From: Scott Allen Jackson
To: Cannon, Steven [AGRON]
Subject: Re: Seattle meeting
Date: Wednesday, February 11, 2015 2:33:47 PM

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ok. will do.
scott

> On Feb 11, 2015, at 2:29 PM, Cannon, Steven [AGRON] <scannon@iastate.edu> wrote:
>
> Hi Scott,
>
> A very minor thing: in subsequent emails about this meeting, can you use my ARS email? That is: steven.cannon@ars.usda.gov
>
> Some of these emails may get copied to the Area office (e.g. for travel request), and they want me to use the ARS email for any official communications. Kind of got my knuckles rapped about this a couple weeks ago.
>
> Otherwise, the data questions are the ones I am thinking about most: appropriate repositories, stable identifiers, handling of full resequencing data and new ab initio assemblies, etc. I think Peter Bretting may weigh in on this.
>
> - Steven
>
> ---
>
> **From:** Scott Allen Jackson <sjackson@uga.edu>
> **Date:** Wednesday, February 11, 2015 at 1:13 PM
> **To:** "Okamuro, Jack" <Jack.Okamuro@ars.usda.gov>, "Nelson, Randall" <Randall.Nelson@ars.usda.gov>, "Bretting, Peter" <Peter.Bretting@ars.usda.gov>, Robert Stupar <stup0004@umn.edu>, Steven Cannon <scannon@iastate.edu>
> **Cc:** "Jones, Jennifer" <jjones@smithbucklin.com>, "Joost, Richard" <RJoost@smithbucklin.com>
> **Subject:** Seattle meeting
>
> US folks only.
>
> Below is a rough agenda. I would like feed back from you all before I send it to the entire group (along with logistics). Randy knows and has dealt with many issues in this community before, so I wanted to get input on things that are missing or that we should avoid. Obviously, germplasm exchange will be an big issue, but much beyond our control. The three Discussion items are things that we will need to discuss and could be thorny. I am missing anything?
>
> Randy, I have you talking briefly about the 50K SNP stuff done with Perry's group. Bob, can you talk about non-SNP variation? (I can give you some epi-variation slides if you need.)

Jack/Steven, I don't have databasing as a discussion item in here. It's obviously an issue, but I don't want to get too sidetracked but it would be good to have some ideas (perhaps relative to DivSeek) on that. If people buy into the overall idea and we move forward as a group then, of course, databasing will be an issue at some point.

proposed agenda

Agenda
Introductions
Peter Wenzl: introduction to DivSeek initiative (www.divseek.org)
Short 8 minute reports by country/collection on a) collection, b) application of genomics/high density markers for characterization, c) phenotyping and d) utilization.
Brazil
China
Japan
Korea
United States
CGIAR
Randy Nelson: 50K SNPs on US collection
Lijuan Qiu: sequence analysis of soybean and G. soja
Robert Stupar: non-SNP variation
Discussion 1: How to collectively characterize collections
Discussion 2: Data sharing
Discussion 3: Germplasm issues: redundancy, sharing, etc.

Thanks, Scott Jackson