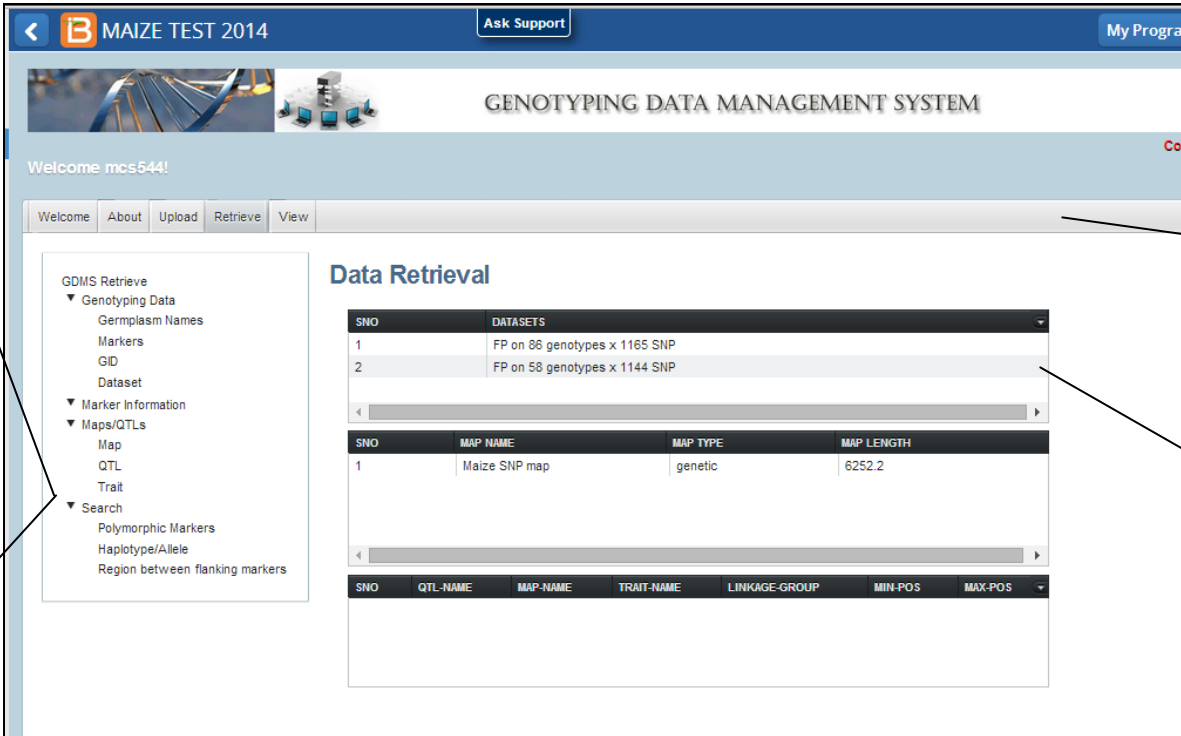


Genotypic Data Management System (GDMS)

Quick View

A Breeding Management System
core functionality

This functionality is embedded in the BMS to enable you to store, search and retrieve molecular marker information, genotyping data and genetic maps, such as low level fingerprinting data ('000s), and marker trait association (MTA) information for breeding traits (QTL data and diagnostic markers) to facilitate decisions required in day-to-day breeding activities. Data can easily be retrieved, visualised and manipulated in various ways, including the easy creation of genotyping orders for third party service providers.



The screenshot shows the 'MAIZE TEST 2014' interface of the Genotyping Data Management System (GDMS). The top navigation bar includes 'Ask Support' and 'My Program'. The main header displays 'GENOTYPING DATA MANAGEMENT SYSTEM' and a welcome message 'Welcome mcs544!'. A sidebar on the left lists navigation options: 'GDMS Retrieve' (Genotyping Data, Germplasm Names, Markers, GID, Dataset), 'Marker Information', 'Maps/QTLs' (Map, QTL, Trait), and 'Search' (Polymorphic Markers, Haplotype/Allele, Region between flanking markers). The main content area, titled 'Data Retrieval', contains two tables. The first table, 'DATASETS', lists two datasets: 'FP on 86 genotypes x 1165 SNP' and 'FP on 58 genotypes x 1144 SNP'. The second table, 'MAP NAME', lists a 'Maize SNP map' with a 'genetic' map type and a 'MAP LENGTH' of 6252.2. A third table at the bottom shows columns for SNO, QTL-NAME, MAP-NAME, TRAIT-NAME, LINKAGE-GROUP, MIN-POS, and MAX-POS. Annotations with arrows point to specific features: 'Create haplotypes and search for lines with particular haplotypes' points to the 'Haplotype/Allele' search option; 'Query for a region of interest e.g., all markers under a QTL region or between flanking markers' points to the 'Region between flanking markers' search option; 'Download genotyping datasets in multiple formats for visualization and analysis in third party applications' points to the 'DATASETS' table; and 'Readily identify and select polymorphic markers between parental lines' points to the 'MAP NAME' table.

“GDMS is very user-friendly... a hassle-free data management tool to integrate huge, complex information like marker data, genotyping data and genetic maps into simple graphical visualisation that helps me as a breeder to take better decisions in my crop improvement programmes. - Dr Muraleedhar Ask, Scientist, lentil and mung bean breeder, Indian Agricultural Research Institute (IARI), New Delhi, India.”

Description	Development phase	What's new	Related support tools
Connect germplasm to genotypic data	Incremental improvements	<ul style="list-style-type: none"> Handle duplicate germplasms while uploading and retrieving genotypic data Upload genotyping data from importing a germplasm list MTA upload, retrieval and deletion Improved validation and error reporting 	<p>Online: www.integratedbreeding.net/22/breeding-management-system/breeding-decision-tools</p> <p>Ask for a demo: ibp@cgiar.org</p>