**Drivers of population genetic structure in plants: global, regional and local scales.**

Population genetic structure has long been recognized to be a critical component of plant biodiversity, including local adaptation, conservation, and incipient speciation. However, its drivers remain poorly understood, especially across different spatial scales. Here I examine mechanisms that affect plant population genetic structure at global, regional, and local scales. At the global scale, I performed a meta-analysis of genetic differentiation (FST) in seed plants, based on a 337-species dataset with data on FST and species traits. I found that FST is higher for tropical, mixed-mating, non-woody species pollinated by small insects, and lower for temperate, outcrossing trees pollinated by wind. At regional and local scales, I focused on understory flowering plants in the Andean biodiversity hotspot. At the regional scale, I tested the effect of flowering asynchrony on genetic differentiation among conspecific allopatric subpopulations. I found that species with higher flowering asynchrony between their subpopulations also show greater genetic differentiation. At the local scale, I examined the effect of insect vs. hummingbird pollination modes on the spatial genetic structure of subpopulations. I found that insect pollination results in a stronger pattern of spatial autocorrelation among closely related individuals. Overall, my findings shed light on the global drivers of genetic divergence in seed plants, and point to important mechanisms for regional genetic divergence and local genetic connectivity in Andean flowering plants.