

Thursday, October 8, 1:30-2:20 p.m.

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Genomics of parallel local adaptation to serpentine and toxic copper mine soils in the wildflower *Mimulus*

A major challenge in 21st century biology is to understand how organisms adapt to complex and often unpredictable environments. Evolutionary ecologists have studied plant adaptation to extreme edaphic environments such as serpentine soils and heavy metal contaminated mine tailings for decades and this classic work provides some of our best examples of “natural selection in action.” These extreme soils impose such strong selection that plant populations occurring on serpentine/mine soils and adjacent “normal” soils are often locally adapted over a scale of meters despite substantial gene flow. Throughout western North America local populations of the yellow monkeyflower *Mimulus guttatus* have repeatedly adapted to patches of serpentine soils or toxic copper mine tailings. Using a combination of reciprocal transplants in the field and lab, QTL mapping, physiological experiments, and population genomic approaches, we are beginning to identify the most important evolutionary genetic changes that have enabled this plant species to survive and reproduce on serpentine soils or mine tailings throughout its range. Serpentine soils and copper mine soils are patchily distributed and vary substantially in their physiochemical properties, and it is not known whether widespread species, such as *M. guttatus*, repeatedly adapt to different patches via the same or different molecular mechanisms. Even if the same gene is repeatedly used, is this due to new mutations or repeated use of standing variation? Are serpentine or Cu mine adapted alleles and pathways selectively equivalent on soils from different serpentine or mine regions, or uniquely suited to each particular habitat? This talk will highlight some of our initial discoveries that answer some (but not all!) of these basic questions about evolutionary plant solutions to ecological challenges.