Evolution of the dehydration tolerance in land plants and role of the ABA-JA crosstalk in desiccation tolerance

BACKGROUND

An algal ancestor of all land plants colonised land 500 million years ago. In order to survive in the new terrestrial environment, dehydration tolerance was crucial for success. Therefore, **the first land plants had to enhance their tolerance to dehydration tolerance**. In land plants, abscisic acid (ABA) is the key signalling molecule regulating plant adaptation to abiotic stresses, including dehydration. The components of the ABA pathway are well conserved in land plants: the PYL/PP2C receptor complex, the SnRK2 protein kinases and key bZIP transcription factors (TF). In contrast, although algae synthesise ABA, they do not respond to it. This has led to the hypothesis that acquisition of ABA-modulation of an ancient desiccation tolerance pathway by an aero-terrestrial algal ancestor paved the way for the evolution of land plants.

The first land plants, such as extant non-vascular Bryophytes, evolved a strong dehydration tolerance. In contrast to Bryophytes, in plants such as angiosperms, desiccation tolerance is mostly restricted in seeds. Indeed, in angiosperms such as the model *Arabidopsis thaliana*, the bZIP transcription factors key in promoting ABA-mediated desiccation tolerance are only expressed in seeds. ABI5 is the primary TF mediating ABA-mediated tolerance. AtABI5 belongs to a functional redundant gene family of at least 6 members. Therefore, we proposed to analyze ***Marchantia polymorpha*, a new model non-vascular plant enabling to infer features of the common ancestor of extant land plants**, that evolved more than 450 million years ago. Marchantia encodes for only 2 ABI5, making it easier to characterize the redundant function of the ABI5 family.

In addition, all core elements of the jasmonate (JA) pathway are conserved in Marchantia, including the COI1-JAZ receptor complex and the MYC transcription factors. However, Marchantia do not synthesise JA-Ile, and the bioactive hormone and ligand of the Marchantia COI1-JAZ co-receptor is dn-OPDA. Recently, the interaction of ABI5-JAZ and MYC2-ABI5, key elements of the ABA- and JA-pathway, has been reported. However, **the functional outcome of the interaction of key components of the ABA- and JA-pathway, and the stress responses regulated by the resulting ABA-JA crosstalk has not been addressed to date**.

HYPOTESIS

We hypothesize that desiccation tolerance in seeds of angiosperm evolved from a general desiccation mechanism of vegetative tissues in ancient Bryophytes, the first land plants. We also propose that the same TFs regulate desiccation tolerance in angiosperms and Bryophytes.

OBJECTIVES

Here, **the PhD researcher aims to study the role of key ABA regulators such as ABI5 on desiccation tolerance in the novel Bryophyte model *Marchantia polymorpha***. The early-stage researcher aims to functionally characterize the 2 Marchantia homologs ABI5 by studding the single and double loss-of-function mutants as well as the over-expressors lines. Functional complementation of ABI5 TFs of Arabidopsis and *Marchantia* regulating desiccation tolerance will be carried out.

In addition, **the PhD researcher will study the role of the ABA-JA crosstalk in the evolution of desiccation tolerance.** The interaction of the key elements of the Marchantia ABA- and JA-pathway will be studied to evaluate the ABA-JA crosstalk in Arabidopsis and Bryophytes (based on the recently reported AtABI5-AtJAZ and AtMYC2-AtABI5 interactions).

EXPECTED OUTCOME

Addressing these hypotheses will increase our limited knowledge on evolution of desiccation tolerance and it will open the way to develop innovative desiccation tolerance biotechnological tools.

EXPERIMENTAL TASKS

- Classical and gateway-based cloning.
- CRISPR/Cas9-based genome editing in Marchantia polymorpha to generate knock-out mutants.
- Generation of over-expression lines in Marchantia polymorpha.
- Functional complementation of TFs of higher and ancestral plants regulating desiccation tolerance.
- Stress tolerance assays, such as dehydration assays and pathogen infections.
- Transcriptional analyses (qPCR and RNA-seq).
- Hormone profiling.
- Protein-protein interaction by Yeat-2-Hybryd (Y2H).
- Metabolomic analyses.