Breeding Management System



Integrated Breeding Platform Today's tools for tomorrow's crops



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The BMS helps in making plant breeding an easier and shorter process. It has been instrumental in making us more efficient breeders in bringing products to end-users, i.e. farmers and families.

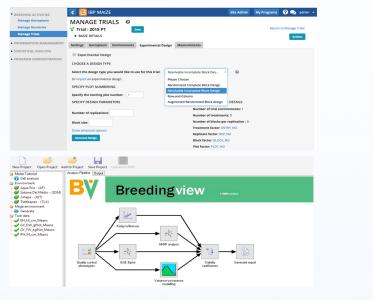
— Lilian Njeri Gichuru, maize breeder, Kenya Agricultural Research Institute

Introduction

Created by the not-for-profit Integrated Breeding Platform (IBP), the Breeding Management System (BMS) software is designed to support plant breeders manage a diversity of data: genealogy, inventory, nurseries, trials, genetic markers, and data analysis. The BMS is available as a single user desktop application, as well as in high-performance multi-user server edition suitable for institutional breeding programs. The BMS has an open source breeding API (BrAPI), developed in collaboration with other publically funded software initiatives, like GOBii, which allows plug-and-play interoperability with external applications. Improved data management and analysis increases breeding efficiency, thus reducing the time and resources required to improve crops under local target conditions. Standardized data terminology through curated crop ontologies facilitates data exchange and comparison across teams, enabling meta-analyses. Large projects, like the Tropical Legumes 3 (TLIII), are using the BMS to standardize their trial designs, data collection, and analysis among participating breeders and technicians. In the developing world, BMS implementation and maintenance are subsidized by government and donor funds. Many national programs, CGIAR centers, universities, and private companies in Africa and SE Asia are using the BMS to efficiently manage breeding activities and data. In the developed world, application and support packages are commercially available for private sector, government agencies, and educational use. The IBP has extensive experience providing professional support to plant breeders, and offers a customizable BMS service package that can include support for system administrators and users.

Studies & Analysis

The BMS will randomize experiments based on common experimental designs. Data collected can be exported to Breeding View (BV) for statistical analysis. BV was created by VSNi, the makers of GenStat, to provide a simple and rapid pipeline for line evaluation. The BMS also accepts experimental designs imported from external randomizations and data can be exported for analysis by any statistical package.



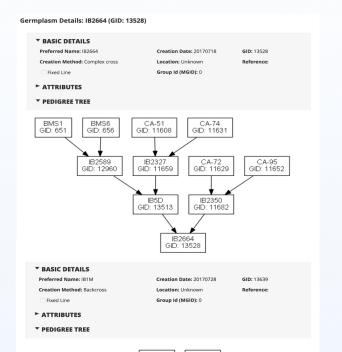
Ontology

The BMS defines phenotype by the property, method, and scale of the observation - giving breeders the freedom to refer to traits by any name. This allows for data uniformity, even for crop initiatives that span the globe and multiple languages.

BREEDING ACTIVITIES	Reference and the second secon	Site Admin My Programs	? 喿 admin 👻
INFORMATION MANAGEMENT Import Germplasm	Ontology Browser @		

Genealogy & Names

The main advantage of the BMS is automated pedigree recording of all crosses and advancements. Pedigrees in the BMS are germplasm units connected by breeding methods. Germplasm units are uniquely defined by GIDs, database specific numbers, which can be connected to multiple names. While names are not the core database identifiers, customizable naming conventions offer breeders human readable details of breeding history. Naming conventions are highly customizable to suit the needs of any breeding institute. A simple naming convention will consists of a cross code, referencing the last application of a generative breeding method in the genealogy. Additional naming information can be applied as descendants are generated through the breeding program. A breeder is also free to change the preferred name of germplasm, such after advancement to performance trials.



Cross & Advance

GIDs are created in the BMS during the processes of crossing and advancement, which correspond to two categories of breeding methods. (1) Generative methods, like crossing and transformation, increase genetic diversity in the offspring. (2) Advancement by derivative and maintenance methods, like selfing and cloning, reduce or maintain genetic diversity.

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	MANA	GE NUI	RSERIES	0								
Manage Nurseries Manage Trials	👻 Nurse	ry: Crossii	ng Nursery 20	017 5***							Return to I	Manage Nurse
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FORMATION MANAGEMENT	Nursery Set	tings Germ	plasm & Checks	Measurements	Des	igned Crosses: [F1] X	Stock	List: (F1) X	≡ ×	Save nursery	
ATISTICAL ANALYSIS	Cross List:		Not					DX	port crossing temp	late	Crossing opti	ons
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	rotar ename.	c / J Juncing						De	sign new crosses	_	Data collectio Advance nurs	
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	1	182589	BMS1/BMS6	BMS1	651	BMS6	656 1	2960 C	rossing Nursery 2	017:1/Cr	ossing Nurse	ry 2017:6
	2	182590	BMS1/BMS7	BMS1	651	BMS7	657 1	2961 0	rossing Nursery 2	017:1/Cr	ossing Nurse	ry 2017:7
	3	182591	BMS1/BMS8	BMS1	651	8M58	658 1	2962 0	rossing Nursery 2	017:1/Cr	ossing Nurse	ry 2017:8
	4	182592	BMS1/BMS9	BMS1	651	BM59	659 1	2963 C	rossing Nursery 2	017:1/Cr	ossing Nurse	ry 2017:9
	5	102593	BMS1/BMS10	BMS1	651	BMS10	660 1	2964 0	rossing Nursery 2	017:1/Cr	ossing Nurse	ry 2017:10
	6	182594	BMS1/BMS11	BMS1	651	BMS11	661 1	2965 C	rossing Nursery 2	017:1/Cr	ossing Nurse	ry 2017:11
	7	102595	BMS1/BMS12	BMS1	651				rossing Nursery 2			
	8	182596	BMS1/BMS13	BMS1	651				rossing Nursery 2			
	9	182597	BMS1/BMS14	BMS1	651				rossing Nursery 2			
	10	182598	BMS1/BMS15 BMS1/BMS16	BMS1 BMS1	651	BMS15 BMS16			rossing Nursery 2 rossing Nursery 2			
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	Cross List:	F1 🖸 Bree					ingle seed	descer	nt - DSD	×	0	v List De
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	1	IB2 LINES										17:6
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	3	182 Lines	elected per Plot:			1						17.8
	4	10.2										17:9
	5	182	ST DETAILS									17:10
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Inventory

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Harvest amounts and details are recorded within the originating nursery or trial, but most inventory functions are located under Manage Germplasm. Inventory withdrawal is a two-part process: reserve and withdraw. Seed preparation lists and labels can be generated based on reserved inventory. All inventory transactions are available for review, allowing others to know who has reserved and withdrawn from an inventory lot.

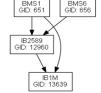
Site Admin 🛛 My Programs 🕜 突 admin 👻

Manage Genotyping Data	Variables	Properties Method	ds Scales		Add New
Browse Studies	Program Favourite			Q. Search	
Head to Head Query	There are no favourite variab			- annona	
Manage Ontologies	Variables				
Import Datasets					
STATISTICAL ANALYSIS	Name	Property	Method	Scale	
	ACCNO	Germplasm id	Assigned	Accession name	
PROGRAM ADMINISTRATION	AD	Anthesis time	Computed	days	
	Aflatox_M_ppb	Aflatoxin content	Aflatox - Measurement	PP8	
	AflavER_1_5	Aspergillus flavus ear rot	AflavER scoring	1-5 disease scoring scale of AflavER_1_5	
	AflavERSev_E_1to5	Aflatoxin content	Visual scoring	Score (1-5) of Aspergillus_flavus1_5	*
	AflavERSev_E_1to5	Aspergillus flavus ear rot severity	AflavERSev - Estimation	1-5 disease scoring scale for AflavERSev_E_1105	
	ALB_pct_CV	Anthracnose leaf blight incidence	Method for CV	Percent	
	ALB_pct_EDF	Anthracnose leaf blight incidence	Method for EDF	Percent	

Roles & Permissions

Administrators control user access to the system by assignment of customizable roles and permissions. Roles are assigned to users at the crop and program level. For example, a single user might have an administrative role for all programs in a crop database and more restricted access to a program in another crop database.





Labels

The BMS supports labeling of study plots and inventory packets with unique identifiers, plot id and stock id.

Nursery Name :	SID36-35 DESIGNATION : IB2623	Nurser			
Plot No. : 1 ENTRY_NO : 1	GID : 12994 StockID : SID36-35 AMOUNT : 300.0	ENTRY			
	Nursery Name : Crossing Nursery 2017 Plot No. : 1	Nursery Name : DESIGNATION : Crossing Nursery 2017 IB2623 Plot No. : 1 GID : 12994 ENTRY No. : 1 StockID : SID36-35			

-35	
30 23 : 12994 kID : SID36-35 9UNT : 300.0	Nursery Name : Crossing Nursery 2017 ENTRY_NO : 35

🕄 List Details Lot Details for BMS1 (GID:651) Lot 77

Location :	Defau	ult Seed Store	Scale :	SEED_AMOUNT_g	
Creation Date	e: 20170	0119	Lot Status :	Active	
Actual Balan	ce: 2075.	Og	Available Balance :	2050.0g	
The table belo	w shows the trans	action details for l	ot 77		
DATE	ТҮРЕ	AMOUNT	SEED SOURCE	LIST NAME	USER
20170119	Deposit	2465.0g		Parental Germplasm	admin
20170119	Withdrawal	-200.0g		Parental Germplasm	admin
20170317	Withdrawal	-100.0g		Parental Germplasm	Shawn
20170405	Withdrawal	-90.0g		Parental Germplasm	Michel
20170728	Reservation	-25.0g		Parental Germplasm	admin

REFERENCES

Leonelli S., Davey R. P., Arnaud E., Parry G. and Bastow R. (2017) Data management and best practice for plant science. Nature Plants: 3:17086. DOI 10.1038/nplants.2017.86

Varshney R, V.K. Singh, J. Hickey, X. Xun, D.F. Marshall, J. Wang, David Edwards and J.-M. Ribaut (2015) Analytical and decision support tools for genomics-assisted breeding. Trends in Plant Science: http://dx.-

doi.org/10.1016/j.tplants.2015.10.018

Ribaut, J.-M., Delannay, X, McLaren, G, Okono, F (2012). "Molecular Breeding Platforms in World Agriculture". In Robert A. Meyers (ed.) Encyclopedia of Sustainability Science and Technology, Springer Verlag. Volume 9, pp. 6692 –6720

API

The Integrated Breeding Platform, in collaboration with other publically funded software initiatives, is developing an open source breeding application program interface (BrAPI) to define how developers to create interoperable plant breeding applications. The BMS is BrAPI compliant to support the development of plug-and-play extensions.