

**Transcript of the Q and A “chat” from the T3/Oat “Speaking of Oats...” webinar, 21 Jan 2021:**

Q. from Stephen Harrison:

**Can data on T3 be restricted or is everything that is uploaded public access?**

Reply from Jean-Luc Jannink:

At the moment, everything that is uploaded is public. This is a feature that we have wanted to add for a while. It's complicated. No guarantees, but I think we will have some privacy features in the next 18 months or so.

We do prefer public data, though.

Q. from Nick Tinker:

**Great presentation!**

**Here in Canada, there has always been pushback from both industry and recommending committees on the automated, public accessibility of variety registration and performance data, and especially its use in automated recommendations. Reasons given are:**

- Data and results need to be interpreted by experts
- Industry partly funds data collection and doesn't want data on their varieties to be public ...

**because it might be misinterpreted in ways that might harm them**

**Can you comment?**

Reply from Jean-Luc Jannink:

Good question, Nick. We have not thought a whole lot about possible downsides yet, since we are just coming out with the tool. Some of the “Data needs to be interpreted by experts” will happen when we meet with seed companies and processors toward the end of the year. So the variety selector tool will not show directly the results of Lucia's analysis, but a bit of a curated output from it. I could imagine there will be some contention on that curation: the future will tell.

Q. from Stephen Harrison:

**I agree with the need to have data interpreted by someone who knows how the data was collected and what may have influenced the results.**

Q. from Nick Tinker:

**I've always felt this is insulting to modern (and even traditional) farmers who understand data.**

Q. from Stephen Harrison:

**Nick: Farmers may or may not understand the data. My concern is that the selection tool may or may not take into account all variables that are important to them. Is the selection based on yield and maturity or does it also consider the numerous disease and quality variables?**

Reply from Jean-Luc Jannink:

Stephen has a good point here, and I think the tool will improve as we have more experience with it, and farmer feedback / other stakeholder feedback, from it. At the moment, the ranking is based only on yield. There will be a tradeoff between how straightforward / user-friendly we can make the tool and how customizable it is by different farmers.



Q. from Nick Tinker:

**Steve: Fair points.... Metadata is relevant, and any summary hides it... But a final interpretation is such a small part of what data can provide. The whole point of T3. It's complicated, but we need to evolve!**

Q. from Bruce Roskens:

**Is there any legal "disclaimer" associated with the data if for instance a seed company should choose to use yield data from the website as a sales tool? Whether it is relevant to a particular zone/area or not?**

(live answered)

Additional reply from Jean-Luc Jannink:

At this time, there is no legal disclaimer. Users do have to accept the terms of the Toronto Agreement (<https://oat.triticeatoolbox.org/about/index.pl>).

Q. from Kevin Smith:

**In terms of uploading data from Field Book to T3, you would normally want to do some error checking before adding the data to the database. Is it better to download locally and do curation or could you do some curation in T3?**

Reply from David Waring:

We can do curation on T3. So, I guess, whatever works best for you is going to be OK. You can also upload from Field Book to the T3 sandbox then use the tools on T3 sandbox to check your data. Some corrections are best done offline.

Q. from Kevin Silverstein:

**Do you have an extensive API so that data can be extracted via an Python or R interface?**

Reply from Clay Birkett:

The BrAPI is very extensive and I know of several people that access the API using R script. I am not sure about Python.

Q. from Stephen Harrison:

**One concern that I have with T3 is standardization of trait ratings. In the old T3, if you typed crown rust, for example, you got 47 different variables and it is very difficult to combine those across trials.**

(live answered)

Additional reply from Jean-Luc Jannink:

Trait ontologies (<https://www.croponontology.org/>) are used as a standard as much as possible.

Q. from Wayne Xu:

**Is it possible to batch download the genotype and a particular trait data for the whole database?**

Reply from David Waring:

The Search Wizard can be used to batch download data. For example, you could just select a trait as the first and only filter and the download will include all of the data for that trait. You could then



select all of the accessions as the 2nd filter and it will download all of the genotype data for those accessions.

Q. from Jose Costa:

**Nice presentation!**

**Any further collaboration/integration with Graingenes?**

Reply from Jean-Luc Jannink:

We plan to improve the resources using JBrowse provided by GrainGenes. We are discussing how to best present pan genome data.

Q. from Steve Eichten:

**What is the current size of the user base, breeding programs, year-to-year increases in data? I see 38 users in the 'People' tab.**

Reply from David Waring:

The Content Status page (under the About menu) has a very general count of the data currently in the database (number of breeding programs, number of trials, etc.).

Q. from Wayne Xu:

**What is the largest number of a trait which has genotype available in T3?**

(live answered)

Additional reply from David Waring:

The top three were what we were expecting: grain yield, test weight, and plant height. Following that are heading date and a couple of lodging traits. Out of a total of 46910 accessions for oat, 5349 of them have genotype data.

Comment from Jim Dyck:

**Breeders and specialists are always available to comment or interpret data if a grower needs or wants it. "Please consult your local oat breeder!" :)**

Q. from Stephen Harrison:

**Can you delete data from T3 once it has been uploaded, suppose you decide the data was compromised and want to edit it?**

(live answered - yes)

Q. from Steve Eichten:

**Is there a slack / forum / github / etc for which one can talk further regarding T3?**

Reply from Clay Birkett:

<https://github.com/solgenomics/sgn>

We use this for issues and features related to breedbase

Comment from Roger Caspers:

**Jean-Luc, perhaps you want to mention the Youtube videos, which have helped me with specific T3 functions.**

(live answered - <https://www.youtube.com/channel/UC3jrvvzGKKEHzOriDBgnj0A> These talk about the wheat database, but also apply to the oat one.)