T3/Oat: Status update
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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 tools for data analysis (http://triticeaetoolbox.org/oat/).

Figure 1. An example T3/Oat marker report.

T3/Oat marker reports and Haplotag

There are currently 862,438 markers stored in T3/Oat. The T3 marker record summarizes the information that is available for each individual marker.

Marker records can be reached by typing a marker name into the "Quick Search" box in the "Quick Links" sidebar, or when browsing T3/Oat.
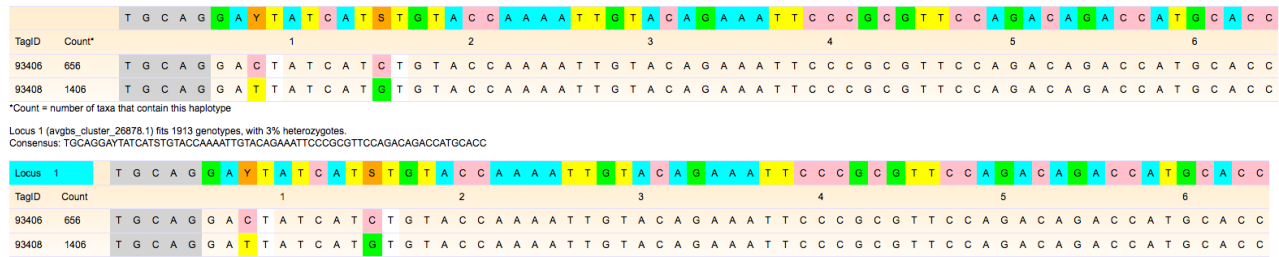
Marker records contain sequence information and map locations when available, and provide a link to the existing allele data for T3 lines (Figure 1). Individual markers may be added to the "Current Selection" using a button on the marker report.

The marker records of GBS markers that were called using HaploTag (Tinker *et al.*, 2016); e.g., during the 2015 Public Oat Genotyping Initiative (POGI), also contain a link to the HaploTag passport file (Figure 2).

Figure 2. An example of a HaploTag passport file. Here, two tags (potential haplotypes) are identified. The positions of the two SNPs (Y and S) are identified by color. The table shows the tag counts at the presumed haplotypes within the locus. Counts greater than or equal to one are shaded; i.e., scored as "present".

View Haplotypes

Select haplotype combination

Show missing   Show haplotypes with missing data

Save line selection   Combine selected haplotype with currently selected lines

Figure 3. The T3 "Select Lines by Haplotype" tool interface. The three chosen markers are closely linked to Qdon.umb-17A/7C, a deoxynivalenol QTL located on chromosome 17A/7C (He et al., 2013).

Featured T3/Oat tool: Select lines by haplotype

T3 lines can be selected by haplotype, based on up to five markers of interest, using the "Select Lines by Haplotype" tool. First, select a set of markers using the "Select Markers" tool (see T3/Oat Status Update: August 2016 for a summary of this tool). Next, navigate to the "Select" menu, and choose "Lines by Haplotype". The tool displays haplotypes within all T3/Oat lines, not just those lines in the current selection. Finally, check the box(es) next to the desired haplotype to add the lines to the current selection.

Current line selections are displayed in the "Quick Links" sidebar, and can be replaced or combined with subsequent line selections. In this manner, T3's line selection tools can be used together to create a customized dataset for download or for analysis using one of T3's integrated analytical tools.

An up-to-date summary of all of the data that is 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.

References

He X, Skinnes H, Oliver R.E., Jackson E.W., Bjornstad A. (2013) Linkage mapping and identification of QTL affecting deoxynivalenol (DON) content (*Fusarium* resistance) in oats (*Avena sativa* L.). Theoretical and Applied Genetics. 126(10):2655-70.

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.