

Dear Oat Breeders,

To further oat improvement and begin to make better use of the T3/oat resource that we are developing, we would like to propose ongoing high-density genotyping of breeding lines from public sector oat breeding programs. The results of this genotyping would be made available through T3/oat. The data would be public. The quid pro quo is: you get the genotyping for free but the results are public for all to use. There is no obligation to make the germplasm available, nor to make phenotypes available. Nevertheless, we would hope and prefer both to occur. We would also prefer the pedigrees of germplasm to be made available to POOL. Please do not submit germplasm developed by someone else without their permission. This initiative subscribes to the International Oat Workers' Code of Ethics. NOTE: this is a North American (not just USA) initiative. We would definitely benefit from Canadian participation.

This note is to ask whether you would be interested in participating in this initiative, and, if so, at what level. You do not have to have an active molecular breeding program to participate. We are interested in capturing as much of the diversity of elite oat in North America as we can, including from traditional programs. Initially, we would prefer samples that represent the diversity of your program, as opposed to, for example, progeny of a biparental cross. If we cover this diversity over the first couple years, we can begin to work with more specific populations.

A basic sketch of how this would work follows:

The genotyping platform would be genotyping by sequencing (GBS). At the moment, 45,000 GBS loci are placed on a consensus genetic map (Huang et al. 2014). We would fund the sequencing of 8 plates of oat lines (i.e., 380 to 760 lines).

Clare Saied, the T3/oat curator in Ithaca, NY, sends out a call for submissions to the genotyping initiative. The breeders send a list of names of the breeding lines to be genotyped to Clare. She enters the line information into T3/oat. A date is determined when Shiaoman Chao would receive plates of dried tissue in Fargo. Shaioman does the library construction and sequencing and would send the resulting sequences to Nick Tinker in Ottawa. He is refining a GBS pipeline called Haplotag that improves on UNEAK, that distinguishes reads at homeologous sites, and that will be submitted for publication soon. He would do the bioinformatics of the SNP calling and send the SNP allele data to T3/oat in Ithaca, NY. Breeders would retrieve their data from T3/oat. If this works well this year, we would continue the program for the next few years to build up a substantial resource of genotyped lines in the public sector in oat.

First, some general interest questions:

1. Would you be interested in participating?

If not, why not?

If yes, how do you envision using the data?

2. We propose GBS for this genotyping because it is less expensive and we think that it has greater potential for the future. Do you agree / disagree? Should we consider doing this with SNP chip technology instead?

Second, some coordinating questions:

1. How many lines would you be interested in submitting? Priority would be given to lines that have been evaluated in the Uniform Nurseries. We would probably set a limit of 95 lines for any single breeding program, depending on the overall demand.

2. Assuming you would want to submit fewer than 95 lines, two possibilities:

— If there is insufficient demand to fill up 4 plates you could put selected lines in >1 well, to fill up a plate.

— You would coordinate with another breeding program to fill up a plate prior to sending it to Shiaoman.

In addition to these questions, please let us know if you have thoughts / comments on how this initiative could run.

Thanks,

Jean-Luc

--

Jean-Luc Jannink

USDA-ARS, Robert W. Holley Center for Agriculture and Health

Phone: +1 607 255 5266

Fax: +1 607 255 6683

Cornell University

Dept. of Plant Breeding and Genetics

258 Emerson Hall

Ithaca, NY 14853

USA