

RNAPO

RNA methylation and reproductive modes in plants: characterization of molecular factors involved in the transition between sexual reproduction and apomixis

ABSTRACT

Nowadays, 800 million persons are underfed and demographic projections indicate that agricultural systems will have to face an exponentially growing demand until 2050. In addition, strategies to fulfill these demands will have to integrate the effects of global warming, environmental changes (water and land limitation) and social demands (biodiversity preservation, food quality).

One essential aspect to meet these challenges is the establishment of efficient tools for plant breeding. Among these, the development of reproductive systems alternative to sexuality, such as haploidisation or clonal reproduction through seeds (apomixis), may revolutionize plant breeding and farming, especially in Southern countries.

Keywords : Developing the plant of the future, Plant, Operation, Apomixy, Protein/proteomic, 1. Exclu de la photothèque

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Project type : AAP MOBILITE

Research units in the network :

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End date : 2017-08-31

Flagship project : no

Project leader : Olivier Leblanc

Project leader's institution : IRD

Project leader's RU : DIADE

Budget allocated : 90000 €

Total budget allocated (including co-financing) : 90000 €

Funding : Labex

GOAL

Recently, REDG/UNR partners identified *tgs1*-like as a strong candidate for apomixis in the tropical forage *Paspalum notatum* (Siena et al., BMC Plant Biology, 2014). TGS1 proteins belong to the RNA cap guanine-N2 methyltransferases family involved in both RNA methylation and transcriptional activation. They are encoded by a single gene in non-photosynthetic organisms and loss of function causes severe reproductive defects in mammals, yeast and *Drosophila*. In plants, TGS1 proteins are encoded by two genes possessing different domains and their function has remained unexplored.

The main objective of this project is to characterize biochemically and functionally TGS1 proteins in plants.

ACTION

Both biochemical and cytological approaches, complementary to on-going functional analyses in *Arabidopsis thaliana* (see figure below on right) will be performed:

biochemical and enzymatic characterization through complementation in yeast and in vitro assays; in situ studies of TGS1 and TGS1-like protein accumulation during reproductive development in *Paspalum notatum* and in the model species *Arabidopsis thaliana*, and; identification of TGS1 and TGS1-like protein partners by co-immunoprecipitation coupled with mass-spec analyses.

RESULTS

- (1) to confirm new proteins involved in RNA cap guanine-N2 methyltransferases in plants;
- (2) to produce a temporal and cellular atlas of TGS1 and TGS1-like protein accumulation in reproductive organs of *P. notatum*;
- (3) to confirm TGS1-like differential protein accumulation between sexual and apomictic plants;
- (4) to identify protein partners, which will provide clues for TGS1 and TGS1-like functions in plants;
- (5) to determine which function, regulation of transcription vs. RNA methylation, is most critical for apomixis in *P. notatum*.