

Jeanmaire Molina's Research Interests

My research interests encompass plant evolution, community ecology, conservation and ethnobotany. The versatility of phylogenetics in elucidating plant evolutionary relationships, dating origins and understanding the mechanisms that have produced current plant distributions, as well as its application in community ecology and herbal medicine make it indispensable to my research.

Phylogenetics and Biogeography of Philippine Plants. Originally from the Philippines, which has over 7,000 islands of varying sizes and geological histories, I am interested in understanding how the Philippine islands have been colonized by plant taxa throughout its geological history and how much phylogenesis (in situ speciation) has contributed to current species richness. This may be addressed through a comparative phylogeographic approach wherein phylogenies from multiple endemic plant taxa are compared, with topological congruence to suggest that similar geological and environmental processes shaped species' phylogenetic history. Do the phylogenies reflect the chronology of geological changes in the Pacific during the Tertiary (65-2 million years ago/mya)? Or did the Pleistocene glaciations (2 mya-12000 years ago), characterized by repeated fragmentation and coalescence of islands left more of a phylogenetic imprint? In the plant family Leeaceae, the phylogeny shows support for Miocene (5-23 mya) species diversification (Molina et al. 2013, *Bot. J. Linn. Soc.*)

Phylogenetic Community Structure of Philippine Forests. In collaboration with the Smithsonian's Center for Tropical Forest Science (CTFS) we have collected DNA barcodes from tree species in the 16-hectare Palanan Forest Dynamics Plot to facilitate taxonomic identifications. We are also using these barcodes to reconstruct the community phylogeny to better understand what shapes community assembly in this Philippine lowland forest constantly beleaguered by typhoons. Can we expect phylogenetic clustering of windward tree species resulting from habitat filtering of conserved traits? At the scale of the plot community, windward tree species seem to be scattered throughout the phylogeny, suggesting that the windward-adapted phenotype is not phylogenetically conserved, but has evolved in various unrelated lineages (Molina et al., in prep).

Evolutionary Genomics and Reproductive Biology of Philippine Rafflesia. The panda of the plant world—*Rafflesia* is found only in Southeast Asia, with Philippines as the seat of diversity. *Rafflesia* produces the biggest flowers (as seen in photo). *Rafflesia* is a parasite solely feeding off the tropical grapevine *Tetrastigma*, and why this host is yet another mystery. In collaboration with New York University, we have sequenced the whole genomes of Philippine *Rafflesia* species to understand the evolutionary genomics of parasitism. We have published evidence for the possible loss of the plastid genome in *Rafflesia* with recovered plastid-like sequences phylogenetically determined to be horizontally transferred from the host (Molina et al. 2014, *Mol. Bio. Evol.*). I am also working with the US Botanic Garden (USBG) to propagate Philippine *Rafflesia* for ex situ conservation. We now have the host plants at USBG, and these can be used for grafting of *Rafflesia*-infected cuttings and seed inoculation experiments (Molina et al. In press. *Sibbaldia*). To have *Rafflesia* bloom here in the US for the first time will draw not only tourism, but much needed conservation awareness in the Philippines, a biodiversity hotspot.



DNA Barcoding and Ethnobotany of Herbal Medicines. The confluence of diverse immigrant cultures in the United States and the accessibility of many of their traditional herbal medicines here make the US an interesting venue to understand the dynamics of urban ethnobotany. Increased demand for these alternative medicines and lack of oversight from the US Food & Drug Administration (FDA) encourages

unscrupulous herbal substitutions that may be revealed by DNA barcoding, which I have been conducting in my lab to taxonomically validate herbal products sold in the US. Borrowing techniques from community phylogenetics, I am also exploring phylogenetic patterns in traditional herbal medicine use that may guide drug discovery efforts. This is seen below for the family Burseraceae, with different species co-opted by various immigrant cultures (represented by colored phylogenetic branches) for addressing the same concern—treating muscle-skeletal pain (indicated by red boxes). This pattern of cultural convergence (Xavier and Molina 2016, *J. Herb. Med.*; Alrashedy and Molina 2016, *PeerJ*) reflects the inherent healing phytochemistry of members of this family, independently discovered by different cultures for the same purpose. An outlier in my Philippine-based research projects, but nonetheless important, my growing interest in ethnobotany is driven by its importance in drug discovery, and the role of phylogenetics in uncovering novel drug sources from phylogenetic patterns of cultural convergence.

