Supplementary Material – Text S1: Description of the deterministic model

In this supplementary material, we describe our epidemiological model in its deterministic form, for a field composed only of susceptible (S) plants, without quantitative resistance. It is used to attribute meaningful values to a parameter representative of the intensity of epidemics in a reference field before deployment of R plants. In a second part, we describe this deterministic model with the introduction of R plants, and in a third part we describe the stochastic model. To summarise how we model the infection process, we consider bottlenecks undergone by viruses from host-to-host transmission to subsequent within-host infection (until the onset of systemic infection, see Fig. S1). The global effect of all bottlenecks is summarised in a unique effective population size, denoted N_e^R in R plants and N_e^S in S plants. During these steps, selection and mutation forces are neglected. Then, upon systemic infection, only selection and mutation are considered, and we assume that virus populations reach instantaneously their equilibrium, consisting of a frequency f_{RB} of resistance-breaking (RB) variant in S plants and of 100% of the RB variant in R plants.

1 Fully susceptible field

In this situation, the host carries no resistance at all (qualitative or quantitative) and the virus effective population size N_e^S accounting for bottlenecks from host-to-host transmission to within-host progression is very large (10^4). The dynamics of the number of infected S plants I^S accross the n_d days of the cropping season in the field composed of N^S S plants is assumed to follow a healthy - infected type ordinary differential equation (ODE), as:

$$\frac{dI^S}{dt} = \beta_0 \frac{I^S(N^S - I^S)}{N^S} \left(1 - e^{-N_e^S}\right).$$

(1)

A single S plant is infected initially, i.e. $I^S(0) = 1$. β_0 is the basic contact rate from an infected plant to a healthy one through insect vectors. The last term of eq. 1 accounts for bottlenecks experienced by viruses. We suppose that S plants get infected if and only if at least one virus

particle (or infectious unit) passes through all bottlenecks. Assuming that the number of virus particles surviving all bottlenecks results from a Poisson distribution of mean N_e^S, it follows that the probability that at least one virus particle survives all bottlenecks is the opposite of the event leading to zero virus particles surviving, that is $1 - e^{-N_e^S}$. In fact, as the S plant carries no quantitative resistance (i.e. $N_e^S = 10^4$) we have $1 - e^{-N_e^S} \simeq 1$. Hence the impact of bottlenecks on the success of infection in this simple model is negligible.

The analytic integration of the proportion of infected S plants $p_i^S(t) = I^S(t)/N^S$ over n_d days through equation 1 provides the area under the disease progress curve (AUDPC) in the field, $A_0 = \int_0^{n_d} p_i^S(t)dt = \frac{1}{\beta_0} \ln \left(1 + p_i^S(0) \left(e^{\beta_0 n_d} - 1 \right) \right)$. Following Fabre *et al.* (2012) [1], we use the AUDPC to attribute meaningful values to the epidemic parameter β_0. For this purpose, we introduce a new parameter, the intensity of epidemics Ω_{int}, giving the average proportion of plants infected along a cropping season in a fully S field. Thereby we have the relationship $\Omega_{int} = A_0/n_d$, from which we can infer values of β_0 for given epidemic intensities.

2 Deployment of resistant plants

Let us now consider the introduction of R plants in the field, with I^R the number of infected R plants and N^R the total number of R plants (the total number of plants is $N^p = N^S + N^R$). The model describing the epidemics then reads as:

$$
\begin{cases}
\dfrac{dI^S}{dt} = \left(\beta_0 \dfrac{I^S(N^S - I^S)}{N^p} + \beta_0 \dfrac{I^R(N^S - I^S)}{N^p} \right) \left(1 - e^{-N_e^S} \right) & (2) \\[3mm]
\dfrac{dI^R}{dt} = \beta_0 \dfrac{I^R(N^R - I^R)}{N^p} \left(1 - e^{-N_e^R} \right) + \beta_0 \dfrac{I^S(N^R - I^R)}{N^p} \left(1 - e^{-N_e^R f_{RB}} \right) & (3) \\[3mm]
I^S(0) = 1 \, , \, I^R(0) = 0. & (4)
\end{cases}
$$

Initially, a single S plant is infected and no R plant is infected. S and R plants can be infected either by S or R plants, at a basic contact rate β_0, as described previously. The mechanism of survival of viruses through bottlenecks is modelled similarly as in eq. 1 for infection of S plants ($1 - e^{-N_e^S}$, eq. 2) and for infection of R plants when the vector comes from a R plant ($1 - e^{-N_e^R}$, left-hand part of eq. 3). Indeed, as we assume that the RB variant is present at a frequency of 1 in R plants, the vector transmitting viruses from an infected R plant to a healthy R plant is necessarily inoculating the RB variant to the target R plant, and we also assume that the survival of at least one RB particle is sufficient to infect the R plant. If a S plant gets infected by a R plant, only the RB variant can be transmitted but we assume that the virus population

instantaneously evolves towards an equilibrium frequency f_{RB} of RB variant through mutation and selection. The bottleneck survival term for the infection of a R plant from a S plant is slightly different ($1 - e^{-N_e^R f_{RB}}$, right-hand part of eq. 3). We suppose that the target R plant will be infected if and only if at least one RB particle survives the bottlenecks. We model this condition with the probability density of a Poisson distribution of mean $N_e^R f_{RB}$. Indeed, if on average N_e^R virus particles survive all bottlenecks, only $N_e^R f_{RB}$ of these virus particles correspond to the RB variant because the infection comes from a S plant. The probability density that at least one RB particle survives all bottlenecks is found by taking the opposite of the event leading to zero RB variant surviving, that is $1 - e^{-N_e^R f_{RB}}$. When f_{RB} is low, i.e. when the qualitative resistance is hardly breakable, this probability is at most $1 - e^{-10^4 \times 10^{-6}} \simeq 10^{-2}$ ($N_e^R = 10^4$ and $f_{RB} = 10^{-6}$). On the opposite, when f_{RB} is high, i.e. when the qualitative resistance is easily broken down, this probability is at least $1 - e^{-1 \times 0.1} \simeq 10^{-1}$ ($N_e^R = 1$ and $f_{RB} = 0.1$), and increases very fast with N_e^R.

3   Stochastic model description

Continuous time Markov chains and birth processes were chosen for the stochastic form of the model [2]. We follow the dynamics of the number of S and R infected plants, I^S and I^R respectively, along the cropping season. A single S plant is infected initially, i.e. $I^S(0) = 1$ and $I^R(0) = 0$. Transition rates π^{ij} for the 'birth' of a new infected plant by contact from an infected i (i = S or R) to a healthy j (j = S or R) plant are defined as $\pi^{ij} = \beta_0 \dfrac{I^i(N^j - I^j)}{N^p}$. The waiting time until the next infection attempt [3] was modelled with the Gillespie algorithm [4]. Once the waiting time is known, the varieties (S or R) of the actual source and target plants are determined according to the probabilities π^{ij} of each event to occur. Then, the number of virus particles surviving the bottlenecks is drawn from a Poisson distribution, as $X_e^S \sim Pois(N_e^S)$ for a target S plant, and $X_e^R \sim Pois(N_e^R)$ for a target R plant. A target S plant gets infected if and only if $X_e^S \geq 1$ (it otherwise remains healthy). For a target R plant, if $X_e^R \geq 1$, two cases are to be distinguished. If the source plant is R, the plant necessarily gets infected. If the source plant is S, the plant will get infected if and only if at least one RB particle is part of the X_e^R surviving the bottlenecks. We assume that the number of RB particles surviving the bottlenecks follows a Binomial distribution, as $n_{RB} \sim Binom(X_e^R, f_{RB})$. To highlight the match with the deterministic form of the model, let us note that a draw of X_e^R in a Poisson distribution of mean N_e^R followed by a draw in a Binomial distribution of parameters X_e^R and f_{RB} is indeed equivalent a single draw draw in a Poisson distribution of

parameter $N_e^R f_{RB}$.

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Supplementary Material – Text S2: Computation of the relative damage and additional relative benefit

In this supplementary material, we describe in details how we compute the relative damage and additional relative benefit. We rely on these two variables to analyse our simulations and assess the impact of deploying qualitative and quantitative resistances on yield benefits.

1 Measuring the yield increase in comparison with the fully susceptible scenario

We analysed the benefit for farmers of deploying resistant (R) plants based on the associated yield increase. This quantity was measured thanks to the area under the disease progress curve (AUDPC), a good proxy of the yield losses caused by a pathogen [1, 2]. Calculations were done for each:

- deployment strategy $\boldsymbol{\delta} = (\varphi, f_{RB}, N_e^R)$, involving a proportion φ of R plants, a frequency of the resistance-breaking (RB) variant in S plants f_{RB} and a virus effective population size N_e^R in R plants,

- and epidemiological context before deployment of R plants Ω_{int}, i.e. a value of the intensity of epidemics.

For one simulation over one cropping season, the AUDPC for a particular epidemiological context and deployment strategy is $A(\Omega_{int}, \boldsymbol{\delta}) = \int_0^{n_d} \left[(1 - \varphi)p_i^S(t) + \varphi p_i^R(t) \right] dt$, integrating the weighted proportions of susceptible (S) and R infected plants, $p_i^S(t) = I^S(t)/N^p$ and $p_i^R = I^R(t)/N^p$, respectively. This AUDPC is compared to the one obtained in the reference field before deployment of R plants with the same epidemiological context, $A_0(\Omega_{int}) = n_d\Omega_{int}$ (see Text S1). For this purpose, we define the percentage of relative damage for a particular deployment strategy in a specific epidemiological context as:

$$D(\Omega_{int}, \boldsymbol{\delta}) = 100 \times \frac{A(\Omega_{int}, \boldsymbol{\delta})}{A_0(\Omega_{int})} \tag{1}$$

For example, $D = 30\%$ means that, in epidemiological context Ω_{int}, deploying R plants according to strategy $\boldsymbol{\delta}$ reduces the total number of infected plants to 30% of the crop damages before R plants deployment.

2 Evaluating the benefit of narrowing bottlenecks to increase yield

From the relative damage we can assess the additional yield benefit provided by using a pyramided resistance, i.e. combining quantitative resistance reducing virus effective population size with a qualitative resistance, compared to a monogenic resistance, i.e. a R cultivar without such quantitative resistance. Strategies using a monogenic, resp. pyramided, resistance cultivar are denoted $\boldsymbol{\delta}_{Rm}$, resp. $\boldsymbol{\delta}_{Rp}$. The reference value of N_e^R for $\boldsymbol{\delta}_{Rm}$ strategies was set to 10^4 (Tab. [1] in main text). For $\boldsymbol{\delta}_{Rp}$ strategies, N_e^R was varied from 1 to 100, thereby reducing virus effective population size by a factor 100 to 10^4. We evaluated the added value of narrowing bottlenecks for yield benefit by comparing $\boldsymbol{\delta}_{Rm}$ and $\boldsymbol{\delta}_{Rp}$ strategies differing only by parameter N_e^R, i.e. with the same values of φ, f_{RB} and Ω_{int}. Following Fabre *et al.* (2015) [3], we define the additional relative benefit of the pyramided resistance strategies as:

$$\Delta(\Omega_{int}, \boldsymbol{\delta}_{Rp}) = \bar{D}(\Omega_{int}, \boldsymbol{\delta}_{Rm}) - \bar{D}(\Omega_{int}, \boldsymbol{\delta}_{Rp}), \tag{2}$$

with $\bar{D}$ the mean relative damage over the n_{iter} stochastic simulation iterations for one set of parameter values. For example, $\Delta = 20$ percentage points means that using the pyramided resistance reduces the total number of infected plants by 20 percentage points compared to using the monogenic resistance, in the same epidemiological context Ω_{int} and with the same proportion of R plants φ and frequency of RB variant in S plants f_{RB}.

References

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Supplementary Material – Text S3: Epidemic dynamics

Here we present a description of model outputs, which consist of single season epidemic dynamics in a field. The output variables are the proportions of infected susceptible (S) and resistant (R) plants, and the total proportion of infected plants (S and R). In Fig. S2, the reference intensity of epidemics in the fully S field Ω_{int} was set to 0.3. In this reference fully S field, the epidemic took off around 40 days after sowing and 95% of the plants were infected at the end of the season (Fig. S2). Deploying a monogenic resistance cultivar (virus effective population size in R plants $N_e^R = 10^4$) at a proportion $\varphi = 0.8$ with a resistance gene characterized by a frequency of the resistance-breaking (RB) variant in S plants $f_{RB} = 0.01$ slightly reduced the epidemic in S plants, with 86% of S plants infected at the end of the season, on average. In R plants, the epidemic took off approximately at the same period and 85% of R plants were infected at the end of the season on average. Hence, the RB variant quickly invaded the field. Overall, in both S and R plants, adding plants with monogenic resistance only slightly decreased the epidemic intensity, from 0.3 to 0.25, and the mean proportion of infected plants at the end of the cropping season was approximately 10 percentage points less than in the fully S field. Adding quantitative resistance reducing N_e^R to 5 (pyramided resistance) drastically slowed down the epidemic. At the end of the cropping season the proportion of infected plants dropped to 11% in S plants, 7% in R plants, and 8% in the field (S and R plants), on average. With this strategy, the intensity of epidemics was reduced to 0.02. This example shows the potential benefit of pyramiding quantitative resistance reducing virus effective population size in R plants. In that case, the qualitative resistance alone reduces the damage by $(0.3 - 0.25)/0.3 = 16.7\%$, and pyramiding a quantitative resistance accounts for an additional $\Delta = 100 \times \frac{0.25 - 0.02}{0.3} = 76.7$ percentage points decrease.

Demographic bottlenecks bring stochasticity to the dynamics of virus populations, and in return also to the epidemics. Hence, it is important to also look at the variability between epidemic simulations. Yet, Fig. S2 shows that the stochastic model intrinsically generates a large variability in the dynamics of the proportion of infected plants, looking at deployment strategies of monogenic resistance, i.e. with negligible bottlenecks. The density of curves at the last day of the cropping season shows that 21% of the curves are concentrated around a peak of density at 96-98% of infected plants (Fig. S2C). The epidemic curves show slightly less variability in simulations of pyramided vs. monogenic resistance deployment. This is explained by the strong decrease in epidemics spread, leading to flat epidemic curves around 0% of infected plants, generating a so-called saturation effect. The peak of density at the last day of the season is located

around 0-2% of infected plants for 61.6% of the simulations (Fig. S2C).

Supplementary Material – Text S4: Impact of the choice of the resistance gene on the relative damage

In this supplementary material, we describe our results on the relative damage (see Text S2), which allow us to disentangle the effects of deploying a qualitative resistance alone from those of deploying resistant (R) plants pyramiding qualitative and quantitative resistances decreasing virus effective population size in R plants N_e^R. We then briefly discuss those results.

Results

We represented the relative damage D as a function of the choice of the qualitative resistance gene (frequency of resistance-breaking - RB - variant in S plants f_{RB}) for two fixed values of the proportion of resistant plants φ (0.2 and 0.8) and of the intensity of epidemics Ω_{int} (0.2 and 0.8), and four N_e^R values, one corresponding to monogenic resistance strategies ($N_e^R = 10^4$), and the other three to pyramided resistance strategies ($N_e^R = 1$, 10 and 100, Fig. S3). Stronger epidemic intensities (Ω_{int}=0.8) generate larger relative damage on average. When φ is small (0.2), relative damages start on average around 36-37% for the lowest f_{RB} value and low Ω_{int} (0.2), against 73-74% for high Ω_{int} (0.8). The pattern remains the same as f_{RB} increases.

When φ is large (0.8), epidemics can become extinct (i.e. nearly all plants remain healthy over the cropping season), as D approaches 0% for the lowest f_{RB} values. The relative damage curves take off from these epidemic-extinction cases for smaller f_{RB} values when Ω_{int} is stronger. Typically, the departure from epidemic-extinction case is located around $f_{RB} = 10^{-6}$ (resp. 10^{-4} for pyramided resistance strategies) when $\Omega_{int} = 0.2$ against $f_{RB} = 10^{-8}$ (resp. 10^{-6} for pyramided resistance strategies) when $\Omega_{int} = 0.8$.

A striking result is the effect of Ω_{int} on the variability of D. The stronger Ω_{int}, the smaller the variability of D. Also, for the lowest Ω_{int} value, D can reach values larger than 100%. It means that the corresponding simulations generated more crop damage than in the fully S field. Yet, the mean relative damage never gets above 100%, showing that on average deploying R plants is beneficial.

The additional relative benefit Δ is evaluated by the distance between the curves corresponding to the pyramided resistance strategies to the ones of the monogenic resistance strategy ($N_e^R = 10^4$). When f_{RB} is small, all the curves are close to each other at a small to moderate damage level, hence no additional benefit is provided by adding quantitative resistance. This is especially true when Ω_{int} is low (0.2), as the curves stay close for a larger range of f_{RB} values

than when Ω_{int} is high. The result of low Δ when $f_{RB} = 0.5$ in figure 1 is here split in two cases. It is true when $N_e^R = 10$ or 100, but less so when $N_e^R = 1$. In that latter case, it is true only when Ω_{int} is high (0.8) and φ is small (0.2); otherwise the relative damage still gets reduced. As in figure 1, we can see that intermediate values of f_{RB} lead to the largest reduction in relative damage when adding quantitative resistance. We can go further here by noticing that a larger φ (0.8) leads to more additional relative benefit.

Discussion

The model shows an interesting combined effect of the intensity of epidemics Ω_{int} and the proportion of R plants φ on relative damage D (Fig. S3). When the majority of plants is S ($\varphi \leq 0.5$), higher epidemic intensities generate larger relative damage on average. Indeed, high epidemic intensities are associated with high contact rates β_0. As the majority of plants is S, higher epidemic intensities lead to a higher number of successful infections along the season, and hence to larger relative damages.

When the majority of plants is R ($\varphi \geq 0.5$), higher epidemic intensities lead to significantly positive values of additional relative benefits for intermediate RB variant frequencies in S plants f_{RB}. When Ω_{int} and f_{RB} are low, epidemic-extinction cases are observed for both pyramided and monogenic resistance strategies. In those cases, decreasing virus bottleneck size cannot provide more yields. When epidemic intensity is high, the relative damage of the monogenic resistance strategy takes off from the epidemic-extinction cases for lower f_{RB} values. More trials of infection are attempted, leading to overall higher successful infection probabilities. In return, as the epidemic does not become extinct anymore, quantitative resistance can provide additional benefit again.

The variability in relative damages decreased with epidemic intensity. The stronger the intensity of epidemics, the sooner all plants get infected, a point beyond which the dynamics necessarily remain constant.

We reported cases where the relative damage got above 100% when epidemics intensity is small. This does not necessarily imply that deploying R plants was harmful, as one major change from fully S field simulations was the use of a stochastic model, which can lead to such a result simply because of the intrinsic variability in epidemic dynamics. In any case, the additional relative benefit hardly ever went below 0 percentage points for the set of parameters used in figure 2, showing that on average deploying R plants is beneficial. The few cases of negative additional

2

relative benefit were most probably due to the intrinsic stochasticity of the model and not to a harmful effect (for resistance durability) of decreasing virus bottleneck size.