



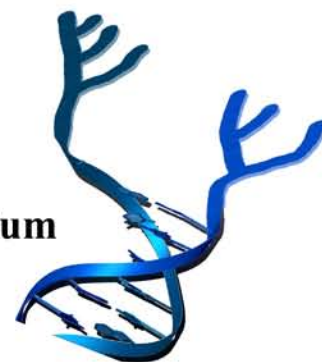
Smithsonian

"Genome-scale Phylogenetics"

Frontiers in Phylogenetics 3rd Annual Spring Symposium

Day 2 - Discussion

Baird Auditorium, National Museum of Natural History
Washington, DC, Tuesday May 21, 2013



Time	Session Topic; focal taxon (if any)	Speaker/Discussion Leader
9:00 - 9:30	workflow for phylo-transcriptomics; RNA from very small samples; Ostracoda	Todd Oakley, <i>University of California Santa Barbara</i>
9:30 - 10:00	Informatics workflow for phylo-transcriptomics; insects	Adam Bazinet, <i>University of Maryland</i>
10:00 - 10:30	"Transcriptome assembly, annotation and challenges : A case study in corals"	Shaadi Pooayei-Mehr, <i>American Museum of Natural History</i>
11:30 - 11:00	BREAK	
11:00 - 11:30	"Challenges facing next generation phylogenetics: Monsters under the bed"	Gavin Naylor, <i>College of Charleston</i>
11:30 - 12:00	"Exon capture and assembly for bony fish phylogenetics: is paralogy a problem?"	Guillermo Orti, <i>George Washington University</i>
12:00 - 13:30	LUNCH	
13:30 - 14:00	generation and analysis of RAD-seq data; cichlid fish	Catherine Wagner, <i>Swiss Federal Institute for Aquatic Science and Technology</i>
14:00 - 14:30	UCEs, RAD-seq, amplicon-seq on MiSeq/HiSeq	Brant Faircloth, <i>University of California Los Angeles</i>
14:30 - 15:00	informatics workflow for bacterial phylogenomics	Marc Allard, <i>U.S. Food and Drug Administration</i>
15:00 - 15:30	BREAK	
15:30 - 16:00	"Whole genome phylogeny of Archaea as an example of how to tackle the extremes: ancient divergences, long branches, and missing data"	Rebecca Dikow, <i>National Zoological Park & National Museum of Natural History</i>
16:00 - 16:30	"New approaches to species tree estimation in the presence of Incomplete Lineage Sorting"	Tandy Warnow, <i>University of Texas at Austin</i>
16:30 - 17:00	"Phylogenomics of insects - the impact of matrix composition"	Sabrina Simon, <i>American Museum of Natural History</i>