

The Triticeae Toolbox Tutorial

Lesson Two. How to submit phenotype experimental data

This tutorial will guide a curator/user to create the files to upload phenotype experiment annotation and data onto T3.

Updated December 2012. Any [feedback](#) is welcome!

Sections

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2. [Complete the Annotation Form](#)
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6. [Submit Data to the Production T3](#)

Section One. Download the Template Files

Point your browser to the T3 Participants page at a wheat or barley sandbox or production database. For example, http://malt.pw.usda.gov/t3/barley/curator_data/instructions.php

Figure 1. Participant's page.

The screenshot shows the Triticeae Toolbox website interface. At the top, there is a navigation bar with buttons for Home, Select, Analyze, Download, and About T3. A 'Contact Us' link is visible in the top right corner. The main content area is titled 'Data Submission' and contains the following information:

- Quick Links:** Login/Register
- Current selections:** Lines: 0, Markers: All, Traits: 0, Trials: 0
- Quick search...** (input field)
- What's New:** A list of recent updates including 'Winterhardiness, F3 Lines from LTT GS Cycle 1, St. Paul, MN', 'Faculty Winter 6-row, NUE High N, Corvallis, OR', '2006, Fort Collins, CO LTT', '2006, Pendleton, OR LTT', '2009, St. Paul, MN LTT', '2011, St. Paul, MN LTT', '2012, Minn. SC3, FHB VC', '2011, Minn. SC2, FHB VC', and '2011, Minn. SC1, FHB VC'.
- Data Submission:** A section explaining that data templates are .csv, .txt, or Excel worksheets. It lists several templates and their purposes:
 - Instructions:** [Steps_in_Data_Submission_to_T3.docx](#) - Rules for filling in the templates, and sequence of submission
 - Data templates:**
 - Germplasm lines** - Name, properties, pedigree, GRIN accession... [[Tutorial T3_Lesson1_LineUpload.html](#)]
 - Wheat [LineSubmissionForm_Wheat.xls](#)
 - Barley [LineSubmissionForm_Barley.xls](#)
 - Macros [T3NameConversion.xlsm](#) for converting line names to T3 format
 - Phenotyping...** [[Tutorial T3_Lesson2_Phenotype.html](#)]
 - Experiment annotation ([new 04Dec2012](#)) [TrialSubmissionForm.xls](#) - Location, planting date, experimental design...
 - Experiment results [PhenotypeSubmissionForm.xls](#) - Values for all traits for test lines and checks, summary statistics
 - [Traits trait_template.xls](#) - Only necessary for new traits. Please discuss with the [curators](#) before adding a new trait.
 - Genotyping ...** [[Tutorial T3_Lesson3_GenotypeUpload.html](#)]
 - Experiment annotation [Geno_Annotation_Sample.txt](#) - Description of the assay
 - Line translation [LinesTrialCode_Sample.txt](#) - Line Name and Trial Code
 - Experiment results [TCAPbarley9K-sample.txt](#) - 2D table of alleles for lines and markers
 - Experiment results [genotypeData_T3.txt](#) - 1D version
 - Markers**
 - Sequence [Generic_SNP.txt](#)
 - Map location [mapupload_example.txt](#)
 - Gene function [Marker_import_sample4.txt](#) - Annotations and synonyms

Once filled in, the resulting Excel files are to be uploaded directly into the T3 software. Some values are checked for validity, most are not. Some seemingly optional rows at the top aren't. To make updates or corrections, edit your file and load it again.

The Sandbox databases, [wheat](#) and [barley](#), are available for test-loading your data files. Once they're ready, click below to submit them officially.

Save and Open the Experiment Annotation Form (Figure 2) and Phenotype Data Form (Figure 3).

Figure 2. Phenotype experiment annotation form

The screenshot shows the PhenotypeSubmissionForm Excel spreadsheet. The main data area is a table with the following structure:

*Line Name	*Check	Filial Gen (0-9)	Seed Stock Year	Seed Stock Experiment	Seed Stock ID	grain yield	plant height
*Trial Mean						4519	74
*Std. Error						549.19	3.4
*Replications						2	2
Trial information goes above this row. Line and check mean information goes below this row							
FE6195-04		0				4869	78
HARRINGTON		1				5262	68

Notes on the right side of the spreadsheet:

- Columns and rows with an asterisk are REQUIRED INFORMATION.** At least one phenotype column and one line row are required. All lines must also have been submitted to T3 via the Line submission form.
- Crop:** Barley or Wheat
- Breeding Program Code:** See 'Search by Breeding Program' on the T3 homepage.
- Trial Code:** Phenotypes come from a single trial. Information about the trial must have been previously submitted to T3 using the Trial Submission Form and assigned a Trial Code (Experiment_YYYY_Location).
- Trait names** in the green cells of row 5 must be the names of Allowed Traits with uniform protocols vetted by TCAP. See 'Trait Descriptions' under the 'About T3' menu, or click on a trait from the 'Search by Trait' dropdown menu on the homepage for a complete description and links to previous experiments. Add as many columns as necessary to accommodate your data. The summary statistics in rows 6 - 8 are for the trial as a whole.
- Trial Mean.** The exact definition of the trial mean is not critical. For example, whether this mean includes the checks or not will not be very important. Therefore submit a trial mean that gives a general sense of the value for that trial, whether it includes checks or not or is weighted or not by replication number.
- Standard Error.** In the case of an augmented design where experimental lines are unreplicated but there are replicated checks, the checks are used to estimate the error variance. The standard error for the experimental lines is then the square root of the error variance. In the case of experiments where experimental lines are replicated, the standard error should be $\sqrt{\text{error_var} / \text{num_rep}}$.
- Replications.** This value refers to the number of individual reps on which a particular trait was measured for normal entries (not checks: if there are repeated checks, checks may have more replications than normal entries).
- Line Name.** T3 will accept any previously submitted primary line name or alias.

Figure 3. Phenotype data form

The screenshot shows the TrialSubmissionForm Excel spreadsheet. The main data area is a table with the following structure:

TRIAL #1	TRIAL #2
PYT2_2009_StPaul	PYT6_2009_StPaul
2009	2009
CAP-2	CAP-6
St Paul, MN	Aberdeen, ID
47.824	47.824
96.616	96.616
Kevin Smith	Kevin Smith
2-Row CAP Lines	6-Row CAP Lines
5/11/2009	5/12/2009
8/9/2009	8/10/2009
no	no
200	200
RCBD	RCBD
50	50
3	3
6.5	6.5
4.6	4.6
yes	yes
Spring was cool and wet	Spring was cool and wet.

Notes on the right side of the spreadsheet:

- Cells with blue background are required, others optional.
- Crop.** barley or wheat
- Breeding Program Code.** Program responsible for data collection (barley: 2-letter code; wheat: 3-letter code) Find codes at the T3 Homepage 'About T3' menu, 'CAP programs'.
- Trial Name.** Format: "Experiment_YYYY_Location", where Experiment is short but descriptive, YYYY=Trials Year. Trial Names should be unique across T3 for a crop. A trial is carried out at one location in one year.
- Trial Year.** Year in which the trial was or would have been harvested.
- Experiment Name.** Optional. The experiment is one hierarchical level above the trial. An experiment may have several trials with similar or identical entry lists, performed at different locations and/or different years. Experiment Name should be short and unique across T3 for a crop.
- Location.** Format: "<city/town>, <state/province/country abbreviation>".
- Lat/Long of field.** Decimal Degrees format, without a degree symbol. There is a converter at <http://boulter.com/gps/>. GPS coordinates can be found by address at <http://itouchmap.com/latlong.html>.
- Collaborator.** Name of principal scientist.
- Experiment description.** Optional. Agreed upon for TCAP-funded experiments, self-assigned otherwise. Limit 300 characters.
- Planting date.** This should be the one date on which planting was begun. Use Excel "Text", not "Date", format. The value should be given as m/d/yyyy with no leading zeros, e.g. "5/7/2012".
- Harvest date.** Use Text format. If the trial was not harvested, use the date of last data collection.
- Begin weather date.** Optional, if T3 should store weather data starting at some point before planting (e.g., to track soil moisture status).
- Seeding rate (seeds/m2).** This is the target density for the trial, not the actual rate for each line.
- Experimental design.** Description of the design.
- Number of entries.** Include the checks in this number.
- Number of replications.** Number of individual reps on which each trait was measured for test entries, not checks.
- Plot size, Harvested area:** Not required for greenhouse trials.
- Other remarks.** Optional. Adjustments to means in data analysis or other specifics of statistical analysis. Other notes that may help in interpretation of results, for example

Section Two. Complete the Annotation Form

Figure 4 is an example of a completed Phenotype Experiment Annotation Form for a 2006 and 2007 evaluation for the barley National Small Grains Collection (NSGC) in Montana.

Breeding program codes, two-letter (barley) or three-letter (wheat) acronyms, can be found on the 'About T3 -- CAP data programs' dropdown menu on the T3 homepage.

The note box on the template spreadsheet details the information required and the preferred format. More than one trial can be detailed on one form as long as the 'trial code' names are unique. Highlighted cells are required.

Important! Be sure you are using the most up-to-date template. As of the update of this tutorial, the current version reads 4Dec12 in cell B2.

Figure 4. Completed phenotype experiment annotation form

	A	B	C	D
1	Trial Submission Form			
2	Template version	9Jul12		
3	Crop	barley		
4	Breeding Program Code	NB		
5		TRIAL #1	TRIAL #2	TRIAL #3
6	Trial Name	NSGCcore_2006_BozemanDry	NSGCcore_2007_BozemanIrr	NSGCcore_2007_BozemanDry
7	Trial Year	2006	2007	2007
8	Experiment Name	NSGC core pre-CAP Montana	NSGC core pre-CAP Montana	NSGC core pre-CAP Montana
9	Location	Bozeman, MT	Bozeman, MT	Bozeman, MT
10	Latitude of field	45.675	45.675	45.675
11	Longitude of field	-111.127	-111.127	-111.127
12	Collaborator	Tom Blake	Tom Blake	Tom Blake
13	Trial description	Spring Barley Core Collection agronomic data	Spring Barley Core Collection agronomic data	Spring Barley Core Collection agronomic data
14	Planting date	5/4/2006	5/8/2007	5/7/2007
15	Harvest date	9/10/2006	9/8/2007	9/7/2007
16	Begin weather date			
17	Greenhouse trial? (yes or no)	no	no	no
18	Seeding rate (seeds/m ²)	approx. 200plants/m ²	approx. 200plants/m ²	approx. 200plants/m ²
19	Experimental design	non replicated	non replicated	non replicated
20	Number of entries	1917	1917	1917
21	Number of replications	1	1	1
22	Plot size (m ²)	6	6	6
23	Harvested area (m ²)	6	6	6
24	Irrigation (yes or no)	no	yes	no
25	Other remarks			
26				

Section Three. Complete the Data Form

Headers: Complete cells B2-B4 on the Data Form header.

B2 - Crop. wheat or barley

B3, B4 - Breeding Program Code and Trial Code (Trial Name) must match the annotation file (Fig. 4).

Edit the column headers (green background) for the traits measured in your trial.

Specific trait names can be found on the 'About T3 -- Trait Descriptions' dropdown menu, or the 'Search by Trait' list on the T3 homepage.

Column headers must match the trait descriptions exactly.

Data: Provide the trial mean, standard error and replication number in the cells above the gray bar for each trait and line information and data below the gray bar as shown.

Only line name and check (0=no, 1=yes) are required in each row.

Figure 5. Data from a 2006 agronomic evaluation of the barley NSGC core in Bozeman, MT

	A	B	C	D	E	F	G	H
1	Phenotype Experiment Results							
2	*Crop	barley						
3	*Breeding Program Code	NB						
4	*Trial Code	NSGCcore_2006_BozemanDry						
5	*Line Name	*Check	Filial Gen (0-9)	Seed Stock Year	Seed Stock Experiment	Seed Stock ID	heading date (Julian)	plant height
6	*Trial Mean						186.55	79.46
7	*Std. Error						0.07	0.44
8	*Replications						1	1
9	Trial information goes above this row. Line and check mean information goes below this row.							
10	PI8809	0	9	2005	NSGC core stock	PI8809		36.00
11	PI5846	0	9	2005	NSGC core stock	PI5846	182.00	92.00
12	PI5873	0	9	2005	NSGC core stock	PI5873	181.00	101.00
13	CIho424	0	9	2005	NSGC core stock	CIho424	182.00	81.00
14	CIho455	0	9	2005	NSGC core stock	CIho455	183.00	78.00
15	CIho497	0	9	2005	NSGC core stock	CIho497	193.00	77.00
16	CIho521	0	9	2005	NSGC core stock	CIho521	181.00	90.00
17	PI19894	0	9	2005	NSGC core stock	PI19894		59.00
18	PI20909	0	9	2005	NSGC core stock	PI20909	182.00	93.00
19	PI26179	0	9	2005	NSGC core stock	PI26179		84.00
20	PI28624	0	9	2005	NSGC core stock	PI28624	181.00	84.00
21	PI29004	0	9	2005	NSGC core stock	PI29004	184.00	76.00
22	PI30842	0	9	2005	NSGC core stock	PI30842	183.00	80.00
23	PI34314	0	9	2005	NSGC core stock	PI34314		81.00
24	PI34424	0	9	2005	NSGC core stock	PI34424	184.00	85.00
25	PI37707	0	9	2005	NSGC core stock	PI37707	184.00	87.00
26	PI5975	0	9	2005	NSGC core stock	PI5975	185.00	89.00

Section Four. Upload Trial Annotations.

Phenotype-related files must be loaded sequentially. Log on as a Curator/User at the **SANDBOX** version of your preferred T3. (Fig. 6 and Fig. 7)

- Wheat User Sandbox : malt.pw.usda.gov/t3/sandbox/wheat
- Barley User Sandbox : malt.pw.usda.gov/t3/sandbox/barley

Figure 6. Barley Sandbox homepage with login link highlighted

The Triticeae Sandbox

Home Select Analyze Download About T3

Quick Links
[Login/Register](#)
 Current selections:
 Lines: 0
 Markers: All
 Traits: 0
 Trials: 0

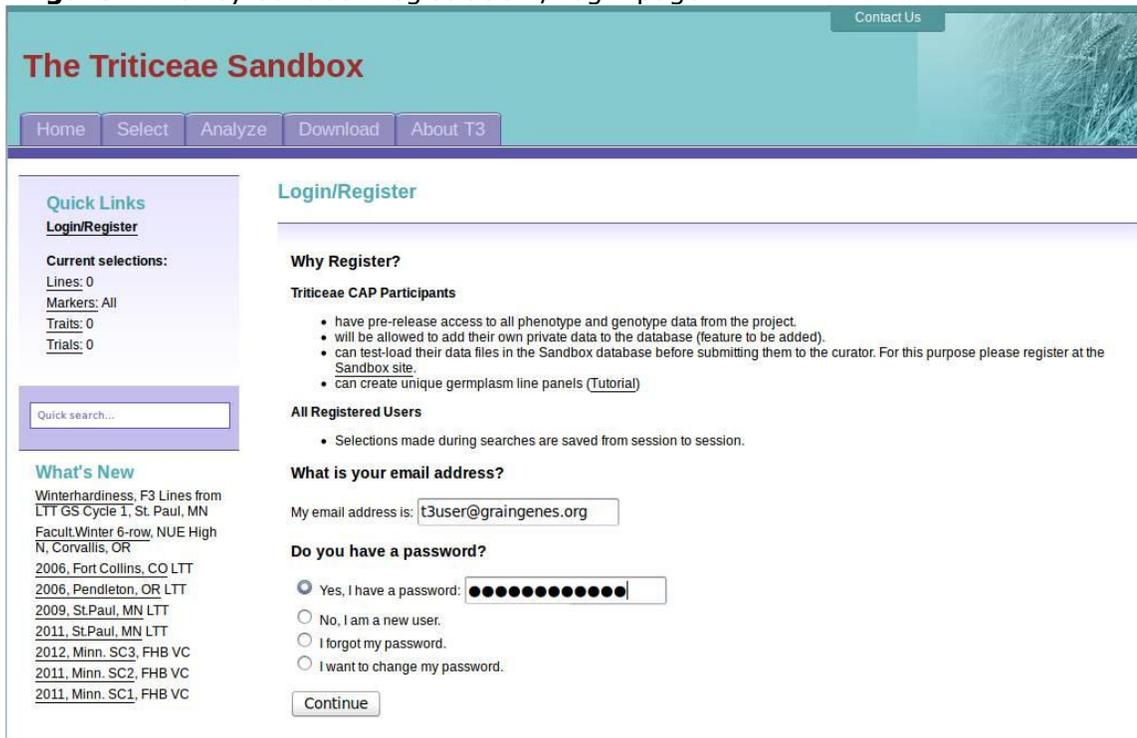
Home: T3 Barley Sandbox

This version of T3 is for hands-on learning, practice, and data experiments.

Anyone can load data here as long as they have registered, and anyone can register. Note that you must register again here even if you've done it already on any other T3 website.

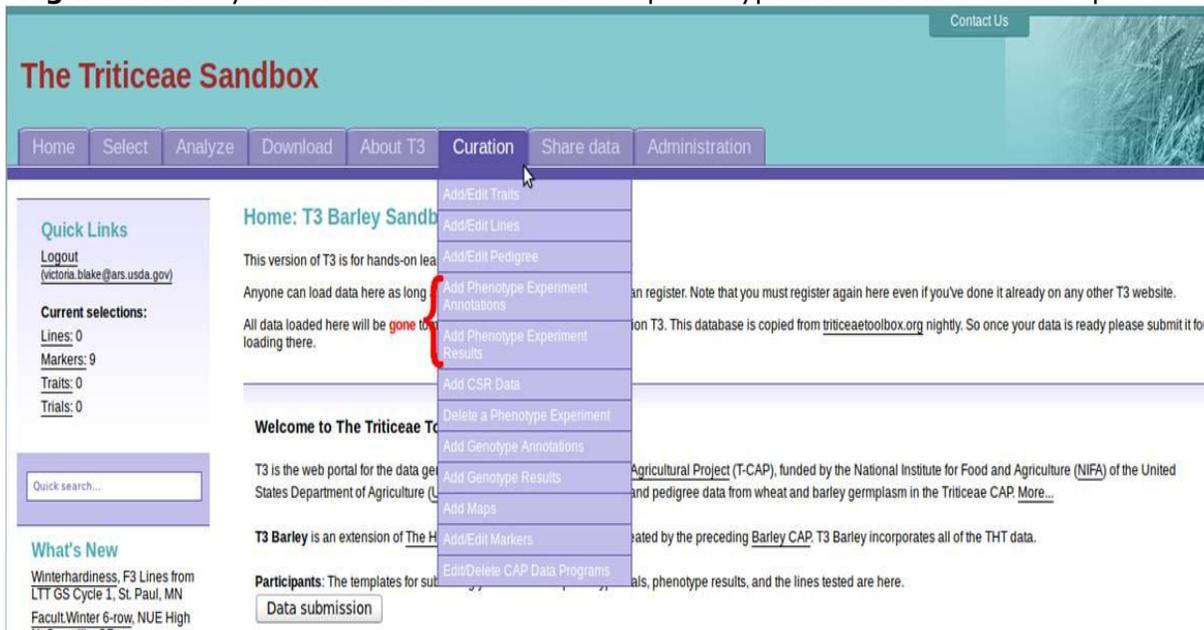
All data loaded here will be **gone** tomorrow, unless loaded into the production T3. This database is copied from triticaeatoolbox.org nightly. So once your data is ready please submit it for loading there.

Figure 7. Barley Sandbox registration / login page



Once logged in, note that new tabs are now available on the top menu bar. Data upload tools are found under Curation menu tab (Fig. 8)

Figure 8. Barley Sandbox curation menu with phenotype annotation and data upload links highlighted



Select 'Add Phenotype Experiment Annotations' from the Curation dropdown menu. Select Upload an Excel file from the menu.

Figure 9. Phenotype trial annotation upload and editing gateway.

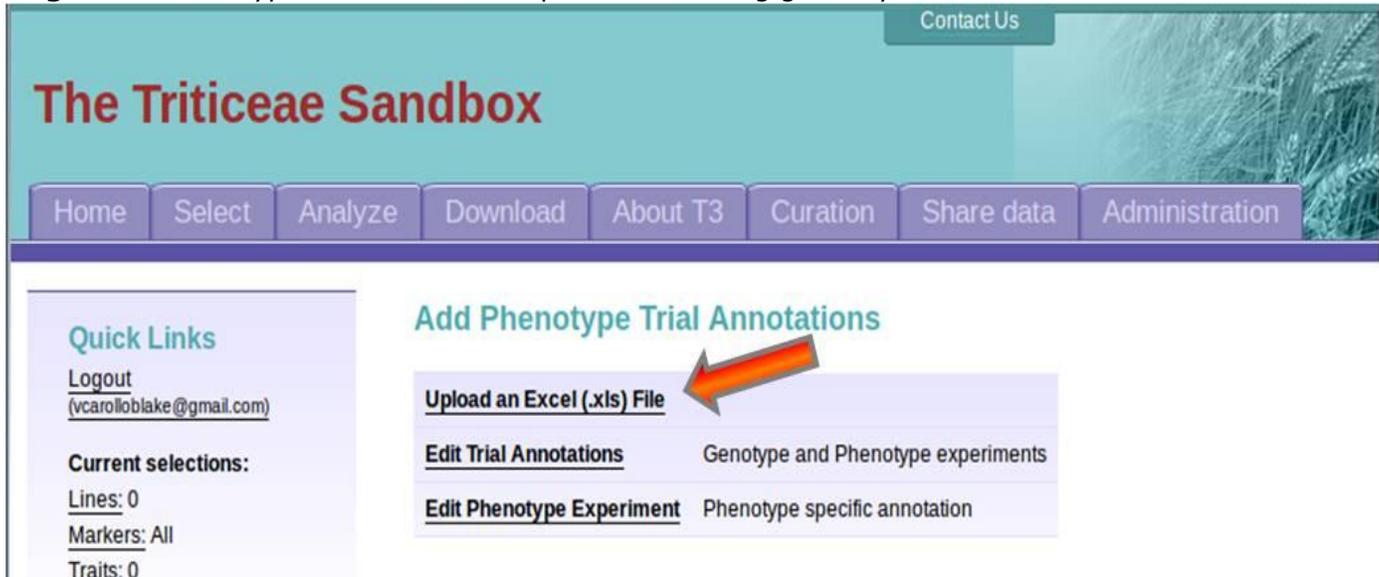
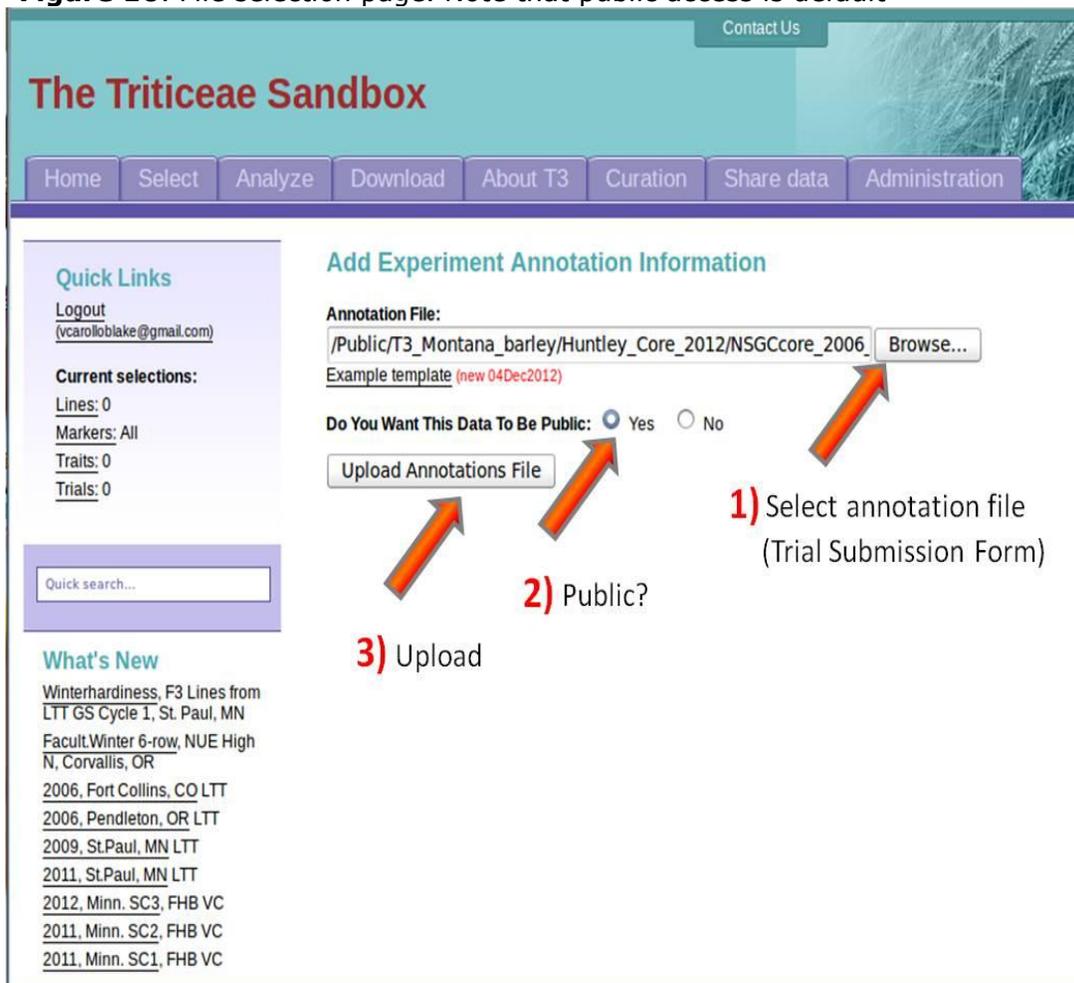


Figure 10. File selection page. Note that public access is default



If the data is properly loaded, a validation table will be created for the submitter to review. (Fig. 11) Click "Accept" to load the data as it appears on the validation table onto T3. Alternatively, if you find an error, the "Cancel" cell will cancel the process.

Figure 11. Data validation page

The Triticeae Sandbox

Home Select Analyze Download About T3 Curation Share data Administration

Quick Links
Logout (vcaroloblake@gmail.com)
Current selections:
Lines: 0
Markers: All
Traits: 0
Trials: 0

Quick search...

What's New
Winterhardiness, F3 Lines from LTT GS Cycle 1, St. Paul, MN
Facult.Winter 6-row, NUE High N, Corvallis, OR
2006, Fort Collins, CO LTT
2006, Pendleton, OR LTT
2009, St.Paul, MN LTT
2011, St.Paul, MN LTT
2012, Minn. SC3, FHB VC
2011, Minn. SC2, FHB VC
2011, Minn. SC1, FHB VC

Add/Update Experiment Annotations: Validation
User's submitted template version: 4Dec12
Current version: 4Dec12

The following data were found in the uploaded file.

Status	Trial Name	Experiment	Breeding Program	Collaborator	Location	Latitude	Longitude	Planting date	Harvest date
New	NSGCcore_2006_BozemanDry	NSGC core pre-CAP Montana	NB	Tom Blake	Bozeman, MT	45.675	-111.127	5/4/2006	9/10/2006
New	NSGCcore_2007_Bozemanlrr	NSGC core pre-CAP Montana	NB	Tom Blake	Bozeman, MT	45.675	-111.127	5/8/2007	9/8/2007
New	NSGCcore_2007_BozemanDry	NSGC core pre-CAP Montana	NB	Tom Blake	Bozeman, MT	45.675	-111.127	5/7/2007	9/7/2007

If Status is "Update", this Trial has been loaded previously and the values shown will replace the existing ones.

Accept Cancel

If the experiment annotation data is loaded onto the database with no internal software errors, a message is generated to assure the user.

Figure 12. Successful Upload message

The Triticeae Sandbox

Home Select Analyze Download About T3 Curation Share data Administration

Quick Links
Logout (vcaroloblake@gmail.com)
Current selections:
Lines: 0
Markers: All
Trials: 0

New entry added for NSGCcore_2006_BozemanDry to **experiments** table.
New entry added for NSGCcore_2006_BozemanDry to **phenotype_experiment_info** table.
New entry added for NSGCcore_2007_Bozemanlrr to **experiments** table.
New entry added for NSGCcore_2007_Bozemanlrr to **phenotype_experiment_info** table.
New entry added for NSGCcore_2007_BozemanDry to **experiments** table.
New entry added for NSGCcore_2007_BozemanDry to **phenotype_experiment_info** table.
Data inserted or updated successfully.

[View](#)

Section Five. Upload Trial Data.

Next, upload the results data.

Select 'Add Phenotype Experiment Results' from the Curation dropdown menu (see Fig. 8).

On the phenotype results upload gateway (Fig. 13), "Browse" to select the Means data file (i.e. Phenotype Submission Form, Fig. 5)

Although the Sandbox will accept it, the raw data should be sent to the T3 curator for archiving without further processing.

Figure 13. Phenotype trial results upload gateway.

The Triticeae Sandbox [Contact Us](#)

Home Select Analyze Download About T3 Curation Share data Administration

Quick Links
[Logout](#)
(vcarolloblake@gmail.com)

Current selections:
Lines: 0
Markers: All
Traits: 0
Trials: 0

Quick search...

What's New
[Winterhardness, F3 Lines from LTT GS Cycle 1, St. Paul, MN](#)
[Facult.Winter 6-row, NUE High N, Corvallis, OR](#)
[2006, Fort Collins, CO LTT](#)
[2006, Pendleton, OR LTT](#)
[2009, St.Paul, MN LTT](#)
[2011, St.Paul, MN LTT](#)
[2012, Minn. SC3, FHB VC](#)
[2011, Minn. SC2, FHB VC](#)
[2011, Minn. SC1, FHB VC](#)

Add Phenotype Experiment Results

Here you can load the results of a single field or greenhouse Trial. The Annotation describing the conditions of the Trial must already have been loaded. Please see the [tutorial](#) for step by step instructions.

Add a Means File

The Means file contains, for each trait, one value for each line in the Trial: the mean over all plots for that line.

Means file: [Browse...](#)

[Example Means file](#)
[Upload](#)

Add Raw Files **2) Upload**

One or more files of additional information maybe be attached to each Trial. The files are archived for downloading but their contents are not loaded into the database.

Trial [Go](#)

or choose from below...

1) Select data file
(Phenotype Submission Form)

3) Send raw data to the curator,
not necessary for the Sandbox

Successfully uploaded phenotype trial data will be tabulated and presented for validation. (Fig. 14)
Double check your data, and if you find no errors, click the 'Accept' button to load into the database.

Figure 14. Phenotype trial data pre-upload validation table.

The Triticeae Sandbox

Home Select Analyze Download About T3 Curation Share data Administration

Phenotype Data Validation

We are reading the following data from the uploaded data file.

*Line Name	*Check	Filial Gen (0-9)	Seed Stock Year	Seed Stock Experiment	Seed Stock ID	grain yield	plant height	heading date	test weight	breeders plump grain	breeders grain protein
*Trial Mean						55.426358837209	70.043411821705	189.77130395349	46.88914803876	70.677518449612	15.046125271318
*Std. Error						1.0173968590824	0.65697920455253	0.50303772311125	0.31656057239457	1.830205847273	0.15800504665939
*Replications						1	1	1	1	1	1
Trial information goes above this row. Line and check mean information goes below this row.											
06WA-42	999		2010	MN CAP	06WA-42	45.1006	75.9936	178.5361	49.9322	83.6655	14.9567
06WA-57	999		2010	MN CAP	06WA-57	72.5816	78.8799	182.1868	51.0656	101.1711	14.5689
06WA-25	999		2010	MN CAP	06WA-25	40.398	60.0316	196.2813	45.0206	57.8663	16.3139
06WA-53	999		2010	MN CAP	06WA-53	64.352	74.8521	192.0453	41.2425	38.6219	15.3445
06WA-63	999		2010	MN CAP	06WA-63	87.2773	62.9179	194.017	46.3429	61.8227	17.2833
06WA-93	999		2010	MN CAP	06WA-93	62.7355	55.1088	196.2813	47.6653	72.1579	15.3445
06WA-38	999		2010	MN CAP	06WA-38	67.1442	74.8521	190.07363	49.5543	100.2431	15.3445
06WA-29	999		2010	MN CAP	06WA-29	25.1144	59.5841	198.253	40.4868	56.0102	15.15058
09AB-62	999		2010	MN CAP	09AB-62	62.8824	85.2946	184.1585	44.265	65.3492	14.9567

Accept Cancel

Figure 15. A successful phenotype data upload!

The Triticeae Sandbox

Home Select Analyze Download About T3 Curation Share data Administration

Quick Links

Logout (vcaroloblake@gmail.com)

Current selections:

Lines: 0
Markers: All
Traits: 0
Trials: 0

The data was inserted/updated successfully.
[View](#)
[Go Back To Main Page](#)

Section Six. Submit Your Data to the Production T3 Database.

Return to the Participant's Page (Fig. 16) and click the 'Submit' button. Complete the file information page (Fig. 17). A message will confirm that the curators are notified (Fig. 18).

Please feel free to contact the curators directly at tht_curator@graingenes.org.

Figure 16. Participant's Page with "Submit" button highlighted

The screenshot shows the 'The Triticeae Sandbox' website. At the top, there is a navigation bar with buttons for 'Home', 'Select', 'Analyze', 'Download', and 'About T3', and a 'Contact Us' button. The main content area is titled 'Data Submission' and contains the following text and links:

The data templates are .csv, .txt or Excel worksheets with column headers for the data T3 can accept or requires, some example values to be replaced with yours, and notes about the restrictions for valid data are included.

- **Instructions** - Rules for filling in the templates, and sequence of submission
- **Data templates**
 - **Germplasm lines** - Name, properties, pedigree, GRIN accession... [[Tutorial](#)]
 - [Wheat](#)
 - [Barley](#)
 - [Macros](#) for converting line names to T3 format
 - **Phenotyping**
 - [Experiment annotation \(new 04Dec2012\)](#) - Location, planting date, experimental design... [[Tutorial](#)]
 - [Experiment results](#) - Values for all traits for test lines and checks, summary statistics
 - [Traits](#) - Within T-CAP the traits, protocols and units will be specified by the project.
 - **Genotyping** ... [[Tutorial](#)]
 - [Experiment annotation](#) - Description of the assay
 - [Line translation](#) - Line Name and Trial Code
 - [Experiment results](#) - 1D table of alleles for lines and markers
 - [Experiment results](#) - 2D table of alleles for lines and markers
 - **Markers**
 - [Sequence](#)
 - [Map location](#)
 - [Gene function](#) - Annotations and synonyms

Once filled in, the resulting Excel files are to be uploaded directly into the T3 software. Some values are checked for validity, most are not. Some seemingly optional rows at the top aren't. Errors in data you've already loaded in T3 can usually be corrected by editing your file and loading it again.

The Sandbox databases, [wheat](#) and [barley](#), are available for test-loading your data files. Once they're ready, click below to submit them officially.

[Submit](#)

A red arrow points to the 'Submit' button.

Figure 17. Data Submission information page

Quick Links
Logout
(victoria.blake@ars.usda.gov)

Current selections:
Lines: 0
Markers: 9
Traits: 0
Trials: 0

Quick search...

What's New
Winterhardness, F3 Lines from LTT GS Cycle 1, St. Paul, MN
Facult.Winter 6-row, NUE High N, Corvallis, OR
2006, Fort Collins, CO LTT
2006, Pendleton, OR LTT
2009, St.Paul, MN LTT
2011, St.Paul, MN LTT
2012, Minn. SC3, FHB VC
2011, Minn. SC2, FHB VC
2011, Minn. SC1, FHB VC

Data Submission

Please submit a data file for the curator to load into the production database.

Data Type

- Germplasm lines
- Phenotyping
 - Experiment annotation
 - Results
- Genotyping
 - Experiment annotation
 - Results

Comments

Data for 2006 NSGC agronomic trials in Bozeman, MT

This file loads successfully in the Sandbox. Yes No

File: /Public/T3_Montana_barley/

- 1) Select file type
- 2) Add Comments
- 3) Does it load?
- 4) Select file
- 5) Click Upload

Figure 18. Confirmation of T3 curator notification