

BIMS (Breeding Information Management System) for efficient management and analysis of breeding data

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GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement



GENOME DATABASE FOR VACCINIUM

Genomics, genetics, and breeding resources for blueberry, cranberry, bilberry, and lingonberry research



CITRUS GENOME DATABASE



Resources for citrus genomics, genetics, breeding and disease research



PULSE CROP DATABASE

Genomic, Genetic, and Breeding Resources for Pulse Crop Improvement

Abstract

Breeding programs produce a large amount of data that require efficient management systems to keep track of performance, pedigree, geographical and image-based data as well as genotyping data. The integration of breeding data with publicly available genomic and genetic data, as well as the integration of each breeder's own genotypic and phenotypic data in a database enhances genetic understanding of important traits and maximizes the marker-assisted breeding utility by breeders and allied scientists. We report the progress on BIMS which we have implemented in the Genome Database for Rosaceae, CottonGEN Citrus Genome Database, Pulse Crop Database and the Genome Database for Vaccinium. BIMS allows individual breeders to integrate their phenotypic and genotypic data with public genomic and genetic data and at the same time have complete control of their own breeding data and access to tools such as data import/export, data analysis and data archive. BIMS incorporates the use of the Android App Field Book, an open-source software for phones and tablets which allows breeders to replace hard-copy field books, thus alleviating the possibility of transcription errors while providing faster access to the collected data. The use of Field Book and BIMS promotes the use and development of standard trait descriptors and metadata as well. New functionality includes searching/loading SNP genotype data and haplotype data, cross search and bulk data editing.

BIMS Component

- Archive
- Manage Breeding
- Data Import
- Search and Download
- Field Book App Management
- Data Analysis Tools

Search Accession

Properties: Name, Trial, Location, Cross, Parent

Traits: AREA (%), BWT (g), E1 (%), FUI (%), LI (g), LP (%), LY (lb/acre), MIC (unit), QS (1,1,3,5), QS (2,1,4,3), QS (4,5,2,5,0,3), QS (5,2,5,1,1,5)

Summary for LY (lb/acre): # Data: 4421, Max: 2742.75, Min: 147.36, Mean: 1199.77, STD: 406.95

Maximum: 2742.75
Minimum: 147.36

Filtered By: Trial - matched 329 accession, BWT (g) - matched 269 accession

Manage Program

Current members: rburrel - EDIT, sook - EDIT

Add Members: Non-member

Permission: READ ONLY, EDIT

Generate a field file

Generate an input file for Field Book.

New Trial, Existing Trial, Cross

Generate

Field Book custom columns: Trait, accession and sample properties

Data Templates

Template name	Details	Download	Description
Property	view	download	Properties
Contact	view	download	Contact information
Dataset	view	download	Trials of your program
Descriptor	view	download	Traits used in phenotyping data
Site	view	download	Locations of the phenotyping
Accession	view	download	Accessions of your program
Cross	view	download	Crosses of your program
Progeny	view	download	Progeny
Marker	view	download	Markers of your program
Phenotype	view	download	Evaluation data (Phenotype)
Phenotype (Long Form)	view	download	Evaluation data (Phenotype) in long form
Genotype (Long Form)	view	download	Genotyping data in long form
Image	view	download	Images for trait, accession and site

Statistical Analysis

Categories: Data Year, Cross, Trial, Stock List

Traits: Foliar_PM, FreeStone, Fruit_Dim, Fruit_L, Fruit_Shape, Fruit_Wd2, Fruit_Wt, Harvest_Date, Harvest_Days, Harvest_Time, Perc_Cracking, Perc_Pitting, pH, Pit_Lh, Pit_Wd1, Pit_Wt, Pull_Force

Statistics: Sweet_cherry_CRS_phenotyping_2010, Sweet_cherry_CRS_phenotyping_2011, Sweet_cherry_CRS_phenotyping_2012

Selection	# Data	Max	Min	Mean	STD
Sweet_cherry_CRS_phenotyping_2010	100	13.94	9.40	11.52	0.85
Sweet_cherry_CRS_phenotyping_2011	255	13.78	8.18	11.11	1.13
Sweet_cherry_CRS_phenotyping_2012	354	13.93	8.44	10.97	1.03

BIMS Vision

Provide individual breeders with a secure and comprehensive online breeding management system to:

- Store, manage, archive and analyze their private breeding program data
- Fully integrate their data with publicly available genomic, genetic and breeding data in the community database
- Manage data from the Field Book App, an android app for collecting phenotype data in the field
- BrAPI compatible
- Available for any Tripal-based database to implement

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