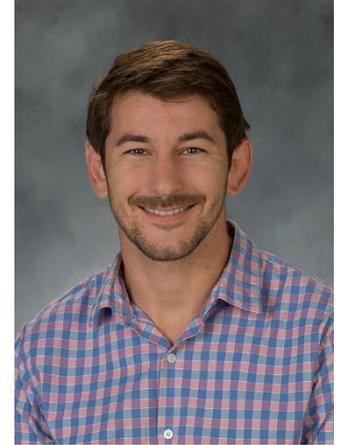


Grant Title: Collaborative Research: RUI: Understanding the effects of ploidal level on responses to global change in plants

Funding Agency: National Science Foundation: Integrative Organismal Systems

PI and Co-PIs: Emily Sessa (University of Florida - Lead institution), Eddie Watkins (Colgate University), Clayton Visger (CSU Sacramento)

Description: Polyploidy, or whole genome duplication, occurs when an organism has one or more extra copies of all its chromosomes. This phenomenon is particularly common in plants, and recent estimates suggest that 15-30% of plants are polyploid. Polyploid species include a vast number of crop and other plants with economic and agricultural uses (e.g., cotton, wheat, potato, soybean). Polyploidy is known to influence a wide range of genetic and physiological features of plants, including physiological traits related to water use and photosynthesis. Polyploid plants can be more vigorous than diploids, have broader ecological niches, wider geographic distributions, and increased ability to invade new habitats, all driven by novel genetic combinations or gene expression patterns that can produce extensive changes in many traits.



Our study is focused on the nature and magnitude of hypothesized differences across ploidy in an experimental setting, using integrated analyses of demography (Emily Sessa), physiological ecology (Eddie Watkins), and transcriptomics (Clayton Visger). We have chosen a set of fern species found in forests throughout the eastern U.S. This is a naturally occurring plant system where polyploidy is prevalent, and whose members are ecologically important in the ecosystems where they occur. Gametophytes of six *Dryopteris* species, including two pairs of a polyploid and its parent taxa, will be grown in a multifactorial experiment with drought and temperature treatments. Data will be collected on reproductive and physiological ecology to determine how changes in temperature and water availability influence demographics and sporophyte recruitment from gametophytes as well as ability to recover from environmental stress. RNAseq will be used to generate transcriptome-wide gene expression profiles to evaluate differences between unstressed, dehydrated, and rehydrated gametophytes in different temperature treatments. Data will be analyzed using new bioinformatic methods developed by Visger for performing differential gene expression analyses on per-cell, per-biomass, and per-transcriptome bases. The results of this work will improve the understanding of how ploidal level may influence species' responses to environmental change.

Sac State Student impact: This project will provide financial support for one graduate student, four undergraduate students, and support travel to conferences (domestic and international) for five students. Two students will also travel to University of Florida for a week-long project meeting and training session, where they will experience an R1 research environment.

Visger Lab: <https://cvisger.github.io/Visger-Lab/>