

Functional characterization of *ROOT MEANDER CURLING*, a rice gene known to be responsive to biotic and abiotic stress

Rice production is highly affected by biotic and abiotic stress conditions worldwide. The plant adaptation to stress relies on the plant perception and transduction of the environmental cues. The rice *Root Meander Curling* (*OsRMC*) gene encodes a receptor-like kinase (without kinase domain) described as a negative regulator of jasmonate and salt responses, and known to be a negative regulator of root curling. However, the exact function of this protein is unknown. This project aims to further characterize *OsRMC* function in biotic and abiotic stress responses. To identify the downstream regulated genes in the *OsRMC* pathway, a transcriptomic analysis will be performed in rice suspension cells over-expressing and/or silencing this gene and different assays (e.g. TAP-tag, pull down) will also be carried out to identify proteins interacting with *OsRMC*. Downstream genes and *OsRMC*-interacting proteins will be validated and studied at different levels to better understand the role of *OsRMC* and their function in stress response.

The following tasks are set:

- 1- Construction of the necessary plasmids to transform rice cells
- 2- Transformation of rice cells and identification of genes / pathways regulated by *OsRMC* (transcriptomic analysis)
- 3- Identification and characterization of proteins that directly interact with the *OsRMC* protein

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