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

OBJECTIFS

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.

ACTIONS

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 charac-terization 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.

RESULTATS

(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.

Responsable :