Note S1. Supporting information on materials and methods

S1.1 Statistical analysis of PLACL-time curves PLACL-time

curves in Figure S3 were fitted using the logistic function

$$f(t; n_0, r, K) = \frac{n_0 K \exp[r(t - t_0)]}{K + n_0(\exp[r(t - t_0)] - 1)}. \tag{1}$$

The shape of the curve described by Eq. (1) is determined by three parameters: n_0, r and K. The parameter n_0 represents the initial value at time t_0, i.e. $f(t = t_0; n_0, r, K) = n_0$. The parameter r is the rate of increase in necrotic area that corresponds to exponential increase during the initial phase. The parameter K represents the stationary value of $f(t; n_0, r, K)$ reached at large times, i.e. $f(t \to \infty; n_0, r, K) = K$.

We determined which of these three parameters differ in different treatments by using model selection approach [1] based on Bayesian information criterion (BIC) [3] and least square fitting. BIC balances the goodness of fit with the number of parameters (or complexity) of the model. We conducted the analysis independently for cultivars Drifter (Figure S3, upper panels) and Chinese Spring (Figure S3, lower panels), as we were not interested in quantitative differences in PLACL between the two cultivars. We started by fitting the most complex model, M_c, that allowed each of the three parameters to vary independently in each treatment. We decided to use the logistic function Eq. (1), because it fitted the data well for this model. Next, we fitted an hierarchy of models of decreasing complexity. The simplest model in this hierarchy (M_0) that fits a single logistic curve to data from all treatments pooled together was rejected due to a poor fit in both cultivars.

To make the analysis feasible, we considered a subset of all possible models in the hierarchy guided by patterns we observed in the data. In particular, for cultivar Drifter, the initial values (characterized by n_0) and the final values of PLACL (characterized by K) appear to be very close in different treatments. We tested this hypothesis by comparing the model M_c with a simpler model, in which n_0 and K were restricted to be the same in different treatments. Indeed, this simpler model proved to be better than M_c, according to BIC. Consequently, we fixed the parameters n_0 and K to be the same in all treatments and equal to their globally optimal values. In cultivar Chinese Spring, we fixed the parameter K to its optimal value restricted to be same in all treatments. We observed strong differences with respect to initial values of PLACL in Chinese Spring. For this reason, in treatments in which the initial values were considerably larger than zero, we set them to the mean values of PLACL observed at the initial time point. In all other treatments, n_0 was set to its optimal value, equal in those treatments.

In both cultivars, we found that the best model based on BIC was of intermediate complexity between M_0 and M_c. Curves in Figure S3 show fits according to the best models and the corresponding parameter values are given in Table S1. The most interesting differences between different treatments within each panel of Figure S3 were found in terms of rates of increase in necrotic area r. Column 2 in Table S1 presents r-values corresponding to the best models.

To corroborate the analysis based on BIC, we also conducted more conservative likelihood ratio tests using the statistic $D_{ij} = -2 \log[\mathcal{L}(m_j)/\mathcal{L}(m_i)]$, where $\mathcal{L}(m_j)$ is the likelihood of a null model and $\mathcal{L}(m_i)$ is the likelihood of an alternative model. Here, we only considered differences in rates of increase in necrotic area, r. Each of the considered cases (different rows in Table S1 correspond to different panels in Figure S3) had three treat-ments: two pure strains and their mixture). In each of these cases, we conducted pairwise comparisons of possible "local" models: $LM_0 : r_1 = r_2 = r_3$, $LM_1 : r_1 \neq r_2, r_2 = r_3$, $LM_2 : r_2 \neq r_1, r_1 = r_3$, $LM_3 : r_3 \neq r_1, r_1 = r_2$, $LM_4 : r_1 \neq r_2, r_2 \neq r_3$. In all cases, the best model was either LM_1, LM_2 or LM_4 and in none of the cases the models LM_0 and LM_3 were better than other models. The fact that the model LM_3 was never the best means that the rates of the four strains inoculated individually were significantly different. Therefore, for conciseness in Table S1, columns 3 and 4, we present only the outcomes of comparison between models LM_1, LM_2 and LM_4. Columns 3 and 4 show the statistics D_{41} and D_{42} that compare the "null" (less complex) models LM_1, LM_2 with the "alternative" (more complex) model LM_4.

Likelihood ratio tests with confidence level $\alpha = 0.05$ gave same results as the model selection analysis based on BIC except for one case: the comparison of PLACL in strains 3D1, 1A5 and their mixture 1A5+3D1 in cultivar Chinese Spring. There, model selection assigned the model LM_4 in which all three rates are different to be the best. But according to the likelihood ratio test, there is not enough evidence to reject the null hypothesis (model LM_2) in favor of the alternative hypothesis LM_4, meaning that the rates r_1 (3D1) and r_3 (1A5+3D1) are not significantly different.

We also compared, PLACL-time curves between the mixture of the four strains ("mix") and each of the individual strains (Figures S3G and S3N) using BIC and the likelihood ratio test (Table S2). Here, we determined whether the rate of increase in the necrotic area in the "mix" was different from the rate in each individual strain. Hence, the relevant models are L4-M_1: $r_5 = r_1, r_5 \neq r_2, r_5 \neq r_3, r_5 \neq r_4$, L4-$M_2$: $r_5 = r_2, r_5 \neq r_1, r_5 \neq r_3, r_5 \neq r_4$, L4-$M_3$: $r_5 = r_3, r_5 \neq r_1, r_5 \neq r_2, r_5 \neq r_4$, L4-$M_4$: $r_5 = r_4, r_5 \neq r_1, r_5 \neq r_2, r_5 \neq r_3$. Column 2 in Table S2 shows the best model according to BIC and columns 3-6 show the outcomes of likelihood ratio tests that compare the four models listed above.

			best model	D_{41}, p	D_{42}, p
cv. Drifter					
	strain				
1	2	3			
3D1	1E4	3D1+1E4	LM$_4$: $r_1 = 1.29$, $r_2 = 0.81$, $r_3 = 1.08$	25.9, 3.7×10^{-7}	6.5, 0.01
3D7	1E4	3D7+1E4	LM$_2$: $r_1 = r_3 = 1.09$, $r_2 = 0.81$	23.4, 1.3×10^{-6}	2.6, 0.1
1A5	1E4	1A5+1E4	LM$_4$: $r_1 = 2.54$, $r_2 = 0.81$, $r_3 = 1.89$	144.7, 2.5×10^{-33}	18.3, 1.9×10^{-5}
3D1	3D7	3D1+3D7	LM$_4$: $r_1 = 1.29$, $r_2 = 1.09$, $r_3 = 2.09$	81.3, 2.0×10^{-19}	45.8, 1.3×10^{-11}
3D7	1A5	1A5+3D7	LM$_4$: $r_1 = 1.09$, $r_2 = 2.54$, $r_3 = 1.62$	39.5, 3.2×10^{-10}	51.8, 6.2×10^{-13}
3D1	1A5	1A5+3D1	LM$_1$: $r_1 = 1.29$, $r_2 = r_3 = 2.54$	0.19, 0.66	67.0, 2.8×10^{-16}
cv. Chinese Spring					
	strain				
1	2	3			
3D1	1E4	3D1+1E4	LM$_4$: $r_1 = 1.16$, $r_2 = 0.33$, $r_3 = 1.79$	294.6, 4.8×10^{-66}	24.4, 7.9×10^{-7}
3D7	1E4	3D7+1E4	LM$_2$: $r_1 = r_3 = 1.28$, $r_2 = 0.33$	205.6, 1.3×10^{-46}	1.9, 0.17
1A5	1E4	1A5+1E4	LM$_4$: $r_1 = 3.35$, $r_2 = 0.33$, $r_3 = 2.15$	311.1, 1.2×10^{-69}	22.3, 2.3×10^{-6}
3D1	3D7	3D1+3D7	LM$_4$: $r_1 = 1.16$, $r_2 = 1.28$, $r_3 = 0.63$	23.5, 1.3×10^{-6}	14.3, 1.5×10^{-4}
3D7	1A5	1A5+3D7	LM$_1$: $r_1 = 1.28$, $r_2 = r_3 = 3.35$	2.3, 0.12	101.7, 6.4×10^{-24}
3D1	1A5	1A5+3D1	LM$_4$: $r_1 = 1.16$, $r_2 = 3.35$, $r_3 = 0.67$	9.2, 0.0024	3.4, 0.065

Table S1: Outcomes of model selection analysis and likelihood ratio tests for PLACL-time curves in Fig. S3A-F and Fig. H-M. Values $n_0 = 0.7$, $K = 96.3$ were optimal in cv. Drifter and values $n_0 = 0.05$, $K = 92.75$ were optimal in cv. Chinese Spring.

					best model	D_{51}, p	D_{52}, p	D_{53}, p	D_{54}, p
cv. Drifter									
		strain							
1	2	3	4	5					
3D1	3D7	1A5	1E4	mix	L4-M$_5$	51.6 6.9×10^{-13}	33.4 7.4×10^{-9}	129.9 4.3×10^{-30}	4.5 0.03
cv. Chinese Spring									
		strain							
1	2	3	4	5					
3D1	3D7	1A5	1E4	mix	L4-M$_3$	37.0 1.2×10^{-9}	117.2 2.6×10^{-27}	0.52 0.47	375.8 1.0×10^{-83}

Table S2: Outcomes of model selection analysis and likelihood ratio tests for PLACL-time curves in case of 4-way strain mixtures.

References

[1] Johnson, J. B., and K. S. Omland. 2004. Model selection in ecology and evolution. Trends Ecol. Evol. **19**:101–8.

[2] Schwarz, G. 1978. Estimating the Dimension of a Model. Ann. Stat. **6**:461–464.