



HAL
open science

A plant-specific homolog of DP1/Yop1 family proteins plays a proviral role in potyvirus infection

Mingshuo Xue, Luc Sofer, Vincent Simon, Roxane Lion, Nathalie Arvy, Jens Tilsner, Sylvie German-Retana, Mamoudou Diop, Jean-Luc Gallois

► **To cite this version:**

Mingshuo Xue, Luc Sofer, Vincent Simon, Roxane Lion, Nathalie Arvy, et al.. A plant-specific homolog of DP1/Yop1 family proteins plays a proviral role in potyvirus infection. The 41st ASV Annual Meeting, Jul 2022, Madison (US-WI), United States. hal-04648013

HAL Id: hal-04648013

<https://hal.inrae.fr/hal-04648013v1>

Submitted on 15 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

A plant-specific homolog of DP1/Yop1 family proteins plays a proviral role in potyvirus infection

Mingshuo Xue¹, Luc Sofer¹, Vincent Simon¹, Roxane Lion¹, Nathalie Arvy¹, Mamoudou Diop², Jean-Luc Gallois², Jens Tilsner^{3,4} and Sylvie German-Retana¹

¹ UMR 1332, Biologie du Fruit et Pathologie, INRAE, Univ. Bordeaux, Equipe de Virologie, 71 avenue Edouard Bourlaux, CS 20032, 33882 Villenave d'Ornon Cedex, France

² UR 1052, GAFL Domaine St Maurice – CS, 60094 - F-84143, Montfavet Cedex

³ Cell and Molecular Sciences, James Hutton Institute, Dundee, DD2 5DA, Scotland, U.K.

⁴ Biomedical Sciences Research Complex, University of St Andrews, North Haugh St Andrews, Fife KY16 9ST, Scotland, U.K.

The *Potyvirus* genus is one of the largest genera of plant RNA viruses responsible for serious diseases in vegetable and fruit crops worldwide [1]. As potyviruses have developed strategies to hijack the host secretory pathway and plasmodesmata (PD) for their transport, the goal of this study was to identify membrane and/or PD-proteins that interact with one of the viral proteins involved in the cell-to-cell movement of turnip mosaic virus (TuMV) the “second 6 kDa molecular-weight membrane anchoring protein” (6K2). The 6K2 induces the formation of endoplasmic reticulum (ER)-derived viral vesicles, important not only for replication but also for intra- and intercellular movement of TuMV [2]. In *Arabidopsis thaliana*, AtHVA22a (*Hordeum vulgare abscisic acid* responsive gene 22) belongs to a multigenic family of transmembrane proteins, homologous to DP1/Yop1 family proteins in yeast and interactors of reticulons, which are responsible for the constriction of ER tubules. The role of HVA22 gene family has been poorly studied in plants, even if its potential involvement in response to abiotic stresses was highlighted [4]. Recent proteomics analysis of PD fractions purified from *Arabidopsis thaliana* suspension cells showed that AtHVA22a is highly enriched in plasmodesmata proteome [3]. Here, using a Split-ubiquitin membrane Y2H assay we screened an *Arabidopsis* cDNA library and identified AtHVA22a as an interactor of the 6K2 protein of TuMV. We further confirmed this interaction in yeast and *in planta* using bimolecular fluorescence complementation (BiFC) and showed that the 6K2/AtHVA22a interaction occurs at the level of the viral replication complexes during TuMV infection and partially at PD levels. Furthermore, overexpression of *AtHVA22a* increases TuMV propagation in *Nicotiana benthamiana* while TuMV propagation is slowed down in *AtHVA22a-CRISPR/Cas9* mutants. Altogether, our results indicate that AtHVA22a plays an agonistic effect on TuMV propagation.

[1] doi:10.1099/jgv.0.000740. [2] doi:10.3389/fmicb.2013.00351. [3] doi:10.15252/embr.201847182. [4] DOI: 10.1023/a:1015593715144