



T3/Oat status update, April 2016

Clare Saied¹, David Matthews, Clay Birkett, Shiaoman Chao, Nicolas A. Tinker and Jean-Luc Jannink

¹T3/Oat curator, Cornell University
crs298@cornell.edu

T3/Oat is the repository of oat phenotype and genotype data for the Oat Global Initiative (www.oatglobal.org) and provides flexible queries for extracting desired datasets for analysis, as well as integrated analysis tools (<http://triticeatoolbox.org/oat/>).

2015 North American Public Oat Genotyping Initiative

The Public Oat Genotyping Initiative (POGI) is an ongoing project carrying out high-density genotyping of oat breeding lines submitted by public sector breeding programs. The results from the 2015 POGI are now publicly available through T3/Oat.

Fourteen North American breeding programs submitted a total of 1,427 lines. Pedigree information is available through T3/Oat and will soon be available through the Pedigree Of Oat Lines (POOL) database (https://triticeatoolbox.org/POOL/index_db.php). The Haplotag pipeline developed by Tinker, *et al.* (2016) was used for GBS SNP calling, and genotype data for over 240,000 markers are now available for download or for analysis using the tools available through T3.

Featured T3/Oat tool: Select Lines by Properties

The 'Select Lines by Properties' tool is used to make line selections based on information held in a T3 line record. Line information is submitted to T3 using an Excel template, which can be found on the 'Data Submission' page under the 'About T3' menu. The same template is used both to add new line records and to amend or supplement the information held about existing T3 lines. The fastest way to access a single T3 line record is by entering the line name into the 'Quick Search' box in the 'Quick Links' sidebar.

Table 1 outlines the fields from a T3 line record that can be used to search for and select lines using the 'Select Lines by Properties' tool, which can be found under the 'Select' menu. Selections can be made from more than one field, and multiple selections can be made in each field, so it is important to 'Clear' the tool if selections are made in error.

The selected lines will be displayed in the 'Current selections' section of the 'Quick Links' sidebar. The current line selections can be replaced or combined with additional line selections using any of the T3 selection tools. Additionally, individual lines can be removed from the current line selection using the 'Select Lines by Properties' tool. In this manner, the T3 selection tools can be used together to create a customized dataset for download or for analysis using T3's integrated tools.

An up-to-date summary of all of the data that are available in T3/Oat can be obtained from the 'Content Status' page, which can be reached through the 'About T3' menu. Please contact the curator with any suggestions or questions, or to discuss uploading data to T3/Oat - any feedback will be gratefully received.



Table 1. The selection fields that can be used in the T3 ‘Select Lines by Properties’ tool. Queries that specify optional fields may return limited results.

Field	Required field?	Description
Line name	Yes	The unique identifier for a T3 germplasm record. Lists of names can be pasted into the ‘Name’ search box. If a search term is considered a synonym in T3, then the primary line name will be returned in the results. An asterisk can be used as a wildcard character to expand the search.
Breeding program	Yes	Breeding programs are ordered alphabetically by the 3-letter T3 breeding program code. The table on the ‘Contributing Data Programs’ page, which can be found under the ‘About T3’ menu, orders breeding programs alphabetically by institution.
Trial year	N/A	The year that a line was included in a T3 phenotype trial or genotype experiment.
Species	Yes	<i>Avena</i> species. An ‘unknown’ value is available.
Genetic characters/ line properties	No	These fields cover some common defining properties of oat lines. The complete list of line properties can be found on the ‘Genetic Character Descriptions’ page under the ‘About T3’ menu. Users are invited to suggest additional line properties or to supplement existing line information.
Preselected line sets	N/A	Predefined line panels created to help make line selection easy; for example, the panel of lines that were genotyped during the 2015 Public Oat Genotyping Initiative (POGI). Registered users can create their own private line panels, which are displayed alongside the public panels.

Reference:

Tinker, N.A., Bekele, W.A., and Hattori, J. (2016) Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. *G3: Genes, Genomes, Genetics*. **6**: 857-863.