**Poinsettias to pitcher plants: deciphering the genomic basis of extreme plant adaptation**

**Modern transcriptomic and genomic techniques offer the ability to explore the patterns and drivers of plant diversification on a scale never before possible. Using a data set of over 300 transcriptomes across Caryophyllales, we found evidence for at least 21 ancient genome duplication events, which is more than previously known in all of angiosperms. From the data set of >15,000 genes per species, we discovered that many gene duplication events were associated with key adaptive trait changes, such as evolution of pigmentation and plant carnivory. This work integrates not only new molecular phylogenomic and computational methods, including several developed for this study, but also field- and collection-based research to connect phenotypic shifts to their genetic and genomic bases.**