



Browse by

Summary Table

Presenting Author

All Authors

Author's Institutions

Abstract Title

Abstract Keywords

Program/Schedule

Programs At-A-Glance

Detailed Programs

Custom Schedule

Sessions

Date/Time

Locations

Search

Botany 2014 Home

View Attendees

Login

## Abstract Detail

Like  Tweet  Share  G+1

Genomics / Proteomics

[Marques, Isabel](#) [1], [Les, Don](#) [2], [Macfarlane, Terry D.](#) [3], [Conran, John G.](#) [4], [Rudall, Paula](#) [5], [Logacheva, Maria](#) [6], [Sokoloff, Dmitry D.](#) [7], [Remizowa, Margarita V.](#) [7], [Graham, Sean W.](#) [8].

### The root of the flowering plants, re-re-revisited.

Most molecular evidence points to a root of flowering-plant phylogeny that divides the angiosperm crown group into *Amborella* vs. all remaining species. However, a subset of analyses have persistently recovered alternative arrangements, typically connecting the root node between *Amborella* plus water lilies, vs. all other angiosperms. These results may be a result of low taxon density in angiosperms or outgroups, but concern seems warranted about this issue given the large phylogenetic distance that separates angiosperms from the other extant seed plants, a possible source of strong systematic error. Some recent publications have focused on using whole plastid genome samplings to investigate this problem (for analysis of the subset of protein-coding plastid gene regions, the plastid gene set). However, the number of relevant lineages that have had their plastid genomes sequenced is still relatively sparse. Here we revisit this question with an expanded sampling of plastomes from multiple lineages around the root node of angiosperm phylogeny. We are aiming for a complete genus-level sampling from the ANITA grade of angiosperms, and currently have 12 of the ~15 genera represented, which we generated using genome-survey sequencing and de novo assembly. Our sampling includes multiple outgroups and other angiosperms, in addition to multiple representatives of the aquatic family Hydatellaceae (Nymphaeales). We also sequenced full plastid circles for a representative subset of taxa to investigate genome structural evolution among these lineages, which define the earliest splits in angiosperm phylogeny.

[Log in](#) to add this item to your schedule

- 1 - University Of British Columbia, Dept of Botany, 3529-6270 University Blvd, Vancouver, BC, V6T1Z4, Canada
- 2 - University of Connecticut, Department of Ecology and Evolutionary Biology, 75 N. Eagleville Road, Unit 3043, Storrs, CT, USA
- 3 - Western Australian Herbarium,, Department of Parks and Wildlife,, Brain Street,, Manjimup, WA, 6258, Australia
- 4 - The University Of Adelaide, ACEBB EEB/EES, Benham Bldg, DX650 312, Adelaide, N/A, SA 5005, Australia
- 5 - Jodrell Laboratory, Royal Botanic Gardens KEW, Richmond, N/A, TW9 3DS, United Kingdom
- 6 - Moscow State University, Evolutionary Biochemistry, Leninskie Gory 1/40, Moscow, N/A, 119991, Russia
- 7 - Department of Higher Plants,, Faculty of Biology,, M.V. Lomonosov Moscow State University,, Moscow,, 119234, Russia
- 8 - University of British Columbia, Department of Botany, 3529 - 6270 University Boulevard, Vancouver, BC, V6T1Z4, Canada

#### Keywords:

*none specified*

**Presentation Type:** Oral Paper:Papers for Topics

**Session:** 35

**Location:** Pines South/Boise Centre

**Date:** Wednesday, July 30th, 2014

**Time:** 11:45 AM

**Number:** 35015

**Abstract ID:**534

**Candidate for Awards:**Margaret Menzel Award