

P19: An analysis of the roles of MADS-box and *KNOX* genes in *Physcomitrella patens*

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MADS-box genes are involved in many ontogenetic processes including differentiation of floral meristems and determination of floral organ identities. *KNOX* genes, a group of plant homeobox genes, are essential for the generation and/or maintenance of shoot apical meristems. Since flowers are the hallmark of angiosperms and since all above-ground parts of a flowering plant are derived from the shoot apical meristem, phylogenetic and functional analyses of members of these gene families from non-flowering plants should impart a more profound understanding of the origin and evolution of the various major land plant groups and the structures that characterize each of them. *Physcomitrella patens* is an attractive system for studying the functions of MADS-box and *KNOX* gene homologues, as in addition to its phylogenetically basal position, simple life cycle and similarities to higher plants, it is especially amenable to gene targeting. We have generated single, double and triple knock-out strains involving the three known *P. patens* *KNOX* genes (*MKN1-3*, *MKN2* and *MKN4*), and confirmed their knocked out status at the molecular level. We have also confirmed the knocked out status of strains in each of which one of two MADS-box genes (*PPM1* and *PPM2*) has been targeted. The phenotypes of all *MKN* and most *PPM* knock-out strains are normal, probably because of functional redundancy within each gene family. However, in one *PPM* knock-out strain, the production of sporophytes is delayed. This agrees with the observation that *PPM1* antisense strains also exhibit delayed sporophyte production, indicating that *PPM1* may function in moss reproductive development.