T3 Input / Output

Germplasm
- Breeders GRIN

Phenotypes
- Nursery trials Quality Labs

Genotypes
- USDA Genotyping Labs

Genetic Maps
- Mapping Labs GrainGenes

Processing & Curation

User-Defined Data Set Assembly

T3

Combined genotype/phenotype data for association analysis with TASSEL

Clustered lines by genotype

Pedigree trees

Haplotype views

Genotype data for graphical genotyping with FlapJack
T3 is Two Independent Databases for Barley and Wheat to support the T-CAP project

<table>
<thead>
<tr>
<th>Barley</th>
<th>Wheat</th>
</tr>
</thead>
<tbody>
<tr>
<td>triticeaetoolbox.org/barley</td>
<td>triticeaetoolbox.org/wheat</td>
</tr>
<tr>
<td><strong>Database</strong> is a continuation of The Hordeum Toolboox (THT), developed for the Barley CAP project (2006-2010)</td>
<td><strong>Database</strong> is new, built on the THT model</td>
</tr>
<tr>
<td><strong>Genotype Data</strong></td>
<td><strong>Genotype Data</strong></td>
</tr>
<tr>
<td>&gt; 13.5M BOPA datapoints from THT</td>
<td>&gt; 24.5 M datapoints from Infinium 9K analysis of the Wheat Core Collection</td>
</tr>
<tr>
<td>&gt; 16 M datapoints from Infinium 9K analysis of the Barley Core Collection</td>
<td></td>
</tr>
<tr>
<td><strong>Phenotype Data</strong></td>
<td><strong>Phenotype Data</strong></td>
</tr>
<tr>
<td>&gt; 100K datapoints from THT</td>
<td>~4K datapoints from a Stripe Rust assay on the Wheat Core Collection</td>
</tr>
<tr>
<td><strong>Blue/Purple</strong> color scheme</td>
<td><strong>Red/Orange</strong> color scheme</td>
</tr>
</tbody>
</table>
The Triticeae Toolbox

Overview
CAP Data Programs
Content Status
Acknowledgments
Terms of Use

Quick Links
Login/Register
Download
Genotype/Phenotype (Tassel format)
Download Genotype/Phenotype (Flapjack format)

Quick search...

Participants: The templates for submitting your data about phenotype trials, phenotype results, and the lines tested are here.

Data submission

Search Type

| Search by Breeding Program | All experiments containing data from the program's lines |
| Search by Trait | All experiments that measure the trait |
| Search by Year | All experiment data from the selected year |

The Triticeae Toolbox (T3)!

Data generated by the Triticeae Coordinated Agricultural Project (T-CAP), funded by the National Institute for Food and Agriculture (USDA). T3 contains SNP, phenotypic, and pedigree data from wheat and barley lines from the CAP. More...
### T3wheat Data Submission Report 2012-09-06

#### Trials
- Phenotype Trials submitted: 160
- Genotype Trials submitted: 31
- CAP data programs: 5

#### Lines
- Line records: 5812
- Breeding programs: 23
- Lines with genotyping data: 4892
- Lines with phenotype data: 5225
- Species: aestivum, durum, other
- Last addition: 09-06-2012

#### Genotype Data
- Markers SNP: 9505
- Markers SSR: 106
- Markers with genotyping data: 7123
- Markers without genotyping data: 2488
- Total genotype data: 25,778,672
- Last addition: 08-07-2012

#### Phenotype Data
- Traits: 78
- Total phenotype data: 127228
- Last addition: 09-04-2012

### T3barley Data Submission Report 2012-09-06

#### Trials
- Phenotype Trials submitted: 388
- Genotype Trials submitted: 98
- CAP data programs: 23

#### Lines
- Line records: 13515
- Breeding programs: 16
- Lines with genotyping data: 10913
- Lines with phenotype data: 6185
- Species: barley
- Last addition: 06-20-2012

#### Genotype Data
- Markers OPA SNP Name: 4608
- Markers DArT Marker: 722
- Markers Historical: 279
- Markers SNP: 5032
- Markers GBS: 55782
- Markers with genotyping data: 8942
- Markers without genotyping data: 57481
- Total genotype data: 33,083,256
- Last addition: 03-14-2012

#### Phenotype Data
- Traits: 71
- Total phenotype data: 225334
- Last addition: 08-30-2012
<table>
<thead>
<tr>
<th>Agronomic</th>
<th>Ontology</th>
<th>Description</th>
<th>Min Value</th>
<th>Max Value</th>
<th>Unit</th>
<th>Unit Info</th>
</tr>
</thead>
<tbody>
<tr>
<td>grain yield</td>
<td>TO:0000390</td>
<td>The grain yield, measured in kilograms per hectare at 14 percent moisture.</td>
<td>0</td>
<td>20000</td>
<td>kg ha⁻¹</td>
<td></td>
</tr>
<tr>
<td>head drop (0-9)</td>
<td>TO:0020077</td>
<td>0-9 rating scale</td>
<td>0</td>
<td>9</td>
<td></td>
<td>head drop rating scale (0-9)</td>
</tr>
<tr>
<td>head shattering</td>
<td>TO:0000473</td>
<td>head shattering percent</td>
<td>0</td>
<td>100</td>
<td>percent</td>
<td></td>
</tr>
<tr>
<td>heading date</td>
<td>TO:0000137</td>
<td>Number of days required for 50% of the heads to emerge completely from the boot.</td>
<td>0</td>
<td>250</td>
<td>days from planting</td>
<td></td>
</tr>
<tr>
<td>lodging</td>
<td>TO:0000066</td>
<td>Measure of percentage of plants that lodged.</td>
<td>0</td>
<td>100</td>
<td>percent</td>
<td></td>
</tr>
<tr>
<td>plant height</td>
<td>TO:0000207</td>
<td>Actual measurement of plant height from soil surface to the highest point in plant as identified in the study.</td>
<td>0</td>
<td>150</td>
<td>centimeter</td>
<td></td>
</tr>
<tr>
<td>spikes per area</td>
<td></td>
<td>Number of flowering stems per given area</td>
<td>0</td>
<td>1000</td>
<td>spikes</td>
<td>flowering heads</td>
</tr>
<tr>
<td>straw breakage</td>
<td></td>
<td>Measure of percentage of plants with broken straw</td>
<td>0</td>
<td>100</td>
<td>percent</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Disease</th>
<th>Ontology</th>
<th>Description</th>
<th>Min Value</th>
<th>Max Value</th>
<th>Unit</th>
<th>Unit Info</th>
</tr>
</thead>
<tbody>
<tr>
<td>BYD Rating (0-8)</td>
<td>TO:0020067</td>
<td>Rating from 0-8 in the field indicating percentage of plants showing foliar discoloration/stunting: 0 = no symptoms, 1 = &gt; 0-3%, 2 = 4-14%, 3 = 15-25%, 4 = 30-49%, 5 = 50-59%, 6 = 60-84%, 7 = 85-95%, 8 = 90-100%.</td>
<td>0</td>
<td>8</td>
<td>Disease Rating 0-8</td>
<td></td>
</tr>
<tr>
<td>CRR Severity</td>
<td>TO:0020058</td>
<td>Common root rot is a fungal disease of barley caused by Cochliobolus sativus, Fusarium culmorum and F. graminearum</td>
<td>0</td>
<td>100</td>
<td>percent</td>
<td></td>
</tr>
<tr>
<td>DON</td>
<td>TO:0000069</td>
<td>Levels of the mycotoxin deoxynivalenol (DON)</td>
<td>0</td>
<td>200</td>
<td>parts per million</td>
<td></td>
</tr>
<tr>
<td>FHB incidence</td>
<td>TO:0000062</td>
<td>Fusarium Head Blight (FHB) Incidence is reported as the percentage of the number of spikes out of 10 that had at least one infected kernel.</td>
<td>0</td>
<td>100</td>
<td>percent</td>
<td></td>
</tr>
</tbody>
</table>
Current T3 Team

Jean-Luc Jannink    USDA-ARS, NAA, RWHCAH, Ithaca, NY.  Project coordinator
Mark Sorrells      Cornell University, Ithaca, NY      Project coordinator
Clay Birkett     USDA-ARS, NAA, RWHCAH, Ithaca, NY.  Database programming and development

Victoria Carollo Blake    USDA-ARS, WRRC, Albany, CA  Data curator
Dave Matthews USDA-ARS, PWA, Ithaca, NY      Database development, GrainGenes collaborator
Shiaoman Chao USDA-ARS Biosciences Research Lab, Fargo, ND  SNP data production and curation
Peter Bradbury USDA-ARS, NAA, RWHCAH, Ithaca, NY      Pedigree information and links to TASSEL
Mike Bonman USDA-ARS, Aberdeen, ID  GRIN collaboration
Harold Bockelman USDA-ARS, Aberdeen, ID  GRIN collaboration
Tim Close Botany and Plant Sciences, UC Riverside. Assembly and SNP context information from HarvEST barley

T3T Developers throughout the U.S.A - Data Collection and Contribution

Julie A. Dickerson Electrical and Computer Engineering, Iowa State University. Principal Investigator

Roger P. Wise USDA-ARS Department of Plant Pathology, Iowa State University. Principal Investigator

Jennifer Kling Dept. of Crop and Soil Science Oregon State University  Phenotype and pedigree data curation
Shreyartha Mukherjee Bioinformatics and Computational Biology, Iowa State University. Developer/Bioinformatics
Kartic Ramesh Computer Science, Iowa State University  Developer
Gavin Monroe Software Engineering, Iowa State University  Developer
Ethan Wilder Computer Engineering, Iowa State University  Developer
Yong Huang Bioinformatics and Computational Biology, Iowa State University  Developer/Bioinformatics

Collaborators

SCRI Germinate Development Team (David Marshall and Paul Shaw)
PLEXdb Development Team (Ethy Cannon and Sudhansu Dash)
Gramene Database (Doreen Ware Lab)
GrainGenes Database USDA/ARS (David Matthews, Gerard Lazo)