T3/Oat progress report

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

The database has now been populated with data from The North American Collaborative Oat Research Enterprise (CORE). The aim of the CORE project was to identify marker-trait associations within elite North American oat varieties. Germplasm was contributed by collaborating breeding programs in North America and Northern Europe, and was subsequently divided into spring and winter panels, with an additional panel chosen to represent the worldwide diversity of cultivated oat. Sixty-eight phenotypic traits were recorded in 82 CORE phenotyping trials, which involved around 700 lines (Table 1). The CORE collaborators have chosen to make these data publically available to encourage integrative analysis, data-mining, and molecular breeding decisions. However, much of these data remain unpublished, and we ask that all users allow CORE members to take priority in publishing initial foundation papers.

Table 1. T3/Oat content status (11/21/2014).

Trials	
Phenotype trials submitted	82
Genotype trials submitted	1
Lines	
Breeding programs	59
Lines with genotype data	635
Lines with phenotype data	702
Species	sativa, strigosa
Phenotype Data	
Traits	68
Total phenotype data	124,188
Genotype Data	
Markers with genotyping data	1932
Markers without genotyping data	3043
Total genotype data	2,166,608

One of the first challenges of the T3/Oat project was to establish a protocol for standardizing phenotypic traits, so as to maximize the compatibility of CORE

data with data contributed from other phenotyping trials. Our approach has been to use Gramene trait ontologies whenever possible. This approach should also maximize cross-compatibility with other oat data platforms in the future. The same process will be undertaken for new traits that are added to the database as new trial data are uploaded.

In addition to the lines that were phenotyped by the CORE project, 635 lines were also genotyped, and the genetic structure of these lines can be analyzed using T3/Oat's integrated analytical tools. The next step will be to upload a genetic map to T3/Oat to allow the utilization of the site's built-in genomic association and prediction tools. The first map to be uploaded will be the oat consensus map published in Oliver, *et al.* (2013).

The "What's New" sidebar on the website is used to highlight recent developments and, in particular, newly available datasets, and will be used to announce when the first genetic map has been uploaded. Additionally, trial data from The Uniform Early and Midseason Oat Performance Nurseries (1996-2014, http://wheat.pw.usda.gov/ggpages/UE-MOPN.html) are currently being curated and will soon be uploaded to the database, followed by historical data from the Uniform Winter Oat Yield Trials (http://www.ars.usda.gov/Main/docs.htm?docid=8419&page=4).

Data are uploaded to T3 using a series of data submission templates (http://triticeaetoolbox.org/oat/curator_data/instructions.php), and trial results can be uploaded in the form of pre-calculated trial means or as plot-level data. Plot-level data can be collected using the Android Field Book app, and data collected in this way can be uploaded to T3 directly without further processing. We encourage UOPN collaborators to submit their plot-level data to T3/oat, making these data available to all and allowing spatial analysis to be carried out on these datasets.

T3/Oat was developed after the success of T3/Barley and T3/Wheat, and tailoring the information provided on the web portal to cater to oat users is an ongoing process. Please contact the curator (crs298@cornell.edu) with any suggestions or questions, or to discuss uploading data - any feedback will be gratefully received.