Breeding Management System

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

credit (photo in tablet): Neil Palmer/CIAT

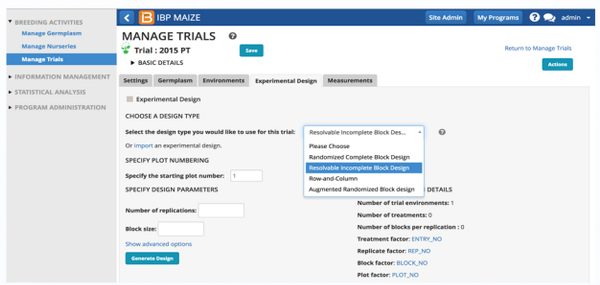
> The BMS helps in making plant breeding an easier and shorter process. It has been instrumental in making us more efficient breeders in bringing products to end-users, i.e. farmers and families.
>
> — Lilian Njeri Gichuru, maize breeder, Kenya Agricultural Research Institute

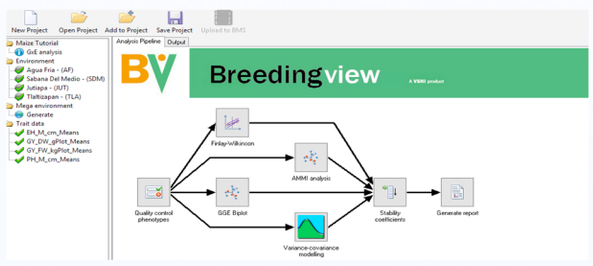
Introduction

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

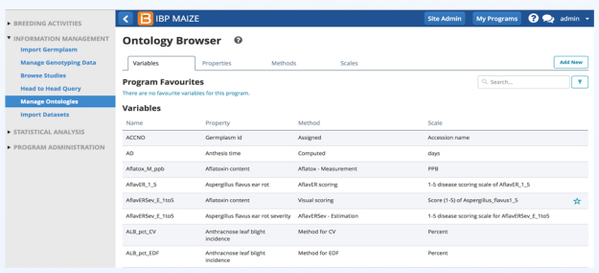
The BMS will randomize experiments based on common experimental designs. Data collected can be exported to Breeding View (BV) for statistical analysis. BV was created by VSNi, the makers of GenStat, to provide a simple and rapid pipeline for line evaluation. The BMS also accepts experimental designs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





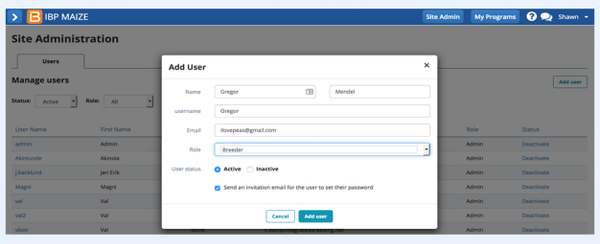
Ontology

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.



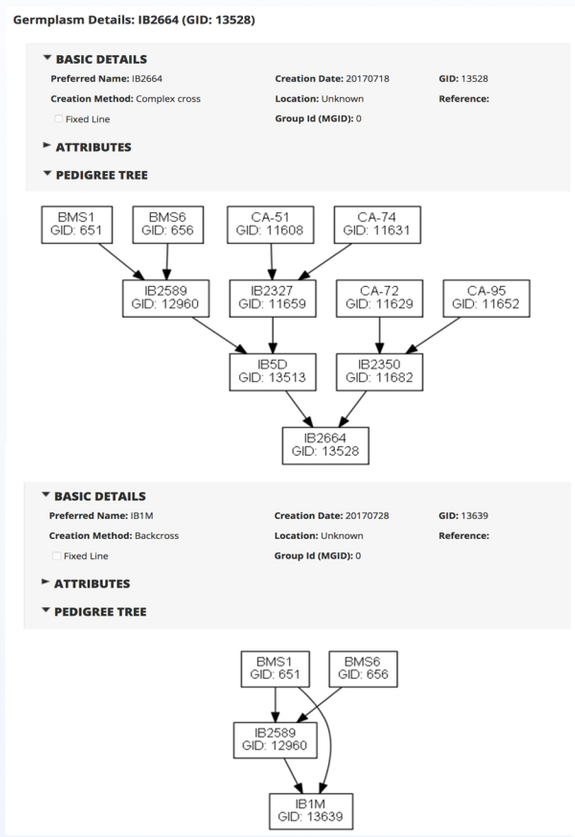
Roles & Permissions

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.



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.



Labels

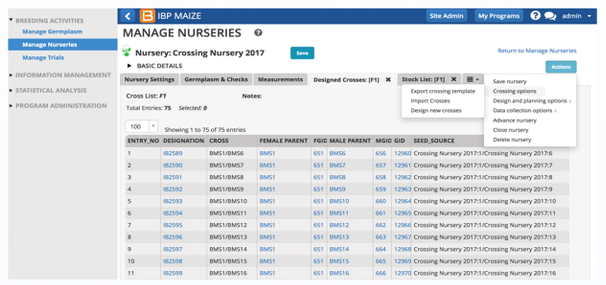
The BMS supports labeling of study plots and inventory packets with unique identifiers, plot id and stock id.

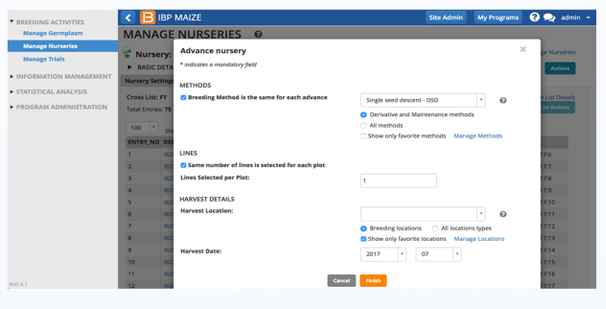
API

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.

Cross & Advance

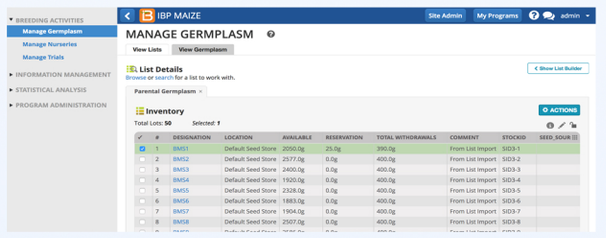
GIDs are created in the BMS during the processes of crossing and advancement, which correspond to two categories of breeding methods. (1) Generative methods, like crossing and transformation, increase genetic diversity in the offspring. (2) Advancement by derivative and maintenance methods, like selfing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

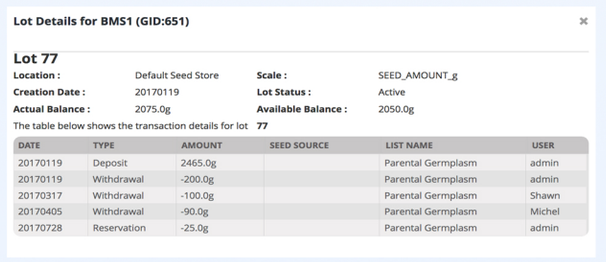




Inventory

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.





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