



[Home](#) [Forum](#) [Objectives](#) [Events](#) [View](#) [Edit](#)

[Home](#) > ... > [Application 2.2.1 Tool 2.10 GDMS V2](#)

[Graham McLaren](#) [Log out](#)

Search

Application 2.2.1 Tool 2.10 GDMS V2

Structure of the ICIS GDMS database:

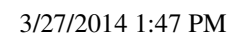
Introduction:

GDMS (Genotyping data management system): GDMS aims to provide a comprehensive public repository for marker information, genotype, linkage map and QTL data from crop species.

The underlying database is MySQL. The datasets available for each crop species are displayed with dimension and type descriptions, can be stored and queried and allele data matrices. Access to datasets requires user login.

Data may be currently exported to the following formats: 2x2 matrix, flajack format and ISMAB formats. Data submission is through templates; upload templates are available for genotype data (separate templates for diversity and mapping populations, type of markers - SNP and SSR data), and mapping populations and marker data templates. The templates are in the form of excel sheets. The GDMS schema will be integrated into the IBDB v2 schema. This schema links to the GMS and DMS tables for the germplasm information and trait and studies information.

GDMS Relationships



Description of Database Tables:

gdms_dataset: This is the primary table of the GDMS database. It stores all the key information of uploaded files like dataset id, dataset name, dataset description etc.

| Field Name | Description | Data type | Size |
|------------------------|---|-----------|------|
| dataset_id | Unique identifier for dataset | int | 4 |
| dataset_name | Name of the dataset | char | 30 |
| dataset_desc | Description of dataset | varchar | 255 |
| dataset_type | Type of the dataset whether it is SSR, SNP, DaRT or QTL etc. | varchar | 10 |
| genus | Genus name for taxon. | char | 25 |
| species | Taxonomic or common name of species analyzed. | char | 25 |
| template_upload_date | The system generates it when a template is uploaded. | date | |
| datatype | Whether uploaded data is int or char or map genotyping data | enmu | |
| missing_data | This is the symbol or characters used by the scientist to represent missing data. | varchar | 20 |
| remarks | Comments on dataset. | varchar | 255 |
| method | Method/Software used to map QTL/MTA ex: PLABQTL (SIM,CIM)/Tassel (GLM,MLM)/ Breeding View | varchar | 25 |
| score | Score type of the QTL/MTA ex: LOD (or) -log10(p) | varchar | 12 |
| institute | Name of the institute | varchar | 75 |
| principal investigator | Name of the principal investigator | varchar | 45 |
| email | Email id | varchar | 45 |
| purpose_of_study | Description of the reason for the study. | varchar | 225 |

gdms_dataset_user: This table shows the relation between the user table that exists in the GMS database and dataset table of GDMS database. It stores dataset ids and user ids.

| Field Name | Description | Data type | Size |
|------------|-----------------------------|-----------|------|
| dataset_id | Identifier for the dataset. | int | 4 |
| user_id | User identification | int | 4 |

gdms_char_values: It stores genotyping values of character type.

| Field Name | Description | Data type | Size |
|------------|---|-----------|------|
| ac_id | Unique identifier for allelic (nucleotide) data. | int | 4 |
| char_value | The allele value, which is normally the expected nucleotide call for SNP data | char | 4 |
| dataset_id | Identifier for the dataset. | int | 4 |
| gid | Germplasm identifier. | int | 4 |
| marker_id | Marker identifier. | int | 4 |

gdms_allele_values: It stores genotyping values of numeric type.

| Field Name | Description | Data type | Size |
|------------------|---|-----------|------|
| an_id | Unique identifier for allelic (fragment) data. | int | 4 |
| allele_raw_value | The raw allele value, which is normally the expected size of SSR fragment. | char | 20 |
| allele_bin_value | The binned allele value, which is normally the expected size of SSR fragment. (binned values ex: after Allelobin) | char | 20 |
| dataset_id | Identifier for the dataset. | int | 4 |
| Gid | Germplasm identifier. | int | 4 |
| marker_id | Marker identifier. | int | 4 |
| peak_height | Height of chromatogram peak | int | 4 |

gdms_mapping_pop: This table stores metadata for mapping population.

| Field Name | Description | Data type | Size |
|------------|-----------------------------|-----------|------|
| dataset_id | Identifier for the dataset. | int | 4 |

| | | | |
|-----------------|--|---------|-----|
| mapping_type | Type of mapping population ex: Allelic or ABH. | varchar | 10 |
| parent_a_nid | nid for parent a (usually female) in the population. | int | 4 |
| parent_b_nid | nid for parent b (usually male) in the population. | int | 4 |
| population_size | Number of individuals in the mapping population. | int | 4 |
| population_type | Type of population used for mapping. | varchar | 50 |
| mapdata_desc | Description of map. | varchar | 150 |
| scoring_scheme | The name of the scoring scheme used. | varchar | 150 |
| map_id | Unique identifier for map. | int | 4 |

gdms_mapping_pop_values: It stores genotyping data values for a mapping population.

| Field Name | Description | Data type | Size |
|----------------|--|-----------|------|
| mp_id | Unique identifier for genotyping data of a mapping population (nucleotide) data. | int | 4 |
| map_char_value | The called genotype value ex: A , B or H | char | 20 |
| dataset_id | Identifier for the dataset. | int | 4 |
| Gid | Germplasm identifier. | int | 4 |
| marker_id | Marker identifier. | int | 4 |

gdms_dart_values: It stores genotyping values of DArT type.

| Field Name | Description | Data type | Size |
|-----------------|---|-----------|------|
| ad_id | Unique identifier. | int | 4 |
| dataset_id | Identifier for the dataset. | int | 4 |
| marker_id | Marker identifier. | int | 4 |
| clone_id | Clone identification number | int | 4 |
| Qvalue | It is an estimate of marker quality, which reflects how well the two phases (Present = 1 vs Absent = 0) of the marker are separated in this sample set. It measures the fraction of the total variation across all individuals due to bimodality. Q is based on ANOVA. | float | 4 |
| reproducibility | Measure in % how reproducible the scoring for replicated samples is. (100 means 100% reproducible). A small number of markers were also analysed in duplicate. A score of X means a scoring discordance between 2 copies of an extract or between 2 copies of a marker. | float | 4 |
| call_rate | Percentage of valid scores in all possible scores for a marker. | float | 4 |
| pic_value | Polymorphism information content (PIC): a maximum of 0.5 when a marker scores 50% 0 and 50% 1. | float | 4 |
| discordance | Measure of reproducibility expressing overall variation of scores within replicated samples. | float | 4 |

gdms_marker: It stores primary information of marker.

| Field Name | Description | Data type | Size |
|-----------------|---|-----------|------|
| marker_id | Unique identifier for marker. | int | 4 |
| marker_type | Type of marker for ex: SSR, SNP, DArT. | char | 10 |
| marker_name | Name of the marker. | char | 40 |
| genotype | Name of the genotype/accession/germplasm on which the marker was originally discovered. | char | 40 |
| Ploidy | Ploidy of the species ex: haploid, diploid etc. | varchar | 25 |
| Species | Name of species | char | 25 |
| db_accession_id | Gen Bank ID or any other public database ID | varchar | 50 |
| reference | Publication / citation details | varchar | 255 |
| primer_id | Name of the primer | varchar | 70 |
| remarks | Comments on marker | varchar | 255 |
| assay_type | Type of assay ex: golden gate, kaspar etc. | varchar | 50 |
| Motif | Motif values ex: Actual SNP [G/T] or SSR (AT) ² | varchar | 250 |
| forward_primer | Forward Primer/Left flanking sequence for KASPar or Golden Gate assay. | varchar | 100 |
| reverse_primer | Reverse primer/Right flanking sequence for KASPar or Golden Gate assay. | varchar | 100 |
| product_size | Size of the Product. | varchar | 20 |
| annealing_temp | Annealing Temperature. | float | 4 |

| | | | |
|---------------|-----------------------|---------|----|
| amplification | Amplification status. | varchar | 12 |
|---------------|-----------------------|---------|----|

gdms_marker_details: It stores additional information of marker.

| Field Name | Description | Data type | Size |
|--------------------------------|--|-----------|------|
| marker_id | Unique identifier for marker. | int | 4 |
| no_of_repeats | Number of repeats. | int | 4 |
| motif_type | Type of motif ex: di, tri, tetra, etc... | varchar | 20 |
| sequence | Sequence in which motif is identified Marker. | varchar | 2500 |
| sequence_length | Number of base pairs. | int | 4 |
| min_allele | Minimum allele value. | int | 4 |
| max_allele | Maximum allele value. | int | 4 |
| ssr_nr | Number of identified SSR out of the total number of identified SSRs. | int | 4 |
| forward_primer_temp | Melting Temp of forward primer. | float | 4 |
| reverse_primer_temp | Melting Temp of reverse primer. | float | 4 |
| elongation_temp | Elongation Temperature. | float | 4 |
| fragment_size_expected | Expected size of fragment in bp. | int | 4 |
| fragment_size_observed | Observed size of fragment bp. | int | 4 |
| expected_product_size | Expected product size. | int | 4 |
| position_on_reference_sequence | Position number of SNP on reference sequence. | int | 4 |
| restriction_enzyme_for_assay | Restriction enzyme. | varchar | 25 |

gdms_map: This stores metadata about the maps (genetic / sequence / physical)

| Field Name | Description | Data type | Size |
|------------|--|-----------|------|
| map_id | Unique identifier for map. | int | 4 |
| map_name | Name of the Map. | varchar | 30 |
| map_type | Type of map ex: genetic, sequence, physical. | varchar | 20 |
| mp_id | Unique identifier for genotyping data of a mapping population (nucleotide) data. | int | 4 |
| map_desc | Description of the map | varchar | 225 |
| map_unit | Linkage group units ex: cm(Centimorgan), bp(basepair) | varchar | 15 |

gdms_qtl: This stores metadata about the QTL.

| Field Name | Description | Data type | Size |
|------------|-----------------------------|-----------|------|
| qtl_id | Unique identifier for QTL | int | 4 |
| qtl_name | Name of the QTL | char | 30 |
| dataset_id | Identifier for the dataset. | int | 4 |

gdms_qtl_details: It stores information about QTL.

| Field Name | Description | Data type | Size |
|-----------------------|--|-----------|------|
| qtl_id | Unique identifier for qtl | int | 4 |
| map_id | Unique identifier for linkage map | int | 4 |
| linkage_group | Chromosome number/ Linkage group number | varchar | 20 |
| min_position | Minimum position of QTL | float | 4 |
| max_position | Maximum position of QTL | float | 4 |
| tid | The ID of the trait name | int | 4 |
| experiment | dataset id from DMS or qtl mapping s/w or location or environment; mandatory field | char | 100 |
| left_flanking_marker | Marker which is left of the QTL | varchar | 50 |
| right_flanking_marker | Marker which is right of the QTL | varchar | 50 |

| | | | |
|--------------|---|---------|-----|
| effect | +ve effect or --ve effect on the trait numeric value. | float | 4 |
| position | Position of QTL | float | 4 |
| score_value | Value of Log 10 base ratio | float | 4 |
| r_square | % of total phenotypic variation | float | 4 |
| interactions | Epistatic or environmental conjunction | varchar | 255 |
| clen | Chromosome length | float | 4 |
| se_additive | Standard error of additive effect | varchar | 15 |
| hv_parent | Parent of High value allele | varchar | 225 |
| hv_allele | High value allele for particular | char | 20 |
| lv_parent | Parent of Low value allele | varchar | 225 |
| lv_allele | Low value allele for particular | char | 20 |

gdms_markers_onmap: It stores the map information and the marker loci.

| Field Name | Description | Data type | Size |
|----------------|---|-----------|------|
| map_id | Unique identifier for map | int | 4 |
| marker_id | Unique identifier for marker | int | 4 |
| linkage_group | Chromosome number/ Linkage group number | varchar | 50 |
| start_position | Start position of marker | double | 8 |
| end_position | End position of marker | double | 8 |

gdms_marker_user_info: It stores the contact details of principal investigator of the marker.

| Field Name | Description | Data type | Size |
|------------------------|-----------------------------------|-----------|------|
| marker_id | Unique identifier for marker | int | 4 |
| principal_investigator | Principal investigator name | varchar | 50 |
| contact | Address of principal investigator | varchar | 200 |
| institute | Institute name | varchar | 100 |

gdms_marker_alias: Marker alias names are stored in this table.

| Field Name | Description | Data type | Size |
|------------|------------------------------|-----------|------|
| marker_id | Unique identifier for marker | int | 4 |
| Alias | Alias name of marker | char | 40 |

gdms_acc_metadataset: It stores accession/germplasm ids of each dataset.

| Field Name | Description | Data type | Size |
|------------|---|-----------|------|
| dataset_id | Identifier for the dataset. | int | 4 |
| gid | Germplasm identifier | int | 4 |
| nid | Unique identifier for the name from GMS database. | int | 4 |

gdms_marker_metadataset: It stores marker ids of each dataset.

| Field Name | Description | Data type | Size |
|------------|------------------------------|-----------|------|
| dataset_id | Identifier for the dataset. | int | 4 |
| marker_id | Unique identifier for marker | int | 4 |

gdms_track_data: It stores the previously retrieved data upon prompting the user.

| Field Name | Description | Data type | Size |
|------------|---|-----------|------|
| track_id | Unique identifier for data track | int | 4 |
| track_name | Name for the selected group of markers / accessions | int | 4 |

| | | | |
|---------|---------------------|-----|---|
| user_id | User identification | int | 4 |
|---------|---------------------|-----|---|

gdms_track_markers: It stores the marker ids.

| Field Name | Description | Data type | Size |
|------------|----------------------------------|-----------|------|
| track_id | Unique identifier for data track | int | 4 |
| marker_id | Marker identifier | int | 4 |

gdms_track_acc: It stores the germplasm ids.

| Field Name | Description | Data type | Size |
|------------|--|-----------|------|
| track_id | Unique identifier for data track | int | 4 |
| nid | Unique identifier for the name. Links to Names table of GMS. | int | 4 |

gdms_mta: It stores information about Marker trait association.

| Field Name | Description | Data type | Size |
|---------------|--|-----------|------|
| mat_id | Unique identifier for mta | int | 4 |
| marker_id | Unique identifier for marker | int | 4 |
| dataset_id | Identifier for the dataset. | int | 4 |
| map_id | Unique identifier for linkage map | int | 4 |
| linkage_group | Chromosome number/ Linkage group number | varchar | 20 |
| position | Position of QTL | float | 4 |
| tid | The ID of the trait name | int | 4 |
| experiment | dataset id from DMS or qtl mapping s/w or location or environment; mandatory field | char | 100 |
| hv_allele | High value allele for particular | char | 20 |
| effect | +ve effect or -ve effect on the trait numeric value. | float | 4 |
| score_value | Value of Log 10 base ratio | float | 4 |
| r_square | % of total phenotypic variation | float | 4 |

VIEWS:

gdms_dataset_size: This view shows number of markers and germplasms contained in each dataset.

gdms_genotypes_count: This view contains the number of genotypes screened for a particular marker.

gdms_mapping_data: It contains marker position on map, marker name, and map name.

gdms_marker_retrieval_info: It contains marker information like marker id, name, principle investigator of the marker, and number of genotypes screened for a particular marker.

Downloads:

[Central GDMS Database Script version 2.0](#)

[Central GDMS-DB Changelog](#)

[Local GDMS Database Script version 2.0](#)

[Local GDMS-DB Changelog](#)

[Generation Challenge Program \(GCP\)](#) Integrated Breeding Platform

[Adaptavist Theme Builder](#) (3.3.3-conf210) Powered by [Atlassian Confluence](#) 2.10.3, the [Enterprise Wiki](#).

Free theme builder license