

From: [Scott Allen Jackson](#)
To: [Steven Cannon](#)
Cc: [Peter Wenzl](#); [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](#); [Francois Belzile](#)
Subject: Re: Follow Up: Glycine meeting Seattle, April 15-17
Date: Wednesday, May 06, 2015 2:40:52 PM

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> 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

Steven Cannon, PhD
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From: Scott Allen Jackson <sjackson@uga.edu>
Date: Thursday, April 30, 2015 at 8:00 PM
To: Peter Wenzl <peter.wenzl@croptrust.org>
Cc: Suk-Ha Lee <sukhalee@snu.ac.kr>, Jones Jennifer <jjones@smithbucklin.com>, "Abberton Michael (IITA)" <m.abberton@cgiar.org>, Steven Cannon <scannon@iastate.edu>, Joost Richard <RJoost@smithbucklin.com>, "Nelson, Randall - ARS" <Randall.Nelson@ARS.USDA.GOV>, "Okamuro, Jack" <Jack.Okamuro@ARS.USDA.GOV>, "邱丽娟 QIU, Lijuan" <qiulijuan@caas.cn>, 李英慧 <liyingshui@caas.cn>, Masao Ishimoto <ishimoto@affrc.go.jp>, Akito Kaga <kaga@nias.affrc.go.jp>, Robert Stupar <stup0004@umn.edu>, Ricardo Abdelnoor <ricardo.abdelnoor@embrapa.br>, "Bretting, Peter" <Peter.Bretting@ARS.USDA.GOV>, "marcelofernandes.oliveira@embr" <marcelofernandes.oliveira@embrapa.br>, Steven Cannon <steven.cannon@ars.usda.gov>, François Belzile <Francois.Belzile@fsaa.ulaval.ca>
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> 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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Peter Wenzl
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Securing our Food, Forever

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

Dear Scott,
Thanks for sending summary of our activity at Seattle. I enjoyed the meeting.
Sincerely 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

