

EXECUTIVE SUMMARY: Desiccation tolerance (DT) is the remarkable ability to suspend metabolic activity and survive near complete loss of cellular water. DT is relatively common in the mosses, but DT is only present in the seeds and pollen in most flowering plants. The genetic and molecular basis of DT in mosses has garnered great interest in the field of agricultural biotechnology, as this trait has important implications for the improvement of economically important crop plants in the context of global aridification and climate change. Researchers in this field have focused their efforts on one moss, *Syntrichia ruralis*, which has emerged as the primary model for understanding moss DT. However, pilot studies have suggested that, like many traditional moss species, *S. ruralis* may actually represent a heterogeneous amalgam of evolutionarily divergent cryptic lineages. Genetic data can be used to identify such cryptic lineages and clarify their evolutionary relationships. This information is critical for the prudent use of *S. ruralis* as DT model, particularly if cryptic lineages differ in their levels of DT. This grant will support a graduate student, who will be trained in current molecular and analytical methods to test the following hypotheses: (1) *S. ruralis* contains multiple cryptic lineages; (2) these lineages vary in their levels of DT; and (3) changes in the coding sequence of a DT candidate gene (*Tr288*) are correlated with these lineage-specific differences in DT. The results of this study will benefit the community of DT researchers currently utilizing *S. ruralis*, and also serve as the basis for future research on the distribution of variably desiccation tolerant moss lineages across California, with the ultimate aim of utilizing these unique organisms as indicators of both historical and contemporary climate change.