

Supplementary Material and Methods

Search for proteins similar to *P. viticola* WY-domain-containing proteins in other oomycetes.

The 68 WY-domain-containing proteins from *P. viticola* were used as a query in a BLAST search at low stringency (Evalue<10e-5) against the proteomes of *Phytophthora infestans* T30-4 (PRJNA17665; Haas et al, 2009), *Phytophthora parasitica* INRA-310 (PRJNA259235), *Peronospora tabacina* 968-S26 (PRJNA285243; Derevnina et al, 2015), *Plasmopara halstedii* OS-Ph8-99-BIA4 (PRJEB6932; Sharma et al, 2015), *Plasmopara halstedii* 710 (PRJNA412027; Pecrix et al, 2019) and *Hyaloperonospora arabidopsidis* Emoy2 (PRJNA30969; Baxter et al, 2010). The BLAST output was analyzed with SignalP4 and TMHMM 2.0, and proteins lacking a signal peptide or possessing a transmembrane domain outside the first 70 amino acids were discarded. Remaining proteins were aligned with MUSCLE and proteins carrying RXLR or RXLR-like motifs were identified by visual inspection of the alignments. The presence of dEER or dEER-like motifs was determined based on the visual inspection of alignments of proteins lacking RXLR motifs. Alignments in Supplementary Figure 1 show proteins lacking RXLR or RXLR-like motif that possess dEER or dEER-like motifs.

Transient expression of 33ΔSP in grapevine leaves using a syringe.

Agrobacterium suspensions were prepared as described in the manuscript, excepting the addition that Silwet-L77. Infiltrations were performed with a needleless 1 ml syringe as described in Zottinni et al. (2008). The infiltration was limited to the area of the leaf in contact with the syringe.

References

- Haas B, Kamoun S, Zody M, Jiang R, Handsaker R, et al. (2009) Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*. *Nature* 461: 393–398.
- Zottini, M. *et al.* (2008) Agroinfiltration of grapevine leaves for fast transient assays of gene expression and for long-term production of stable transformed cells. *Plant Cell Reports* **27**, 845-853.