

Gramene’s Diversity Advanced Search: Highly-Flexible User Front-End Built on GDPC Middleware

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Gramene’s Genetic Diversity databases contain genetic data (i.e. SNPs, SSRs, sequences), phenotypic data (i.e. trait measurements), environment data (i.e. planting location, experiment), and germplasm data (i.e. stock, pedigree, passport). Currently three crops (maize, wheat, and rice) are stored with varying amounts of those data types. Several web-based tools provide access to these cereal databases which meet the needs of many users. Although in instances where more complex queries are required, Gramene’s Diversity Advanced Search (www.gramene.org/diversity/gramene_gdpc.html) gives users more flexibility when retrieving data.

The Advanced Search (a.k.a. GDPC Browser) uses the GDPC middleware (www.maizegenetics.net/gdpc) to access databases. The middleware is a communications layer that makes it possible to retrieve data remotely via web services. The middleware also masks the complexities of various databases making it possible to query and integrate data from multiple data sources.

Although the middleware is important infrastructure, users of the Advanced Search only need to understand the various controls to construct a query and retrieve data. After choosing which crop database to access, users can build lists of data. This data is retrieved based on search criteria specified by the user. Once retrieved, the data can be manipulated in various ways including exporting to standard file formats.

Short example to get started...

- Go to: http://www.gramene.org/diversity/gramene_gdpc.html
- Click on “Get Maize Diversity Data.” NOTE: This may take a few minutes the first time.
- When it asks “Do you want to run the application?”, click “Run.” The application should start-up and show that it is connected to “Gramene Diversity Maize Database.”
- Each labeled tab corresponds to a type of data that you can retrieve. First go to the tab labeled “Taxa.”
- Check the box next to “Germplasm Type,” and then select the germplasm type “Inbred.” Also, check the box next to “Source,” and then select the source “CIMMYT.”
- Then click “Get Data” to retrieve all inbred taxa with source CIMMYT.
- Next go to the tab labeled “Loci.”

- Check the box next to “Chromosome Name,” and then select chromosome name “1.”
- Click “Get Data” to retrieve all loci on chromosome 1.
- Next click on the tab labeled “Genotype Experiments.”
- The list labeled “Locus (working list)” will contain all the loci that you retrieve in the previous steps. Highlight all the loci in this list by first clicking (to highlight) any of the loci. Then press <Ctrl> <a> to select all loci in the list.
- Check the box next to “Polymorphism Type,” and select polymorphism type “SNP.”
- Click “Get Data” to retrieve all the genotype experiments associated with loci on chromosome 1 designed to score SNPs.
- Next click on the tab labeled “Genotypes.” Items in both lists “Taxa (working list)” and “Genotype Experiment (working list)” result from the actions above. All items in both lists should already be highlighted.
- Click “Get Data” to retrieve all genotypes for the given taxa and genotype experiments.

Please feel free to experiment with other functionality of the Advanced Search. Notice that some search criteria may result in very large data sets, causing long wait times. Send any problems to tmc46@cornell.edu.