34-Banana plants use post-transcriptional gene silencing to control banana streak virus infection.

Chabannes M.[1], Duroy PO.[1], Seguin J.[2,3], Rajendran R.[2], Laboureau N.[1], Pooggin M.[2], Iskra-Caruana ML.[1]

[1] CIRAD, UMR BGPI, F-34398 Montpellier Cedex 5.
[2] Institute of Botany, University of Basel, Schoenbeinstrasse 6, 4056 Basel, Switzerland
[3] FASTERIS SA, Ch. Du Pont-du-Centenaire 109, 1228 Plan-les-Ouates, Switzerland

matthieu.chabannes@cirad.fr

Banana streak virus (BSV), the causative agent of banana streak disease, is a plant pararetrovirus belonging to the family *Caulimoviridae*, genus *Badnavirus*. The genome of BSV is a circular double-stranded DNA of 7.4 kbp made of three ORFs and like other pararetroviruses replicates via reverse transcription of viral pregenomic RNA (Lockhart, 1990). While the first two ORFs encode two small proteins of unknown function, the third ORF (~210 kD) encodes a polyprotein that can be cleaved to yield the viral coat protein and proteins with homology to aspartic protease, reverse transcriptase and RNaseH. Little information is available about antiviral defense response of the host plant on BSV or other members of *Caulimoviridae*. RNA silencing, also known as RNA interference (RNAi), is an ancient gene regulation and cell defense mechanism, which exists in most eukaryotes (Xie and Qi, 2008). Plants have adapted the RNA silencing machinery into an antiviral defense system. Interestingly, Arabidopsis plants infected with *Cauliflower mosaic virus* (CaMV), a type member of the genus *Caulimovirus* in the family *Caulimoviridae*, accumulate siRNAs of 21, 22 and 24 nt size classes, where the 24 nt species are the most predominant ones (Blevins et al., 2006; Moissiard and Voinnet, 2006). Further analysis showed that, the leader region (600 nt) of CaMV pregenomic RNA produces massive amounts of siRNAs with several hot and cold spots of siRNA generation (Blevins et al., 2011) to function as a decoy for the RNA silencing defense system of the plant. To determine whether the viral decoy strategy was universally used among viruses belonging to the family *Caulimoviridae*, we have performed a deep sequencing of total siRNAs of 6 Cavendish banana plants infected independently with one of the 6 BSV species we own in the laboratory. We obtained for the first time, experimental evidence of virus-derived small RNA (vsRNA) from those 6 BSV species by blasting sequencing data against the 6 BSV species genomes. vsRNA are enriched in 21-nt class thus BSV are likely silenced at the post-transcriptional level. Besides, our data unequivocally show that the decoy strategy used by the CaMV is not employed by the BSV since most of the hot spots of siRNA production are located in ORF1 and 2.
Information generated about siRNAs derived from BSV genome could help us to design silencing-based transgenic and non-transgenic (RNA vaccination) approaches to obtain BSV resistance in banana crop.

Keywords : banana, silencing, BSV, siRNA

References:

Blevins T. et al., (2006) Nucleic Acids Res. 34(21):6233-46.
Blevins T. et al., (2011) Nucleic Acids Res. 39(12):5003-14.
Lockhart B.E.L. (1990) Phytopathology, 80: 127-131
Moissiard G. and Voinnet O. (2006) Proc. Natl. Acad. Sci. 103(51):19593-8.
Xie Z. and Qi X. (2008) Biochim. Biophys. Acta 1779(11):720-4.