

Gramene Diversity

Gramene Genetic Diversity database contains SSR and SNP allelic data and passport descriptions for rice, maize and wheat germplasms. It also holds phenotypic data for maize.

The ultimate goal is to make this database a source of rice, maize, and wheat bio-information from/for evolutionary, domestication, association, and genetic diversity studies. It also could potentially be useful for applications such as germplasm management, marker assisted selection and DNA-based variety identification.



3/22/07



A Comparative Mapping Resource

GRAMENE

Tutorial Help



If you are viewing this tutorial with Adobe Acrobat Reader, click the "bookmarks" on the left hand side of the Reader for easier navigation.

Note! Although we continually work to make Gramene compatible with all browsers, there are problems with some browser versions. If you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through Gramene Feedback.

www.gramene.org

From either of the search or quick start menus, click on Diversity.

Diversity Home: Search

(by Germplasm name)

General search
does NOT
search Diversity

The screenshot shows the GRAMENE Diversity website interface. At the top, there is a green header with the GRAMENE logo and the word 'Diversity'. Below the header is a navigation bar with links: Search, Genomes, Species, Download, Resources, About, Help, and Feedback. A search bar is located in the top right corner with the text 'Find anything' and a 'Search' button. Below the navigation bar, there is a section titled 'Gramene: Genetic Diversity Database'. This section contains a search form with three main fields: 'Search for:', 'Search in:', and 'Species:'. The 'Search for:' field has a dropdown menu with options: 'Similarity Search', 'Markers', and 'Germplasm'. The 'Search in:' field has a dropdown menu with options: '--Any--', 'Markers', and 'Germplasm'. The 'Species:' field has a dropdown menu with options: 'Rice', 'Maize', 'Rice', and 'Wheat'. Below the search form, there is a 'Submit' button. A red starburst graphic is located on the left side of the page. Several yellow callout boxes provide instructions: 1. 'Enter germplasm name, accession number or marker name to view allelic data.' points to the 'Search for:' field. 2. 'optional' points to the 'Search in:' field. 3. '2. Select species' points to the 'Species:' field. 4. '3. Click "Submit"' points to the 'Submit' button. 5. 'Example searches' points to the text 'E.g., Germplasm "IRGC 3575", RA4969, Basmati'. 6. 'Click for database species summaries (see Slide 13)' points to the 'Species:' field. 7. 'General search does NOT search Diversity' points to the top search bar. 8. '3/22/07' is in the bottom left corner.

GRAMENE Diversity

Find anything

[Search](#) [Genomes](#) [Species](#) [Download](#) [Resources](#) [About](#) [Help](#) [Feedback](#)

[Diversity Home](#) [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Gramene: Genetic Diversity Database

Search for: Search in: Species:

☐ Similarity Search

E.g., Germplasm "IRGC 3575", RA4969, Basmati

Database contains SSR and SNP allelic data and passport descriptions. The database can be searched by germplasm accession number, accession name, or marker name. You can also search for germplasm accessions "IRGC 3575", PI 400000, or RA4969, or marker RM22. Specify the species of your interest from pull-down menu before you press the submit button. For search tips, please see the [help document](#).

To perform advanced queries, click the [Advanced Search](#) here or above. Advanced search provides access to SNPs, SSRs, sequences, etc. and phenotypic data that may be collected in field, gene, and physiological experiments. Data are saved in various formats, data integrated from multiple sources, etc.

We welcome your questions, comments and suggestions. Please email us at [diversity@gramene.org](#) or use the pages to send us your remarks.

For data summary of the database, click [here](#).

Example searches

Click for database species summaries (see Slide 13)

3/22/07

Error messages?

 [Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Error

Search for: Search in: Species:

☒ Similarity Search

E.g., [IRGC 3575](#), [RA4969](#), [Basmati 1](#), [RM22](#).

Error:

No search term long enough (3) to be indexed

*For accession numbers
with IRGC prefix, use
quotations : "IRGC 3575".*

*Error message
gives hint*

*For small names (<3
letters/word) with a space,
remove the space : IR36*

*For small names (<3 letters)
double the name : T1T1*

(Germplasm Name)

Click to begin new
search (home page)

Collection Information

View Germplasm IR36"

Click to view taxonomic details (*See Gramene Ontology tutorial*)

Click to view allele data on
germplasm (see next slide)

Experiment Information

Click to view general
marker type details

Links to abstract

[Show Allele Data](#)

Allele Data for one Germplasm

Allele data for germplasm "1594" from the experiment "Genetic structure and diversity in *Oryza sativa* L.".

[Search Again](#)

Items 1 to 25 of 169.

Page 1 of 7 | Next

| Accession Number | | Subsp. & subtaxa | Country of Origin | Accession Number | Stock Number | Locus name | Genotype |
|------------------|--|---------------------------------------|-------------------|------------------|--------------|------------|----------|
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM1 | 86, 108 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM2 | 167 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM5 | 112 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM7 | 181 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM11 | 139 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | OSR13 | 94 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM13 | 139 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM16 | 181 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM17 | 157, 183 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM19 | 225 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM21 | 159 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM22 | 195 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM25 | 145 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM31 | 138 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM44 | 103 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM55 | 22 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM72 | 15 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM85 | 10 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM87 | 151 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM104 | 238 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM105 | 126 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM1 | 86, 108 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM2 | 167 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM5 | 112 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM7 | 181 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM11 | 139 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | OSR13 | 94 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM13 | 139 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM16 | 181 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM17 | 157, 183 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM19 | 225 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM21 | 159 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM22 | 195 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM25 | 145 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM31 | 138 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM44 | 103 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM55 | 22 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM72 | 15 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM85 | 10 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM87 | 151 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM104 | 238 |
| IR36 | | Group II (indica, cross-bred basmati) | NA | 1594 | RA5352 | RM105 | 126 |

Markers assayed for a germplasm

Click hyperlinked column headings to sort table by that column

Click for allele
data on this
marker from all
experiments
(Slide 8 & 9)

Click to return to
Germplasm Data
(*Previous Slide*)

*Allele(s) for the
corresponding loci*

Click for all allele data on this marker from this experiment (see Slide10)

Download results

Experiments for one Marker

View Marker "OSR13"

There is allele data for locus "OSR13" from 2 experiments.

[\[Click here for primer sequences, mapping and other details on OSR13 \]](#)

| Title | Design | Polymorphism Type | Allele Scoring Protocol | PI(s) | Comments | Data |
|--|--|---------------------|--|--|--|----------------------------------|
| Genetic structure and diversity in <i>Oryza sativa</i> L. | 234 rice accessions from wide geographical regions of the world | SSR | PCR products were size separated by capillary electrophoresis using ABI 3700 DNA analyzer; SSRs were analysed with GenScan 3.1.2 software and scored with Genotyper 2.5 software. | McCouch, S. and Tai, T. H. | Prediction of population structure was model-based (STRUCTURE) and based on data from 169 genomic SSRs. For more information, see the paper by Garris et al., 2005 . | Show Allele Data |
| Population Structure and Breeding Patterns of 145 U.S. Rice Cultivars Based on SSR Marker Analysis | 115 U.S rice cultivars and 30 ancestral rice accessions introduced from Asia were genotyped by means of 169 genomic SSR markers. | SSR | PCR products were size separated using ABI 3700 DNA analyzer; SSR fragment sizes were estimated with GenScan 3.1.2 software. Alleles were scored with Genotyper 2.5 software using the LocalSouthernMethod, and binned manually. | McCouch, S. and Tai, T. H. | Population structure was inferred using distance method with 169 SSR markers. For more information, please read the paper by Garris et al., 2005 . | Show Allele Data |

[\[Click here for primer sequences, mapping](#)

Click to view all allele data for marker from experiment.
(Slide 10)

Click to view marker details in Gramene Marker DB. (See Slide 9)

3/22/07

Marker Detail from Marker DB

[Markers Home](#) | [Markers Search](#) | [View Map Sets](#) | [SSR Markers Resource](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Search

Name: Type:

Markers menu indicates you are not in Diversity database anymore

E.g., "AG840697,AG841134", "rm*", Oat RFLPs like "CDO*", or view [help](#).

View Rice SSR "OSR13"

| Details | Source/Library | Map Positions (7) | Associations (1) | Images (0) |
|----------------------------------|---------------------|-------------------|------------------|------------|
| ID | 17488683 | | | |
| Name | OSR13 | | | |
| Synonyms (2) | OSR13(K) RM14643 | | | |
| Type | SSR | | | |
| Species | Oryza sativa (Rice) | | | |
| Germplasm | UNKNOWN | | | |
| Description | | | | |
| Repeat Motif | (GA)n | | | |
| Anneal Temperature | 55 | | | |
| Expected PCR Product Size | 0 | | | |
| Sequence Source | | | | |
| Remarks | | | | |

Marker Data in Gramene Marker DB. See Markers Tutorial

Allele Data for One Marker from One experiment

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [Advanced Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Allele data for marker "OSR13" from the experiment "Genetic structure and diversity in *Oryza sativa* L.".

[Search Again](#)

Items 1 to 25 of 234. Page of 10 | [Next](#)

| Germplasm Accession Name | Subsp. & subtaxa | Country of Origin | Accession Number | Stock Number | Locus name | Genotype | View All Genotypes on Germplasm |
|---------------------------------|-----------------------------------|-------------------|------------------|--------------|------------|----------|--|
| Pagaiyahan | admix (indica, tropical japonica) | Taiwan | IRGC 8267 | RA5013 | OSR13 | 98 | All Genotypes On "Pagaiyahan" |
| Peh-Kuh-Tsao-Tu | indica, indica | Taiwan | IRGC 8237 | RA5009 | OSR13 | 98, 104 | All Genotypes On "Peh-Kuh-Tsao-Tu" |
| JC93 | indica, indica | India | IRGC 9175 | RA4922 | OSR13 | 98 | All Genotypes On "JC93" |
| Honduras | japonica, tropical japonica | Honduras | IRGC 1717 | RA5129 | OSR13 | 98 | All Genotypes On "Honduras" |
| Romeo | japonica, temperate japonica | Italy | PI 433512 | RA5371 | OSR13 | 98 | All Genotypes On "Romeo" |
| Ai-Chiao-Hong | indica, indica | China | IRGC 51250 | RA4922 | OSR13 | 94 | All Genotypes On "Ai-Chiao-Hong" |
| Basmati 1 | aus | Pakistan | IRGC 27 | RA4922 | OSR13 | 112 | All Genotypes On "Basmati 1" |
| | indica, indica | Vietnam | | 4870 | OSR13 | 116 | |
| | | | | | OSR13 | 104 | |
| | | | | | OSR13 | 94 | |

Click for Germplasm Data – as in slide 6.

All alleles for marker on all germplasms in an experiment

Click to view all allele data on all markers/loci on a germplasm (as in slide 7).

Search by Marker

Enter Marker name.

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Gramene: Genetic Diversity Database

Search for: Search in: Species:

☐ Similarity Search

E.g., Germplasm "IRGC 3575", RA4969, Basmati 370, or marker RM22.

The Gramene Genetic Diversity database contains SSR and SNP allelic data and parent descriptions for rice, maize and wheat germplasms. It also holds phenotypic data for maize. The database can be searched by germplasm accession number, accession name or marker/locus name. For example, in the rice database you can search for germplasm accessions "IRGC 3575", "IRGC 3604", or RA4969, or marker RM22. Please specify the species of your interest from pull-down menu before you press the submit button. For more information, please read the [help document](#).

For more complex queries, you can use [The Genomic Diversity and Phenotype Connection Browser](#). Click [here](#) to download and get documentation on how to use the GDPC Browser.

We welcome your questions, comments and suggestions. Please use the [contact form](#).

For data summary of the database, click [here](#).

Search result is the same as slides 8-10.

Click for database summary by species (*see Slide 12*)

Data Summary

DATA SUMMARY

RICE DATABASE

| | |
|---------------------------------|--|
| Species: | <i>Oryza sativa</i> , <i>O. glaberrima</i> , <i>O. rufipogon</i> |
| Total no. of germplasms: | 695 |
| Data type: | SSR data and passport descriptions |
| Total No. Loci: | 572 SSR loci (Note: All loci are not necessarily unique.) |
| Project website: | Part of the data was obtained from McCouch Lab |

MAIZE DATABASE

| | |
|--|--|
| Species: | <i>Zea spp.</i> |
| Data type: | SSR, SNP, sequence, and phenotype data and passport descriptions |
| Germplasms with sequence data: | 229 |
| Germplasms with SNP data: | 449 |
| Germplasms with SSR data: | 1544 |
| No. of loci with sequence data: | 3683 |
| No. loci with SNP data: | 1435 |
| No. of loci with SSR data: | 520 |
| Project website: | Molecular and Functional Diversity of the Maize Genome |

WHEAT DATABASE

| | |
|---------------------------------|--|
| Species: | <i>Triticum aestivum</i> , <i>Aegilops spp.</i> |
| Data type: | SNP and sequence data and passport descriptions |
| Total no. of germplasms: | 48 |
| Total SNP markers: | 3802 |
| Total sequence assays: | 3802 |
| Project website: | Haplotype Polymorphism in Polyploid Wheats and Their Diploid Ancestors |

*Summary of information
in the current release of
Gramene. (Linked from
home page)*

Germplasm search

Options are based on species

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [FAQ](#) | [Release Notes](#)

Germplasm Search

Please select the database of your interest first.

From this search utility you can download information about germplasms from each database, including germplasm type, countries of origin, geographical parameters of the lines' collection locations, and where the seed can be obtained.

To obtain this information, use the search form at the right. To obtain a complete list of the germplasms in the databases, leave all the search parameters in their default state, choose the output format you would like, and click Submit. To change the sorting order of the resulting output, modify the 'Sort by' parameters before clicking Submit. To limit the search by your criteria of interest, use the text input fields and drop-down menus to specify your criteria.

The text input fields (Accession name, Source, Racename, State/Province, Collector, Collection) search for an exact match ('equals'). These searches can be modified to contain the text that you enter ('contains') or matching the text that you enter ('matches'). The wildcard '?' stands for a single character and '*' for zero or more characters. The search is not case sensitive.

Results in HTML format will appear below the search form on a refreshed page, containing a subset of the available fields in the database. For a complete table, including information on population, locality, elevation, longitude and latitude, choose a format other than HTML. Alternative formats for downloading and saving the complete result table include Excel or three different text formats: fixed-width, comma-separated or tab-delimited.

[View germplasm search tutorial](#)

Database:

Accession:

Source:

Germplasm Type:

Genus:

Species:

Subspecies:

Racename:

Country:

State/Province:

Collector:

Collection:

Sort by (#1):

Sort by (#2):

Sort by (#3):

Output Format:

Rice
Wheat
Maize

Rice

equals

equals

equals

contains

matches

ALL

ALL

ALL

ALL

equals

equals

equals

equals

ascending

ascending

descending

Accession

Source

- Select -

HTML

Submit

Reset

- Select -
Accession
Source
Genus
Species
Subspecies
Racename
Country
State/Province
Collector
Collnumb

HTML
Excel
text (fixed-width)
csv (comma-separated)
tsv (tab-delimited)

For more help with this screen, see the Panzea tutorial.

Select options and click submit

Molecular Diversity Search

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Molecular Diversity Search

Please select the database of your interest first.

From this search utility you can download information about all the markers used for the crop of your interest, including name of the marker, name of the gene/locus, and type of the marker, as well as primer sequences and repeated element for SSR markers (for maize and wheat). Please read this [help document](#) for how to obtain details of the markers assayed for rice.

To obtain a complete list of the markers in a database, leave all the search parameters in their default state, choose the output format you would like, and click Submit. To change the sorting order of the resulting output, modify the 'Sort by' parameters before clicking Submit. To limit the search by marker name, gene/locus name or marker type, use the text input fields to specify the marker name or gene/locus name, or the drop-down menu to specify the marker type.

The text input fields (Marker and Gene/Locus) are set by default for an exact match (modified to find marker or gene/locus names either containing characters or matching the text/wildcard combination that you enter). The asterisk (*) stands for a single character while "*" stands for zero or more characters. The search is case-sensitive.

The results of your molecular diversity search will appear below the search form on a refreshed page. To view the genotypes (or sequence alignments) corresponding to a marker, follow the link (displaying the marker type) in the Assays column of the HTML output table. The complete results of your molecular diversity search can also be downloaded and saved in Excel format or in one of three different text formats: fixed-width, comma-separated or tab-delimited.

[View](#) a molecular diversity search tutorial.

Options are based on species

Database:

Rice
Wheat
Maize
Rice

Marker:

equals

Gene/Locus:

equals

Marker Type:

equals

ALL

Sort by (#1):

ascending

Marker

Sort by (#2):

ascending

Gene/Locus

Output Format:

ascending

HTML

descending

HTML

Submit

Reset

For more help with this screen, see the Panzea tutorial.

Select options and click submit

HTML
Excel
text (fixed-width)
csv (comma-separated)
tsv (tab-delimited)

Gene/Locus Search

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Gene/Locus Search

Please select the database of your interest first.

From this search utility you can download information about all the loci assayed for the crop of your interest, including name and type of the loci. For the maize loci, you can also view their location within the maize genome. To obtain this information, use the search form at the right. To obtain a complete list of the loci from a database, leave all the search parameters in their default state, choose the output format you would like, and click Submit. To change the sorting order of the resulting output, modify the 'Sort by' parameters prior to clicking Submit.

To limit the search by your criteria of interest, use the drop-down menus and text boxes to specify your criteria. Types of loci include Mapped, Unmapped, and cytological loci. If you wish, the search can be confined to only those genes or loci for which at least one assay was performed for a marker of a given type (SSRs, SNPs, Sequencing, etc). However, the other marker types present in the resulting loci will also be listed. In addition, the search can be confined to a particular chromosomal region, relative to the IBM2 2004 Neighbors

For more help with this screen, see the Panzea tutorial.

The search is set by default for an exact match ('equals'). The search loci names either containing the text that you enter or the text/wildcard combination that you enter ('matches'). The character while '*' stands for zero or more characters. The search is not case sensitive.

Output tables in HTML format will appear below the search form on a refreshed page. Alternatively, the complete results of your search can be downloaded and saved in Excel format or in one of three different text formats: fixed-width, comma-separated, or tab-delimited.

[View](#) a gene/locus search tutorial.

Try a Maize Locus Search at [MaizeGDB](#)

Database:

Rice
Wheat
Maize
Rice

Options are based on species

Gene/Locus:

equals

Locus Type:

equals
contains
matches

Containing Marker(s) of Type:

ALL

IBM2

ALL

Chromosome:

Position (from cM):

Position (to cM):

Sort by (#1):

ascending

Sort by (#2):

ascending

Sort by (#3):

ascending

Output Format:

descending

HTML

Submit

Reset

Select options and click submit

- Select -
Gene/Locus
Locus Type
Unigene Name
IBM2 Chr
IBM2 Position
Genetic Bin
FPC Contig
FPC Chr.
FPC Start
FPC Stop

HTML
Excel
text (fixed-width)
csv (comma-separated)
tsv (tab-delimited)

3/22/07

Phenotype Search

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#)
[Notes](#)

Phenotype Search

Database:

Rice
Wheat
Maize
Rice

Options are based on species

From this search utility you can download the maize phenotype data gathered in the course of the maize genome project from a variety of germplasm accessions and lines for use in association and QTL studies.

To obtain this information, use the search form at the right. To obtain the complete set of data far in our project, leave all the search parameters in their default format you would like, and click Submit. To change the output, modify the 'Sort by' parameters before clicking Submit. To filter by area of interest, use the drop-down menus to specify your

For more help with this screen, see the Panzea tutorial.

Tables in HTML format will appear below the search form on a refreshed page. Alternatively, the complete results of your search can be downloaded and saved in Excel format or in one of three different text formats: text (fixed-width), csv (comma-separated), or tsv (tab-delimited).

[View](#) a phenotype search tutorial

Try a Phenotype Search at [MaizeGDB](#)

Phenotype Name: in

Evaluation Locality: in

Planting year: in

ALL
ALL
ALL
- Select -
Phenotype Name
Evaluation Locality
Planting Date
Rep
Accession
Source

Sort by (#1): ascending Phenotype Name

Sort by (#2): ascending Evaluation Locality

Sort by (#3): descending Planting Date

Sort by (#4): ascending Rep

Sort by (#5): ascending Accession

Sort by (#6): ascending Source

Output Format: HTML

Submit

Reset

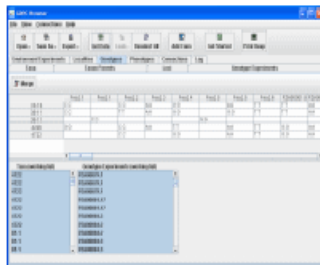
HTML
Excel
text (fixed-width)
csv (comma-separated)
tsv (tab-delimited)

Select options and click submit

GDPC Browser

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [Advanced Search Tools](#) | [Tutorial](#) | [FAQ](#)

Diversity Advanced Search



The advanced search provides access to genomic data such as SNPs, SSRs, sequences, etc. that may be collected in field, genetic, or physiological experiments. Complex queries can be executed in various formats, data integrated from multiple sources.

*For more complex queries, you can use **The Genomic Diversity and Phenotype Connection (GDPC) Browser**. Here you can download and get documentation how to use the GDPC Browser.*

Advanced Search

[Get Rice Diversity Data](#)

[Get Wheat Diversity Data](#)

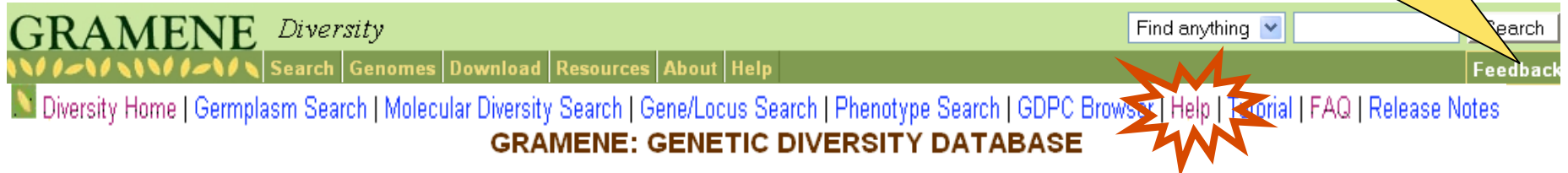
[Get Maize Diversity Data](#)

Starting the Advanced Search with the links above requires [Java version 5.0](#) and [Java Web Start](#). Java Web Start is bundled with Java version 5.0. If you are unsure which download to choose, the latest update of the "Java Runtime Environment (JRE) 5.0" will likely be what you need. To download go to:

<http://java.sun.com/javase/downloads/index.jsp>

Help

Use Feedback to ask questions or make comments to Gramene



Gramene Genetic Diversity module is a repository for SSR and SNP allelic and phenotypic data for cereal crops. Currently, there is SSR data for rice, SNP and phenotypic data for maize, and SNP data for wheat. Please read the data summaries for more detail.

The Genetic Diversity module allows you to view allelic variation at particular loci across multiple germplasms from a specific experiment, as well as genome-wide allelic variation in particular germplasms.

HOW TO SEARCH:

On the [Diversity home page](#), use the search text field to retrieve allele data.

What search keywords to use:

Searches can be done using germplasm accession name, accession number, or marker/locus name. For example, to search for the marker [M22](#).

Tips:

- If an accession number (with > 3 characters) has a space between the letters and numbers, then enclose the name in quotes to return the exact matching germplasm. Eg. For IRGC 3575, use "[IRGC 3575](#)".
- If a germplasm name has more than 3 characters and is with a space between the characters, then spell the name with out the characters, eg. for IR 36 use [IR36](#).
- If the accession name has only two characters, then double the name, eg. for germplasm T1 use [T1T1](#).
- Select the species of your interest from the species pull-down menu before you press "submit".

Help documents assist in how to conduct a search and to define your results.

SEARCH RESULTS:

A: Search by germplasm accession name or accession numbers will provide the following information.

Passport description:

3/22/07

Tutorials

 [Diversity Home](#) | [Germplasm Search](#) | [Molecular Search](#) | [GDPC Browser](#) | [Help](#) | **Tutorial** | [FAQ](#) | [Phenotype](#)

Tutorials are available in PDF or Powerpoint

Diversity Tutorial

Select your preferred format:

- ◆ [PowerPoint Tutorial](#)
- ◆ [Adobe PDF Tutorial](#)

Release Notes

Navigate to other Gramene Tutorials.

Gramene Tutorials: [Navigation](#) | [Overview](#) | [Genomes](#) | [GrameneMart](#) | [BLAST](#) | [Maps](#) | [Mappings](#) | [Proteins](#) | [Ontologies](#) | [Genes](#) | [QTL](#) | **Diversity** | [Pathways](#) | [Literature](#)

Free associated software:



[PowerPoint viewer](#)

Download free software for viewing tutorials.

FAQ's

Submit a question to
Gramene

Gramene FAQ

- Moderator: cer17@cornell.edu
- Gramene FAQ's may be browsed by category (based on datasets) or may be searched by keyword. (see search on bottom left of page)
- Subcategories:
 - Maps and CMap
 - BLAST
 - Proteins
 - Ontologies
 - Genomes
 - Markers
 - QTL
 - Genes
 - Literature
 - Data Curation
 - Gramene Program
 - Diversity
 - GrameneMart
 - Pathways

Answers in this category:

 [New Item](#)

- 2006-Aug-15 3:45am

This document is: <http://dev.gramene.org/cgi-bin/fom?file=1>

[\[Search\]](#) [\[Appearance\]](#) [\[Show This Entire Category\]](#) [\[Show Expert Edit Commands\]](#) This is a [Faq-O-Matic](#) 2.721.

Select a module to view it's FAQ's

Search FAQ

Release Notes

 [Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)



Diversity Release Notes

The Gramene Genetic Diversity database contains SSR allelic data for rice, SNP data for Wheat, and phenotypic, SSR and SNP data for maize. Allelic variation on loci of multiple germplasms of a species and genome-wide allelic variation of germplasms can be viewed by searching for locus/marker name, germplasm name or accession number.

On this release:

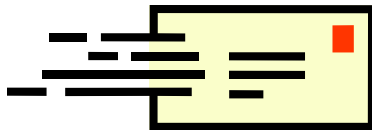
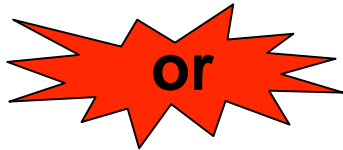
- Rice: 695 germplasm accessions (651 unique); 572 SSR markers (254 unique).
- Wheat: 48 germplasm accessions; 3802 SNP markers.
- Maize: 449 germplasm accessions with SNP data; 1544 germplasm accessions with SSR data. 1435 SNP and 520 SSR markers.

Click [here](#) for database summary.

Contact Gramene



Use the feedback button, located at the top of every page, to provide feedback or to ask questions about Gramene.



Email Gramene at gramene@gramene.org