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Effects of allelic forms of the Potato virus Y (PVY) resistance gene *va* on infection kinetics and viral population structures **Abstract N° 851**

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Viruses are obligate parasites sharing a high mutation rate when replicated, leading or not to genetic diversity. Indeed, one of the major constraints in the evolution of viral populations is the interaction with the host. Potato virus Y (PVY, *Potyvirus* genus), a single stranded positive sense RNA virus, infects a wide host range including cultivated Solanaceous species. This plant virus is transmitted by aphids and is worldwide distributed. This pathogen is the most damaging virus affecting tobacco crops. Considering its economical importance and the lack of efficient methods to control aphid transmission, genetic resistance is a solution to limit the PVY spreading in the fields. Three allelic forms (conferring different level of resistance to PVY) of a recessive resistant gene (*va*) have been described and introduced in numerous cultivars of *Nicotiana tabacum*. However, such partial resistant hosts can not totally prevent the viral replication in the plants which can consequently result in the selection of virulent variants. Indeed, some variants of PVY able to overcome these resistance sources have been reported in many countries. Hence, the objective of our study is to better characterise the PVY resistance sources and to understand their role in both the emergence and the spread of such virulent PVY isolates. A fully characterized PVY isolate was inoculated to two couples of tobacco near isogenic lines, differing in allelic state at the locus of the *va* gene. The kinetics of viral particles accumulation during the infection process was recorded in order to determine the impact of the different alleles of the *va* gene on viral multiplication. Moreover, the molecular analysis of the viral population was performed on different regions of the PVY genome. The nucleotide sequence diversity of each of these genomic regions was compared between inoculated hosts plant in order to determine the impact of the resistant gene *va* on the structure of viral population. Data related to infection kinetics and molecular changes of viral sequences will be presented.

Keywords : Potato virus Y, tobacco plant, genetic resistance, viral population