

T3/Oat status update, May 2017

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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://triticeaetoolbox.org/oat/>).

Uniform Oat Performance Nursery 2016: Seed characteristics

The data available from the 2016 Uniform Early & Midseason Oat Performance Nurseries (UEOPN & UMOPN) have now been supplemented with seed characteristic data: groat protein content, groat oil content, and beta-glucan content. The seed characteristic data include data from Urbana, IL; Waseca, MN; Volga, SD; and Arlington, WI (UEOPN); and from Urbana, IL; Crookston, MN; Arlington, WI; and Fargo and Minot, ND (UMOPN).

Featured T3/Oat tool: Selection index

The “Selection Index” can be used to rank lines in the current selections based on two or more phenotypic traits of interest. To use the Selection Index tool, first select a set of lines and phenotypic traits using the T3 selection tools; for example, the “Selection Wizard” can be used to select a complementary set of lines, phenotypic traits, and phenotype trials (please see the [T3/Oat status update from March 2016](#) for help using the Selection Wizard). Next, navigate to the “Selection Index” tool, which is located under the “Analysis” menu. Finally, choose the relative weights for each of the selected traits and a scaling method (Figure 1).

Selection Index

Choose relative weights and a scaling method to combine the traits into an index.
If smaller values of a trait are better, reverse the scale.
Data will come from the currently selected trials.

Trait	Weight	Reverse scale
grain yield	50	<input type="checkbox"/>
beta glucan dwb	50	<input type="checkbox"/>

Scaling of trait values

- Normalized, subtracting the trial mean and dividing by the standard deviation
 Actual measured value
 Percent of common line:
 Rank in trial

Figure 1. The “Selection Index” tool requires the user to choose relative weights for each of the selected phenotypic traits and to choose a scaling method.

The tool ranks the lines in the current selections across all of the selected trials, as well as showing individual trait values for each trait used in the analysis (Figure 2). A table ranking the lines within each trial appears below the table summarizing the average selection index across trials.

Selection Index

Scaling method: **normalized**. Weights: **50, 50**.

Selection Index values

Individual trait values, after scaling and averaging over trials, are also shown.

Line	Index	grain yield	beta glucan dwb
ND100046	1.04	-0.24	2.32
ND121901	1	-0.12	2.13
ND121207	0.56	0.37	0.75
IL09-6937	0.55	0.31	0.79
CDC_NORSEMAN	0.44	0.68	0.21
MN11231	0.43	0.18	0.67
ND101473	0.43	-0.2	1.06
WIX10055-8	0.29	0.64	-0.06
LEGGETT	0.28	0.11	0.45
WIX10045-12	0.26	0.05	0.48
OT3083	0.19	0.47	-0.09
NEWBURG	0.17	-0.08	0.41
SD120098	0.17	-0.34	0.69
WIX10045-9	0.14	-0.09	0.38
CDC_RUFFIAN	0.14	0.87	-0.59
SD120261	0.14	0.23	0.05
HA07-02X22-1	0.13	-0.1	0.36
OT3063	0.13	0.61	-0.35
WIX9878-3	0.13	-0.01	0.27
MNBT1021-1	0	0.6	-0.59
ND122321	-0.03	-0.12	0.07
HA08-03X29-1	-0.05	-0.62	0.53
MN11211	-0.13	0.76	-1.02
SD120640	-0.22	0.12	-0.55
SD120419	-0.25	0.5	-1
WIX9528-1	-0.33	0.13	-0.79
ND121730	-0.33	-0.84	0.17
OGLE	-0.37	-0.28	-0.47
SD120553	-0.41	-0.06	-0.76
IL09-5508	-0.45	-0.56	-0.34
CLINTLAND64	-0.49	-0.78	-0.2
MNBT1020-1	-0.55	0.43	-1.54
ND111357	-0.57	-0.23	-0.91
SD120665	-0.59	0.55	-1.72
IL10-9872	-0.66	-0.42	-0.9
GOPHER	-1.09	-1.97	-0.2

Figure 2. An example output from the “Selection Index” tool.

A 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 “Resources” menu. Please contact the curator with any suggestions or questions, or to discuss uploading data to T3/Oat; any feedback will be gratefully received.