**Steps in the submission of data to T3**

1. Submit all the line names and properties using the Line Submission Form.
2. If lines are to be genotyped, submit the Genotyping ID Submission Form.
3. Submit trial information using the Trial Submission Form.
4. Submit phenotypic data using the Phenotype Submission Form. Step 4 can be iterated several times without going back to Step 3.

Notes on what information is needed on each form are given below.

**Line Submission Form**

Line Names are unique identifiers for a line within a crop. If a line with that name exists already within T3, the new submission will not be accepted but its breeding program, aliases, pedigree and properties will be displayed for confirmation (or not) that it is the same as the new submission.

*Line Names*

In order to be able to search the database for specific lines, we have to use consistent formats. Use the following naming conventions for Line Names:

• Use all capital letters: BARONESSE

• Dashes within names can be maintained: 6B97-2245

• Spaces cannot be used in a name.  
Spaces will be replaced with an understroke “\_” if they occur between two letters (e.g., AC METCALFE –> AC\_METCALFE) or if they occur between two numbers (e.g., IA95 506 –> IA95\_506) but will be deleted if they occur between a number and a letter (e.g., SHORT 2 –> SHORT2 or IA95506 X10 –> IA95506X10). For any line that contains spaces or understrokes, an alias will automatically be created with both characters removed so that that line will turn up in a global search for the name.

*Pedigree Formats*

Breeders can submit pedigrees in text format:

Mentor/Minerva//Vada\_mutant/4/Carlsberg/Union//Opavsky/Salle/3/Ricardo/5/Oriol/6153P40

We are using standard Purdy notation (Purdy et al., Crop Sci 8: 405-406).

Pedigrees in this format will be stored in a text field for reference by breeders. It is not necessary for the text version of pedigrees to be all caps with no spaces. Use the text format that is easiest for you to read.

Where possible, provide names of intermediate parents in the pedigrees. If a parent is already in the database, then it is not necessary to expand the pedigree to include earlier generations.

*Filial Generation*

This is the filial generation (number of generations of selfing since the hybrid + 1) of the single plant which is the common ancestor of all seeds that form this line. Possible values for Filial Gen. are single digits: integer from 1 to 8 corresponds to seeds from F1 to F8 derived plants ; anything greater than 8, use 9; if the seeds were from a doubled haploid (DH) plant, use 0.

*Values for descriptive variables:*

Barley

Growth Habit: winter, spring, or facultative

Row Type: 2 or 6

Primary End Use: malt, feed, food, fuel, or other. Indicate the intended use. At the F4-F5 stage, the quality of a line for malting may not be known yet.

Hull: hulless, hulled, or empty (assumed to be hulled)

Wheat

Grain Hardness: hard or soft, if unknown, NA

Color: Red or White, if unknown, NA

Growth Habit: Spring, Winter or Facultative

Species: aestivum or durum

Awned or awnless: A or N (No awns)

Comments: general text field to say something about the line (cannot be used as a query to sort lines)

**Genotyping ID Submission Form**

Breeders initiate the process by contacting the genotyping lab to request the number of plates and labels to be sent, and the time frame for them to receive the plates.

The labs send plates to breeders that have plate ids already assigned. The breeder prepares a shipment to the genotyping lab.

The breeder uploads a Genotyping ID Submission Form to T3 with crop, breeding program code, and name of the genotyping lab in the header and plate id, well id, line names, stock names, and whether or not the sample is a TCAP sample in rows. A name must be filled in for every well, though “empty” is acceptable for empty wells. A hard copy of this Genotyping ID Submission Form should be included with the samples when they are sent to the genotyping lab.

Prior to uploading to T3 the Genotyping ID Submission Form, all line names will have been submitted to T3 using the Line Submission Form. The line names will be checked against T3. If there are any names not in T3 the user will be notified and the Genotyping ID Submission Form not be uploaded. If any line names on the Genotyping ID Submission Form match aliases, the user will be notified of those.

The lab downloads the Genotyping ID Submission Form from T3.

The lab processes the samples and submits the genotypes to T3 using the plate id and well id as the identifier. Since T3 already knows which sample names goes with which plate and well id’s it associates the genotypes with the correct sample name.

Instructions:

Plate ID: must match the names given by the genotyping lab

Well ID: use IDs going from A01 to H12 in the order given. If multiple plates are on the same form, repeat A01 to H12 for each plate.

Line Name: use names matching previously submitted names

Filial Gen.: This is the filial generation of the single plant from which plant tissue was sampled for DNA extraction for genotyping. Possible values for Filial Gen. are single digits: integer from 1 to 8 corresponds to F1 to F8 derived plant tissue; anything greater than 8, use 9; if the tissue was from a doubled haploid (DH) plant, use 0.

TCAP sample?: This is for genotyping lab accounting and determines who should be charged for this genotyping.

**Trial Submission Form**

The following information can be entered in the form. Cells with a red background are required, others are optional.

Trial Code. Required. Experiment\_YYYY\_Location, where Experiment is short but descriptive, YYYY=Year Harvested, and Location is self-explanatory. Trial Codes should be unique across T3 for a crop.

Experiment Code. Optional. The experiment is one hierarchical level above the trial. The trial is carried out at one location in one year. The experiment may have several trials with similar (may be identical) entry lists, performed at different locations in different years. The Experiment Code should be short, descriptive, and unique across T3 for a crop.

Breeding Program. Required. Program responsible for data collection (Three letter code).

Calendar Year Harvested. Required.

Location. Required.

Lat/Long of field. Required. DO NOT use a degree symbol! Just put a number. We have found four coordinate standards:

|  |  |  |
| --- | --- | --- |
|  | Latitude | Longitude |
| Decimal Degrees (WGS84) | 42.4375 | -76.504167 |
| Degrees, Minutes & Seconds | N42 26 15 | W76 30 15 |
| GPS | N 42 26.250 | W 76 30.250 |
| UTM (X and Y) | 18N 376284 | 4699449 |

For simplicity, we would like to use the Decimal Degrees standard. There is a converter between these standards at <http://boulter.com/gps/>.

Collaborator. Required. Name of scientist.

Greenhouse trial? (yes or no). Required.

Narrative Description of Experiment. Optional. Agreed upon for TCAP-funded experiments, self-assigned otherwise. 300 characters maximum.

Planting date. Required.

Begin weather date. Optional. If T3 should store weather data starting at some point *before* planting (e.g., to figure out soil moisture status), then put that date here. If blank, weather will be collected starting at planting date.

Seeding rate (seeds/m2). Required. This is the TARGET density for the trial, not the actual rate for each line in the trial. Depending on how seed is packaged, rates may vary. Just give the target rate.

Experimental design. Required. A description of the design. We do not have a strict format for this description at this point.

Number of entries. Required. Include the checks in this number.

Number of replications. Required. 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).

Plot size (m2). Required.

Harvested area (m2). Required.

Irrigation (yes or no). Required.

Harvest date. Required. This is a required information. Therefore you can only submit this form AFTER you have harvested the experiment. If the experiment is not destined to be harvested, put the date of the last data collection event.

Other remarks. Optional. Adjustments to means in data analysis or other particularities of statistical analysis. Other notes that may help in the interpretation of the results, for example, that harvest was delayed due to weather, etc.

**Phenotype Submission Form**

Phenotypes come from a single trial. Information about the trial must have been previously submitted to T3 using the Trial Submission Form and is identified by the Trial Code**.** The Trial Code row is the only row that has no information about the phenotypes, but has just one value, the Trial Code. The Trial Code given on this sheet is just an example.T3 should also have been "made aware" of Line Names via the Line submission form.

The value in the Check column indicates whether that line of data is the average for a line (0), for a standard check (1), or for a summary statistic, i.e., Trial Mean, Std. Error, Std. Error Diff., Prob>F, Coef. Var., or Replications at the top of the sheet (2). We have no rules on what is designated as a check and what is not. Information on whether a line is a check can be used by future analysts. In the meanwhile, breeders should use their informal understanding of what is a check in designating lines as checks. See below for information on the summary statisitics.

Values in the green columns should be means for each line calculated across the experiment, ideally considering lines as fixed effects (I think: this is something to be discussed with the statistics group).

Replace "Pheno1", "Pheno2" etc. with the names of phenotypes given in the T3 phenotype ontology page. Phenotypes without a matching name will not be accepted. If there is no data for a phenotype for a particular line, leave that cell EMPTY. We will develop a protocol for adding new phenotypes as allowable in T3. All phenotypes should have measurement protocols that TCAP scientists agree to adhere to.

The Trial Mean reported should be obtained from the lines being submitted to T3 lines and the checks included in the spreadsheet. If there were additional lines in the trial that are not being submitted to T3, they should be left out of the mean calculation and omitted from the submission form. For simplicity, we will assume a common variance, so the standard error of a mean (Std. Error) and F tests for comparing lines in each trial (Prob>F) can be caluculated from the Mean Square Error (MSE) in the ANOVA (including CAP and non-CAP lines). The formula for the Std Error = sqrt(MSE/r), where r is the number of replications. For incomplete block designs, the standard error of the difference (Std. Error Diff.) will be depend on whether the two lines being compared were in the same incomplete block or not. The value reported here should be for lines in different incomplete blocks.

“Replications” refers to the number of individual reps on which a particular trait was measured for normal entries (not checks: if there are repeated checks, they may have more replications than normal entries). For most agronomic traits, this will be the same as the number of replications in the trial indicated in the Annotations file. For some quality evaluations, breeding programs may submit a single bulk sample, in which case the number of Replications for such traits would be = 1. Unless there are repeated checks in a trial, it may not be possible to provide estimates of standard errors (Std Error) and F statistics for such data. The standard deviation among a set of lines is not a useful measure of precision because it reflects the genetic variation among lines as well as errors in estimation. Breeders are encouraged to review their quality data carefully because they are in the best position to judge if values are reasonable for a given genotype.