

Retrocrop

Mobilome sequencing: a new technique to identify active retrotransposons and analyse their epigenetic impacts on tropical crop phenotypes

ABSTRACT

Transposable elements (TEs) are now recognised as major drivers of plant genome evolution, both through their mutagenic properties and through the epigenetic regulation that they can drive. TEs can be mobilized when plants have to face environmental challenges and this might have phenotypic, genetic, and epigenetic consequences. However, the repertoire of mobile TEs in stressed crops is not known. It is indeed technically challenging to identify mobile TEs that can be mobilized in a subset of the plant cells. To tackle this problem we have developed a new technique to identify the diversity of mobile elements, constituting the mobile part of the genome or “mobilome” in plants. This technique is based on the targeted high-throughput sequencing of the extrachromosomal part of the genome, notably constituted by active TEs. Using this technique we have successfully identified previously known mobile TEs in the model plant *Arabidopsis* and in rice. Furthermore we have identified an interesting novel TE that is active in specific developmental stages in rice.

Keywords : Microscopic (Gene/cell), Gene expression, Method, Tool, Technic, Phenotyping, Rice, *Arabidopsis* (species), Corn

Year : 2012

Project number : 1202-041

Type of funding : AAP OS

Project type : AAP

Research units in the network : LGDP

Start date : 2013-02-01

End date : 2014-06-30

Flagship project : no

Project leader : Marie Mirouze

Project leader's institution : IRD

Project leader's RU : DIADE

Budget allocated : 21840 €

Total budget allocated (including co-financing) : 21840 €

Funding : Labex

PERSPECTIVES

The newly identified TE will be investigated further to better understand its epigenetic control and potential mobility. This new method opens perspectives for the exhaustive identification of the part of the genome that is actively transposing, allowing to assess its impact on the epigenome and the genome and to better understand the phenotypic consequences. This project has resulted in several publications and has opened new collaborations with scientists working on different crops.