

**From:** [Scott Allen Jackson](#)  
**To:** [Robert Stupar](#)  
**Subject:** Re: Seattle Meeting, April 15-17  
**Date:** Friday, February 13, 2015 12:18:22 PM

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Great. 15-17 is good. That's what I'm doing.

Sent from my iPhone

On Feb 13, 2015, at 10:51 AM, Robert Stupar <[stup0004@umn.edu](mailto:stup0004@umn.edu)> wrote:

Hi Scott,

I just booked my room. Thanks for organizing this.

I will be happy to talk about non-SNP variation. Feel free to send along slides on epi-variation.

Should I plan to fly in the evening of the 15th and fly out the morning of the 17th? (I would like to book this flight ASAP.) It seems that all the formal meeting time will be on the 16th. Is that correct?

Thanks,  
Bob

Robert Stupar  
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On Thu, Feb 12, 2015 at 3:54 PM, Scott Allen Jackson <[sjackson@uga.edu](mailto:sjackson@uga.edu)> wrote:

Hi everyone,

Details below on the meeting on the application of genomics for soybean genomic resources.

1) **Hotel:** I have a room block reserved at 15-17 April at the Seattle Downtown Courtyard Marriott (612 2nd Avenue Seattle WA 98104). **You need to immediately register your room** under your name and credit card. You can do so by using the following link: [Book your group rate for Germplasm and Genomics Meeting Room Block](#). The full link is at bottom of email in case the embedded link does not work.

There is a light rail (<http://www.soundtransit.org/Fares-and-Passes/Link-fares>) that will take you from the airport to 0.1 miles from the hotel (get off at Pioneer Square). The cost is \$2.75 USD.

2) **Proposed meeting agenda** (this is a beginning outline. If you have additional ideas/thoughts, please let me know).

Purpose: to explore the possible application of genomics and phenomics to the international soybean genetic resources.

#### 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 (15 min)

\* Lijuan Qiu: sequence analysis of soybean and G. soja (15 Min)

\* Robert Stupar: non-SNP variation (15 min)

Discussion 1: How to collectively characterize collections

Discussion 2: Data sharing

Discussion 3: Germplasm issues: redundancy, sharing, etc.

Thanks and let me know if you have any questions,

Scott Jackson

Link for hotel reservations:

[https://www.marriott.com/meeting-event-hotels/group-corporate-travel/groupCorp.mi?resLinkData=Germplasm%20and%20Genomics%20Meeting%20Room%20Block%5Eseaps%60GGMGMA%60159.00%60USD%60false%604/15/15%604/17/15%603/25/15&app=resvlink&stop\\_mobi=yes](https://www.marriott.com/meeting-event-hotels/group-corporate-travel/groupCorp.mi?resLinkData=Germplasm%20and%20Genomics%20Meeting%20Room%20Block%5Eseaps%60GGMGMA%60159.00%60USD%60false%604/15/15%604/17/15%603/25/15&app=resvlink&stop_mobi=yes)