Branching Out: Generating an Evolutionary Tree of Southeast Asian Plants with Computational Tools

Conner J. Copeland  
University of Montana, Missoula, conner.copeland@umconnect.umt.edu

Travis Wheeler  
University of Montana, Missoula

Jedediah Brodie  
University of Montana, Missoula

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Branching Out: Generating an Evolutionary Tree of Southeast Asian Plants with Computational Tools
Conner Copeland¹, Jedediah Brodie², Travis Wheeler¹

¹Dept. of Computer Science, University of Montana, Missoula, MT, USA; ²Dept. of Biological Sciences, University of Montana, Missoula, MT, USA

Marsupials, Mammals, and Angiosperms: An Untold Tale of Evolutionary History
The islands of the Southeast Asian archipelago are home to a distinctive gradient of animal species. Islands closer to mainland Asia are home to mammals, while those closer to Australia host marsupials. This is illustrated by the figure below, which demonstrates how the region can be divided into sections based on animal populations. However, the islands are home to plant species from the same genera, presenting a unique opportunity to investigate how interactions with different animals have shaped the evolution of the islands’ plants. Efforts to research this phenomenon by the Biology Department’s Dr. Jedediah Brodie have been hampered by a lack of a phylogeny, or evolutionary tree, of these plant species. This project seeks to provide a phylogeny for use in his research, and to fill an important hole in our knowledge of evolutionary history.

Our Pipeline
Our pipeline works similarly to the general method, using 3 sequences (matK, rbCL, and Internal Transcribed Spacers 1 and 2) and 4 MSA-building tools (Opal, MAFFT, Muscle, and Clustal Omega). Multiple tools were used to limit the impact that software bias may have on the alignment input to the phylogeny inference software. In this way, highly supported regions are likely to be found in all alignments, while uncertain regions will differ from tool to tool, receiving less support. The tool FastTree was used to build an approximate Maximum Likelihood phylogeny from the resulting concatenated MSA.

Current Results
The figure to the left represents the phylogeny constructed using the pipeline above, and includes over 1200 species. In the zoomed region shown above, we demonstrate that typical genus-level clusters are largely represented in the tree. Development of this phylogeny will support future analyses of phylogeographic and species-coevolutionary processes.