

Characterization of Brazilian tobacco *Potato virus Y* (PVY) isolates: identification of a new group in the PVY species

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Potato virus Y (PVY, genus *potyvirus*, family *Potiviridae*) is known to be one of the most variable RNA plant viruses. This virus causes severe damages on tobacco plants and induces significant yield and quality losses of the leaf products. The variability and distribution of PVY populations have been extensively studied in Europe and North-America while such type of data is still scarce for PVY isolates from South America. To improve knowledge on PVY diversity, a survey was performed in tobacco fields from three southern states of Brazil. The sampled PVY isolates were characterized using serological, biological and molecular tools applied to study PVY isolates in potato hosts. The characterization procedure starts with the assignment of PVY isolates in serogroup by ELISA using commercial and a library of monoclonal antibodies developed by the laboratory raised against Y^N and Y^{O/C} serotypes. Then, isolates were inoculated to *Nicotiana tabacum* cv Xanthi and to potato cultivars to determine the virulence and aggressiveness of each isolate. The potato cvs. (Nicola, Béa, Désirée, Eersteling and Maris Bard) used in this pathotyping procedure were selected according to their genetic background (i.e. presence of PVY hypersensitive resistance genes *N_{ytbr}* and *N_c*) and/or their ability to express the tuber necrosis symptom induced by some PVY^N isolates. Finally, HC-Pro and coat protein (CP) regions of PVY Brazilian genomes were sequenced. Only few percent of Brazilian PVY isolates were assigned in Y^N or Y^{O/C} serogroups as most of the tested PVY-infected samples were not detected by the used monoclonal serological reagents. Consequently, they were assigned into the unconventional Y^U serogroup. Biological characterization and molecular analyses strengthened the unconventional status of Y^U isolates as they i) are not able to infect the potato cultivars used in the study and ii) share common features within the CP nucleotide sequence. Finally, data from phylogenetic analyses carried out with Brazilian PVY sequences suggest the presence of a new group in the species and make it possible to describe the evolution of PVY life history traits.