The Triticeae Toolbox: Transitioning to Breedbase

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What is T3?

- The Triticeae Toolbox is a centralized database for small grains breeders (wheat, oat, barley)
- Combines accession information, phenotype trial data, and genotype data from various sources
- Allow users to create custom datasets
- Provide summary and analytical tools
The Hordeum Toolbox was developed for the Barley CAP.

The Triticeae Toolbox was expanded from THT for the Triticeae CAP.

Tools have been added periodically to T3.


Blake, V.C., et. al. 2016. The Triticeae Toolbox: Combining Phenotype and Genotype Data to Advance Small-Grains Breeding. Plant Gen. 9:1-10
Transition to Breedbase

What is Breedbase?
Breedbase is a comprehensive breeding management and analysis software. It can be used to design field layouts, collect phenotypic information using tablets, support the collection of genotyping samples in a field, store large amounts of high density genotypic information, and provide Genomic Selection related analyses and predictions. Breedbase supports the BrAPI standard.

How can I use Breedbase?
Breedbase is a web application that only requires a browser. To get your instance, follow this guide to deploy via docker, or contact the Breedbase development team.

What crops are using Breedbase?
There are a number of instances running for diverse crops, including Cassava (https://cassavabase.org), sweet potato (https://sweetpotatobase.org), banana (https://musabase.org), rice (https://ricebase.org), tomato and other Solanaceae (https://solanomics.net/) and many others.

BREEDBASE is located at the Boyce Thompson Institute.
What is Breedbase?

- A "comprehensive breeding management and analysis software"
- Database, analytical tools and website
- Developed by Lukas Mueller’s lab at Boyce Thompson Institute
- Currently used by multiple crops: cassava, sweet potato, banana, rice, Solanaceae crops
Breedbase Features

- Design field layouts
- Store phenotype trial information
  - Tightly integrated with Fieldbook / Pheno Apps
- Store genotype information
- Provides summary and analytical tools
- BrAPI compliant
Why Choose Breedbase?

- **More developers**
  - Core development team at BTI
  - Already being used by multiple crops

- **Unified database**
  - Sharing of ideas, database structures, tools…

- **Unique Features**
  - Trial Design
  - Seedlot Management
  - Barcodes (seedlots, accessions, plots, etc)
Current Status of Transition

- **Wheat:** Data from T3/Classic has been migrated
  Needs some manual reorganization

- **Oat:** Trait ontology created
  Starting to load Accessions

- **Barley:** Coming Soon
The New T3/Wheat

Main Production Site
https://wheat.triticeaetoolbox.org

Sandbox / Test Site
https://wheat-sandbox.triticeaetoolbox.org
T3 Demos

- Live Demos
- Screenshots in presentation
- Presentation will be available:
  - New T3/Wheat website
T3 Demos

- Creating an Account
- The Search Wizard
- Searching Accessions
- Using Lists
- Trial Design Tool
- Uploading Phenotype Data
- Trial Summary Tool
Creating an Account

An account is required to:
- add any data to the database
- view some types of data in the database (such as phenotype trial results)
- use some of the tools (such as summarizing trials)

To check if you already have an account:
- Go to: Search > People to see if your name is already associated with an account

https://wheat.triticeaetoolbox.org/user/new
Creating an Account

Click the “Login” Button in the top right of any page.
Creating an Account

Click the “New User” link in the login pop-up window.
Creating an Account

Fill out the new account registration form.
Creating an Account

You will receive an email (from noreply@graingenes.org - check your Junk/Spam folder) with a link to confirm your email address.

You must open the confirmation link before you can login to your account.
The Search Wizard can be used to:

- Explore the database
- Filter data by 1 or more search criteria
- Download filtered and/or combined datasets

You must have an account to download data
The Search Wizard can be used to filter data by up to 4 different data types:

- Accessions
- Breeding Programs
- Genotyping Protocols
- Genotyping Projects
- Locations
- Traits
- Trials
- Years
Filter by Trials & Traits:

1) Select ‘Trials’
2) Choose (+) Trials to include
3) Select ‘Traits’
4) Choose (+) Traits to include
5) Optionally continue to select specific Accessions...
Download Trial Phenotypes:

1) Click ‘Related Trial Phenotypes’

2) Click the ‘Phenotypes’ button to download a CSV file
The Search Wizard

Example Phenotype Spreadsheet

<table>
<thead>
<tr>
<th>S</th>
<th>W</th>
<th>X</th>
<th>Y</th>
<th>Z</th>
<th>AN</th>
<th>AO</th>
<th>AP</th>
<th>AQ</th>
<th>AR</th>
</tr>
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<tbody>
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</tr>
</tbody>
</table>

*Note: The spreadsheet contains columns for various genetic data points such as `germplasmName`, `observationUnitName`, `replicate`, `blockNumber`, `plotNumber`, `Grain test weight g/CO_321:0001218`, and `Grain yield kg/hajCO_321:0001218`.*
Advanced Search: Accessions

https://wheat.triticeaetoolbox.org/search/stocks

Select “Accessions and Plots” from the Search menu
Advanced Search: Accessions

Search by Genetic Character:

- Select “Advanced Search” then “Genotypes”
- Select a Locus (Genetic Character)
- Select an Allele value
Advanced Search: Accessions

Search by Genetic Character:

- The results table contains Accessions that match all search criteria.
- Results can be saved to a List.
Search by Genetic Character:

- The Accession detail page includes a table of all associated Loci that have been characterized for the Accession.
Advanced Search: Accessions

Search by Pedigree:

- Select “Advanced Search” then “Properties”
- Next to “Search By Another Property” select “pedigree”
Advanced Search: Accessions

Search by Pedigree:

• Select “Advanced Search” then “Properties”

• Next to “Search By Another Property” select “pedigree”
Search by Pedigree:

The results table will only include Accessions that have JERRY in their Purdy pedigree

<table>
<thead>
<tr>
<th>Stock Name</th>
<th>Stock Type</th>
<th>Organism</th>
<th>Synonyms</th>
<th>Owners</th>
<th>organization</th>
<th>pedigree</th>
</tr>
</thead>
<tbody>
<tr>
<td>NDSU-12</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>North Dakota State University</td>
<td>11M225-123-2 = RWG10 (PhB1)/JERRY</td>
<td></td>
</tr>
<tr>
<td>CA9W07-817</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>Falcon/Jerry</td>
<td></td>
</tr>
<tr>
<td>CA9W08-856</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>Jerry/CDC Falcon</td>
<td></td>
</tr>
<tr>
<td>NDSU-11</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>North Dakota State University</td>
<td>11M225-123-2 = RWG10 (PhB1)/JERRY</td>
<td></td>
</tr>
<tr>
<td>15NORD-25</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>CM2036/Jerry</td>
<td></td>
</tr>
<tr>
<td>CA9W07-818</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>Jerry/Falcon</td>
<td></td>
</tr>
<tr>
<td>NDSU-10</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>North Dakota State University</td>
<td>11M225-123-1 = RWG10 (PhB1)/JERRY</td>
<td></td>
</tr>
<tr>
<td>CA9W07-819</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>Jerry/Falcon</td>
<td></td>
</tr>
<tr>
<td>15NORD-58</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>S077W083-Jerry</td>
<td></td>
</tr>
<tr>
<td>15NORD-32</td>
<td>accession</td>
<td>Tritium</td>
<td></td>
<td>USDA-ARS</td>
<td>RWG10/Jerry</td>
<td></td>
</tr>
</tbody>
</table>

Showing 1 to 10 of 19 entries
Using Lists

• Lists are used throughout various parts of Breedbase:
  - List of Accessions are required for creating a trial
  - List of Traits are required for creating a phenotyping spreadsheet
  - Lists can be used in the Search Wizard

• Lists can be generated in many ways:
  - From the Search Wizard
  - From a Search Result table
  - Manually through the List Manager

• Lists can be made public and shared
Using Lists

Create a List - Search Wizard:

Lists can be created directly from the Search Wizard.

Any selected items of any data type can be added to an existing or new List.
Create a List – Search Results:

Lists can be created from most tables (such as search results)

Look for the “Copy Results to a List” section

NOTE: Only the visible items will be added to the list (ie, items on other pages will NOT be added)
Using Lists

Manage Your Lists:

Lists can be created manually, by entering the names of the items.

To manage your Lists, click the “Lists” button from the top right corner of any page.
Using Lists

Create a List – Manually:

Enter the List name and description (optional)

Click the “New List” button to create the List

Click the List Name to edit the List contents
Modify a List (Add Items):

Select the List type

Enter the names of the list items (one item per line)
- The names must match existing items in the database

Click the “Add” button to add the items to the List
Using Lists

Validate the List:

Validating the List ensures all of the List items are valid entries for the specified List Type

Click the “Validate” button under the “Type” section
Using Lists

List Usage – Search Wizard:

Lists can be used as selections in the search wizard.
List Usage – Trial Design:

Lists of Accessions are used to specify the entries and checks used in a phenotyping Trial.
Trial Design

• A Trial must be created before any phenotyping data can be added

• A Trial contains metadata about itself:
  - Trial Name (must be unique)
  - Breeding Program (must already exist)
  - Location (must already exist)
  - Trial Type (phenotyping, greenhouse, Preliminary Yield Trial, Advanced…)
  - Year
  - Plot Dimensions
  - Field Size
  - Description
  - Design Type (Randomized, RCBD, Incomplete Block, Augmented, …)
Trial Design

- A Trial contains information about the physical plot layout

- Each plot has information about itself:
  - Block
  - Rep
  - Row & Column
  - Accession
  - Observations

- The plots can be created:
  - Using the Trial Design wizard
  - Uploading a plot layout template
Before you design a new Trial, make sure you have the following:

- **Breeding Program**
  - Each Trial is associated with a single Breeding Program
  - If your Breeding Program doesn’t exist it will have to be added first

- **Location**
  - Each Trial is assigned to a single location
  - Each Location is associated with one or more Breeding Programs
  - The Location of your Trial needs to exist AND be associated with your Breeding Program

- **Lists of Accessions** for entries (required) and checks (optional)
Manage Field Trials:
Select “Field Trials” from the Manage menu
Create a Trial:

- **Upload Existing Trial**
  - You create and upload a template defining the plot layout

- **Design New Trial**
  - The Trial Design Wizard defines the plot layout
Design New Trial:

Click the “Design New Trial” button from the Manage Trials page

Fill out the basic information about the Trial: location, plot dimensions, design type, etc...

Validate the form

Continue
Design New Trial:

Select the Lists of entries and checks

Enter the number of blocks

Continue
Design New Trial:

Enter the number of rows (needs to be a number that gives rows with an equal number of plots)

Choose plot layout format

Serpentine:
1  2  3
6  5  4
7  8  9

ZigZag:
1  2  3
4  5  6
7  8  9
Design New Trial:

Each block is a rep

Randomly assigns entries to plots within each block / rep

Dark blue plots are checks
Design New Trial:

- Redo Randomization:
  - Will reshuffle the plot assignments with the same parameters

- Confirm
  - Will save the Trial to the database
Trial Design

Design New Trial:

An empty trial now exists

Trial Details can be modified

Field layout can be modified

Phenotype observations can be added
Once the Trial has been added to the database:

- A “phenotyping spreadsheet” can be created for the trial
  - Specific to an individual trial
  - Contains a column for each selected trait

- Observations are added to the phenotyping spreadsheet

- The phenotyping spreadsheet is uploaded for the trial
Phenotype Upload

Open the Trial Detail page:

• Search > Field Trials
  - Filter by name in the Search box
  - Click Trial name

• Manage > Field Trials
  - Expand Breeding Program
  - Double click Trial name

• Search > Wizard
  - Include any filters before Trials
  - Filter by Trial
  - Click Trial name
Create Phenotyping Spreadsheet:

From the Trial Detail page:

- Find the “Upload Data Files” section
- Find the “Data Collection Files” subsection
- Next to “Phenotyping Spreadsheets” click the “Create Spreadsheet” button
Phenotype Upload

Create Phenotyping Spreadsheet:

Select the list of Traits that will be observed in this Trial

Optionally include a column for plot-level notes

Spreadsheet Format:

- **Simple**: includes a plot name column and a column for each trait
- **Detailed**: includes more trial and plot-level information
### Populate Phenotyping Spreadsheet: Simple Format

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td>observationunit_name</td>
<td>Grain test weight g/l</td>
<td>CO_321:00001210</td>
<td>Grain yield kg/ha</td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD12DHA01373_1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD10066_2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD10135_3</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD12DHA03614_4</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD12DHA01556_5</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD12DHA01364_6</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD13052_1_7</td>
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<tr>
<td>TEST_TRIAL-rep1-SD110060_7_8</td>
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<td>TEST_TRIAL-rep1-SD12DHA01328_9</td>
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<tr>
<td>TEST_TRIAL-rep1-SD110038_3_10</td>
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<tr>
<td>TEST_TRIAL-rep1-SD12DHA01024_11</td>
<td></td>
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</tr>
<tr>
<td>TEST_TRIAL-rep1-SD3062_2_12</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD110044_7_13</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>TEST_TRIAL-rep1-SD12008_2_14</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>TEST_TRIAL-rep1-SD10257_2_15</td>
<td></td>
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</tr>
<tr>
<td>TEST_TRIAL-rep1-SD13090_7_16</td>
<td></td>
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</tr>
</tbody>
</table>

**Plot name:** includes trial name, rep number, accession name and plot number

- Enter test weight here
- Enter grain yield here
### Phenotype Upload

#### Populate Phenotyping Spreadsheet: Detailed Format

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
<th>H</th>
<th>I</th>
<th>J</th>
<th>K</th>
<th>L</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Spreadsheet ID</td>
<td>ID3081575492609</td>
<td>Spreadsheet to BasicExcel</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Trial name(s)</td>
<td>TEST_TRIAL</td>
<td>Operator</td>
<td>Enter operator here</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>3</td>
<td>Description(s)</td>
<td>TEST_TRIAL: This is Date</td>
<td>Enter date here</td>
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</tr>
<tr>
<td>4</td>
<td>Trial location(s)</td>
<td>TEST_TRIAL: Ithaca</td>
<td>Design Type(s)</td>
<td>TEST_TRIAL: RCBD</td>
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<td>Predefined Columns</td>
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<td>accession_name</td>
<td>plot_number</td>
<td>block_number</td>
<td>trial_name</td>
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- **Accession Name**
- **Plot Number**
- **Enter test weight here**
- **Enter grain yield here**
Phenotype Upload

Upload Phenotyping Spreadsheet:

From the Trial Detail page:

- Find the “Upload Data Files” section
- Find the “Data Collection Files” subsection
- Next to “Phenotyping Spreadsheets” click the “Upload” button
Phenotype Upload

Upload Phenotyping Spreadsheet:

Select the format of the phenotyping spreadsheet

Choose your phenotyping spreadsheet

Verify the file

Store the observations
Phenotype Upload

After Upload:

Phenotype summary available on the Trial Detail Page

Includes mean, ranges, histograms of each trait
Phenotype Upload

https://wheat.triticeaetoolbox.org/help/phenotype_upload_workflow

Upload Workflow and Instructions:

General steps for uploading data for a phenotyping trial

- Check prerequisites
- Create the Trial
- Create the phenotyping spreadsheet
- Upload the phenotyping spreadsheet
Select “Summarize Trials” from the “Analyze” Menu

https://wheat.triticeaetoolbox.org/tools/trial/summary/list
Select a List that contains 2 or more Trials
Trial Summary Tool

Select 1 or more traits to summarize

Note: Only traits that have been observed in all of the Trials will be shown

Select the Traits to summarize
Trial Summary Tool

Trial Summary Tool Output:

A table with LS Means for each Trait across all Trials

A table summarizing each Trait
Future Work

• Organizing Phenotyping Trials
  - Within Breeding Programs
  - Breeding Programs can contain folders for separate experiments
  - Create Breeding Programs for Cooperative Nurseries?

• Adding Tools / Report Pages from T3/Classic
  - Which ones are most useful?
  - Genomic Selection tool?
Get In Touch:

Email: djw64@cornell.edu

Website: https://wheat.triticeaetoolbox.org/contact/form

What tools do you want to see in the New T3?

How can we make it easier to submit data?
Acknowledgements

The Triticeae Toolbox
Jean-Luc Jannink
Clay Birkett
David Waring

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