

## **T11: A phylogenetic approach to understanding gene relevance to important traits in the evolution of land plants.**

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The use of phylogenetic data to address the importance of individual genes in a complex phenotype, or in the evolution of a particular trait, is an approach that has received relatively little attention. We have initiated a study of the evolution of desiccation tolerance. Phylogenetic analyses suggest that desiccation tolerance was primitively present in the bryophytes (basal-most living clades of land plants), but was lost early in the evolution of tracheophytes. Desiccation tolerance has re-evolved in seeds and pollen and vegetatively in *Selaginella*, the ferns, and at least eight independent evolutions in the angiosperms. In the moss *Tortula ruralis*, we have identified several genes that appear to be intimately involved in desiccation tolerance. One of these genes, a rehydrin Tr 288, accumulates transcripts at high levels in response to desiccation that are only used upon rehydration. This gene has physical properties similar to the stress induced dehydrin proteins. Tr 288 however, has little sequence similarity with dehydrins other than the presence of a rudimentary K-box sequence at its carboxy terminus. Our working hypothesis is that Tr288 is an ancestral dehydrin and as such may be a useful marker in a phylogenetic analysis of desiccation tolerance. We devised a PCR based strategy, utilizing the highly repetitive nature of Tr288, to track the presence of Tr288 homologs (verified by sequence analysis) in other species. We have detected homologs within the *Tortula ruralis* complex and have expanded the analysis into other bryophyte groups and into the tracheophyte lineages. Our findings indicate that this gene, in its present form, does have adaptive relevance in regards to the evolution of desiccation tolerance. Furthermore, Tr288 seems to have evolved after the liverworts branched away from the hornworts, mosses, and tracheophytes, consistent with the current opinion that the liverworts are sister to the remainder of the land plants. The data also reveal that some of the more modern groups of desiccation tolerant mosses that are adapted to hot tropical climates may have mechanisms of tolerance that differ from the more basal clades (this research facilitated by the "Deep Gene" RCN grant NSF-0090227).