

**P3: The ABA- and osmotic stress-response in *Physcomitrella patens*: expression of *Lea* homologues.**

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Late Embryogenesis Abundant (LEA) proteins accumulate in developing seeds during embryonic maturation. Highly hydrophilic and natively unfolded, the ABA- and osmotic stress-induced accumulation of these proteins has been linked with the acquisition of desiccation tolerance that is characteristic in the seeds of most flowering plants. Three major classes of LEA proteins have been described. Group 1 LEA proteins (exemplified by the wheat “Em” protein) remain natively unfolded. Group 2 LEA proteins (“dehydrins”) and Group 3 LEA proteins have the potential to form alpha-helical structures as dehydration proceeds.

Vegetative desiccation tolerance remains widespread among the bryophytes. In some species (*e.g. Tortula ruralis*) tolerance is manifest when plants are subject to rapid desiccation; in others, including *Physcomitrella*, tolerance is induced only after a preparatory period of mild stress. This latter behaviour more closely resembles the mechanisms utilised by higher plants.

Some years ago, we demonstrated that a higher plant desiccation-associated gene – the wheat “Em” gene - was ABA-regulated in *Physcomitrella* using an identical transcriptional mechanism to that seen in cereals. Now, using the resources of the *Physcomitrella* EST databases, we have identified moss homologues of the Group 1, 2 and 3 genes, and analysed their responses to ABA and osmotic stress treatments. All exhibit ABA- and osmotic stress-induction, although with different kinetics. Induction is rapid (detectable within minutes). Isolation and characterisation of genomic and cDNA sequences of the *Physcomitrella* “Em” homologue reveals a putative ABA response element in its promoter. Interestingly, although this gene is massively ABA- and stress-up-regulated, the coding sequence contains an in-frame termination codon, implying that the gene product is translationally truncated.