"Genome-scale Phylogenetics"

Frontiers in Phylogenetics 3rd Annual Spring Symposium
Baird Auditorium, National Museum of Natural History
Washington, DC, Monday May 20, 2013

9:30-9:35  Opening Remarks and Logistics
          Michael Braun, Frontiers in Phylogenetics Program, NMNH

9:35-9:45  Introduction and Welcome to the Smithsonian
          Eva Pell, Undersecretary for Science, Smithsonian Institution

9:45-10:30 My Students Could Do My Thesis in Five Minutes; How to Cope with the Next
          Generation
          Rob DeSalle, Sackler Institute of Comparative Genomics, AMNH

10:30-11:00 Using Whole Genomes to Resolve the Avian Tree of Life
          Erich Jarvis, Duke University Medical Center

11:00-11:30 Break

11:30-12:00 Molecular Phylogenies, Genomics and the Bacterial Species Concept
          Margaret Riley, University of Massachusetts Amherst

12:00-12:30 Phyto transcriptomics to Bring the Understudied Ostracoda into the Fold
          Todd Oakley, University of California Santa Barbara

12:30-14:00 Lunch Break

14:00-14:30 Evolution via the Grape Vine – Insights from Transcriptome Sequence Data
          Jun Wen, Department of Botany, NMNH

14:30-15:00 Genome-scale Phylogenetics of Rapid Adaptive Radiation: RAD Sequence Data
          Illuminates the History of Lake Victoria Cichlids
          Catherine Wagner, Eawag, Swiss Federal Institute for Aquatic Science and Technology

15:00-15:30 Break

15:30-16:00 Shotgun in the Dark or a Rifle in the Daylight? The Case for Using Single Copy
          Orthologous Gene Capture in Phylogenetics
          Gavin Naylor, Hollings Marine Lab, College of Charleston and Medical University of
          South Carolina

16:00-16:30 Achieving Phylogenomic Nirvana: Ultraconserved Elements (UCEs) Capture History
          at the Species, Population, and Individual Levels
          Brant Faircloth, Department of Ecology and Evolutionary Biology, University of
          California, Los Angeles

16:30-17:00 Unsolved Challenges- Panel Discussion on Future Directions