([Howad et al., 2005](#)), is now available in GDR. [CMap](#) displays the prunus bin map with bin names and the first/ last markers of each bin, and the bin-mapped markers are displayed in each bin page. For example, all the bin mapped markers of the first bin in G1 are shown in [bin 1:14 page](#). All the markers in the prunus bin map can be queried through the [GDR marker search page](#).

5. Enhanced SSR server now available with primer generating option.

The online [SSR server](#) at GDR has been enhanced to include an option to have primers generated for the sequences that users wish to data mine for microsatellites.

6. More databases are available for [blast/fasta](#) sequence similarity search.

The databases available for blast/fasta sequence similarity search includes the following: peach ESTs, unigenes and ESTs with SSR's, BAC anchored peach ESTs, mapped peach ESTs, almond ESTs and unigenes (Abbott, Clemson U); peach ESTs and unigenes, peach ESTs with SSR's (Vendramin, CRA ISF); octoploid strawberry ESTs, unigenes, and ESTs with SSRs (Folta, U of Florida); diploid strawberry ESTs and unigenes (Davis, U of New Hampshire); ESTs of Fragaria, Malus, Prunus, Pyrus, Rosa, and entire Rosaceae family from NCBI dbEST; NCBI Rosaceae genomic sequences; NCBI Rosaceae protein sequences; Arabidopsis protein sequences from TAIR. A detailed [description of the databases](#) is available in each search engine. The blast/fasta sequence servers return the output of the searches in both parsed excel file and as a raw output file with visual alignments.

7. Data available for the three peach BACs that are completely sequenced.

Anchored ESTs/markers and the sequences for the three BACs (082118, 028F08 and pPn31C7) can be accessed from [BAC search site](#). An online annotation pipeline is currently under development by the GDR team.

8. New [Rosaceae Executive Committee web page](#) created to provide a communication portal for information and reports generated by the committee.

9. The GDR publications database now contains 242 papers relevant to Rosaceae genetics/genomics. New publications since our last newsletter are listed below:

1. Lazzari B et al. ESTree db: a tool for peach functional genomics. BMC Bioinformatics. 2005 Dec 1;6 Suppl 4:S16.

2. Patocchi A, Walser M, Tartarini S, Broggin GA, Gennari F, Sansavini S, Gessler C Identification by genome scanning approach (GSA) of a microsatellite tightly associated with the apple scab resistance gene Vm. Genome 2005 Aug;48(4):630-6.

3. Oosumi T, Gruszewski HA, Blischak LA, Baxter AJ, Wadl PA, Shuman JL, Veilleux RE, Shulaev V High-efficiency transformation of the diploid strawberry (*Fragaria vesca*) for functional genomics. *Planta*. 2005 Dec 1;:1-12.
4. Gillen, A.M., Bliss, F.A. Identification and Mapping of Markers Linked to the Mi Gene for Root-knot Nematode Resistance in Peach *J. Amer. Soc. Hort. Sci.* 130(1):24-33.
5. Tzanetakis IE, Martin RR New features in the genus Ilarvirus revealed by the nucleotide sequence of *Fragaria chiloensis* latent virus. *Virus Res* 2005 Sep;112(1-2):32-7.
6. Verde I, Lauria M, Dettori MT, Vendramin E, Balconi C, Micali S, Wang Y, Marrazzo MT, Cipriani G, Hartings H, Testolin R, Abbott AG, Motto M, Quarta R Microsatellite and AFLP markers in the *Prunus persica* [L. (Batsch)]x*P. ferganensis* BC(1)linkage map: saturation and coverage improvement. *Theor Appl Genet* 2005 Aug 9;:1-9.
7. Howad W, Yamamoto T, Dirlewanger E, Testolin R, Cosson P, Cipriani G, Monforte AJ, Georgi L, Abbott AG, Arus P Mapping with a Few Plants: Using Selective Mapping for Microsatellite Saturation of the *Prunus* Reference Map. *Genetics* 2005 Aug 22;.
8. Holland D, Larkov O, Bar-Ya'akov I, Bar E, Zax A, Brandeis E, Ravid U, Lewinsohn E Developmental and varietal differences in volatile ester formation and acetyl-CoA: alcohol acetyl transferase activities in apple (*Malus domestica* Borkh.) fruit. *J Agric Food Chem* 2005 Sep 7;53(18):7198-203.
9. Gao ZS, Weg WE, Schaart JG, Arkel GV, Breiteneder H, Hoffmann-Sommergruber K, Gilissen LJ Genomic characterization and linkage mapping of the apple allergen genes Mal d 2 (thaumatin-like protein) and Mal d 4 (profilin). *Theor Appl Genet* 2005 Sep 6;:1-11.
10. Mohapatra A, Rout GR Identification and analysis of genetic variation among rose cultivars using random amplified polymorphic DNA. *Z Naturforsch [C]* 2005 Jul-Aug;60(7-8):611-7.
11. Lalli DA, Decroocq V, Blenda AV, Schurdi-Levraud V, Garay L, Le Gall O, Damsteegt V, Reighard GL, Abbott AG Identification and mapping of resistance gene analogs (RGAs) in *Prunus*: a resistance map for *Prunus*. *Theor Appl Genet* 2005 Sep 30;:1-10.
12. Mehli L, Kjellsen TD, Dewey FM, Hietala AM A case study from the interaction of strawberry and *Botrytis cinerea* highlights the benefits of comonitoring both partners at genomic and mRNA level. *New Phytol* 2005 Nov;168(2):465-74.
13. Lin C, Mueller LA, Carthy JM, Crouzillat D, Petiard V, Tanksley SD Coffee and tomato share common gene repertoires as revealed by deep sequencing of seed and cherry transcripts. *Theor Appl Genet* 2005 Nov 5;:1-17.
14. Xie H, Sui Y, Chang FQ, Xu Y, Ma RC SSR allelic variation in almond (*Prunus dulcis* Mill.). *Theor Appl Genet* 2005 Nov 24;:1-7.

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<http://www.genome.clemson.edu/gdr/MailingList.shtml>

Work in progress

- Online EST sequence processing pipeline
- Annotating peach, plum and apricot BACs.
- Annotating the rosaceae unigene.
- Developing a rosaceae BAC annotation pipeline
- Extending the gene and QTL data available in CMap
- Integrating data from the USDA CSREES NRI projects