

Figure S1. A standard view of the GUI during manual selection of training data

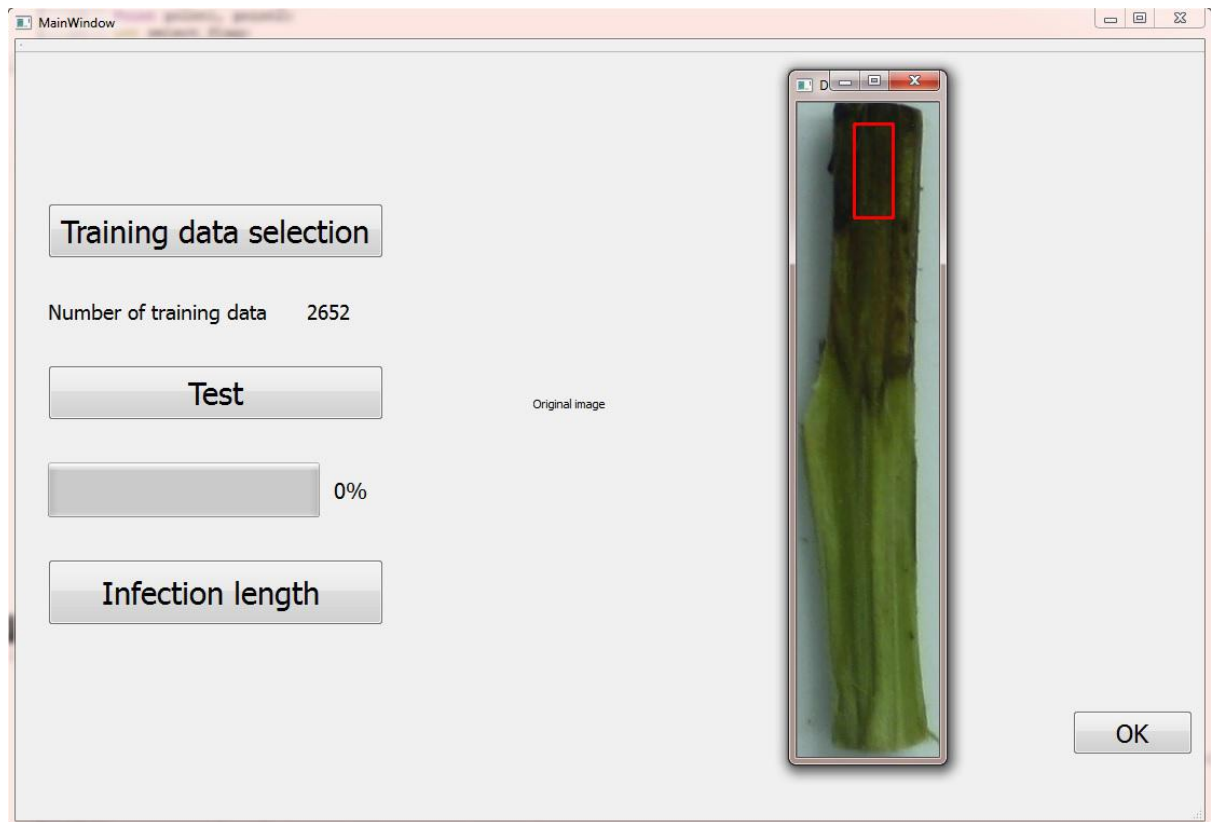


Figure S2. A standard view of the GUI during percentage area of necrosis estimation

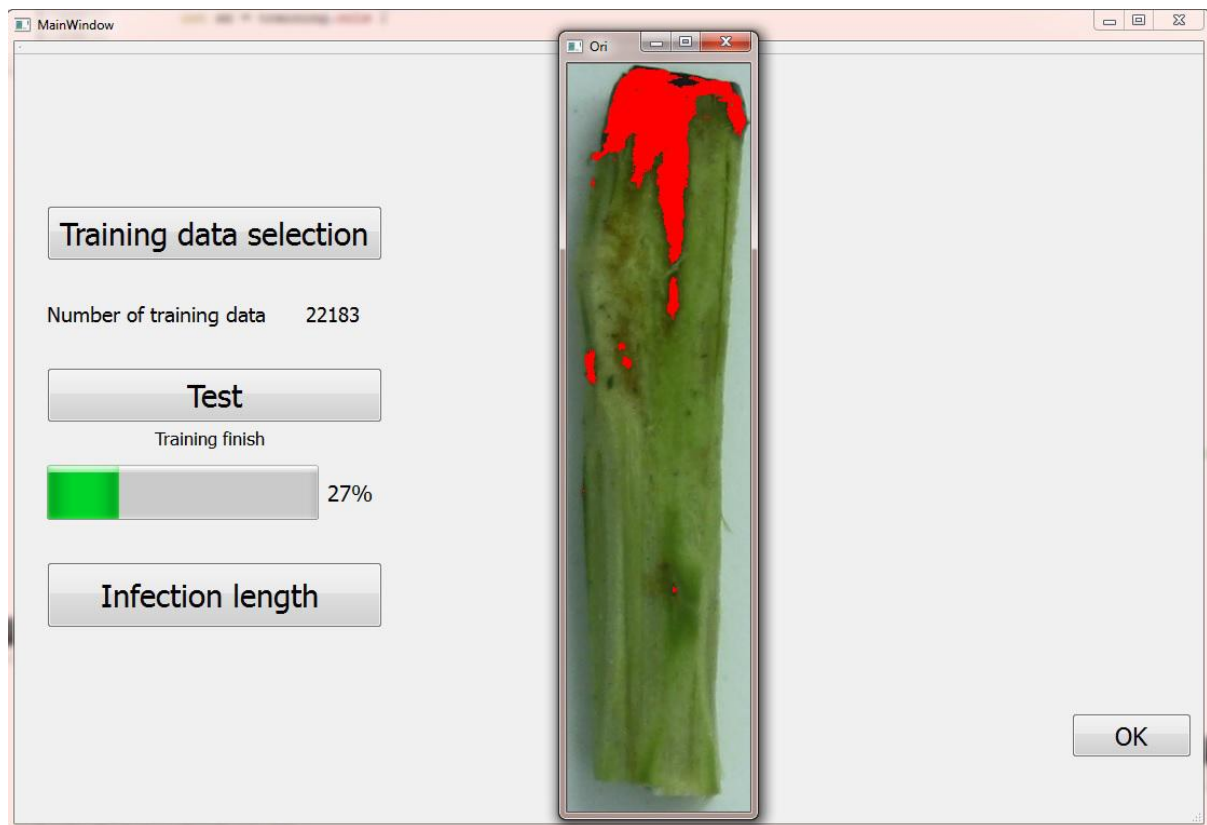


Figure S3. A standard view of the GUI during necrosis length estimation

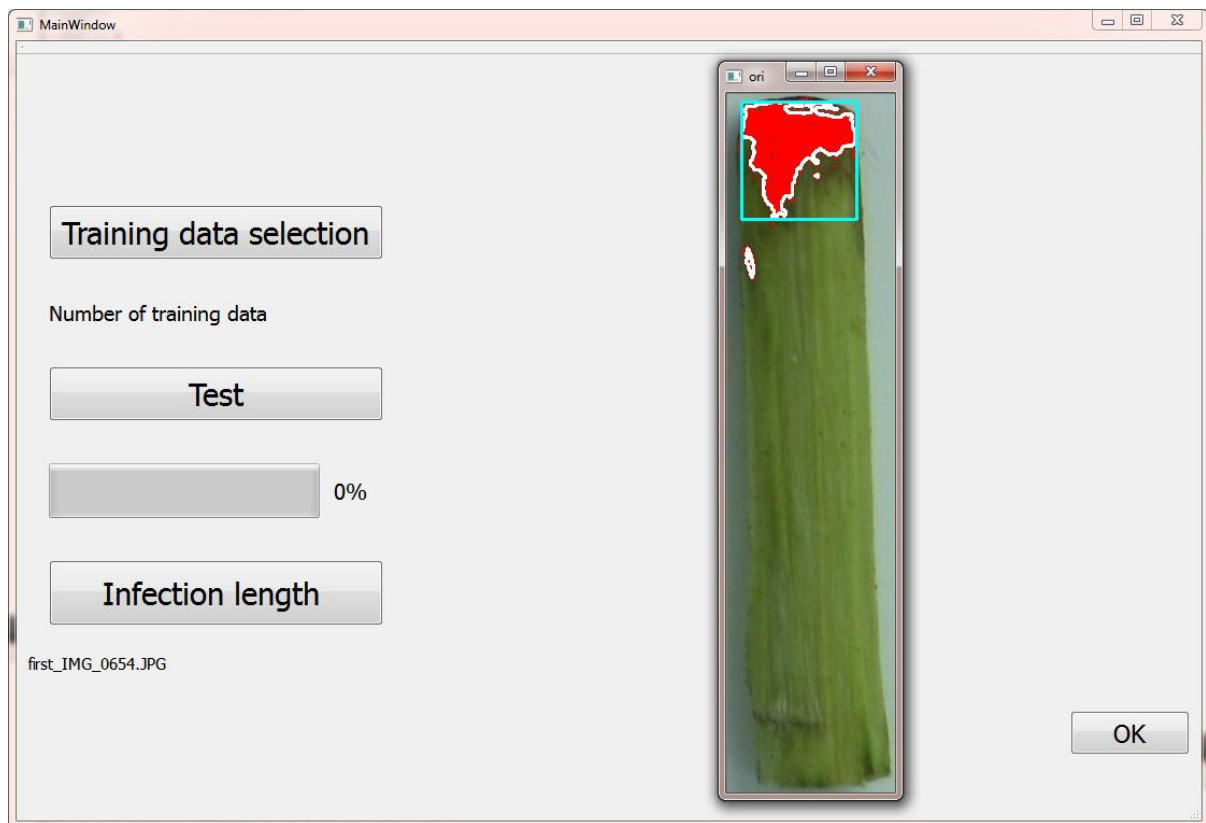


Figure S4. Visual output of ANOVA from Genstat including the histogram of residuals, fitted-value plot and normality plots.

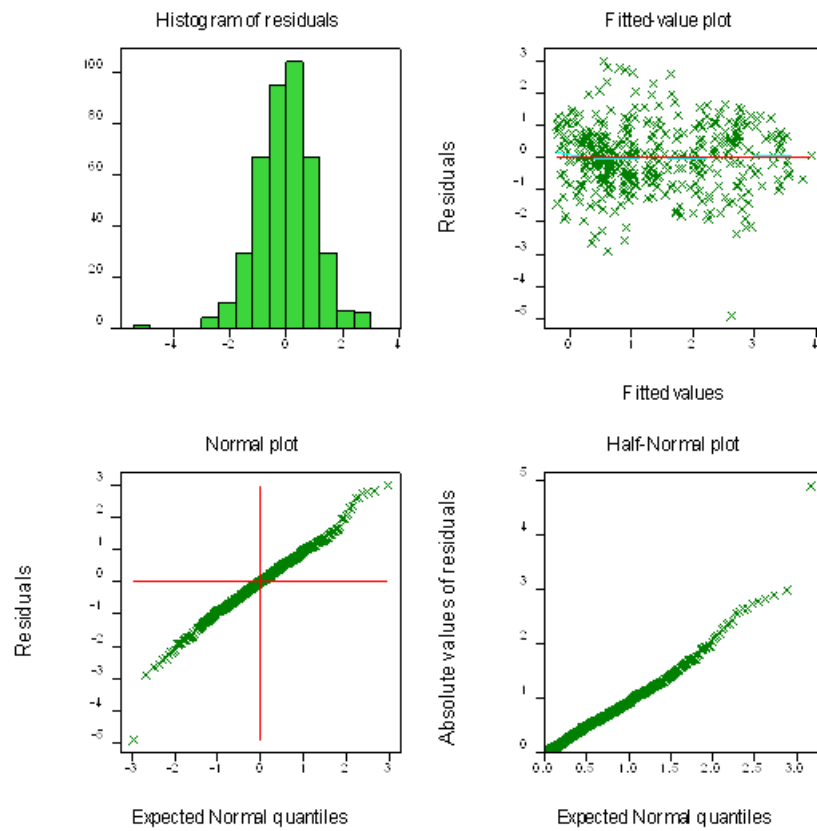


Figure S5. Interaction plot showing percentage necrosis for all *P. syringae* strains on the different *Prunus* species cherry and plum. The mean values from the ANOVA were used and Least Significant Difference bars calculated during the ANOVA. The means are plotted on a log scale with back-transformed values as the scale. Strains isolated from cherry are highlighted in red whilst those isolated from plum are highlighted in purple.

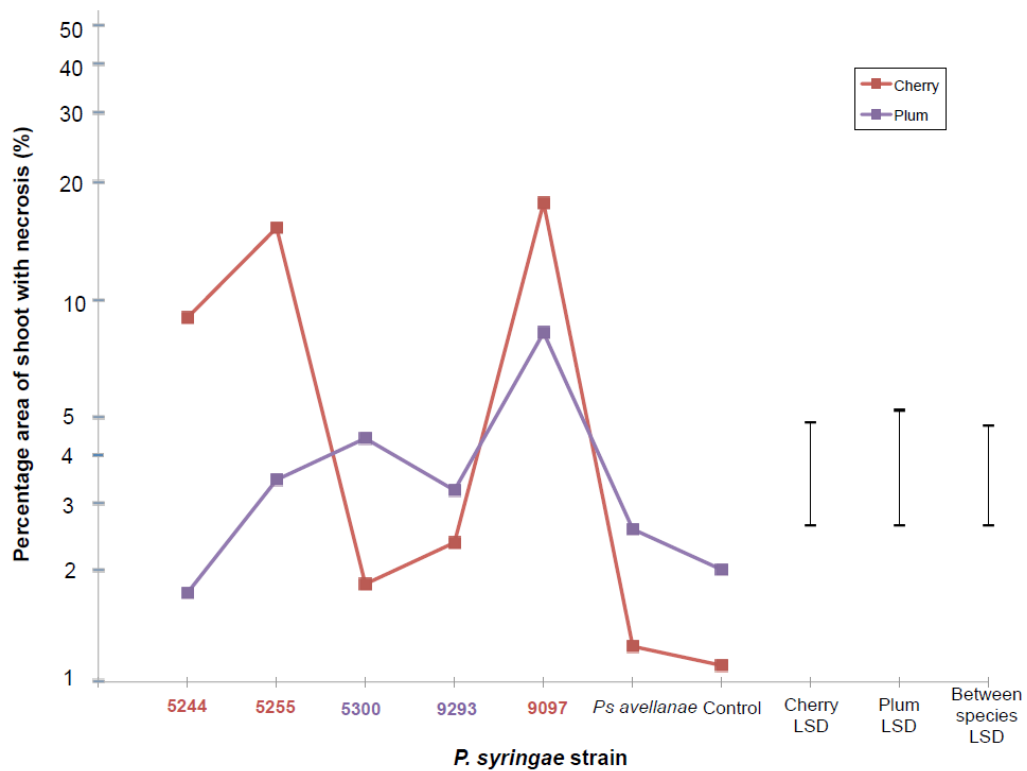


Figure S6. The relationship between the percentage area of necrosis measured using ImageJ or automated image analysis software using fixed thresholding. The linear fitted line indicated the deviation from the ideal calibration line.

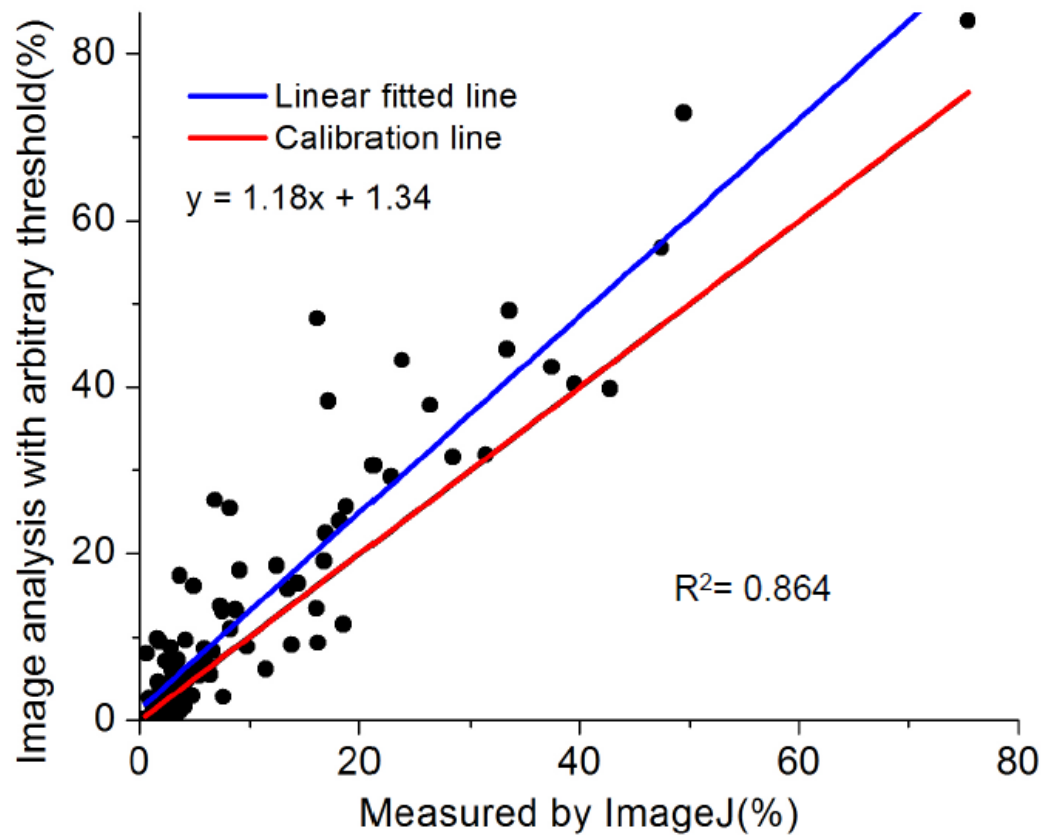


Figure S7. The relationship between the percentage area of necrosis measured using ImageJ or automated image analysis software using adaptive thresholding. The linear fitted line indicated the deviation from the ideal calibration line.

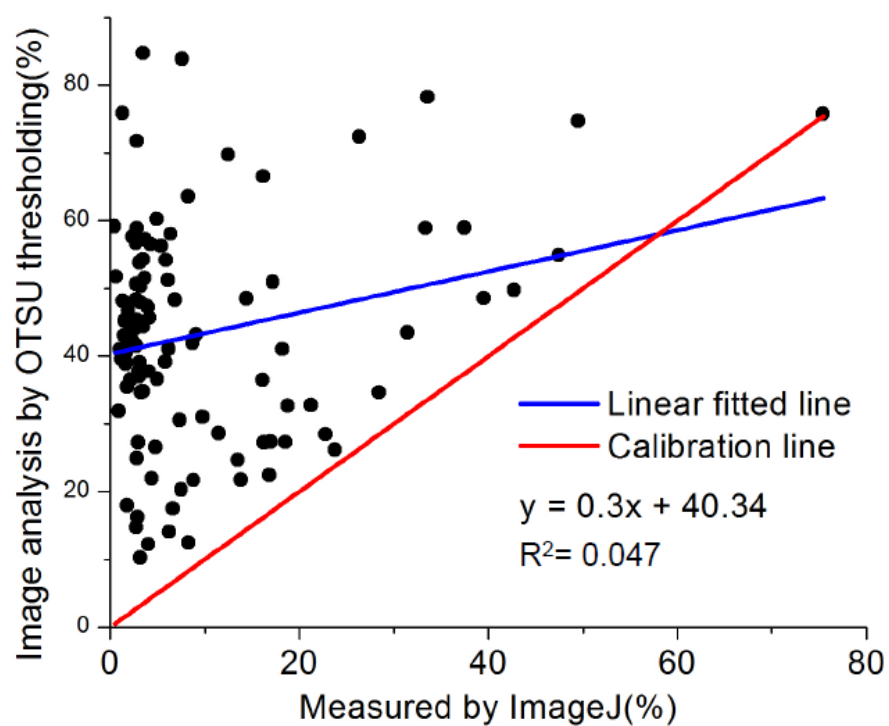


Figure S8. Graphical depiction of an artificial neural network (ANN) model containing one input layer with three neurons, one binary output layer and one hidden layer with sixteen neurons

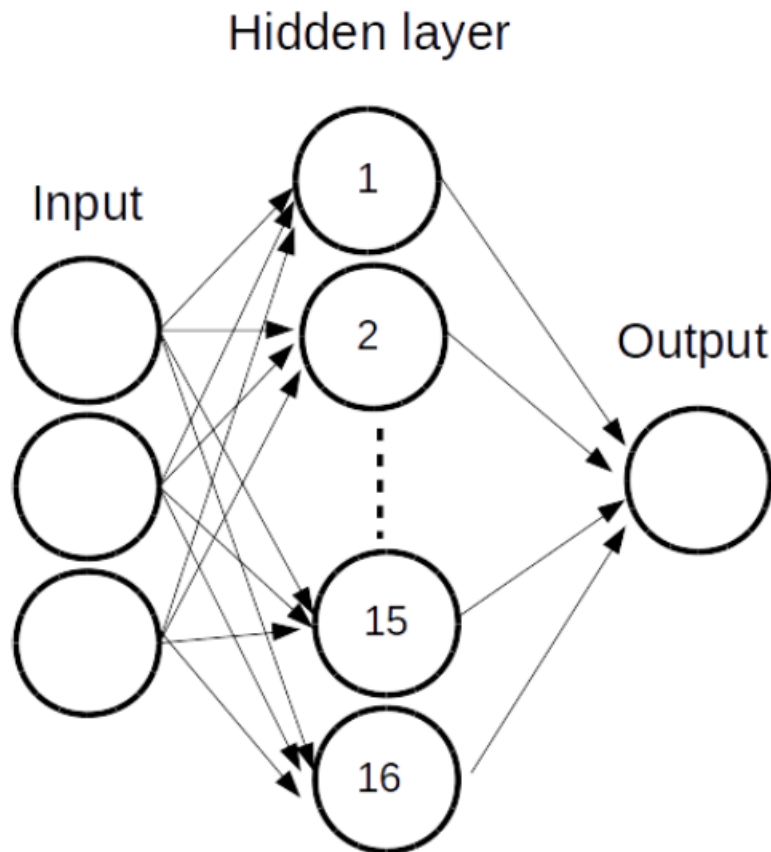


Table S1. ANOVA table generated using Genstat. The ANOVA was performed on the log transformed (+0.1) raw data values. The formula used was aov(strain*(species/cv)+box)

Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.	F pr.
box stratum	9		8.454	0.939	0.82	
box.*Units* stratum						
Species	1		3.895	3.895	3.39	0.066
Strain	6		267.715	44.619	38.82	<.001
species.cv	4		46.591	11.648	10.13	<.001
species.strain	6		87.822	14.637	12.73	<.001
species.cv.strain	24		30.332	1.264	1.1	0.341
Residual	368	1	422.974	1.149		
Total	418	1	867.032			

ANOVA FORMULA: strain*(species/cv)+box

Table S2. Table of means and Least Significant Difference values generated from the ANOVA.

Tables of means from ANOVA								
Variate: LOG((area+0.1))								
Grand mean 1.342								
species	cherry	plum						
	1.41	1.206						
rep.	280	140						
		strain						
species	cv	5244	5255	5300	9293	9097	<i>Ps avellanae</i>	Control
cherry	mgl	1.566	2.541	0.138	0.641	2.383	0.281	-0.08
	nap	2.352	2.727	0.896	1.033	3.399	0.638	0.017
	round	2.129	3.539	0.557	0.501	2.706	-0.057	0.549
	van	2.792	2.132	1.052	1.433	3.029	0.326	0.258
plum	mseed	0.273	0.702	0.893	0.658	1.366	0.626	0.449
	vict	0.946	1.832	2.125	1.755	2.88	1.333	1.04

Least significant differences of means (5% level)					
Table	species	strain	species cv	species strain	species cv strain
rep.	unequal	60	70	unequal	10
d.f.	368	368	368	368	368
l.s.d.	0.2182	0.3849	0.3564	0.6667 min.rep 0.5774 max-min 0.4714 max.rep	0.9428