Getting Your Fill Of Grains Within The GrainGenes Resource

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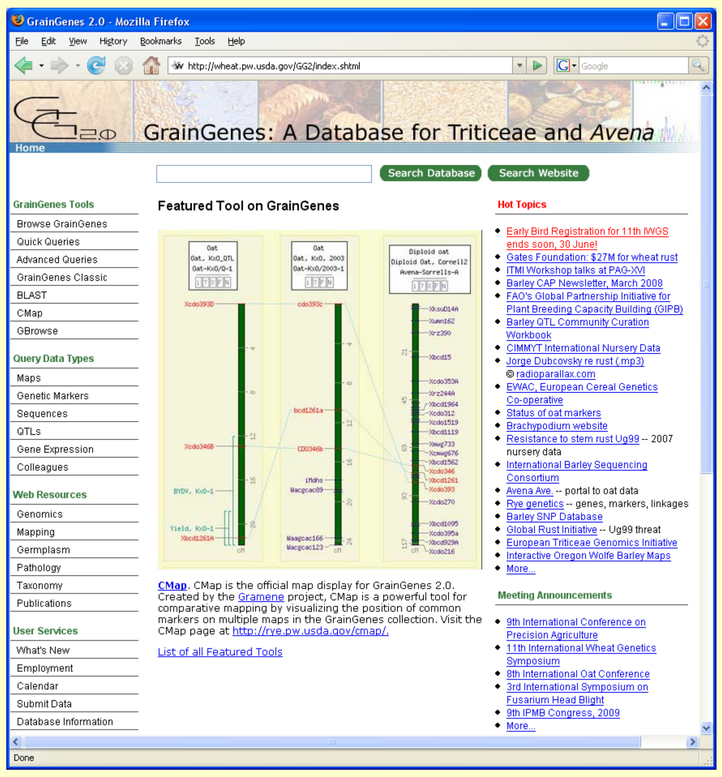


GrainGenes 2.0 Homepage

www.graingenes.org

The GrainGenes resource (http://www.graingenes.org) is a web-portal and database that has been available to the public since 1992 to provide information on the small grain crops of the Triticeae tribe (wheat, barley, rye) and *Avena* species. A convenient web space for discovering oat information available via the GrainGenes resource as well as links to other information can be found on a recently created page called “Avena Avenue”.

As linkage maps are made available, they can be made web-accessible using the CMap visual displays used by the GrainGenes database. Currently there are ten map studies creating over 250 linkage groups for oat. This interface allows the comparative tracking of common molecular markers found among different map studies. Comparative mapping between related species may prove valuable in refining map studies. There are over 1000 RFLP, AFLP, SNP, SSR types of mapped molecular marker records including ancillary information (i.e. primers, PCR conditions, etc...) available within the GrainGenes database. Information from recent DArT marker production is in the process of being integrated into the database. Use of the “Quick Queries” will aid accessing this information.

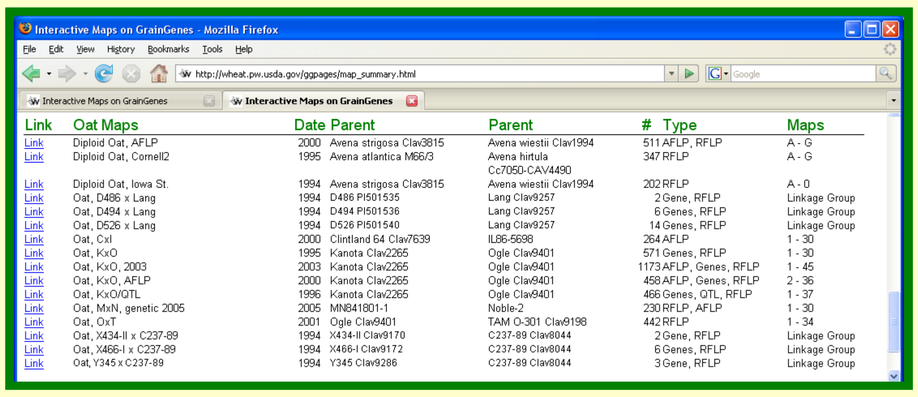
An effort has been launched to input phenotypic data from oat nursery plots. Some of these data are accessible from Avena Avenue. These data, coupled with high-throughput genotyping data will enable researchers to perform association analysis for gene and QTL discovery. A few QTL studies for oat have been entered into the GrainGenes database. Currently about seven different traits have been represented in 376 KxO QTLs distributed across oat maps. A funded project to enrich GrainGenes with barley QTLs have added about 600 new loci and consensus maps are in development for traits such as abiotic stress, quality, pathology, and other agronomic traits. It is hopeful that these will be valuable for comparative mapping studies between species. The database is able to provide the traits, range of phenotype scores among the sample population, and provides a map highlighting the area of the QTL.

GrainGenes also houses information about related grass species which allows the use of comparative maps to determine like-associations among related species. A model organism for the grass species, *Brachypodium distachyon*, is evolving as a research tool and information from this species may help build gaps in the comparative efforts between the related species. The *Brachypodium* species is part of the Pooideae subfamily, and thus can be quite valuable for comparative genomic studies between oat and other grasses, and closely related temperate cereals. We invite you to visit the GrainGenes resource and keep in contact with us. We welcome suggestions on ways to improve this resource for your research needs.

Other tools such as pre-formatted “Quick Queries”, advanced SQL, and Batch Queries have been updated to add user access to the database.

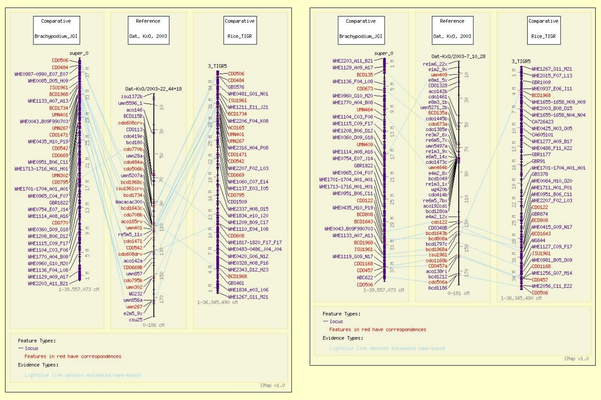
MAPS!

A new Table of Contents page has been created to help organize the 165 Map studies now in GrainGenes. The map display used in GrainGenes 2.0 is CMap, developed by the GMOD group (www.gmod.org). This tool provides an excellent interface both for viewing single maps and for comparing maps. Listed below are the current set of maps for oat.



CMap Display

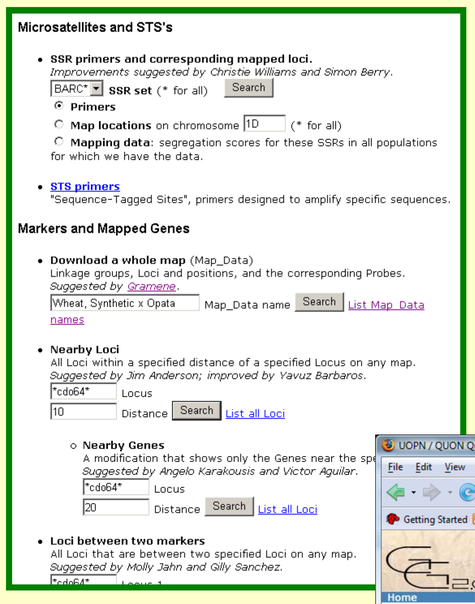
The CMap display is a powerful tool to make comparisons between map studies to determine if markers are shared between maps, or if different cultivars or species share the same results. Below are two sample linkage groups from the KxO, 2003 Map Study which compare common molecular markers shared (as shown by connecting map lines) between the two model grass species, Brachypodium (left) and Rice (right).

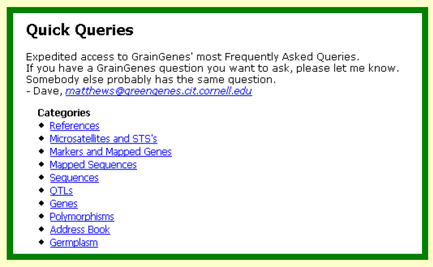


CMap Display: Comparison of two Oat linkage groups to model grasses.

QUERIES!

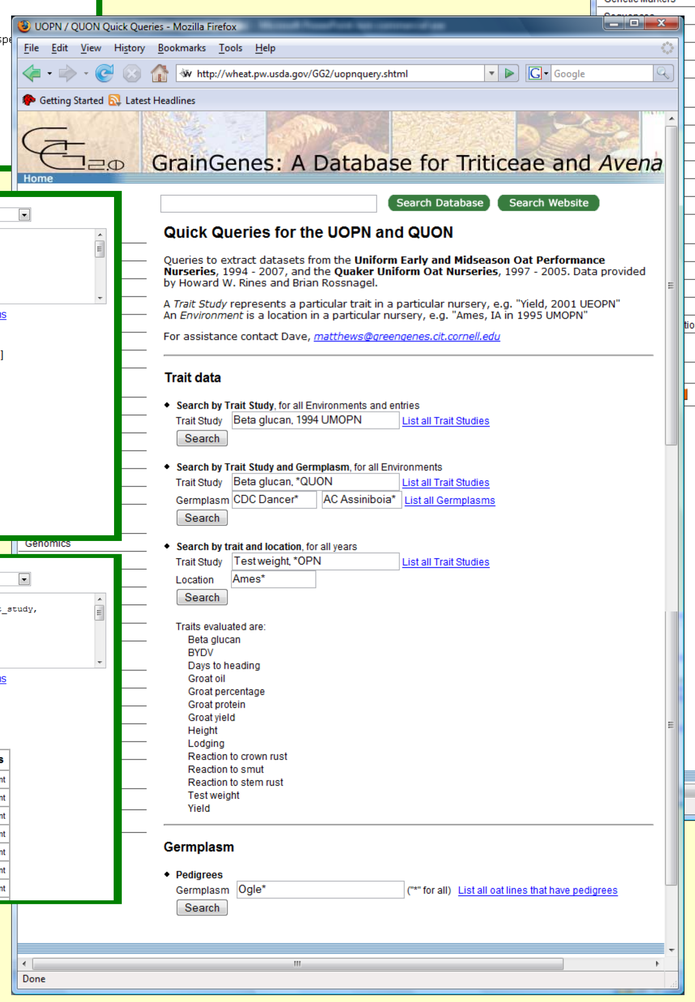
The Quick Queries page from GrainGenes Classic has been updated to use SQL queries. Many of the queries are frequently asked question suggested by GrainGenes users. Selecting a query will execute it and will also provide the SQL query code which may be edited to customize future queries. A few of the queries are shown. **Also available are Batch Queries.** Perform a raw SQL query on a list of up to 10,000 items. Powerful!

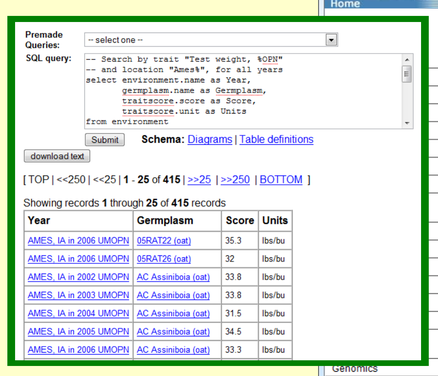


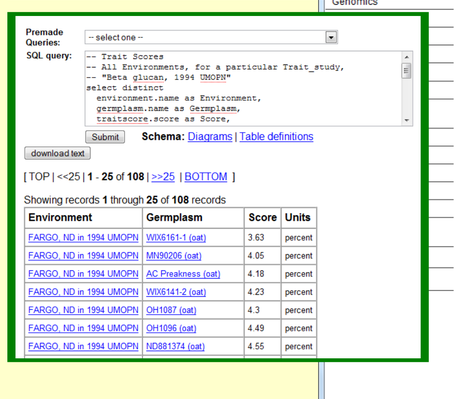


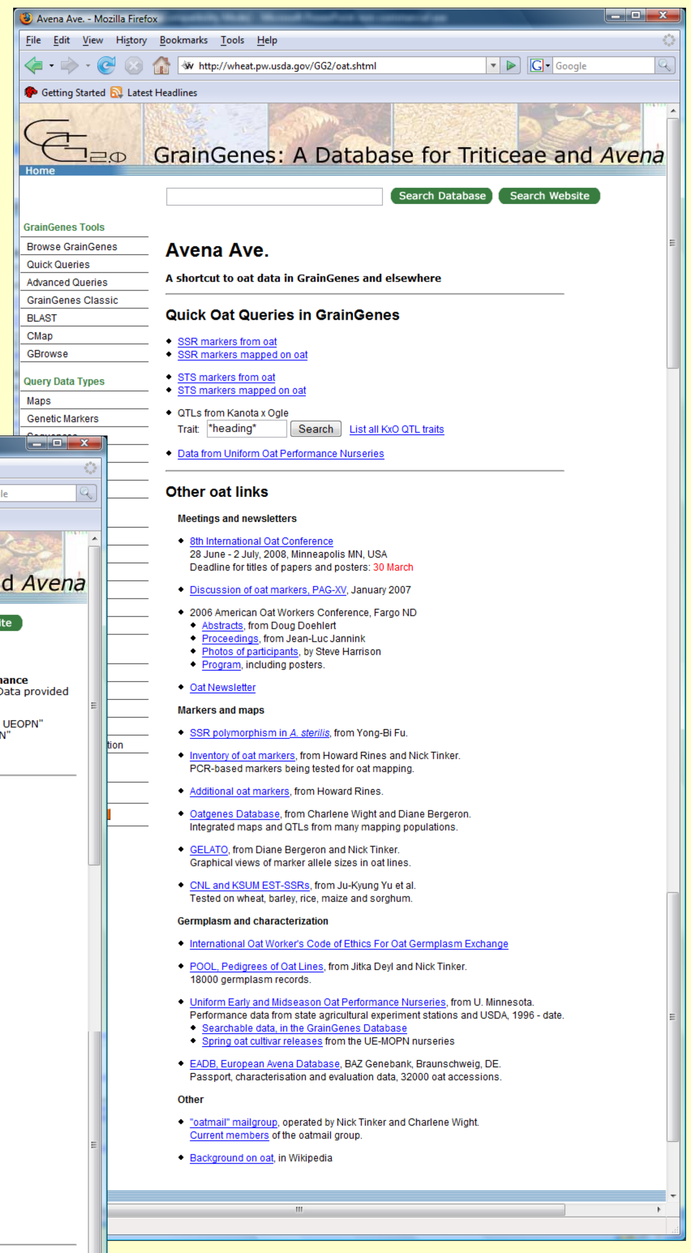
New Queries for Trait Study Data!

A series of sample queries have been created to survey oat nursery data. Shown below are a sample of **UOPN** and **QUON** datasets. These are linked from the ***Avena Avenue*** web area.







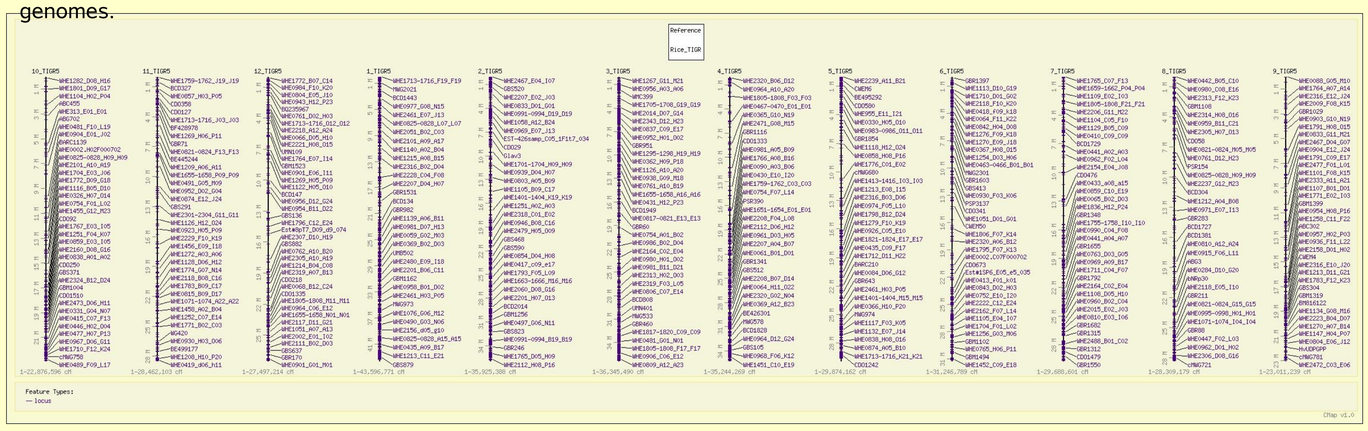


Avena Avenue!

A web area of the GrainGenes resources has been placed to provide quick links to vital oat information. Shown below a list of links now available, from *searching a list of oat markers* to *signing up for the oat e-mail list*.

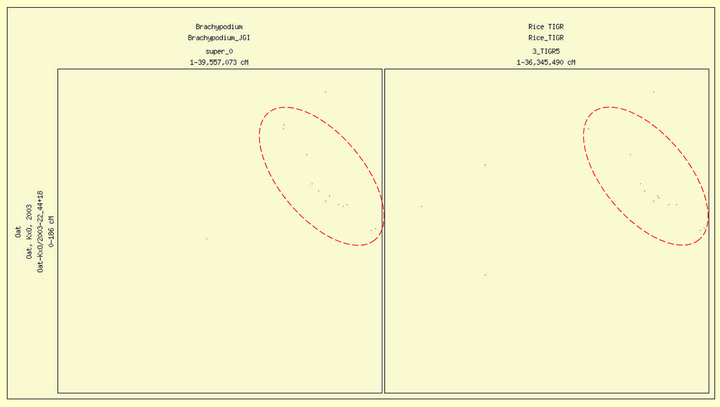
PROBES!

The GrainGenes database houses information on over 30,000 molecular markers, many for which sequence data is available. There are currently only 990 probes listed as being sourced from *Avena* and the rest are from the closely related wheat, barley, and rye species. The rice genome has been sequenced and the Brachypodium distachyon genome is underway. As a test of coverage, molecular probes listed in the GrainGenes resource were matched against the rice genome and the preliminary 4X coverage Brachypodium genome. Below is shown the saturation of the GrainGenes molecular markers against these genomes.

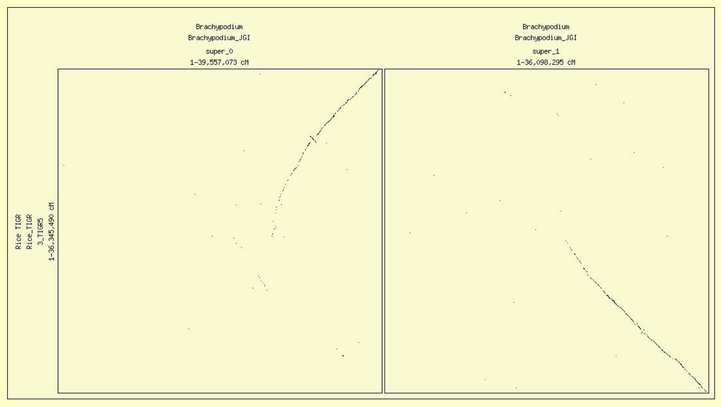


CMap Display: GrainGenes collection of probes compared to the twelve chromosomes of rice (TIGR release 5, 2007).

CMap Display: GrainGenes collection of probes compared to the twelve largest supercontigs of Brachypodium (JGI, brachypodium.org, 2008).



Dot Plot (CMap) of Map Display: Probes shared between Oat linkage group 22_44+18 and model grass species Brachypodium supercontig_0 (left) and Rice chromosome 3 (right). Region of co-linear matches with oar are circled in red.



Dot Plot (CMap) Map Correspondences: Probe matches shared between Rice chromosome 3 (Y-axis) and Brachypodium supercontig_0 (left) and **supercontig_1 (right)**.