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The *Potyvirus* genus is one of the largest genera of plant RNA viruses responsible for serious diseases in crops worldwide. As potyviruses 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 the 6K2 protein, a potyviral protein involved in replication and cell-to-cell movement of turnip mosaic virus (TuMV).

Using Split-ubiquitin membrane Y2H assays we screened an Arabidopsis cDNA library for interactors of the TuMV-6K2. We isolated AtHVA22a (*Hordeum vulgare abscisic acid* responsive gene 22) that belongs to a multigenic family of transmembrane proteins, homologous to DP1/Yop1 family proteins in yeast and interactors of reticulons. HVA22 DP1/Yop1 family genes are widely distributed in eukaryotes, but the role of HVA22 proteins in plants are not well-known, except the role in blast disease resistance recently described in rice [1]. Interestingly, proteomics analysis of PD fractions purified from Arabidopsis suspension cells showed that AtHVA22a is highly enriched in plasmodesmata proteome, making it a good candidate for the virus cell-to-cell movement [2]. We further confirmed the interaction between 6K2 and AtHVA22a in yeast, as well as *in planta* by using bimolecular fluorescence complementation (BiFC). Furthermore, we showed that the 6K2/AtHVA22a interaction occurs at the level of the viral replication complexes (VRC) during TuMV infection and partially at PD. The partial relocalization of AtHVA22a at the VRC during TuMV infection seems to be specific to *potyvirus* infection as it is not induced on *potexvirus* infection. Finally, we showed that the propagation of TuMV in arabidopsis leaves is increased when AtHVA22a is overexpressed in planta but slowed down upon inactivation of *AtHVA22a* by CRISPR-Cas9.

Altogether, our results indicate that AtHVA22a plays an agonistic effect on TuMV propagation.

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[2] doi: 10.15252/embr.201847182.