

## EXPERIMENTAL EVOLUTION OF THE HOST RANGE FOR TWO ISOLATES OF POTATO VIRUS Y

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### ABSTRACT:

Potato virus Y (PVY) remains one of the most economically damaging plant viruses, characterized by high genetic diversity and remarkable adaptability to different hosts. Despite its importance, the role of host species in driving PVY evolutionary trajectories, and eventually resulting in host range expansion, remains poorly understood. Here, we investigated the evolutionary dynamics of two PVY isolates (PVYNb and PVYSt) subjected to serial passages in three solanaceous hosts: *Nicotiana benthamiana*, *Solanum lycopersicum*, and *Solanum tuberosum*. Over ten passages, we monitored changes in infection efficiency, virus accumulation, and host-specific adaptation patterns, combining infectivity assays with high-throughput sequencing of evolved viral populations. Our results revealed isolate-specific and host-dependent evolutionary responses. PVYNb exhibited high adaptability, with robust infection efficiency and sustained viral replication in *N. benthamiana*, which acted as a source host facilitating viral diversification. In contrast, PVYSt displayed restricted infectivity, with tomato acting as a sink host, limiting viral accumulation and reducing the potential for sustained transmission. Serial passage experiments highlighted complex dynamics, with significant interactions between viral genotype, host species, and passage number shaping viral population size and stability. Infectivity assays of evolved lineages demonstrated that PVYNb populations passaged in *N. benthamiana* showed enhanced infectivity across all hosts, suggesting the potential for host generalism driven by a permissive hosts. Conversely, PVYSt populations and lineages evolved in tomato or alternating hosts exhibited reduced fitness, indicative of evolutionary constraints. Genome sequencing revealed higher intra-population diversity and host-specific fixed mutations in PVYNb lineages, while PVYSt populations remained more genetically stable, with few fixed changes across hosts. These findings underscore the critical role of host species as selective environments influencing viral adaptation, host range evolution, and, ultimately, virus emergence potential. This study highlights the key role of host species in shaping PVY evolution and adaptation, with implications for understanding virus evolution and developing effective management strategies for PVY in diverse agricultural systems.

**KEYWORDS:** source-sink dynamics; *Potyvirus*; virus evolution

### SUPPORT

Work in València was supported by grant PID2022-136912NB-I00 funded by MCIU/AEI/10.13039/501100011033 and by "ERDF a way of making Europe" and by grant CIPROM/2022/59 funded by Generalitat Valenciana to S.F.E. In Brazil, the project was funded by CNPq grant 404174/2023-0. I.J.dM. received scholarships from CAPES and later from CNPq. A.K.I-N. is a CNPq fellow.