

From: [Scott Allen Jackson](#)
To: [Nelson, Randall](#); [Bretting, Peter](#)
Subject: Fwd: Genomic characterization of world soybean germplasm collections
Date: Thursday, January 15, 2015 9:06:36 AM

Randy/Peter,

I have received positive responses from all invitees, except the Russians. I've emailed twice with no response. Perhaps Putin is screening their email...

Everyone is interested and would like to have a meeting to discuss the issues (including those that Randy raised—though some are governed politically, not by scientists).

I hope that both of you will be able to make it. Do you have any preference on when/where? I assume international travel will be difficult. Would West coast or Hawaii be good? Would be more accessible for the Asians.

Thanks, Scott

Begin forwarded message:

From: Scott Jackson <sjackson@uga.edu>
Subject: Genomic characterization of world soybean germplasm collections
Date: January 4, 2015 at 8:21:21 PM EST
Cc: <JJones@smithbucklin.com>, "Joost, Richard" <RJoost@smithbucklin.com>, Hannes Dempewolf <hannes.dempewolf@croptrust.org>, Peter Wenzl <pwenzl.personal@gmail.com>, <Peter.Bretting@ars.usda.gov>
To: <i.seferova@vir.nw.ru>, <a-rsri@mail.ru>, 邱丽娟 <qiulijuan@caas.cn>, <rlnelson@illinois.edu>, <Randall.Nelson@ars.usda.gov>, Suk-Ha Lee <sukhalee@snu.ac.kr>, <kaga@affrc.go.jp>, <ishimoto@affrc.go.jp>, Ricardo Abdelnoor <ricardo@cnpso.embrapa.br>, <rakashi@cc.miyazaki-u.ac.jp>

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

Country Contacts:

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