T3/Oat status update, December 2016

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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 analysis tools (http://triticaetoolbox.org/oat/).

T3/Oat year-end content summary

Line records: 16,790
      Lines with phenotype data: 12,898
      Lines with genotype data: 2,037

Phenotype trials: 1,168 (see Table 1 for data sources)

Marker records: 862,438
      Markers with genotype data: 248,637
      Markers with map location: 52,680

Genotype experiments: 19 (see Table 2 for data sources)

Genetic maps: 14 (see Figure 1)

Table 1. The source of T3/Oat phenotype

T3 phenotype experiment	Count
CORE AFRI109 Panel	33
CORE Spring Panel	35
CORE Winter Panel	14
Cornell Metabolomics Trial	4
National Small Grains Collection	12
UMN Founders Trial	4
UMN Variety Trial	8
Uniform Early Oat Performance Nursery	279
Uniform Midseason Oat Performance	527
Uniform Oat Winter Hardiness Nursery	67
Uniform Winter Oat Yield Trial	185
Total	**1168**

Table 2. The source of T3/Oat genotype

T3 genotype experiment source	Count
Collaborative Oat Research Enterprise (CORE)	2
Public Oat Genotyping Initiative (POGI)	10
National Small Grains Collection (NSGC)	1
Oliver mapping data	6
Total	**19**

Featured T3/Oat tool: Select Genetic Map

There are currently 14 genetic maps stored in T3/Oat (Figure 1), which can be downloaded to view offline using the "Download" menu by selecting "Genetic Maps".

The "Select Genetic Map" tool is used to select a genetic map in T3/Oat, and the tool can be used to determine the genetic map with the best coverage of the data held in the "Current Selections" by clicking the button at the bottom of the page labelled "Calculate markers in map for selected lines". The results of this calculation are displayed in the column labelled "markers (in selected lines)" of the tool (see Figure 1).

If a genetic map is selected, the marker positions of selected markers will be included in a download made using the download "Genotype and Phenotype Data" function, which is found in the download menu. The genetic maps can also be selected for use with the "Genomic Association and Prediction" tool, which is found under the "Analyze" menu.

A 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.

Map Sets

This table lists the total markers in each map. If a marker is not in the the selected map set then it will be assigned to chromosome 0.

select	markers (total)	markers (in selected lines)	map set name	comment (select item for complete text)
◉	7202	639	Framework Oat Consensus Map (2015)	Oat consensus map composed of 6K SNP array markers and PstI-MspI-GBS markers, developed by merging 1
○	50668	639	Expanded Oat Consensus Map (2016)	Oat consensus map composed of 6K SNP array markers and PstI-MspI-GBS markers, developed by merging 1
○	1914	243	Kanota x Ogle (2015)	A de-novo genetic linkage map of Kanota x Ogle (KO) that was used in the construction of the Hexaplo
○	888	131	CDC Sol-Fi x HiFi (2015)	A de-novo genetic linkage map of CDC Sol-Fi x HiFi (CH, historically SH) that was used in the constr
○	1508	194	Hurdal x Z-597 (2015)	A de-novo genetic linkage map of Hurdal x Z-597 (HZ) that was used in the construction of the Hexapl
○	2257	161	Ogle x TAMO-301 (2015)	A de-novo genetic linkage map of Ogle x TAMO-301 (OT) that was used in the construction of the Hexap
○	660	114	CDC Boyer x 94197A1-9-2-2-5 (2015)	A de-novo genetic linkage map of CDC Boyer x 94197A1-9-2-2-5 (BG, historically GB) that was used in
○	1166	95	Otana x PI260616 (2015)	A de-novo genetic linkage map of Otana x PI260616 (OP) that was used in the construction of the Hexa
○	1821	173	Provena x 94197A1-9-2-2-5 (2015)	A de-novo genetic linkage map of Provena x 94197A1-9-2-2-5 (PG) that was used in the construction of
○	623	116	IL86-1156 x Clintland 64 (2015)	A de-novo genetic linkage map of IL86-1156 x Clintland 64 (IL4) that was used in the construction of
○	598	105	Provena x CDC Boyer (2015)	A de-novo genetic linkage map of Provena x CDC Boyer (PB) that was used in the construction of the H
○	895	62	Dal x Exeter (2015)	A de-novo genetic linkage map of Dal x Exeter (DE) that was used in the construction of the Hexaploi
○	1366	167	AC Assiniboia x MN841801 (2015)	A de-novo genetic linkage map of AC Assiniboia x MN841801 (AM) that was used in the construction of
○	608	122	IL86-6404 x Clintland 64 (2015)	A de-novo genetic linkage map of IL86-6404 x Clintland 64 (IL5) that was used in the construction of

Selection	Framework Oat Consensus Map (2015)
Comment	Oat consensus map composed of 6K SNP array markers and PstI-MspI-GBS markers, developed by merging 12 component populations. This version of the map includes all framework markers retained during the merging of component maps from 12 bi-parental populations. See "Expanded Oat Consensus Map" for a version that contains approximate positions of additional markers. Contact: Nick Tinker or Jessica Schlueter. Reference: Chaffin et al, 2016.

Figure 1. The T3 Select Genetic Map tool interface.