

**P15: *Physcomitrella patens* as a model for investigating organization and function of the cellulose-synthesizing terminal complex**

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Cellulose is synthesized at the plasma membrane as microfibrils that vary in diameter from about 3 nm in land plants to 25 nm in some algae. Microfibril structure is determined largely by the organization of arrays of integral plasma membrane protein particles known as ‘terminal complexes’. These terminal complexes contain the catalytic subunits of cellulose synthase encoded by a family of genes designated *CesA*. Although the *CesA* gene products of plants and bacteria share conserved regions, their extensive differences may contribute to variation in terminal complex and microfibril structure. We are examining the genetic basis for this variation by comparing the *CesA* genes of algae in which terminal complex structure ranges from rosettes (plant-like) to linear (bacteria-like). In preparation for direct testing of the function of domains potentially involved in terminal complex assembly, we are sequencing and examining the expression patterns of *CesA* genes from *Physcomitrella patens*, which is uniquely suited for targeted transformation and analysis of terminal complex structure by freeze fracture electron microscopy. Degenerate primers were used to amplify and clone 8 fragments representing 5 different *CesA* genes from genomic DNA isolated from *P. patens*. Probes derived from the cloned fragments were used to isolate *CesA* clones from a genomic library from *P. patens* (gift of Stavros Basharides). In seed plants, members of the *CesA* gene family are differentially expressed during primary and secondary cell wall deposition, particularly in vascular tissue, and one group of *CesA-like* genes (*CsIDs*) are expressed in tip-growing cells such as root hair and pollen tubes. Phylogenetic analysis supports the presence of *CsID* genes in *P. patens*, but does not support orthology between primary and secondary cell wall type *CesAs* in mosses and seed plants.