

**From:** [Scott Allen Jackson](#)  
**To:** [Okamuro, Jack](#); [Nelson, Randall](#); [Bretting, Peter](#); [Bob Stupar](#); [Cannon, Steven \[AGRON\]](#)  
**Cc:** [Jones, Jennifer](#); [Joost, Richard](#)  
**Subject:** Seattle meeting  
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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](http://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