ANR PCRI GREENER Gene and REgulatory elements Networks Involved in Rice Cortex and aerenchyma formation

Floods are responsible for around 60% of all agricultural damage and crop loss (FAO, 2015). The perspective of global climate warming will affect cultivated areas and crop growing conditions, impacting the future of food security in the world. The identification of genes controlling flooding tolerance is one of the keys to the development of submergence-tolerant varieties in cereals, a problem that affects an increasing number of cultivated areas worldwide. Rice has aerenchyma, which are air-filled cavities that connect the aerial parts and roots, allowing them to maintain their respiration and growth under submerged conditions. Aerenchyma formation is an adaptive response to submergence in rice but the gene network controlling aerenchyma and cortex formation is still unknown.

The main objective of the project is to identify and characterize transcription factors involved in cortex and aerenchyma tissue differentiation in rice using a systems biology approach. This work will help to identify key genes behind aerenchyma and flooding tolerance in rice. These genes will be future candidates for breeding better-flooding tolerance cultivars in rice but also in cereals.

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