

New mechanisms determining MFT-mediated sensitivity to abscisic acid during the germination of *Medicago truncatula* seeds.

The decision, when the plant should start sprouting, is one of the key developmental steps that can affect the further growth and survival of young seedlings. Thus, in a harsh environment, the seed remains dormant until favorable conditions appear. The germination process is tightly regulated by both internal signals and environmental causes. The two plant hormones abscisic acid (ABA) and gibberellin (GA) play an essential role in tilting the balance towards inhibiting or promoting germination. One of the components of the ABA and GA signaling pathways recruited to control seed germination is MOTHER OF FT AND TFL1 (MFT) protein. Therefore, MFT can be considered as an important factor controlling crucial agriculture traits, such as seed dormancy release and germination.

The MFT from *Arabidopsis* was found to promote germination of after-ripened seeds under unfavorable conditions by tuning seed sensitivity to ABA and regulating the expression of germination-related genes. AtMFT was also proposed to be an important factor in dormancy promotion in freshly matured dormant seeds. However, this issue was not fully addressed and still requires clarification. Given the economic importance of legumes, we propose to perform a comprehensive functional analysis of MFT in model legume *Medicago truncatula* (barrel medic), which has great potential for translational biology. Our preliminary data suggest conservation of *Arabidopsis* and *Medicago* MFT genes, however further studies are necessary to recognize an exact MFT mode of action in *Medicago*, and point at functional similarities and differences across species, especially in the context of ABA sensitivity modulation during the after-ripening process. Therefore, we would like to address in more detail the potential opposite role of MtMFT in seed germination depending on seed dormancy status, and finally, recognize the mechanism(s) underlying this phenomenon.

Of note, MFT-like protein is a member of the phosphatidylethanolamine-binding protein (PEBP) family and is recognized as ancestral to well-explored FLOWERING LOCUS T (FT)-like, and TERMINAL FLOWER1 (TFL1)-like proteins. The latter control flowering timing and function as transcription regulators that interact with other proteins. MFT proteins similarly to FT and TFL1 do not contain any typical DNA binding domain, and possibly require interactions with transcription factors (TFs) to modulate the expression of target genes, during seed germination. Although the potential interactions of MFT with other proteins were suggested, its partners have not yet been identified. Therefore, we are going to use several complementary methods to determine interactor(s) of MtMFT in two biological scenarios (dormant and non-dormant seeds). Additionally, we propose to resolve the crystal structure of MtMFT, which is also unknown. Crystallographic studies might reveal a mechanistic insight of MFT action, indicate potential binding sites, and help form new hypotheses regarding the identification of its cognate partners.

To summarize, in this project, we would like to answer the question of whether MtMFT can interact with different TFs/regulatory proteins depending on seed status (freshly-matured, after-ripened), and as such could differentially modulate the expression of target genes in dormant and nondormant seeds, therefore changing their sensitivity to ABA. This could be a milestone for a better understanding of the MFT-mediated sensitivity to ABA and its altering during the after-ripening process.