

## Weighted Multi-Trait Query

BMS 16.0-17.0 Manual

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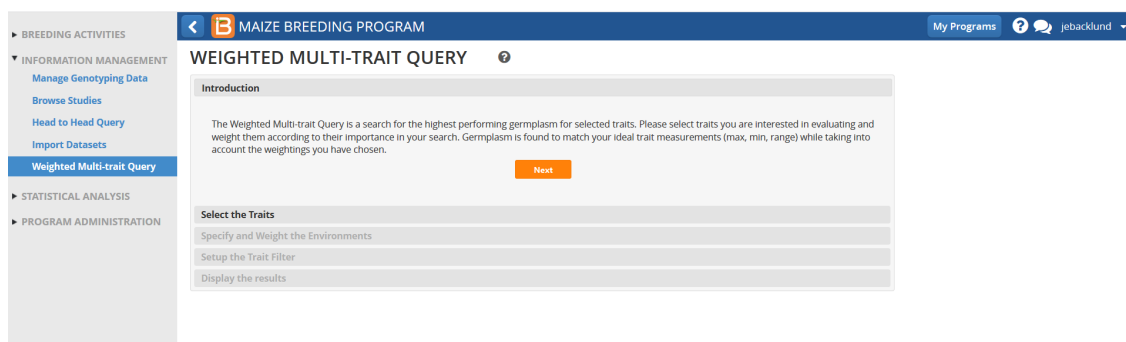
## About

Query germplasm by phenotype across studies and locations. A 'wizard' style user interface allows the user to:

- Query germplasm by phenotype.
- Filter query results by environment, location, and studies
- Filter query results by phenotypic criteria.
- Create summary scores for germplasm.
- Select and save germplasm.

## Select Phenotypic Traits

- Select Weighted Multi-Trait Donor Query from under Information Management. Select **Next**.



The screenshot shows the 'MAIZE BREEDING PROGRAM' interface. On the left is a sidebar with a navigation menu containing: BREEDING ACTIVITIES, INFORMATION MANAGEMENT (with sub-items: Manage Genotyping Data, Browse Studies, Head to Head Query, Import Datasets), Weighted Multi-trait Query (highlighted), STATISTICAL ANALYSIS, and PROGRAM ADMINISTRATION. The main content area is titled 'WEIGHTED MULTI-TRAIT QUERY' and features a 'Next' button. Below this is a section titled 'Select the Traits' with a list of options: 'Specify and Weight the Environments', 'Setup the Trait Filter', and 'Display the results'.

- All phenotypic traits defined in the ontology are available for selection. Select the phenotypic traits to include in the query.

**WEIGHTED MULTI-TRAIT QUERY**

**Introduction**

**Select the Traits**

Get all values for numeric variates

TRAIT	TRAIT NAME	STANDARD VARIABLE NAME
▼ All Traits		
▶ Abiotic stress		
▶ Agronomic		
▶ Biochemical trait		
▶ Biotic stress		
▶ General		
▶ Morphological		
▶ Passport		
▶ Physiological		
▶ Quality		

**Next**

**Specify and Weight the Environments**

Setup the Trait Filter

Display the results

To facilitate choosing among the available traits, they are organized into a tree starting with major groups such as 'Abiotic stress', 'Agronomic', 'Biotic stress', etc.

## Perform Query

- Select Next. The system will search for all of the studies that contain observations for one or more of the traits chosen. Depending on the amount of the data in your database, the query may take several minutes to process.

**WEIGHTED MULTI-TRAIT QUERY**

**Introduction**

**Select the Traits**

Get all values for numeric variates

TRAIT	TRAIT NAME	STANDARD VARIABLE NAME
▼ All Traits	Grain moisture	GMoi_NIRS_pct
▶ Abiotic stress	Grain yield	GY_FW_kgPlot
▶ Agronomic	Aspergillus flavus ear rot	AflavER_1_5
▶ Biochemical trait		
▶ Biotic stress		
▶ Anthracnose leaf blight incidence		
▶ Aphid damage		
▶ Army worm damage		
▶ Aspergillus ear rot severity		
▶ Aspergillus flavus ear rot		
▶ AflavER_1_5		
▶ Aspergillus flavus ear rot severity		
▶ Bacterial leaf stripe severity		
▶ Bacterial stalk rot incidence		

**Next**

**Specify and Weight the Environments**

Setup the Trait Filter

Display the results

Three traits are selected; grain moisture (Gmoi\_NIRS\_pct) , grain yield (GY\_FW\_kgPlot), and Asperillus flavus ear rot (AflavER\_1\_5). Grain moisture and yield are numeric variables and Asperillus flavus ear rot is a categorical variable.

## Filter Query

Query results can be filtered by both location and study. Additional environmental conditions can be added to the query results to assist filtering. The filters can be applied in any order and the effects are cumulative.

## Specify & Weight Environments

- Include or exclude environments from query. Specify the importance of each location by weight: important, critical, desirable, or ignored.

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Introduction

Select the Traits

Specify and Weight the Environments

Environment Filter

NO Environment Filter applied yet

Filter by LocationFilter by Study

Add Environment Conditions columns to the Environment Filter

Choose Environments:

TAG	ENV NO	LOCATION	COUNTRY	STUDY	WEIGHT
<input checked="" type="checkbox"/>	32	CGMSITE01	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	33	CGMSITE02	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	34	CGMSITE03	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	35	CGMSITE04	Zimbabwe	RYT18	Important
<input checked="" type="checkbox"/>	36	CGMSITE05	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	37	CGMSITE06	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	38	CGMSITE07	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	39	CGMSITE08	Zimbabwe	RYT18	Important
<input checked="" type="checkbox"/>	40	CGMSITE09	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	41	CGMSITE10	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	42	CGMSITE11	Kenya	RYT18	Important

Number of Environment selected: 217

Next

217 environments were evaluated for grain moisture (Gmoi\_NIRS\_pct) , grain yield (GY\_FW\_kgPlot), and Asperillus flavus ear rot (AflavER\_1\_5). In this example, all locations are included and all locations are considered important.

- Filter trial environments by location by selecting Filter by Location and specifying the locations of interest. Apply.

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Introduction

Select the Traits

Specify and Weight the Environments

Environment Filter

NO Environment Filter applied yet

Filter by LocationFilter by Study

Add Environment Conditions columns to the Environment Filter

Choose Environments:

TAG	ENV NO	LOCATION	COUNTRY	STUDY	WEIGHT
<input checked="" type="checkbox"/>	32	CGMSITE01	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	33	CGMSITE02	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	34	CGMSITE03	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	35	CGMSITE04	Zimbabwe	RYT18	Important
<input checked="" type="checkbox"/>	36	CGMSITE05	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	37	CGMSITE06	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	38	CGMSITE07	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	39	CGMSITE08	Zimbabwe	RYT18	Important
<input checked="" type="checkbox"/>	40	CGMSITE09	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	41	CGMSITE10	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	42	CGMSITE11	Kenya	RYT18	Important

Number of Environment selected: 217

Next

Filter by Location

Specify filter by checking or unchecking countries/locations.

COUNTRY/LOCATION	# OF ENVIRONMENTS	TAG
Colombia	45	<input type="checkbox"/>
Tanzania	2	<input checked="" type="checkbox"/>
Uganda	40	<input checked="" type="checkbox"/>
Zimbabwe	40	<input checked="" type="checkbox"/>
Mexico	3	<input type="checkbox"/>
Ghana	2	<input type="checkbox"/>
Kenya	40	<input checked="" type="checkbox"/>
Bolivia	1	<input type="checkbox"/>
Costa Rica	3	<input type="checkbox"/>

Cancel

Apply

In this example, the locations have been limited to those in Eastern and Southern Africa.

- Next.

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Select the Traits

Specify and Weight the Environments

Environment Filter

NO Environment Filter applied yet

Filter by LocationFilter by Study

Add Environment Conditions columns to the Environment Filter

Choose Environments:

TAG	ENV NO	LOCATION	COUNTRY	STUDY	WEIGHT
<input checked="" type="checkbox"/>	37	CGMSITE06	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	38	CGMSITE07	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	39	CGMSITE08	Zimbabwe	RYT18	Important
<input checked="" type="checkbox"/>	40	CGMSITE09	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	41	CGMSITE10	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	42	CGMSITE11	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	43	CGMSITE12	Zimbabwe	RYT18	Important
<input checked="" type="checkbox"/>	44	CGMSITE13	Uganda	RYT18	Important
<input checked="" type="checkbox"/>	45	CGMSITE14	Tanzania	RYT18	Important
<input checked="" type="checkbox"/>	46	CGMSITE15	Kenya	RYT18	Important
<input checked="" type="checkbox"/>	47	CGMSITE16	Zimbabwe	RYT18	Important

Number of Environment selected: 161

Next

The original 217 environments have been reduced to 161 environments in Eastern and Southern Africa.

# Setup Trait Filter

Filter and weight the query results by phenotypic parameters. For each trait, every observation included in the environments filter will be scored as passing or failing to meet the phenotypic criteria for that trait. A combined score across all of the traits is also calculated (see details below). The contribution of the individual traits to the combined score can be weighted as being Critical, Important, or Desirable to reflect its importance.

## Numeric Traits

The Numeric Traits tab provides a set of comparison operators for specifying the criteria that will be used to identify germplasm that meets or surpasses the desired levels. To specify criteria between a lower and upper limit, choose 'Between' and enter the two values separated by a dash.

- Specify condition and weights for numeric traits.

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Specify and Weight the Environments

Setup the Trait Filter

Numeric TraitsCharacter TraitsCategorical Traits

Get all values for numeric variates

TRAIT	# OF LOCATIONS	# OF LINES	# OF OBSERVATIONS	MIN	MEDIAN	MAX	CONDITION	LIMITS	WEIGHT
GMol_NIRS_pc	161	103	13560	-41.72	-0.209	37.312	>	20	Important
GY_FW_kgPlot	1	40	120	5.4118	6.75972	7.9122	Keep All		Important

Drop TraitKeep All<<=>=>>BetweenInNot in

Next

The numeric trait, grain moisture has been limited to those germplasm with greater than 20% moisture.

## Categorical Traits

- Reduce the column widths to make the selection criteria visible.

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Introduction

Select the Traits

Specify and Weight the Environments

Setup the Trait Filter

Numeric TraitsCharacter TraitsCategorical Traits

Specify filters for the Categorical Traits

TRAIT	# OF L	# OF LI	# OF OB	CLASS 1	CLASS 2	CLASS 3	CLASS 4	CLASS 5	CONDITION	LIMITS	WEIGHT
AflavE1_1_5	10	40	1200	1 (70)	2 (247)	3 (354)	4 (377)	5 (152)	Keep All		Important

Next

Display the results

- Specify condition and weights for categorical traits. Select Next. Use commas to separate multiple values. To enter a single value, just enter the value with no commas.

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Specify and Weight the Environments

Setup the Trait Filter

Numeric Traits

Character Traits

Categorical Traits

Specify filters for the Categorical Traits

TRAIT	# OF LI	# OF OI	# OF OBSE	CLASS 1	CLASS 2	CLASS 3	CLASS 4	CLASS 5	CONDITION	LIMITS
AflavER_1_5	161	103	13560	1 (2286)	2 (501)	3 (4612)	4 (1523)	5 (122)	In	1,2

Drop Trait

Keep All

In

Not in

Next

Asperillus flavus ear rot (AflavER\_1\_5) has 5 categories. In this example, the results are restricted to those germplasm with Asperillus flavus ear rot scores of highly resistant (1) and resistant (2).

## How Success Ratios Are Calculated

### Individual Trait Success Ratios

Success ratios are calculated based on whether an observed value of the trait meets the criteria set in the 'Setup the Trait Filter' pane. Observations that meet the criteria are assigned a score of +1 while observations that do not meet the criteria are assigned a value of -1. For example, if the trait of interest is Grain Moisture and the criterion is that the observed value is < 19 then an observed value of 18.9 would be assigned a score of +1 and an observed value of 19.1 would be assigned -1. Each observation is weighted based on the weight assigned in the 'Specify and Weight the Environments' pane. The Choices under the WEIGHT column in the 'Setup and Weight Environments' pane are 'Ignored', 'Desirable', 'Important', and 'Critical' which are assigned weights of 0, 1, 2, and 3, respectively.

For each trait, a weighted average is calculated for each line for which there are observations in one or more of the environments selected in the 'Specify and Weight the Environments' pane. The weighted average is presented under the SUCCESS RATIO column for each trait along with the number of observations included in the weighted average.

### Combined Score

A combined score is also provided in the results pane. The combined score is a weighted average of the success ratios of all of the traits included in the query. The weight of each trait is the weight assigned in the 'Setup the Trait Filter' pane. The Choices under the WEIGHT column in the 'Setup the Trait Filter' pane are 'Ignored', 'Desirable', 'Important', and 'Critical' which are assigned weights of 0, 1, 2, and 4, respectively. Note that the number of observations of a trait doesn't factor into the combined score, only the success ratio and the weight assigned to each trait.

### Formulas used to calculate Success Ratios and Combined Scores

Individual trait Success Ratios are calculated based on observations (subscript l) of traits (subscript j) for lines (subscript i) in environments (subscript k). Let  $R_{ijkl}$  be +1 if observation  $O_{ijkl}$  is within limits for trait j, and -1 if it is outside the acceptable limits. Then a score for line i and trait j over all environments k could be  $R_{ij..} = \sum_k E_k \sum_l R_{ijkl} / n_{ijk}$  where  $n_{ijk}$  is the number of observations of trait j for line i in environment k and  $E_k$  is  $1.0/N_{ij}$  (where  $N_{ij}$  is the number of environments where trait j was measured on line i) if all selected environments have equal weight or it is  $W_k / \sum_k W_k$  if the environments have different weights.

Combined Scores are calculated for each line as a weighted average of the trait scores: Combined Score  $R_{i...}$  for line i with weights T for traits j:  $R_{i...} = \sum_j T_j R_{ij.} / \sum_j T_j$

## Results

The results of the Weighted Multi-trait Query are displayed in a table. Note that there are left and right arrow buttons below the table enabling you to page through the results, which may span multiple pages. Also note that if you have selected multiple traits, they may not all fit on the page; there is a scroll bar just above the left and right arrows for scrolling through the trait columns.

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Introduction

Select the Traits

Specify and Weight the Environments

Setup the Trait Filter

Display the results

LINE NO	LINE GID	LINE DESIGNATION	GMOL_NIRS_PCT NO OF OBS	SUCCESS RATIO	GY_FW_KG/PLOT NO OF OBS	SUCCESS RATIO	COMBINED SCORE	TAG
1	352444	MH1	30	0.47	30	0.87	0.54	
2	352453	MH10	30	-0.87	30	1.0	0.11	
3	352454	MH11	30	-0.87	30	1.0	-0.25	
4	352455	MH12	30	-0.53	30	1.0	0.18	
5	352456	MH13	30	-0.93	30	0.87	-0.31	
6	352457	MH14	30	-0.87	30	0.93	-0.27	
7	352458	MH15	30	-0.8	30	0.67	-0.33	
8	352459	MH16	30	0.2	30	1.0	0.13	
9	352460	MH17	30	-0.73	30	1.0	-0.11	
10	352461	MH18	30	-0.53	30	1.0	-0.04	
11	352462	MH19	30	-0.87	30	0.47	-0.47	
12	352445	MH2	30	-0.93	30	1.0	-0.18	
13	352463	MH20	30	-0.33	30	0.93	-0.02	
14	352464	MH21	30	-0.87	30	1.0	0.09	
15	352465	MH22	30	-0.87	30	0.93	-0.22	

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## Sorting

Clicking once on a column header will sort in ascending order; clicking again will sort in descending order.

- Click twice on the COMBINED SCORE column and the table to sort results in descending order from highest to lowest.

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Setup the Trait Filter

Display the results

LINE NO	LINE GID	LINE DESIGNATION	GMOL_NIRS_PCT NO OF OBS	SUCCESS RATIO	GY_FW_KG/PLOT NO OF OBS	SUCCESS RATIO	COMBINED SCORE	TAG
77	352464	MH21	3	1.0	3	1.0	1.0	
87	352473	MH30	3	1.0	3	1.0	1.0	
88	352474	MH31	3	1.0	3	1.0	1.0	
100	352449	MH6	3	1.0	3	1.0	1.0	
93	352479	MH36	3	0.33	3	1.0	0.78	
94	352480	MH37	3	0.33	3	1.0	0.78	
103	352452	MH9	3	1.0	3	1.0	0.78	
65	352453	MH10	3	-0.33	3	1.0	0.56	
67	352455	MH12	3	-0.33	3	1.0	0.56	
75	352445	MH2	3	1.0	3	1.0	0.56	
78	352465	MH22	3	1.0	3	1.0	0.56	
96	352482	MH39	3	1.0	3	1.0	0.56	
64	352444	MH1	3	-1.0	3	1.0	0.33	
66	352454	MH11	3	1.0	3	1.0	0.33	
68	352456	MH13	3	1.0	3	1.0	0.33	

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Save to List

Four germplasm have combined scores of 1.0 and will be selected for inclusion in an upcoming study.

## Tag & Save Germplasm

- Tag germplasm of interest and Save to List.

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LINE NO	LINE GID	LINE DESIGNATION	GMOI_NIRS_PCT NO OF OBS	SUCCESS RATIO	GY_FW_KGPLOT NO OF OBS	SUCCESS RATIO	COMBINED SCORE	TAG
77	352464	MH21	3	1.0	3	1.0	1.0	<input checked="" type="checkbox"/>
87	352473	MH30	3	1.0	3	1.0	1.0	<input checked="" type="checkbox"/>
88	352474	MH31	3	1.0	3	1.0	1.0	<input checked="" type="checkbox"/>
100	352449	MH6	3	1.0	3	1.0	1.0	<input checked="" type="checkbox"/>
93	352479	MH36	3	0.33	3	1.0	0.78	<input type="checkbox"/>
94	352480	MH37	3	0.33	3	1.0	0.78	<input type="checkbox"/>
103	352452	MH9	3	1.0	3	1.0	0.78	<input type="checkbox"/>
65	352453	MH10	3	-0.33	3	1.0	0.56	<input type="checkbox"/>
67	352455	MH12	3	-0.33	3	1.0	0.56	<input type="checkbox"/>
75	352445	MH2	3	1.0	3	1.0	0.56	<input type="checkbox"/>
78	352465	MH22	3	1.0	3	1.0	0.56	<input type="checkbox"/>
96	352482	MH39	3	1.0	3	1.0	0.56	<input type="checkbox"/>
64	352444	MH1	3	-1.0	3	1.0	0.33	<input type="checkbox"/>
66	352454	MH11	3	1.0	3	1.0	0.33	<input type="checkbox"/>
68	352456	MH13	3	1.0	3	1.0	0.33	<input type="checkbox"/>

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Save to List

- Specify the germplasm list details and Save. The germplasm list now available from Manage Germplasm and can be included as a study list.

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LINE NO	LINE GID	LINE DESIGNATION	GMOI_NIRS_PCT NO OF OBS	SUCCESS RATIO	GY_FW_KGPLOT NO OF OBS	SUCCESS RATIO	COMBINED SCORE	TAG
1	352444	MH1	30	0.47	30	0.87	0.54	<input checked="" type="checkbox"/>
29	352478	MH35	30	0.13	30	1.0	0.38	<input checked="" type="checkbox"/>
23	352446	MH3	30	0.27	30	0.53	0.33	<input checked="" type="checkbox"/>
28	352477	MH34	30	-0.47	30	0.87	0.22	<input checked="" type="checkbox"/>
19	352469	MH26	30	-0.67	30	0.93	0.2	<input type="checkbox"/>
36	352448	MH5						<input type="checkbox"/>
39	352451	MH8						<input type="checkbox"/>
4	352455	MH12						<input type="checkbox"/>
30	352479	MH36						<input type="checkbox"/>
8	352459	MH16						<input type="checkbox"/>
2	352453	MH10						<input type="checkbox"/>
14	352464	MH21						<input type="checkbox"/>
17	352467	MH24						<input type="checkbox"/>
22	352472	MH29						<input type="checkbox"/>
27	352476	MH33						<input type="checkbox"/>

Save to List

Save in:

Lists

Change Location

List Name

2018 Stage 2 selections

Description

Lines selected for combined score of yield, moisture, Aflav resistance

Type

GERMPLASM LISTS

Save

Cancel

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