

Developmental gene diversification in the moss clade

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With the near complete sequencing and incipient assembly and annotation of the *Physcomitrella* and *Selaginella* genomes, the comparative analysis of complete developmental gene families in a moss, a lycophyte, and angiosperms will soon be possible. Our studies of Class III HD-Zip and KANADI genes in all land plant lineages, as well as similarity searches for several other developmental genes in *Physcomitrella* and *Selaginella*, have revealed the presence of multiple, highly similar gene family members in *Physcomitrella*. Phylogenetic analyses have revealed that in many cases these genes are the result of duplications of a single gene following the divergence of the moss ancestor from the land plant stem lineage. The high degree of similarity suggests recent duplication events. Phylogenetic analysis of Class III HD-Zip genes in streptophytes produced a topology that was largely consistent with accepted ideas about embryophyte relationships except that a clade of *Physcomitrella* genes was resolved as sister to all other land plant sequences. While different sequence-based phylogenetic analyses have produced conflicting topologies as to the branching order of mosses, hornworts, and liverworts, mosses are not usually resolved as the lineage derived from the basal node. In our Class III HD-Zip data set *Physcomitrella* was the only moss representative. Phylogenetic analyses of mosses indicate that *Physcomitrella* is well-nested within the moss clade, which suggests that long-branch attraction may be a problem when using *Physcomitrella* sequences as sole representatives of the moss clade in gene family phylogenetic reconstruction. In order to get an initial assessment of how common multiple gene family members are in mosses and to determine whether including sequences from members of other major moss clades would affect gene family topology we have begun attempts to clone Class III HD-Zip genes from *Sphagnum* and *Polytrichum*. Initial success with *Sphagnum* indicates the presence of three Class III HD-Zip genes. Preliminary Bayesian analysis indicates that the *Sphagnum* genes form a clade that is sister to a clade including all five *Physcomitrella* genes. Including *Sphagnum* sequences changes the topology of the Class III HD-Zip tree so that moss sequences are no longer sister to all other land plant sequences. This indicates that independent gene diversification events have occurred with different moss clades and that *Physcomitrella*, as a sole representative of the moss clade, may give erroneous results in gene family reconstruction.