

**From:** [Scott Allen Jackson](#)  
**To:** [Peter Wenzl](#)  
**Cc:** [Steven Cannon](#); [Suk-Ha Lee](#); [Jones Jennifer](#); [Abberton Michael \(IITA\)](#); [Cannon Steven \[AGRON\]](#); [Joost Richard Nelson, Randall - ARS](#); [Okamuro, Jack](#); "???" [QIU, Lijuan](#); "???" [Masao Ishimoto](#); [Akito Kaga](#); [Bob Stupar](#); [Ricardo Abdelnoor](#); [Bretting, Peter](#); [marcelofernandes.oliveira@embr](mailto:marcelofernandes.oliveira@embr); [François Belzile](#)  
**Subject:** Re: Follow Up: Glycine meeting Seattle, April 15-17  
**Date:** Tuesday, May 12, 2015 1:34:13 PM

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This looks like a good approach for us.

Randy, are you familiar with this? Instead of you being the conduit for all the accession names/numbers, would this work?

scott

On May 12, 2015, at 11:08 AM, Peter Wenzl <[peter.wenzl@croptrust.org](mailto:peter.wenzl@croptrust.org)> wrote:

Dear all,

I've talked to my colleagues here at the Crop Trust who're developing and maintaining the Genesys portal (<https://www.genesys-pgr.org/welcome>). I hear that it would be quite straightforward to provide room for assembling a global inventory of soybean accessions on this platform, if you wish to do so.

Genesys was designed for the purpose of assembling global inventories of genebank accessions (accession IDs, genebank IDs & passport data). That fact that soybean is not an Annex 1 crop of the International Treaty doesn't matter.

Best regards, Peter

On Wed, May 6, 2015 at 8:40 PM, Scott Allen Jackson <[sjackson@uga.edu](mailto:sjackson@uga.edu)> wrote:

Thanks for following up Steven,

several issues here:

1) on the funding. I think you are right that initially, at least, individual but coordinated efforts will be necessary. As a group, I think we can provide letters of support stating that the proposed research is part of a larger international initiative.

2) On the collection of accessions (both genotype and non-genotyped). Randy Nelson had 'volunteered' to start the process of collecting all the accessions to begin global inventory. Perhaps, as part of that, people could indicate which ones are genotyped and how. I suspect that much of the collections have been genotyped in the past, but probably not sequence-based (e.g. SSRs), so the information may not be of much use for what we envisage.

As an aside, we had discussed having an intern work on the data analysis. But the more I think about it, I think this is going to be more of a postdoctoral project—as you indicate below.

scott

On May 1, 2015, at 12:09 PM, Cannon, Steven  
<[Steven.Cannon@ARS.USDA.GOV](mailto:Steven.Cannon@ARS.USDA.GOV)> wrote:

Speaking for myself: I am still very enthusiastic about the group's plans, but have been swamped, .

I do, however, have a little progress to report. A student group that I have been advising has worked out a very fast GBS variant-calling and imputation pipeline for soybean. It is processing a lane of GBS data (384 samples multiplexed) in about two hours. This uses something like the "flanking sequencing database" concept that we discussed, to help speed the analysis and focus on known, well-assayable SNP locations. This process goes from raw reads through deconvolution of accessions through variant calling and VCF creation and haplotype imputation. I expect they would be willing to share the methods, but after some more documentation and testing.

I have also spoken with Michelle Graham and Bill Beavis here at ISU. Michelle has resequenced about a hundred lines used in the U.S. collection, and Bill Beavis is working with Brian Diers on a genotyping of a set of NAM populations in the U.S.

A next step for my continued involvement would be to find more skilled hands (probably a postdoc). I'm still considering a couple of RFPs: one at my university, and one with the United Soybean Board. It seems to me that others in this group might also seek funds. We could try to get funding for the group – but considering the many institutions and countries involved, it may be easier for each group to try to find a small amount of funding – or otherwise carve out some time from existing staffing – and then pool our efforts.

Another relatively small but important thing that we could do with moderate effort is for each participant in the project to work to assemble a list of their country's accessions, and also a list of accessions that have been (or are being) genotyped. These lists could initially be shared via email to this group – perhaps best, to a designated person who can cross-check and integrate and summarize the lists. I hate to heap more work on Randy, but maybe his group would be in the best position to make sense of the IDs/accessions from the several countries.

Best,  
Steven

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Steven Cannon, PhD

USDA - Agricultural Research Service  
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**From:** Scott Allen Jackson <[sjackson@uga.edu](mailto:sjackson@uga.edu)>  
**Date:** Thursday, April 30, 2015 at 8:00 PM  
**To:** Peter Wenzl <[peter.wenzl@croptrust.org](mailto:peter.wenzl@croptrust.org)>  
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**Subject:** Re: Follow Up: Glycine meeting Seattle, April 15-17

This is great, Peter. I don't have any thing to add. Maybe others do. Please let us know if they have any feedback.

Thanks for taking the time to join us.

scott

On Apr 30, 2015, at 7:15 PM, Peter Wenzl <[peter.wenzl@croptrust.org](mailto:peter.wenzl@croptrust.org)> wrote:

Dear all,

Time's running and it's already two weeks since the meeting in Seattle! I wanted to thank you -and Scott in particular- for having invited me to your meeting. I really enjoyed it and there was a lot I learned from your presentations and the ensuing discussions.

If you don't mind, I would like to report back to the DivSeek Steering Committee some of the key take-away points from the meeting, such as:

- Your plan to assemble a cross-genebank accession inventory
- Your approach to attempt to integrate existing data sets through a community-wide catalogue of GBS sequence tags identified across a broad range of accessions
- The plan to genotype all existing core collections on a single platform to create a global picture of the total diversity available, which could then be used to place individual accessions into a global context
- Your plans to explore opportunities of working with DivSeek in the area of software tools, databases, and hosting large datasets.
- Your quest to at least achieve data-sharing for cases where germplasm sharing is difficult.

In case there're any other important items I've missed here, which you would like me to report back to the Steering Committee, please let me know.

Looking forward to a continuing relationship,

All the best, Peter

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On Mon, Apr 20, 2015 at 5:45 AM, "이석하"  
<[sukhalee@snu.ac.kr](mailto:sukhalee@snu.ac.kr)> wrote:

Dear Scott,  
Thanks for sending summary of our activity at Seattle. I enjoyed the meetign.  
Sincerelyn yours,  
Suk-Ha Lee

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날짜 : 2015년 4월 18일(토) 08:21:44  
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Folks,

First a big thanks to all that attended—  
especially those that flew great distances!  
All of your contribution and inputs are  
greatly appreciated. I think we had a good  
meeting and there are many areas of  
opportunity to work together to better  
exploit our genebank collections to improve  
soybean breeding for the future. We  
identified some first steps where we can  
work together, but I think we will need to  
work hard to keep momentum going.

Please let me know if you have any comments  
or want to make any modifications to the  
attached report.

Sincerely, Scott Jackson

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