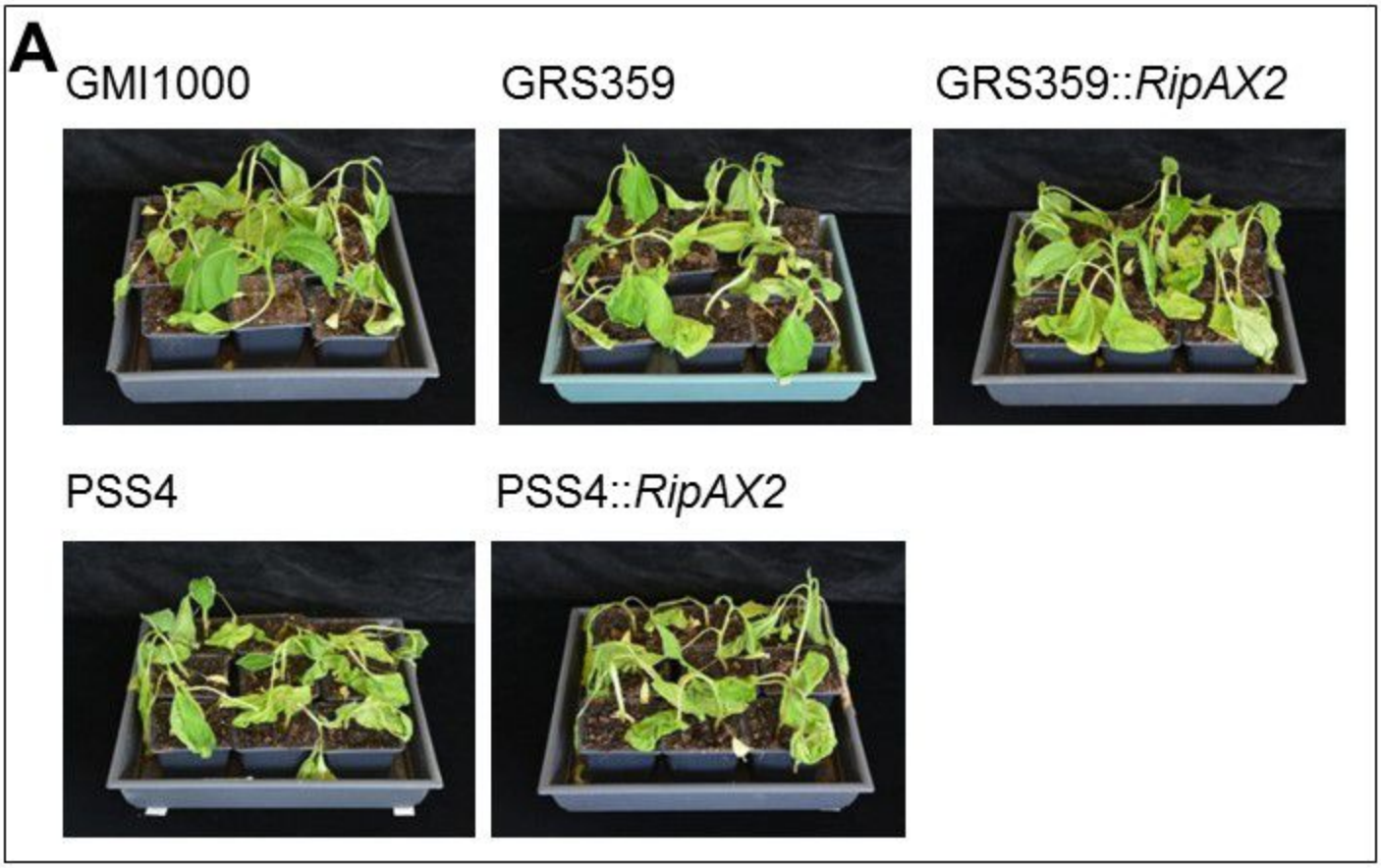
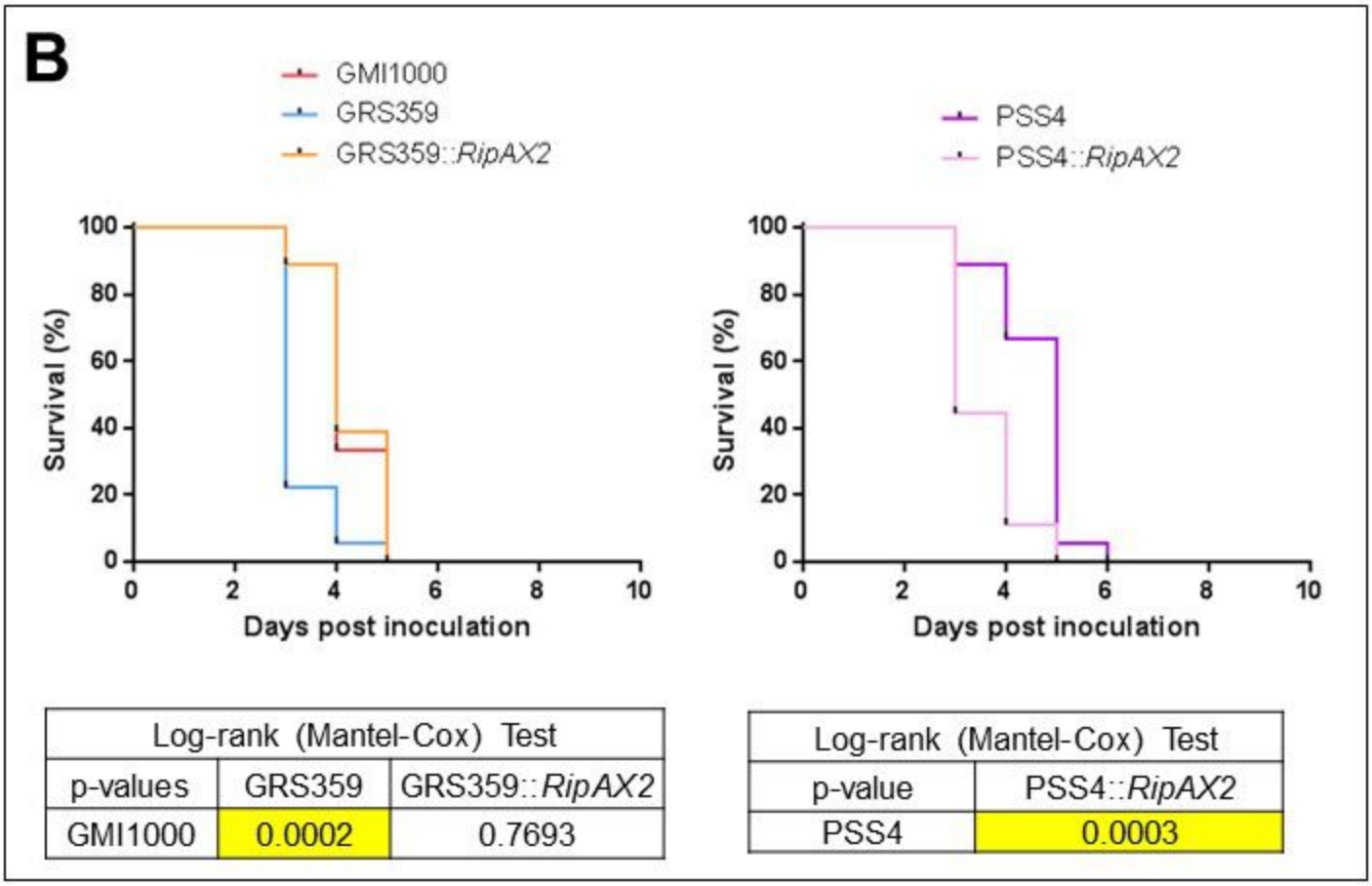


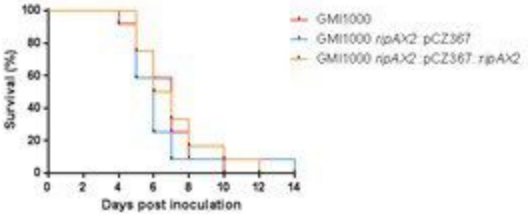


Log-rank (Mantel-Cox) Test		
p-values	GRS359	GRS359::*RipAX2*
GMI1000	0.0002	0.7693

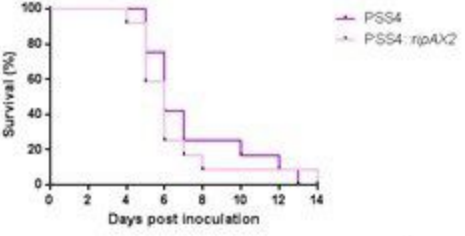
Log-rank (Mantel-Cox) Test	
p-value	PSS4::*RipAX2*
PSS4	0.0003

Figure S1. The RipAX2-triggered eggplant resistance is specific to AG91-25. (A) Pictures taken 6 DPI. All strains, whatever their RipAX2 content, are able to trigger disease on MM738 susceptible plants. (B) Kaplan-Meir survival curves representing the wilting of the MM738 eggplants after inoculation (18 plants per strain). Log-rank (Mantel-Cox) test shows that the wilting rates of the plants inoculated with the different strains are not significantly different.

Repetition 2



Log-rank (Mantel-Cox) Test		
p-values	GMI1000 *ripAX2*::pCZ367	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*
GMI1000	0.4511	0.6094



Log-rank (Mantel-Cox) Test	
p-value	PSS4::*ripAX2*
PSS4	0.6005

Figure S2. Kaplan-Meier survival curves observed on MM738 plants (susceptible control) inoculated with strains GMI1000, GMI1000 *ripAX2*::pCZ367, GMI1000 *ripAX2*::pCZ367::*ripAX2*, PSS4, and PSS4::*ripAX2*, in one supplemental replicate. Log-rank (Mantel-Cox) Test are given with p-value.

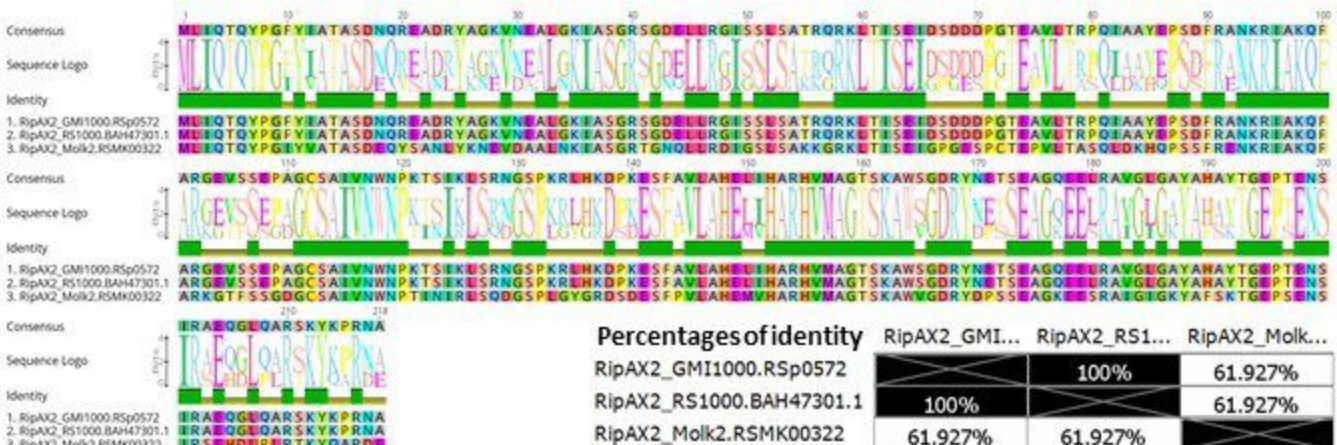


Figure S3. Alignment of the RipAX2 proteic alleles from GMI1000, RS1000, MOLK2, and their percentages of identity.

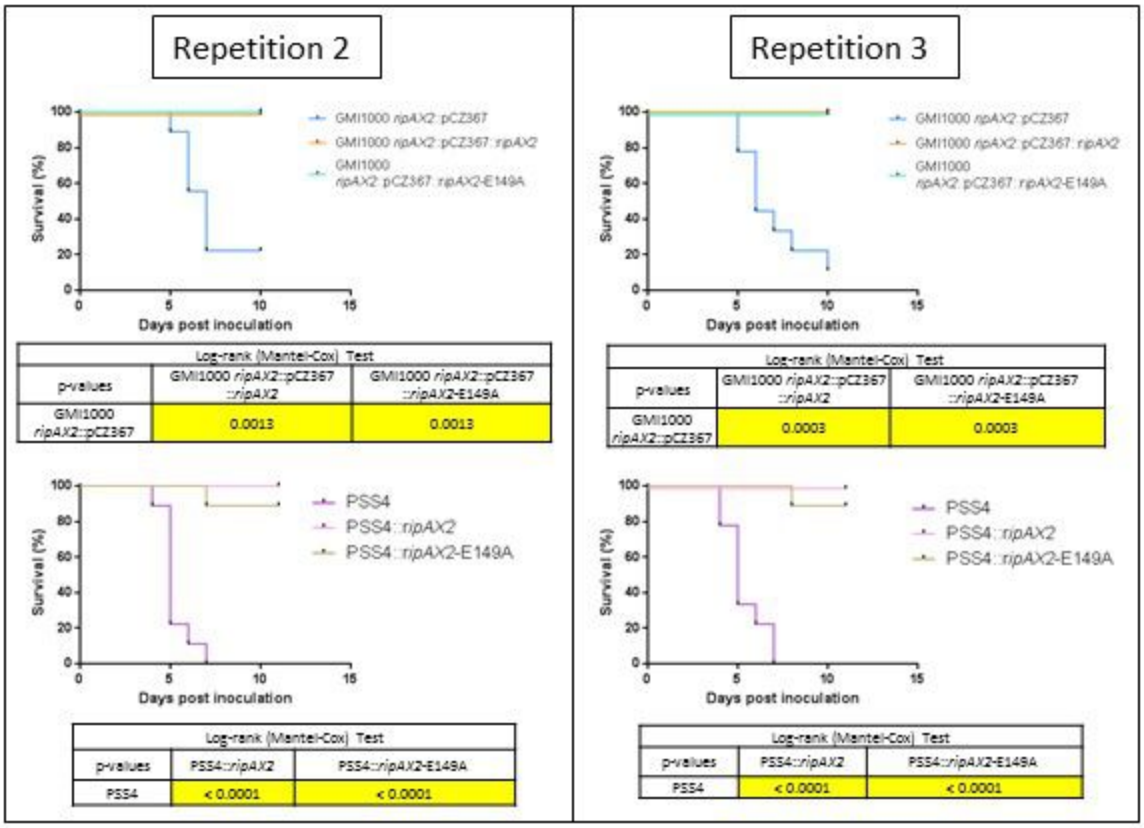
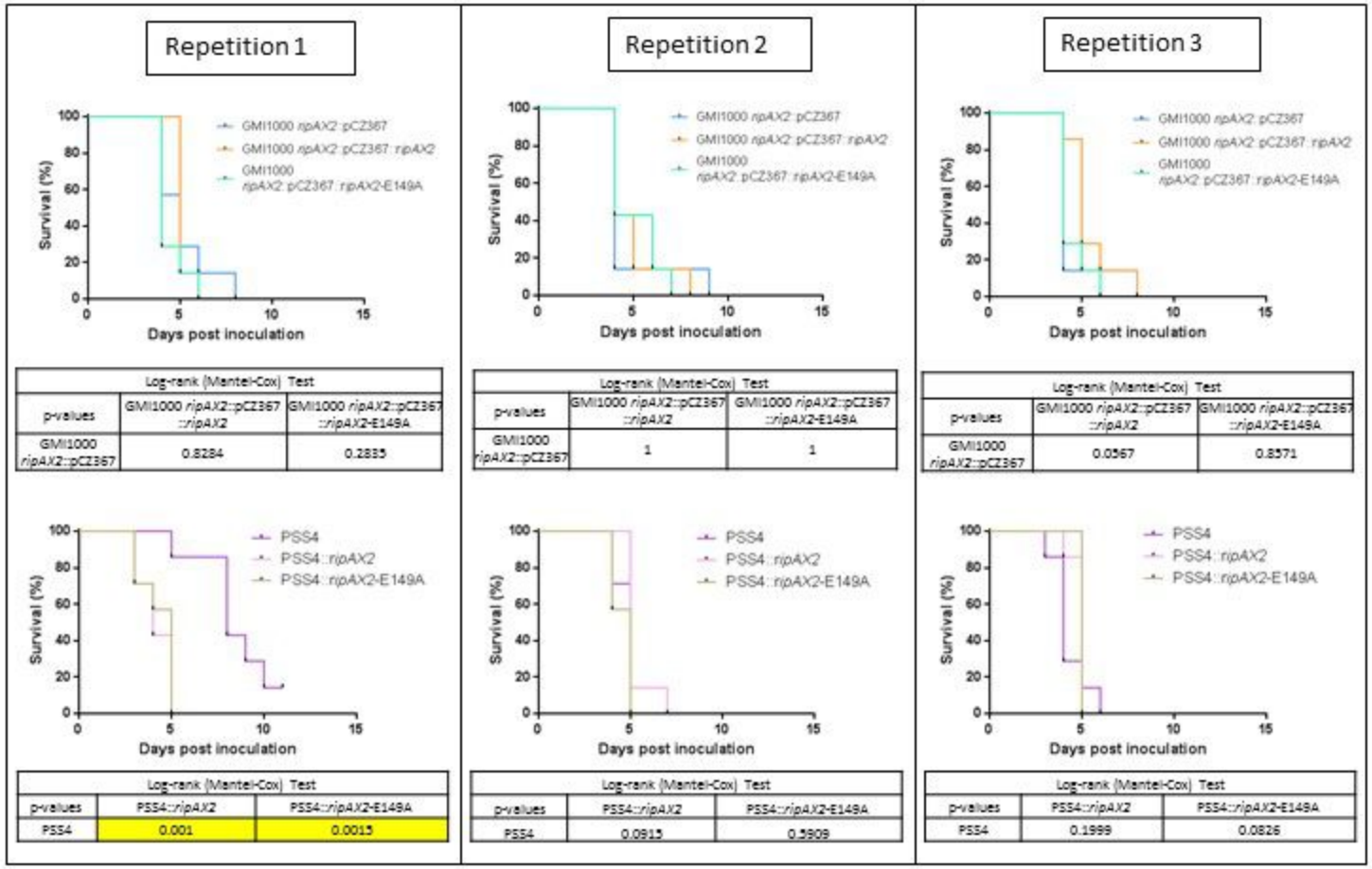


Figure S4. Kaplan-Meier survival curves observed on AG91-25 plants inoculated with strains GMI1000 *ripAX2*::pCZ367, GMI1000 *ripAX2*::pCZ367 ::*ripAX2*, GMI1000 *ripAX2*::pCZ367 ::*ripAX2*-E149A, PSS4, PSS4::*ripAX2*, PSS4::*ripAX2*-E149A, in two supplemental replicates (22 plants and 18 plants per strain, for each respective replicate). Log-rank (Mantel-Cox) tests are given with p-value.



Log-rank (Mantel-Cox) Test		
p-values	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*-E149A
GMI1000 *ripAX2*::pCZ367	0.8284	0.2835

Log-rank (Mantel-Cox) Test		
p-values	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*-E149A
GMI1000 *ripAX2*::pCZ367	1	1

Log-rank (Mantel-Cox) Test		
p-values	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*	GMI1000 *ripAX2*::pCZ367 ::*ripAX2*-E149A
GMI1000 *ripAX2*::pCZ367	0.0567	0.8571

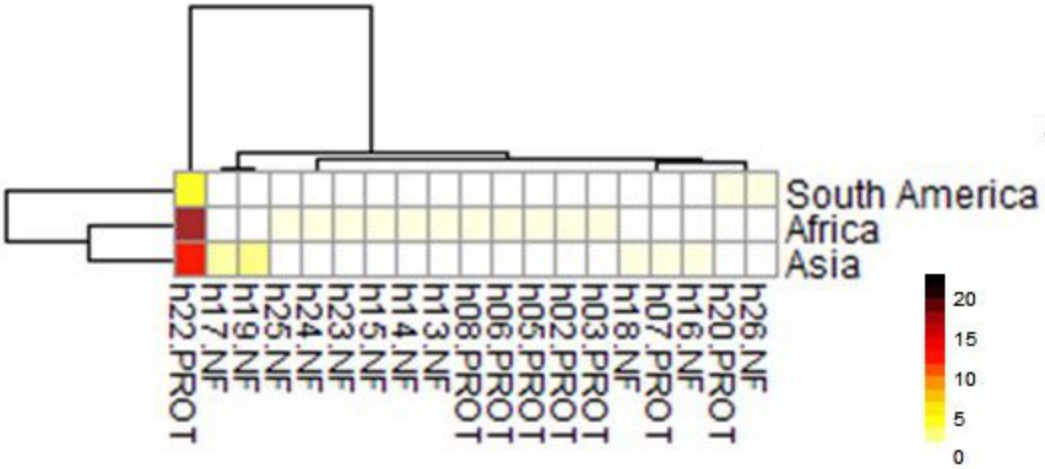
Log-rank (Mantel-Cox) Test		
p-values	PSS4::*ripAX2*	PSS4::*ripAX2*-E149A
PSS4	0.001	0.0015

Log-rank (Mantel-Cox) Test		
p-values	PSS4::*ripAX2*	PSS4::*ripAX2*-E149A
PSS4	0.0815	0.5909

Log-rank (Mantel-Cox) Test		
p-values	PSS4::*ripAX2*	PSS4::*ripAX2*-E149A
PSS4	0.1999	0.0826

Figure S5. Kaplan-Meier survival curves observed on MM738 plants inoculated with strains GMI1000 *ripAX2*::pCZ367, GMI1000 *ripAX2*::pCZ367 ::*ripAX2*, GMI1000 *ripAX2*::pCZ367 ::*ripAX2*-E149A, PSS4, PSS4::*ripAX2*, PSS4::*ripAX2*-E149A, in three replicates. Log-rank (Mantel-Cox) tests are given with p-value.

Figure S6. DNA alignment of the reference *ripAX2* alleles (GMI1000 and RS1000) with the long *ripAX2* alleles amplified within the phylotype I Ivorian strains RUN1546 (sequevar 13), RUN1740 and 1743 (sequevar 31), and in the Guianese phylotype IIA RUN1994 (sequevar 41). Alignments were done using MUSCLE under GENEIOUS v5.5. Each strain is represented by its nucleotide sequence (upper line) and proteic sequence (lower line). Black squares indicate stop codons.



Alleles (G)	Strains (N)	G/N
2	12	0.17
6	26	0.23
6	28	0.21

Figure S7. Geographic distribution of the 19 RipAX2 alleles, either functional (PROT) or non-functional (NF), across regions within the phylotype I strains. The heatmap was built with the R package pheatmap, based on Euclidean distances between observations; the clusters were calculated using the Ward method. For each region, are presented the number of RipAX2 alleles (G), and Phylotype I strains (N). "Africa" gathers Burkina-Faso, Cameroon, Ivory Coast, Reunion Isl., and South Africa; "Asia" gathers Australia, India, Indonesia, Philippines, Taiwan, and Thailand; "South America" gathers French Guiana and Martinique. The heatmap values correspond to numbers of strains.