

QUANTITATIVE AND SYSTEMS BIOLOGY COLLOQUIUM: Integrating phylogenetic and genomic approaches to study fish macroevolution

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About the Speaker:

Originally from Colombia, Ricardo Betancur-R. began his academic career in 1994 with a B.Sc. in Marine Biology from Universidad Jorge Tadeo Lozano, followed by an M.Sc. in Marine Biology from Universidad Nacional de Colombia in 2004. That same year, he moved to the U.S. and completed a Ph.D. in Biological Sciences at Auburn University in 2009. He subsequently conducted postdoctoral research at The George Washington University until 2013 and held a 2-year Peter Buck Postdoctoral Fellowship at the Smithsonian National Museum of Natural History from 2013 to 2014. From 2014 to 2018, Ricardo served as an Assistant Professor at the University of Puerto Rico, Río Piedras campus, and later at the University of Oklahoma, where he became an Associate Professor in 2023. He is currently an Associate Professor at SIO in the Marine Biology division. Ricardo's research focuses on phylogenetic inference and comparative analysis, using fishes as model systems and emphasizing genome-scale approaches for macroevolutionary studies. Fieldwork is a cornerstone of his research, with expeditions spanning four continents.



Abstract:

Macroevolution has traditionally been studied through the lenses of paleontology and paleobiology. However, the growing availability of time-calibrated molecular trees has recently spurred the development of novel approaches to study diversification dynamics (phylogenetic comparative methods) and to uncover the genomic underpinnings of trait origins across the Tree of Life (phylogenetic genotype-to-phenotype mapping). In this seminar, I will present studies that leverage these approaches, using fishes as model systems. Specifically, these studies aim to elucidate how habitat transitions have influenced the macroevolutionary history of fishes. I will demonstrate how transitions along the benthic-pelagic axis in the water column are linked to historical mass extinction events and convergent evolution in traits such as body shape, locomotion, and trophic functions in marine fishes. Additionally, I will discuss how transitions from marine to freshwater environments have driven replicated adaptive radiations in a region characterized by an otherwise depauperate ichthyofauna: the tropical rivers of Australia and New Guinea (AU-NG). These marine-derived adaptive radiations in AU-NG exhibit extraordinary diversification, not only in species richness and morphology but also in genes associated with adaptive traits, which have undergone episodic diversifying selection. Lastly, I will briefly highlight other research conducted by members of my lab, including studies on historical biogeography, comparative phylogeography, and species delimitation in marine fishes.

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Location: SSM 104