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Les éléments transposables : quels rôles dans la structure et l'évolution des génomes dans plantes méditerranéennes et tropicales ?

Transposable elements : which roles in genome structure and evolution in Mediterranean and tropical plants ?

Understanding the evolutionary role of viral integration in banana genome: which similitude with retrotransposons?

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The genome of banana (*Musa* sp.) harbours multiple integrations of several species of *Banana streak virus* (BSV), certainly resulting from illegitimate recombination between host and viral DNA. Surprisingly, this badnavirus does not require integration for its replication. Some integrations, only existing in the *Musa balbisiana* genome (denoted B), are infectious by releasing a functional viral genome following stresses such as in vitro culture and interspecific crosses. To date, four widespread species of BSV (*Goldfinger* -BSGFV, *Imové* -BSImV, *Mysore* -BSMysV and *Obino l'Ewai* -BSOLV) have been reported as integrated into the B genome with three of them as infectious (eBSGFV, eBSImV and eBSOLV). In order to study BSV expression from such viral integrants and to retrace their evolutionary story, a full genomic and genetic characterisation of BSV integrants (eBSV) was undergone including cytogenetic localization on chromosomes. Very low copies of integrations were recorded for each BSV species. The full characterisation of eBSGFV was recently performed in our lab (Gayral et al., 2008). eBSGFV results from a single event of integration corresponding to an allelic insertion of at least one full-length viral genome extensively rearranged with several viral regions duplicated. Although the four BSV species present important differences with each other, the organisation of eBSOLV and eBSImV looks like eBSGFV. Indeed, each of them is more or less extensively rearranged in PKW and is present as allelic insertions at the same locus. In contrary, the non infectious eBSMysV presents two independent insertions sites.

The evolutionary history of each BSV species was studied by analysing their distribution, their insertion polymorphism and their structure evolution among representative banana species, in relation to the phylogeny of *Musa* genus. The early evolutionary stages of infectious eBSV for BSGFV and BSImV were investigated among selected banana genotypes representative of the diversity of 60 wild *Musa* species and genotypes. Both BSV species integrated recently in banana evolution, circa 640,000 years ago, and after speciation between *Musa acuminata* and *Musa balbisiana*, circa 4.5 MYA. These two species were subject to different selective pressures and showed distinct levels of rearrangement within their final structure. Unlike other pathosystems harboring viral integrants, there is no colonization of host genomes by duplication of the viral sequences once integrated. The strong diversity of eBSV in the *Musa* genome could be rather explained by independent integrations from each of the numerous BSV species.

Interestingly, *M. balbisiana* diploid genotypes (BB) such as Pisang Klutuk Wulung (PKW), harbor infectious eBSVs in their genome but are nevertheless resistant to any multiplication of BSV. The mechanisms underlying such resistance are believed to be driven by epigenetic phenomena but no evidence has been obtained so far in banana plants.

1. Iskra-Caruana M.-L., Baurens F.-C., Gayral P., Chabannes M. (2010) A Four-Partner Plant-Virus Interaction: Enemies Can Also Come from Within. *Molecular Plant Microbe Interaction* (11):1394-402
2. Gayral P., Blondin L., Guidolin O., Carreel F., Hippolyte I., Perrier X. and Iskra-Caruana M.-L. (2010) Evolution of endogenous sequences of *Banana streak virus*: what can we learn from banana (*Musa* sp.) evolution? *Journal of virology*. 84(14):7346-59.

