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Oral presentation

**Virulence and adaptation of *Potato virus Y* (PVY) on *Nicotiana tabacum* varieties carrying recessive resistance gene “*va*”.** C. Lacroix, M. Tribodet, L. Glais, E. Jacquot. INRA, Agrocampus Ouest, Univ. Rennes 1, UMR1099 BiO3P (Biology of Organisms and Populations applied to Plant Protection), BP 35327, F-35653 Le Rheu.

*Potato virus Y* (PVY, genus *Potyvirus*) infects a wide range of host plants including solanaceous species. PVY is the most damaging virus affecting tobacco. Three allelic forms (0, 1 and 2) of the “*va*” recessive resistance gene have been introduced in numerous *Nicotiana tabacum* varieties. To test the impact of “*va*” on PVY natural populations, the virulence of 86 isolates collected from French tobacco fields was characterized using susceptible and “*va*” resistant tobacco genotypes as hosts. Most of the tested isolates infect both susceptible and resistant genotypes. Moreover, virulence of PVY isolates collected on various resistant tobacco varieties is broader than the one observed for isolates collected on susceptible ones. To assess the adaptation of PVY isolates to the gene “*va*”, serial passages of a PVY infectious clone were initiated on tobacco genotypes B0 and V2 carrying alleles 0 or 2 of the “*va*” gene, respectively. A first passage of the infectious PVY clone on test plants led to the production of only a few (15/130) V2 infected plants. These viral populations produced in V2 infected hosts were able, after a second passage on test plants, to efficiently infect both B0 (192/450) and V2 (273/450) lineages. This reveals a fast adaptation dynamics of the infectious PVY clone used.

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