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Cai, Liming [1].

Herbariomics-based biodiversity research: from specimen to phylogeny.

Herbarium specimens provide the most reliable links between taxonomy, phenotypic traits, genetic information, and species' distributions. The application of genome sequencing to herbarium specimens (herbariomics) and mounting efforts in digitization provide unparalleled opportunities to investigate phylogenetic diversity in a spatio-temporal context. However, applying herbariomics across large clades can still be challenging due to technical and financial bottlenecks. In this half-day workshop, we will provide hands-on instructions for the design and application of genome skimming technique to herbarium specimens. Participants will be introduced to techniques that enable efficient and economic genomic sequencing across hundreds to thousands of specimens. We will also provide step-by-step instructions to curate and analyze high throughput sequence data with an emphasis on phylogenetic studies. Participants will learn to assemble and annotate sequences from the plastid, mitochondrial, and nuclear ITS regions using the state-of-the-art tool GetOrganelle. Following assembly, we will introduce an efficient pipeline to extract orthologous sequences from genic and intergenic regions for phylogenetic analysis. Participants will learn to reconstruct alignments and phylogenetic trees for large data set containing thousands of tips. For advanced users, we will also introduce strategies to identify and verify structural changes in the plastid genomes by visualizing the assembly graphs produced by GetOrganelle. Prepared datasets will be provided, but attendees may bring their own data. Participants will need to bring a laptop (either Mac or Windows) with a UNIX-compatible operating system such as OS-X or Linux.

Planned Speakers:

Liming Cai, UC Riverside

Hongrui Zhang, Harvard University

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1 - University of California - Riverside

Keywords:

none specified

Presentation Type: Workshop

Session: W16, Herbariomics-based biodiversity research: from specimen to phylogeny

Location: Virtual/Virtual

Date: Sunday, July 18th, 2021

Time: 1:00 PM(EDT)

Number: W16001

Abstract ID:20

Candidate for Awards:None