Appendix S1: estimation of the dominance based on “mortality phenotypes”

A second estimation of dominance was based on the proportion of “mortality phenotypes” (mortality date) that were considered incompatible with the mortality pattern of susceptible individuals. Mortality in the S × S progenies reared on Bt was modeled as a function of time using a Weibull distribution characterized by both a shape parameter \( (k > 0) \) and a scale parameter \( (\lambda > 0) \). Maximum log-likelihood estimations of those parameters set the reference model (henceforth \( \Phi_{ss} \)) which describes the mortality dynamics of susceptible individuals on Bt corn. Then, on the basis of this model, we computed the probability of individual mortality (in the R × R and R × S progenies) to be incompatible with the mortality phenotype of susceptible individuals (\( \Phi_{ss} \)). The density probability associated to the proportion of “non-susceptible” individuals (\( p \) – henceforth \( p_{R\times S} \) and \( p_{R\times R} \) relative to the crosses R × S and R × R, respectively) was calculated on the basis of a binomial distribution. The dominance (\( h_\phi \)) was assessed using the following formula: 

\[
h_\phi = \frac{p_{S\times S} - p_{R\times S}}{p_{S\times S} - p_{R\times R}},
\]

and its associated posterior probability distribution was computed accordingly.

Reference model

The mortality \( M(t) \) in the S × S progenies reared on Bt was modeled as a function of time using to a Weibull distribution:

\[
M(t|k, \lambda) = 1 - e^{-\left(\frac{t}{\lambda}\right)^k}.
\]

where \( k > 0 \) is a shape parameter and \( \lambda > 0 \) is a scale parameter of the distribution.
Under this model, we considered the probability for an individual \( i \), originating from a \( S \times S \) cross \( c \), to die between two observation times \( T_{ci} \) and \( T_{ci}+1 \). The corresponding likelihood function used to fit the Weibull model was:

\[
\ell(k, \lambda) = \prod_{c=1}^{C} \prod_{i=1}^{l_c} \left[ M(T_{ci} + 1|k, \lambda) - M(T_{ci}|k, \lambda) \right]
\]

The maximum likelihood estimations of the parameters \( k \) and \( \lambda \) defined the reference model (henceforth, \( \Phi_{ss} \)) describing the mortality dynamics of susceptible individuals (i.e., originating from \( S \times S \)) on \( Bt \) corn.

**Proportion of “non-susceptible” phenotypes in the \( R \times R \) and \( R \times S \) progeny**

Then, on the basis of this model, we discriminated individuals of the \( R \times R \) and \( R \times S \) progenies whose observed mortality date was not compatible with the phenotype of susceptible individuals (\( \Phi_{ss} \)). We classified as “non-susceptible” any individual mortality events that had, conditionally to \( \Phi_{ss} \), a probability to be observed lower than 0.001. The following criterion was considered:

\[
1 - P(O_{ci} | \Phi_{ss}) > 0.999
\]

where \( O_{ci} \) is the time interval within which the death an individual \( R \times R \) or \( R \times S \) is observed. Individuals surviving up to adult stage were *de facto* considered to meet this criterion.

The density probability of the proportion of individuals meeting this criterion in each cross (\( p \) – henceforth \( p_{R \times S} \) and \( p_{R \times R} \) relative to the crosses \( R \times S \) and \( R \times R \), respectively) was calculated on the basis of a binomial distribution:

\[
\Psi_c \left(p|n_c, N_c\right) = C_{N_c}^{n_c} p^{n_c} (1 - p)^{n - n_c}
\]
where $n_c$ denotes the observed number of individuals which were discriminated as non-compatible with the $\Phi_{si}$ model out of the $N_c$ individuals reared on $Bt$.

The dominance corresponding to those distributions was assessed using the same formula as before: $h_\phi = (p_{S\times S} - p_{R\times S}) / (p_{S\times S} - p_{R\times R})$, and the associated posterior probability distribution was computed accordingly.

**Results**

The maximum log-likelihood fit (-14.02) of the reference Weibull model ($\Phi_{si}$) was obtained with the parameter values $k = 2.511$ and $\lambda = 0.595$ (Figure S1). The maximum log-likelihood estimation of the proportions of individuals which did not die according to the modeled pattern of susceptible insects ($p_{R\times S}$ and $p_{R\times R}$) were comparable: $p_{R\times S} = 0.667$ and $p_{R\times R} = 0.610$.

The interval defining 95% of their probability distribution, [0.539, 0.772] in $R \times S$ and [0.540, 0.676] in $R \times R$ overlapped (Figure S2). The maximum likelihood estimation of the dominance based on the mortality phenotype was close to 1, $h_\phi = 1.088$ with a 95%-interval of [0.854 – 1.327], while the dominance estimation based on larvae survival at the end of the experiment was higher, $h_S = 1.560$ with a 95%-interval [0.874, 2.566] (Figure S3).