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Virulence and adaptation of *Potato virus Y* (PVY) on *Nicotiana tabacum* varieties carrying recessive resistance *va* gene

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Improved tobacco cultivars introgressed with alleles of the recessive resistance gene *va* have been deployed worldwide to limit agronomical consequences associated with *Potato virus Y* (PVY) infections. Unfortunately, necrosis symptoms resulting from PVY infections have been reported on these cultivars suggesting that PVY is able to overcome the resistance. Field surveys were performed in contrasted cultural environments where the use of *va* is old and massive (France) or recent and limited (Brazil) to i) estimate the prevalence of PVY in symptomatic tobacco plants and to ii) characterize PVY isolates present in susceptible and *va*-derived tobacco cultivars. A serological typing procedure, applied to 953 leaves collected from different tobacco growing areas, was performed using polyclonal antisera raised against different viral species including PVY, and monoclonal antibodies anti-PVY^{OC} and -PVY^N isolates. Moreover, 115 PVY isolates were mechanically inoculated on one susceptible and three *va*-derived tobacco cultivars to define virulence of these isolates against alleles 0, 1 and 2 of the *va* gene. Qualitative and quantitative statistical analyses performed using data associated with infection efficiencies showed that i) the probability for a tobacco plant to be infected with PVY is reduced in *va* hosts, ii) most of PVY isolates tested were able to overcome the three alleles of the *va* gene and iii) the monitored biological diversity of PVY isolates was lower in the *va*-derived resistant tobacco hosts than in PVY-susceptible ones. The presented study and associated results helps to understand consequences of the deployment of the *va* gene in tobacco on both diversity and virulence of PVY isolates.