#### 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 "nonsusceptible" 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:  $h_{\phi} = (p_{S\times S} - p_{R\times S}) / (p_{S\times S} - p_{R\times R})$ , 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:

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

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 × 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 × R and R × 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 × S and R × R, respectively) was calculated on the basis of a binomial distribution:

$$\Psi_{c}(p|n_{c},N_{c}) = C_{N_{c}}^{n_{c}} p^{n_{c}} (1-p)^{n_{c}}$$

where  $n_c$  denotes the observed number of individuals which were discriminated as noncompatible with the  $\Phi_{ss}$  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 ( $\Phi_{ss}$ ) 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 × S and [0.540, 0.676] in R × 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).