

Abstract

OFPs (Ovate family proteins) are plant specific proteins, which influence the morphology of all aerial organs. OFPs have been identified as proteins interacting with TALE- (Three aa loop extension) proteins and regulating their cellular localization. TALE-proteins are homeodomain transcription factors, which are involved in processes such as meristem initiation and maintenance, organ development and reproduction in *Arabidopsis thaliana*. This work focused on the role of OFP1 and OFP5 in the development of *Arabidopsis thaliana*. Yeast two hybrid screenings were performed and new interactors of OFPs were identified and an OFP interaction network was generated. Within this network the search for network motives led to identification of several candidates, which were interacting with both OFPs and TALE-proteins. Some of these are the following proteins. TSK associating protein 1 (TSA1) is expressed in the SAM and interacts with TONSOKU (TSK), a prominent player in meristem identity and maintenance. The α -subunit of the Casein Kinase II is a conserved serin threonin kinase, which accumulates in meristematic cells and functions in cell division. MAP65-7, a protein of the conserved microtubule binding protein family MAP65 was also found as an interactor using the OFP network. This protein might mediate the cellular association of OFPs to microtubules. LONGIFOLIA 1 and LONGIFOLIA 2 are two redundant proteins, which participate in longitudinal cell elongation and display a mutant phenotype contrary to OFP1 and OFP5 mutants. For some of these interaction partners colocalization and interaction with OFP1 and OFP5 was shown *in vivo*.

In addition the analysis of loss of function and gain of function mutants could show that OFP1 and OFP5 have a redundant function in cell elongation. By generating *OFP5* amiRNA plants it was possible to study the effect of OFP5 knock down on plant development normally leading to homozygous lethal plants. The observation that OFP5 amiRNA plants show elongated cotyledons and leaves suggested that OFP5 regulates the cotyledon and leaf morphology. Furthermore it was shown that OFP1 as well as OFP5 might have a function in activating cell division. The crossing of OFP1 and OFP5 overexpression lines with a CYCB1;1-GUS markerline showed an increased mitotic activity in root cells compared to wildtype. An increased cell division rate could also be detected in the medio lateral direction in cotyledons of the OFP5 overexpression line. Therefore it is postulated that OFP1 and OFP5 play a role in the maintenance of meristematic activity by inhibiting cell elongation and

promoting cell division. In this way OFPs could have an influence on morphological organ development of *Arabidopsis thaliana*.