Integrated Breeding Platform (IBP)

Advancement

BMS 13.0-14.0 Manual

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Introduction

Advancement and crossing are ways to create new germplasm (GIDs) using the BMS pedigree management (see more Germplasm & Genealogy). Germplasm must reside within a study to be advanced or crossed. Advancement is generally through maintenance or derivative breeding methods, and is expected to result in offspring less than or equal to the parent(s) in terms of genetic diversity. Crossing is generally preformed though generative methods, and the offspring are expected to be more genetically diversity than the individual parent(s).

Advance

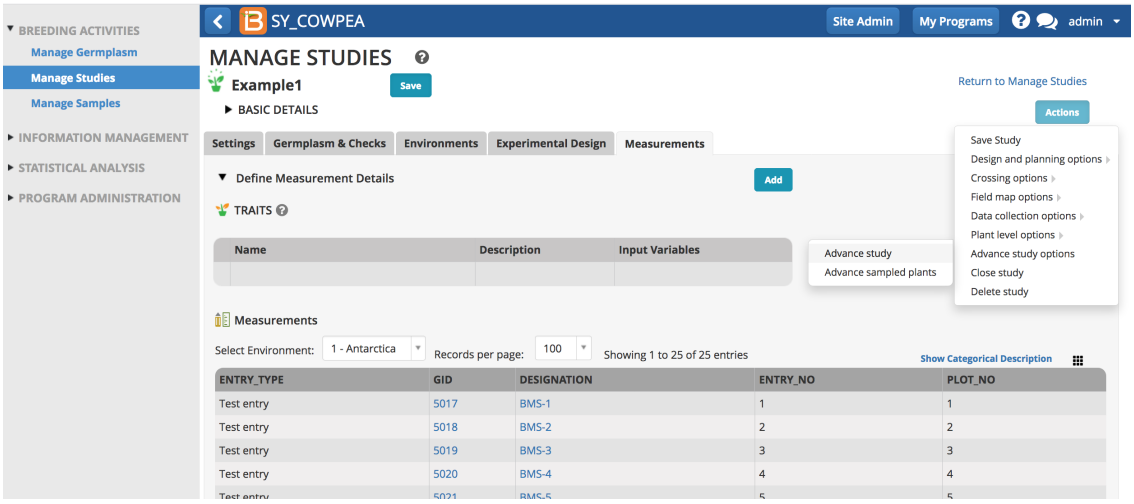
Advances can be made two ways, by plot or within plot selections. A breeder will chose to advance germplasm for a variety of reasons. Examples include:

- Advance F1 generation to create GIDs for F2 offspring
- Advance plants of interest to create GIDs for the offspring or clones
- Advance inbred lines to create GIDs for bulked seeds
- Advance a bag of seed to create GIDs for individual seeds/seedlings

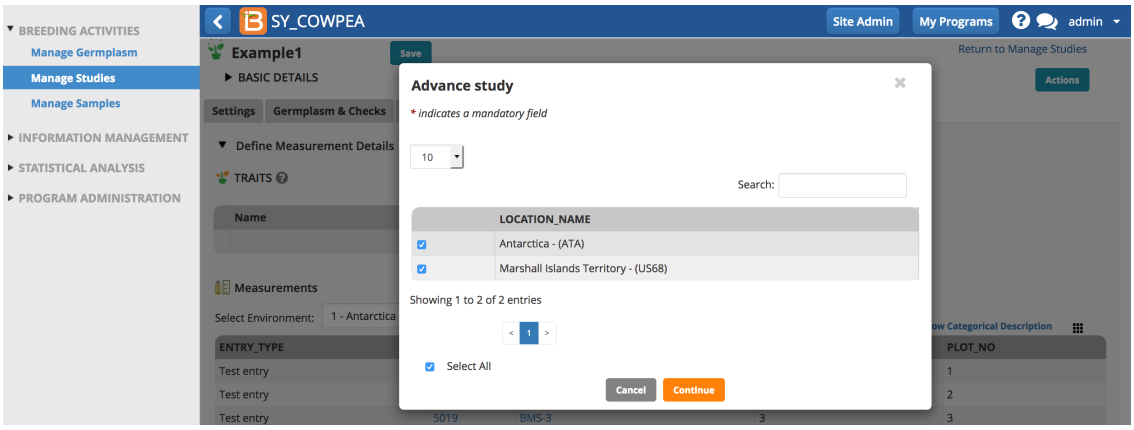
Advance by Plot

The following example every plot will be advanced, such as for a seed bulk.

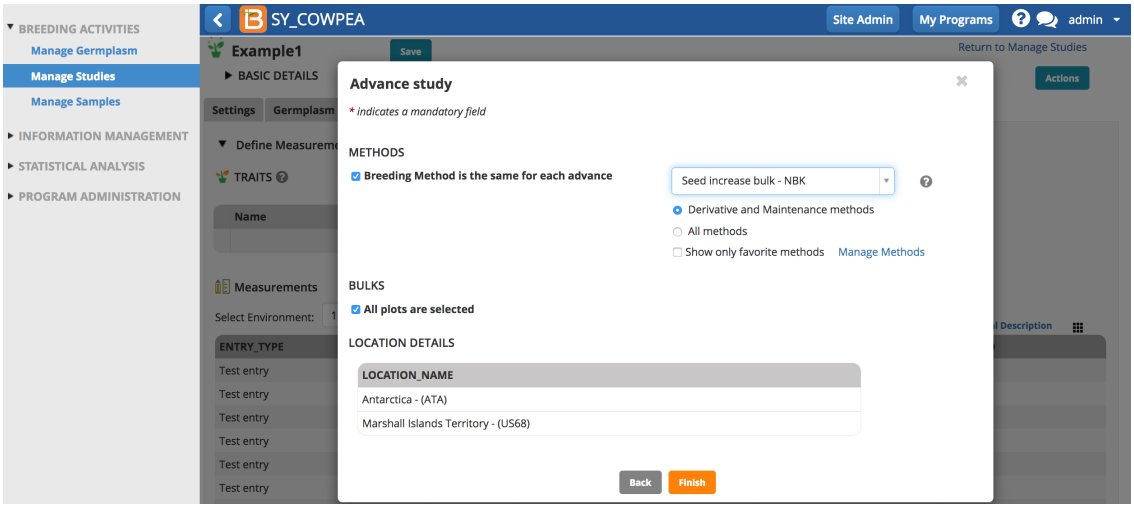
- Open a study measurements tab. Select Advance Study from the Actions button dropdown menu.



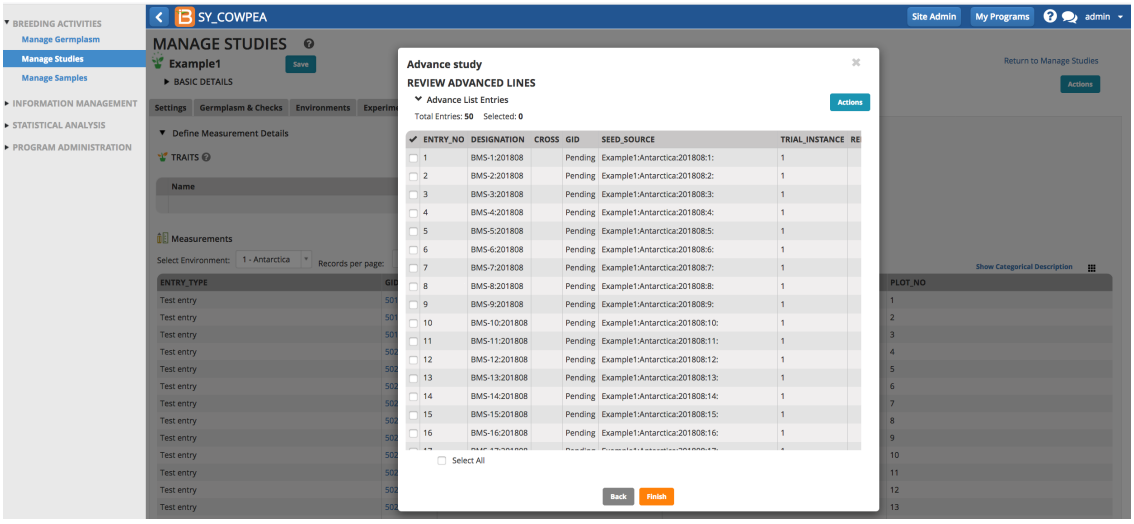
- Select which of the study instances (locations in this case) to advance. Continue.



- Choose a breeding method and Finish. Derivative and maintenance breeding methods are filtered by default since these are the most common for advancements. All plots are selected by default.

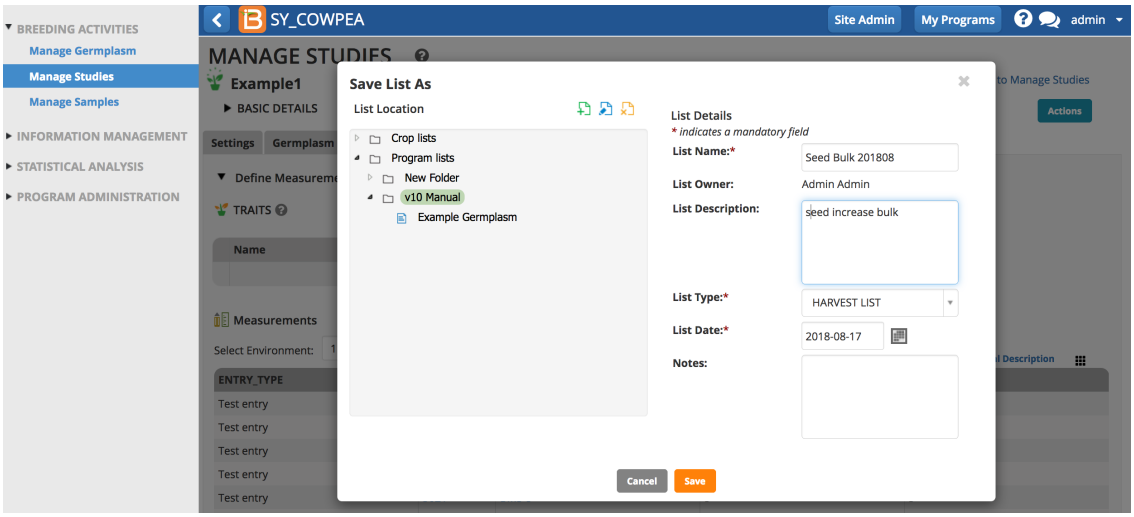


- Review the advanced lines and select Finish.



Notice that the pending lines have been automatically named. For example the designation, BMS-1-201808, is a concatenation of the parent line, BMS-1, and the year and month of creation. This is the default naming convention associated with the breeding method, Seed increase bulk. See your system administrator if you would like to change the default naming conventions.

- Specify the folder where the list will be saved. Name the list and add optional information. Save.



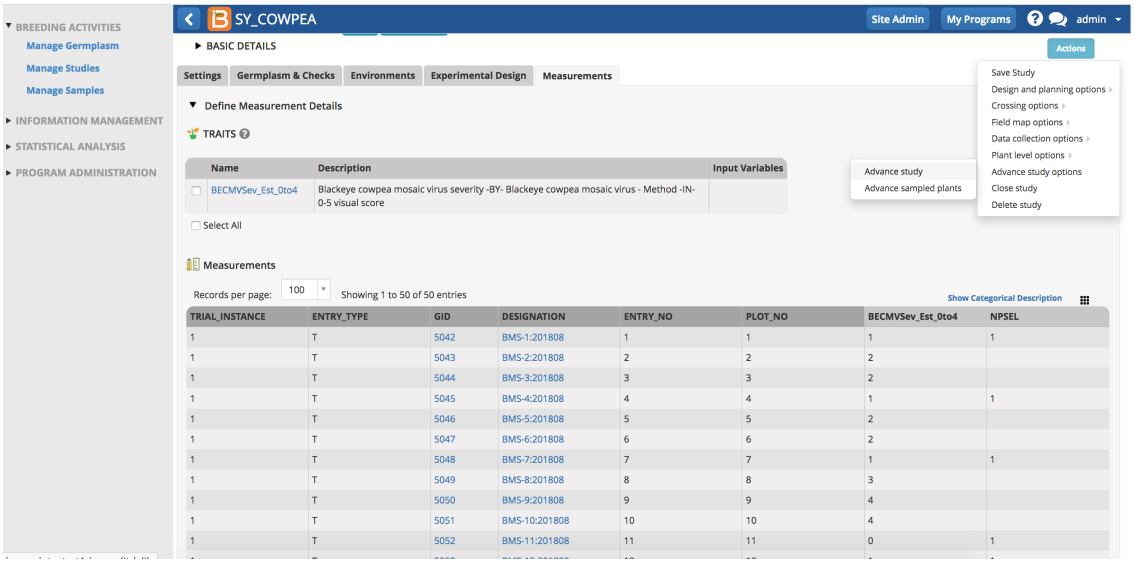
Within Plot Selections

Within plots selections are made based on phenotypic or genotypic criteria. To make within plot selections, the study needs a Selection Variate with selections recorded.

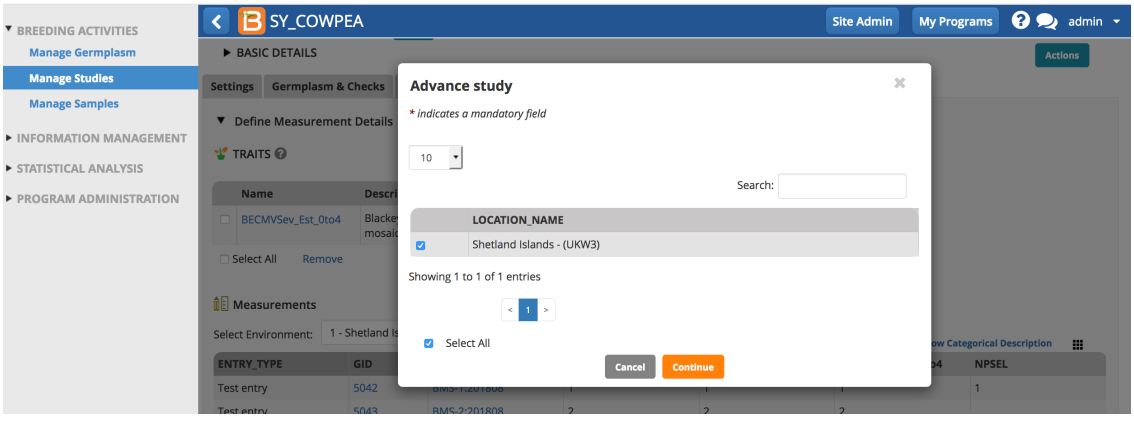
No Plant ID

Selection and advance anonymous plants within a plot.

- From the Actions menu choose Advance Study. In this example, number of plants selected (NPSEL) is a selection variate. A single plant from each plot with disease resistance (zero or one scores for mosaic virus severity) have been selected for advancement.

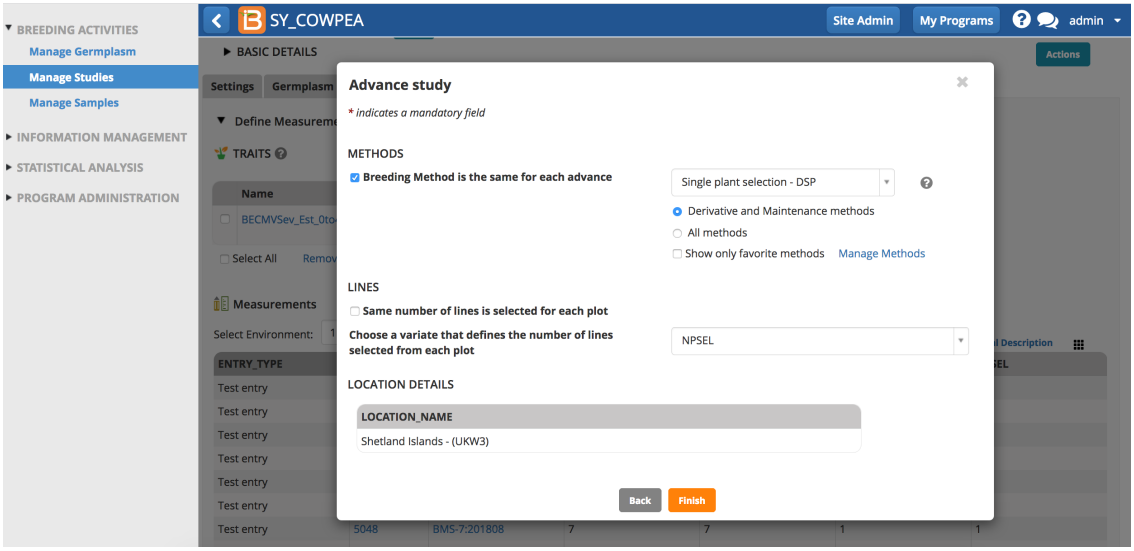


- Select which of the study instances (location in this case) to advance. Continue.

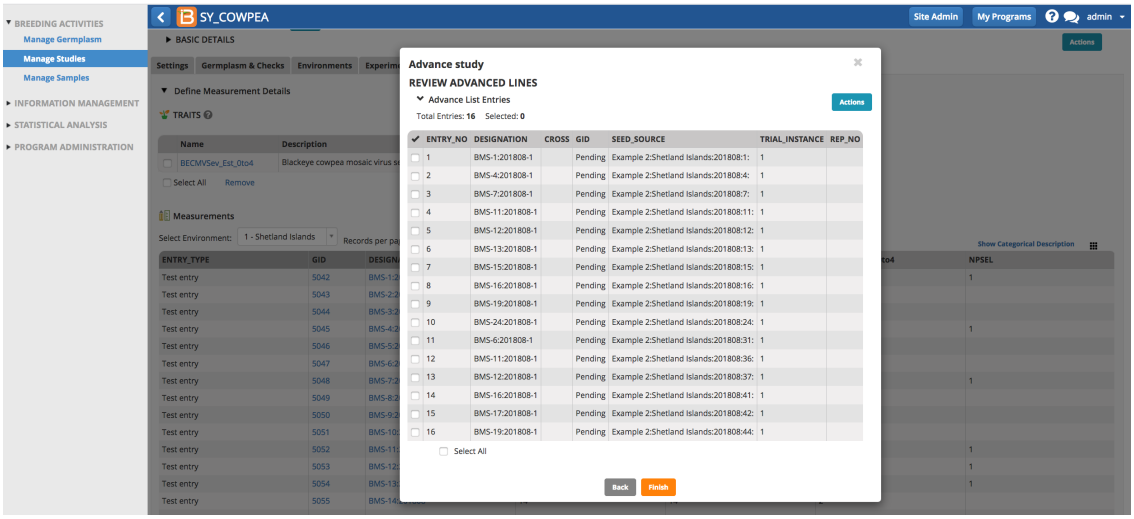


- Choose a breeding method. Derivative and maintenance breeding methods are filtered by default since these are the

most common for advancements. Deselect 'All plots are selected'. Choose the selection variate that defines the number of lines advanced from eah plot. Finish.

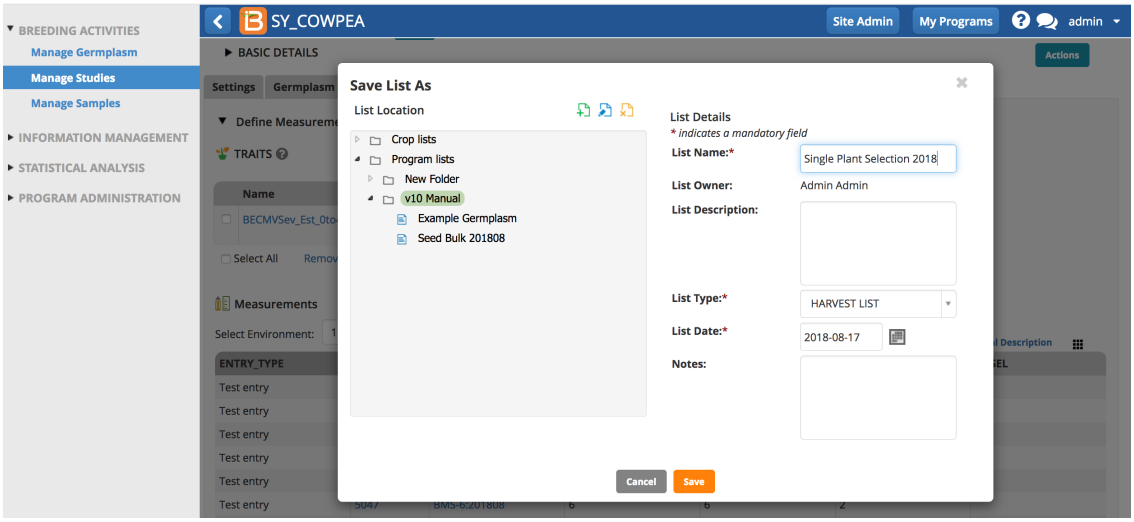


- Review the advanced lines and select Finish.

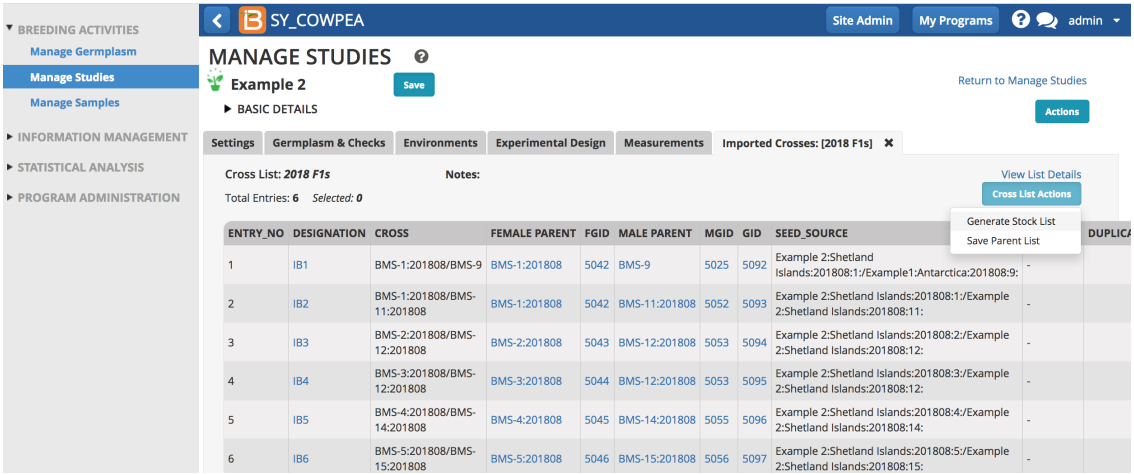


Notice that the pending lines have been automatically named. For example the designation, BMS-1-201808-1, is a concatenation of the parent line, BMS-1-201808, and the plant sequence number, 1). This is the default naming convention associated with the breeding method, single plant selection. See your system administrator if you would like to change the default naming conventions.

- Specify the folder where the list will be saved. Name the list and add optional information. Save.



The advance list can now be viewed in the associated nursery. The stock list can now be generated to record the harvest. (See Add Inventory After Crossing & Advancement).



With Plant ID

Select and advance plants with their own observation number from a plot.

- After creating a plant sub-observation dataset,

Related

- Germplasm & Geneaology
- Manage Inventory
- Crossing