

**Isolation and characterization of novel aldehyde dehydrogenase (ALDH) genes from the desiccation-tolerant moss *Tortula ruralis*.**

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The desiccation-tolerant moss *Tortula ruralis* is an important experimental system for the study of gene control in response to severe water deficit-stress. We have employed EST analysis to discover genes that mediate vegetative desiccation tolerance and have identified two unique members of the aldehyde dehydrogenase (ALDH) gene super family, ALDH7B6 & ALDH21A1. ALDHs represent an important adaptive response to osmotic- and oxidative-stress and are an important pathway for the detoxification of aldehydes by oxidation to their corresponding carboxylic acids. Aldehydes are intermediates in a number of fundamental biochemical pathways that can also be generated in response to a variety of environmental stresses that perturb metabolism such as salinity, cold, heat-shock and desiccation. ALDH7B6 encodes a turgor-responsive ALDH7 protein family homologue with significant similarity to the angiosperm cDNAs 26g, Btg-26 and MF-40. ALDH21A1 encodes a novel ALDH protein. ALDH21A1 is less than 30% identical to known ALDH proteins. Based upon established nomenclature for ALDH proteins, ALDH21A1 describes a novel eukaryotic ALDH protein family designated ALDH21. RNA blot hybridizations were used to analyze expression in response to ABA, UV-C, NaCl and desiccation. ALDH7B6 steady-state mRNA transcript levels are unchanged in response to all treatments and the gene is constitutively expressed. ALDH21A1 steady-state transcript levels increased in response to all treatments and were more abundant within the polysomal mRNA fraction of salt-treated gametophytes. We postulate that ALDH7B6 & ALDH21A1 play an important role in the detoxification of aldehydes generated in response to desiccation-stress, and that ALDH21A1 expression represents a unique stress tolerance mechanism.