

Manage Ontology

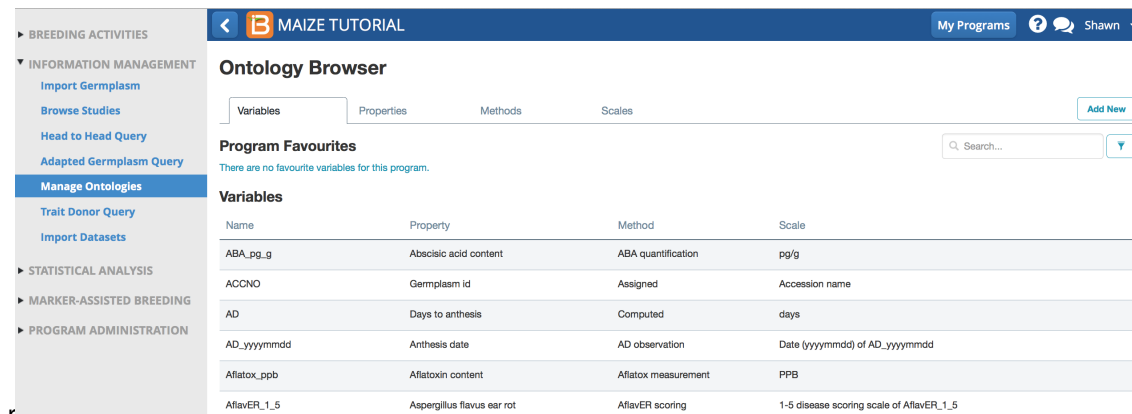
BMS 13.0-14.0 Manual

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Introduction

The Breeding Management System's crop ontology management tool uses a structured vocabulary to allow descriptors to act as variables in database queries and statistical analysis. Core crops come preloaded with a set of variables, or ontology terms, recommended by their community of practice. Preloaded ontologies are fully customizable. The BMS also provides a generic crop database to support any breeding program. Consistent variable definitions are essential for data sharing and collaboration. As you consider ontology customization, we recommend that you coordinate with collaborators and your crop community to similarly define terms to facilitate data sharing and meta analysis. See more about [Crop Ontology Curation](#).

- Select Manage Ontologies from the information management menu to browse, edit, or add ontology terms.



Ontology Browser

Variables | Properties | Methods | Scales | [Add New](#)

Program Favourites
There are no favourite variables for this program.

Variables

Name	Property	Method	Scale
ABA_pg.g	Abscisic acid content	ABA quantification	pg/g
ACCNO	Germplasm id	Assigned	Accession name
AD	Days to anthesis	Computed	days
AD_yyyymmdd	Anthesis date	AD observation	Date (yyyymmdd) of AD_yyyymmdd
Aflatox_ppb	Aflatoxin content	Aflatox measurement	PPB
AflavER_1_5	Aspergillus flavus ear rot	AflavER scoring	1-5 disease scoring scale of AflavER_1_5

Maize Ontology Browser

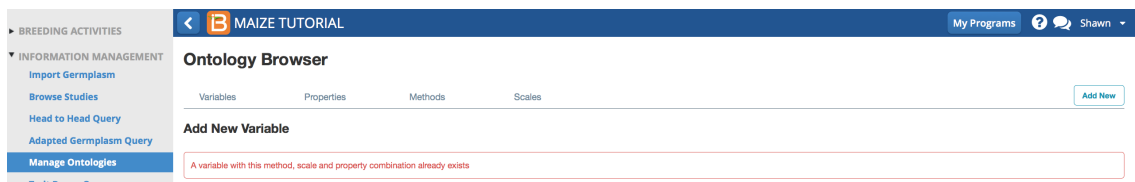
Variable Identity

Each variable name is identified by 3 details. Only one ontology term can be associated with a combination of unique details.

- Property: What is measured
- Method: How the variable is measured
- Scale: Categorical scale or unit of measure for the variable

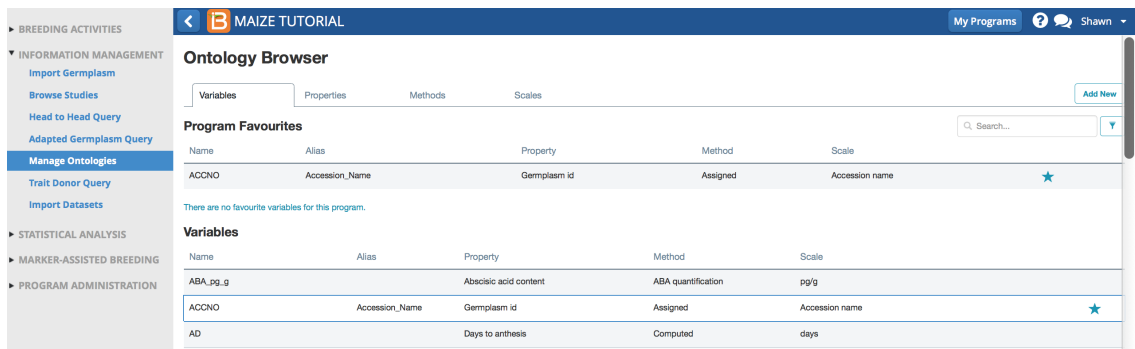
Duplicate Variable Error

The BMS will not allow you to add a new variable with an identical combination of property, method, and scale to other variables.



Aliases & Favorites

Although it is important for crop communities to similarly define traits and share a common vocabulary, the BMS provides the ability to create custom aliases for ontology terms, allowing breeders to communicate variables in familiar language within their breeding programs. Once an alias has been set, the custom alias will replace the variable name in the user interface, data collection files, and the output of statistical analyses. Giving a variable an alias does not change the functional identity (property, method, and scale) of the variable. Variables which are given aliases are automatically added to your program favorites. Any variable can be made a program favorite by selecting the star symbol to the right. Deselect the blue star to remove from favorites.



Add & Edit Variable

Once a variable is used in a study property, method, and scale can not be changed from the user interface. See your system administrator for more information on editing variables in use.

- Select Add New. Choose Variable.



Variable name is generally an abbreviation or acronym describing the variable. Variable names in the default BMS crop ontology will be recognizable between all members of a crop community. Variable name is the ontology term specified in BMS data collection files and the output of statistical analyses. Variable names cannot contain spaces or special characters with the exception of underscore, and cannot start with a number to ensure compatibility with Breeding View (BV) statistical engine and other apps. If variable names exceed 15 characters truncation of variable name will occur in the graphical output of BV. Changing a variable name does not change the functional identity (property, method, and scale) of the variable.

- Name & describe variable. Variable description is a plain language description of the variable. Editing or expanding a variable's definition does not change the functional identity (property, method, and scale) of the variable.
 - Name: B_Carotene
 - Describe: Beta-carotene content, mg/kg dry matter (mg/kg d.m.)
- Property describes what is being measured. The default maize ontology has no property describing beta-carotene content, so a new one must be added. Select Add a New Property.

BREEDING ACTIVITIES

INFORMATION MANAGEMENT

Import Germplasm

Manage Genotyping Data

Browse Studies

Head to Head Query

Manage Ontologies

Import Datasets

Trait Donor Query

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PROGRAM ADMINISTRATION

SY_MAIZE

Site Admin

My Programs

admin

Ontology Browser

VariablesPropertiesMethodsScales

Add New

Add New Variable

NameB_Carotene

DescriptionBeta-carotene content, mg/kg dry matter (mg/kg d.m.)

PropertyAdd a new property

MethodAdd a new method

ScaleAdd a new scale

Variable TypeStart typing

SaveCancel

Find Existing or Add New Property

- Name the property, Beta-Carotene. Tag the classes, Quality and Physiological. Tagging the property helps the ontology search engine provide selections of relevant traits. Save.

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Ontology Browser

VariablesPropertiesMethodsScales

Add New

Add New Property

NameBeta-Carotene

Description

ClassesQualityPhysiologicalStart typing

Crop Ontology ID

SaveCancel

Find Existing or Add New Method

Method describes how the property is measured. Beta-carotene content is measured by high performance liquid chromatography, which is not included in the default maize ontology.

- Select Add a New Method.

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VariablesPropertiesMethodsScales

Add New

Add New Variable

NameB_Carotene

DescriptionBeta-carotene content, mg/kg dry matter (mg/kg d.m.)

PropertyBeta-CaroteneAdd a new property

MethodAdd a new method

ScaleAdd a new scale

Variable TypeStart typing

SaveCancel

- Name and describe the method, HPLC, high performance liquid chromatography.

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Ontology Browser

Variables Properties Methods Scales [Add New](#)

Add New Method

* Name: HPLC

Description: high performance liquid chromatography

[Save](#) [Cancel](#)

Find Existing or Add New Scale

Beta-carotene content is a numeric variable measured in units of milligram per kilogram of dry matter.

- Name: mg/kg d.m.
- Description: milligram per kilogram of dry matter
- Data Type: Numeric
- Valid Range: Numeric scales offer the option of setting a range of valid values for setting limit for all variables sharing a particular scale. It is recommended to set the limits as expected range when creating each variable.

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Ontology Browser

Variables Properties Methods Scales [Add New](#)

Add New Scale

* Name: mg/kg d.m.

Description: milligram per kilogram of dry matter

* Data Type: Numeric

Valid Range: Minimum Maximum

[Save](#) [Cancel](#)

Variable Type

Variable type differentiates traits, or phenotype, from different independent variables. Variable type determines which variables are presented in different BMS tools.

- Types
 - Analysis
 - Environment Detail
 - Germplasm Descriptor
 - Nursery Condition
 - Selection Method
 - Study Detail
 - Treatment Factor
 - Trait
 - Study Detail
- Like most terms in the crop ontology, beta-carotene, is a trait or phenotype. Select Trait from the drop down menu of different variable types. Save.

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Ontology Browser

Variables Properties Methods Scales [Add New](#)

Add New Variable

* Name: B_Carotene

Description: Beta-carotene content, mg/kg dry matter (mg/kg d.m.)

* Property: Beta-Carotene [Add a new property](#)

* Method: HPLC [Add a new method](#)

* Scale: mg/kg d.m. [Add a new scale](#)

* Variable Type: **Trait** Start typing

Expected Range: Minimum Maximum

Note that values must be within the valid range for the selected scale (-).

[Save](#) [Cancel](#)

- Expected Range: Numeric variables offer the option of setting a range of valid values for quality control. Data outside of this range is flagged as a possible error during data import. It is recommended to set minimum and maximum expected values accordingly biological limits of the trait.

Formulas

Traits whose value is derived from calculation will be associated with a formula. See more on [Creating formulas for calculated variables.](#)

Select the variable to which a formula will be added. Select add a new formula.

The screenshot shows the VIGNA_VIRTUAL interface. On the left is a sidebar with navigation options: BREEDING ACTIVITIES, INFORMATION MANAGEMENT (Import Germplasm, Manage Genotyping Data, Browse Studies, Head to Head Query, Manage Ontologies, Import Datasets, Trait Donor Query), STATISTICAL ANALYSIS, and PROGRAM ADMINISTRATION. The main panel is titled 'Ontology Browser' and has tabs for Variables, Properties, and Methods. Under 'Program Favourites', there is a table:

Name	Property
DFDWTKGH	Dry fodder weight
FFODKGHA	Fresh fodder weight
Fod_Moi_pct	Derived

Below this is a 'Variables' section with another table:

Name	Property
AB	AB
ACCNO	Germplasm id
ACNTOMIA	ACTOMIA
ALEC_PLT	Alectra
AlecInf_Est_0to4	Alectra
AlecNo_Count9Wk_Alec	Number of Alectra plants
AlecNo_CountWk_Alec	Number of Alectra plants

On the right, the 'Fod_Moi_pct' configuration panel is shown with the following details:

- Name: Fod_Moi_pct
- Description: (Percent moisture of fodder calculated) = ((dry weight fodder)/(fresh weigh fodder)) *100
- Property: Derived
- Method: Calculated
- Scale: Percent
- Variable Type: Trait
- Expected Range: 0 to 100

At the bottom of this panel are buttons for 'Edit' and 'Add'. Below the configuration panel are sections for 'Formula' and 'Metadata'.

- Enter the formula and Save using the coding described in [Creating formulas for calculated variables.](#)

The screenshot shows the 'Add New Formula' dialog in the VIGNA_VIRTUAL interface. The 'Target Variable' is set to 'Fod_Moi_pct'. The 'Calculation' field contains the formula: $((DFDWTKGH)/((FFODKGHA))) * 100$. There are 'Save' and 'Cancel' buttons at the bottom of the dialog.

The trait is now associated with the formula and can be calculated by the BMS after data for input variables is added.

Algebraic Formula

The screenshot shows the VIGNA_VIRTUAL interface. On the left is a sidebar with navigation options: BREEDING ACTIVITIES, INFORMATION MANAGEMENT (Import Germplasm, Manage Genotyping Data, Browse Studies, Head to Head Query, Manage Ontologies, Import Datasets, Trait Donor Query), STATISTICAL ANALYSIS, and PROGRAM ADMINISTRATION. The main panel is titled 'Ontology Browser' and has tabs for Variables, Properties, and Methods. Under 'Program Favourites', there is a table:

Name	Property
DFDWTKGH	Dry fodder weight
FFODKGHA	Fresh fodder weight
Fod_Moi_pct	Derived

Below this is a 'Variables' section with another table:

Name	Property
AB	AB
ACCNO	Germplasm id
ACNTOMIA	ACTOMIA
ALEC_PLT	Alectra
AlecInf_Est_Oto4	Alectra
AlecNo_Count9Wk_Alec	Number of Alectra plants
AlecNo_CountWk_Alec	Number of Alectra plants

On the right, the 'Fod_Moi_pct' variable is detailed:

- Name: Fod_Moi_pct
- Description: (Percent moisture of fodder calculated) = ((dry weight fodder)/(fresh weigh fodder))*100
- Property: Derived
- Method: Calculated
- Scale: Percent
- Variable Type: Trait
- Expected Range: 0 to 100

There is an 'Edit' button. Below is the 'Formula' section:

Calculation	Input Variables
((DFDWTKGH)/((FFODKGHA))*100	DFDWTKGH, FFODKGHA

There is a 'Metadata' section at the bottom.

Fod_Mod_pct is the percent moisture of fodder calculated by dividing the dry weight (DFDWTKGH) by the fresh weight (FFODKGHA) and multiplying by 100
 Calculation = ((DFDWTKGH)/((FFODKGHA))*100

Date to Days Formula

The screenshot shows the VIGNA_VIVA interface. The sidebar is similar to the previous one. The main panel is titled 'Ontology Browser' with tabs for Variables, Properties, Methods, and Scales. An 'Add New' button is in the top right. The 'Add New Formula' dialog is open:

- Target Variable: FlWT_Day
- Input Variables: Select or search variables in the list...
- * Calculation: fn:daysdiff ({{Pit_Date}} , {{FlWT_Date}})

There are 'Save' and 'Cancel' buttons at the bottom.

Calculate the number of days occurring between 2 dates = fn:daysdiff ({{DATE1}},{{DATE2}})

Average Formula

The screenshot shows the SY_RICE interface. The sidebar has additional options: Manage Germplasm, Manage Studies, and Manage Samples. The main panel is titled 'Ontology Browser' with tabs for Variables, Properties, and Methods. Under 'Variables', there is a table:

Name	Property	Me
ALT_Mean	Plant height	Av
ALT_Means	Plant height	LS
ALT_MeanSED	Plant height	Me
AmyCt_NIRS_Pct_Mean	Amylose content	Ca
AmyCt_NIRS_Pct_Mean_CV	Amylose content	CV
AmyCt_NIRS_Pct_Mean_Heritability	Amylose content	He
AmyCt_NIRS_Pct_Mean_Mean	Amylose content	Av
AmyCt_NIRS_Pct_Mean_Means	Amylose content	LS
AmyCt_NIRS_Pct_Mean_MeanSED	Amylose content	Me

On the right, the 'AmyCt_NIRS_Pct_Mean' variable is detailed:

- Description: mean amylose (%) content from repeated NIRS measures
- Property: Amylose content
- Method: Calculation - Amylose NIRS Means
- Scale: %
- Variable Type: Trait, Study Condition
- Expected Range: All values allowed

There is an 'Edit' button. Below is the 'Formula' section:

Calculation	Input Variables
fn:avg({{AmyCt_NIRS_Pct}})	AmyCt_NIRS_Pct

There are 'Edit' and 'Delete' (trash icon) buttons.

Calculate averages of subsamples of grain quality amylose percent meassures (fn:avg({{AmyCt_NIRS_Pct}})

- Select the garbage can icon to delete a formula. Select delete to confirm that you want to delete the existing formula.
**If you want to edit and existing formula, you can copy the formula before deleting and paste back into the empty formula builder to edit.*

PROGRAM ADMINISTRATION

ACCNO	Germplasm id
ACNTOMIA	ACTOMIA
ALEC_PLT	Alectra
AlecInf_Est_Oto4	Alectra
AlecNo_Count9Wk_Alec	Number of Alectra plants
AlecNo_CountWk_Alec	Number of Alectra plants

Formula

Calculation

Input Variables

(((DFDWTKGH))/((FFODKGHA)))-100

DFDWTKGH, FFODKGHA

Please confirm that you would like to delete this formula.

DeleteCancel

Search Ontology

Searching the maize database for "beta" now reveals the newly added B_Carotene variable.

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Add New

Variables

NameAliasPropertyMethodScale

B_CaroteneBeta-CaroteneHPLCmg/kg d.m.

beta

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Time Series

BMS version 11 does allow a single traits to be associated with mulitple sub-observations to record repeated measures (see more [Observations & Sub-Observations](#)). However, time series is still under development. If the v11 sub-observation solution to time series recording does not suit your needs, you are still able to create individual traits for each time points.

The nomenclature of new traits created to support time series should be standardized for each crop. The following table offers some suggestions for time series nomclature.

Time Code Type	Time Code	Examples
Cereals Zadoks growth/development stages	GS(00-99) or DS(00-99)	<ul style="list-style-type: none">DS65 = headingDS75 = anthesisDS87 = physiological maturity
Maize growth/development stages	Vegetative: VE, V1-Vn, VT Reproductive: R1-R6	<ul style="list-style-type: none">VE = emergenceV3 = third LeafVT = tasselingR1 = silkingR6 = physiological maturity
Soybean growth/development stages	VE, VC, V1-Vn, R1-R8	<ul style="list-style-type: none">VE = emergenceV4 = second trifoliolateR2 = full floweringR8 = full maturity
Generic Codes	<ul style="list-style-type: none">hd = headingflw = floweringant = anthesisvg = vegetative periodprehd = pre-headinggf = grain fillingmat = maturity	
Days after emergence	dae	45dae, 65dae....
Days after sowing	das	45das, 65das...
Days after planting	dap	45dap, 65dap...

Weeks after planting	wap	1wap, 2wap...
Months after planting	map	1map, 2map
Date	yyyymmdd	20150315
Date+hr+min	yyyymmdd	201503151135
Time	t	t1, t2...

- First create a new method with the subsampling code.

Adapted Germplasm Query	ABA quantification	
Manage Ontologies	ABA quantification	ABA quantification
Trait Donor Query	ABA quantification ear 1	ABA quantification subsample

- Second create a new trait with the subsampling code.

BREEDING ACTIVITIES

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Manage Nurseries

Manage Trials

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Ontology Browser

Variables Properties Methods Scales

Add New

Add New Variable

Name

ABA_pg_g_ear1

Description

ABA content ear subsample1

Property

Abscissic acid content

Add a new property

Method

ABA quantification ear 1

Add a new method

Scale

pg/g

Add a new scale

Variable Type

Trait x Start typing

Expected Range

Minimum

Maximum

Note that values must be within the valid range for the selected scale (-).

Save

Cancel

- Repeat. Create a new ontology term for each required sub-sample or time series measurement.

Related

- [Manage Studies](#)
- [Study Measurements](#)