

From: [Scott Allen Jackson](#)
To: [Nelson, Randall](#)
Cc: [Bretting, Peter](#)
Subject: Re: Genomic characterization of world soybean germplasm collections
Date: Monday, January 05, 2015 7:17:16 PM

I'm on board with you regarding pure-lining.

If we do have a meeting, we can outline the exchange issue as one of the key topics.

scott

On Jan 5, 2015, at 5:01 PM, Nelson, Randall
<Randall.Nelson@ARS.USDA.GOV> wrote:

Scott,

I think it would be great to get the curators of the major collections together. I tried, not too hard, to organize that at couple of the WSRGs but never succeeded. I think that it is important to present these issues before we meet so the participants can come prepared.

You remember correctly my discussion with Paul. He was adamantly opposed to pure lining self-pollinated germplasm accessions but that is a commonly held position. I don't see how we can proceed with using our current genetic tools without doing that.

Randy

From: Scott Allen Jackson [<mailto:sjackson@uga.edu>]
Sent: Monday, January 05, 2015 2:36 PM
To: Nelson, Randall
Cc: Bretting, Peter
Subject: Re: Genomic characterization of world soybean germplasm collections

Hi Randy (and Peter),

I realize ARS budgets are tight. If we get an international consortium together, we might be able to shake some money out somewhere....

Per your other comments, I realize exchange is difficult with several countries. I also realize that the US supplies most of the world's germplasm. I'm hopeful that such an initiative, if we stipulate exchange, may shake some of those things free (or more free). It would be one topic for discussion. I was in China at the end of November and they indicated that there is movement in the government to possibly allow some exchange. They indicated it was a result of the President's recent visit. WE'll see if that really happens.

The cost/curation/return on investment are key discussions to be had. It may be that for Glycine, it is not worth the investment—especially if pure lines are needed. (Weren't you part of the discussion in Asilomar on pure lines/single seeds with Paul Gepts?)

I agree that availability is a KEY issue. I'm hopeful that if this does proceed that we would stipulate participation on germplasm availability and that this might shake some things free. If not, we go nowhere.

FYI we have been recommended for funding by the EU and NSF to sequence ~10,000 phaseolus accessions. I hope that you and Peter can help soybean to lead the way:)

scott

On Jan 5, 2015, at 12:23 PM, Nelson, Randall
<Randall.Nelson@ARS.USDA.GOV> wrote:

Scott,

Your email was the first that I had heard of this initiative. According to Peter Bretting, ARS helped plan the initiative but has no money to contribute.

It would be good for the soybean community to be an active participant in this initiative and I would be pleased to be a part of that but there are some very significant barriers to an effective project.

Suk-Ha said he could be a part of the project but in recent years South Korea has refused our requests for germplasm. The restrictions on the Chinese collection are well known. Japan is a bit better but also have restrictions on what you can do with their germplasm. Russia and Brazil have been the most open, but Brazil has a duplicate of our collection with a very few exceptions. For all practical purposes, the USDA Collection supplies the world with soybean germplasm. If other collections are not willing to share their germplasm, characterizing this material will have very limited benefits.

We are the only collection that has pure lined accessions. Our acquisitions from China in the 90s indicate that approximately one third of their accessions are mixed lots with some accessions having as many as 10 different phenotypes. Without pure lined accessions, genotyping is not going to be very useful for these objectives.

Henry Nguyen's project has the potential to sequence 400 accessions from the USDA Collection with the selection based on the SNP data.

Those data will be available relatively soon. Without good phenotypic data on the collections, how much more useful will large scale sequencing be as compared to extensive SNP data relative to the cost and to curating and breeding objectives? I don't know how to answer that question but that would be important to consider.

If resolution of the germplasm availability and pure lining issues is a criterion for meeting, we will not meet, but I think they need to be raised prior to a meeting so all participants understand the problems and can be prepared to address them. How well these issues can be addressed will be a major factor in all future plans.

Thanks,
Randy

From: Scott Allen Jackson [<mailto:sjackson@uga.edu>]
Sent: Sunday, January 04, 2015 7:21 PM
To: i.seferova@vir.nw.ru; a-rsri@mail.ru; 邱丽娟; rlnelson@illinois.edu; Nelson, Randall; Suk-Ha Lee; kaga@affrc.go.jp; ishimoto@affrc.go.jp; Ricardo Abdelnoor; rakashi@cc.miyazaki-u.ac.jp
Cc: JJones@smithbucklin.com; Joost, Richard; Hannes Dempewolf; Peter Wenzl; Bretting, Peter
Subject: Genomic characterization of world soybean germplasm collections

Dear Colleagues,

I'm Scott Jackson from the University of Georgia in the USA. I'm contacting you as persons that have access to or are in charge of germplasm collections in various countries. You may be away of an international initiative to use genomics to characterize crop germplasm collections in order to better curate them and to exploit them for crop improvement (www.divseek.org).

I am wondering if there is interest to organize the soybean community to take advantage of this initiative. We would have to find funding source(s) for data generation, but could work hand-in-hand with Divseek to take advantage of infrastructure that will be put together to make use of the genomic data.

In the US, most of the germplasm collection has been genotyped with a 50K SNP chip. However, this has limitations and sequencing would complement the utility of the data to uncover haplotypes and non-SNP variation. In addition, it would be useful to understand redundancy within and between collections and to better understand the variation among the various collections.

If there is interest, I propose that we organize a workshop/meeting. I don't have money to pay for travel, but we could organize it as inexpensively as possible and possibly raise some money to help coordinate it. Topics might

include: interest to characterize collections at the sequence level; sequencing approaches; utility in curation; funding; etc...

If I have contacted the wrong person, or if someone is missing, please forward this email to the.

Sincerely,

Scott Jackson

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