

Description of Additional Supplementary Files

File name: Supplementary Data S1

Description: Quantitative concentrations in CFU/ml of *X. fastidiosa* detected in the *V. arizonica* accessions used in this study.

File name: Supplementary Data S2

Description: Significant SNPs from the GWAS in hap1 and hap2 and from both methods.

File name: Supplementary Data S3

Description: CNVs detected around the SNP-defined peaks associated with PD resistance.

File name: Supplementary Data S4

Description: Name, sequences, p-values and adjusted p-values of the 115 significant kmers.

File name: Supplementary Data S5

Description: Best hit mapping information of significant kmers to hap1, hap2 and unplaced contigs.

File name: Supplementary Data S6

Description: Gene functional annotation of genes around PD-associated peaks.

File name: Supplementary Data S7

Description: Presence-absence matrix of significant kmers in *V. arizonica*.

File name: Supplementary Data S8

Description: Presence-absence matrix of significant kmers in other species.

File name: Supplementary Data S9

Description: Gene expression of the homologous genes of *V.ari*-RGA14 and *V.ari*-RGA18 (Agüero et al., 2022) in *V. arizonica* b40-14. Transcript abundance is shown as Transcripts per Million (TPM). n = three genotypes for stems. n = 1 for b40-14 leaves.

File name: Supplementary Data S10

Description: Significant SNPs from the multi-locus mixed-model GWAS on hap1.