

Leebens-Mack Lab – Postdoctoral research project opportunities

My lab uses comparative genomics analyses to pursue a wide range of questions relating to the genetic and molecular underpinnings of macroevolutionary innovations such as flowering, the shifts from C₃ photosynthesis to CAM, shifts from hermaphroditism to dioecy, and changes in pollination syndromes. We have several projects that a postdoc could jump into, but I am also open to launching new research that could be pursued using a comparative genomics toolkit. Some more specific research opportunities include the following:

- We are starting an NSF-funded project that is using fast neutron irradiation to identify genes contributing to various developmental traits in weedy morning glories (*Ipomoea purpurea*). This project could be expanded to developing and using functional genomics tools in other morning glory species including sweetpotato (*I. batatas*) and wild relatives (e.g. *I. trifida*).
- My lab has worked on identification of sex determination systems in several dioecious plant species and experimentally identified sex determination genes in garden asparagus (*Asparagus officinalis*). This work is ongoing and there are opportunities to characterize evolutionary, molecular and developmental processes driving sex differences in a variety of dioecious plants. An NSF-funded project is exploring the causes and consequences of sex-based differences in responses to environmental stress including heat and drought stress.
- As part of a large initiative supported by the Department of Energy's Joint Genome Institute, we are sequencing and annotating genomes from a broad range of plant species - see <https://phytozome-next.jgi.doe.gov/ogg/>. This work is yielding new opportunities for comparative analysis of variation in genome structure, gene content, and gene function across land plants. Possible research projects using these data include ancestral genome reconstruction, characterizing the fate of genes following gene and genome duplications, and integrative analyses of gene families with genes involved in specific biological processes (e.g. biosynthesis of cell wall components, diversification of specific biosynthetic pathways, and regulation of plant developmental and physiological processes).