

PhD. thesis:

The role of bZIP transcription factors in the male gametophyte of *Arabidopsis thaliana*

Abstract

Sexual plant reproduction depends on the production and differentiation of functional gametes by the haploid gametophyte generation. Currently, we have a limited understanding of the regulatory mechanisms that have evolved to specify the gametophytic developmental programs. To unravel such mechanisms, it is necessary to identify transcription factors (TF) and their complexes that are part of such haploid regulatory networks. For that reason we selected candidate Arabidopsis bZIP TFs, which have been shown to have critical roles in plants, animals and other kingdoms. Here we describe the putative bZIP TFs regulatory network active in Arabidopsis thaliana pollen and highlight to the greater impact two members of this network - AtbZIP18 and AtbZIP34. We report the complex functional characterization of AtbZIP34 and AtbZIP18, which are widely expressed in both gametophytic and sporophytic tissues, however they possess significantly enhanced expression during late stages of pollen development. We have studied both genes using several genetic and molecular approaches. Several lines of evidence, including the AtbZIP34 expression pattern and the phenotypic defects observed, suggest a complex role of AtbZIP34 in male reproductive development that involves a sporophytic role in exine patterning, and a sporophytic and/or gametophytic mode of action of AtbZIP34 in several metabolic pathways, namely regulation of lipid metabolism and/or cellular transport (Gibalová et al. 2009). Unlike AtbZIP34, AtbZIP18 TF didn't reveal any significant disturbances in mature pollen or earlier developmental stages. Our observations suggest that AtbZIP18 itself cannot cause dramatic changes in pollen phenotype or function, probably caused by redundancy. We have also identified forming of dimers between several members of pollen expressed bZIP TFs.