**Supplementary Text 1.** Further details of generalised linear models fitted, including dispersion tests and adjusted R2 used

For all binomial/quasibinomial models, a ‘weights’ term was included (Gelman and Hill, 2007). For the leaf herbivory analyses, this corresponded to the total number of leaves surveyed at each distance point. For the dummy caterpillar analysis, this was the number of caterpillars recovered at each distance point. For the UM2 data (dummy caterpillars and pitfall traps), Plot ID (‘Plot1’ or ‘Plot2’) was included as a fixed factor in the analysis to control for between-plot differences. Poisson generalised linear models use a log link function, and binomial models a logit link function. Model outputs were back-transformed accordingly for inclusion in the main text.

Models with poisson or binomial families fitted were tested for overdispersion. For binomial models, a function that tests for overdispersion from Bolker (2019) was used. For poisson models, the dispersiontest() function from the package AER in R was used. Quasibinomial/quasipoisson models (as appropriate) were fitted to overdispersed data. Dispersion parameters of all GLMs fitted are reported in Supplementary Table 1; where the dispersion parameter differs from 1, this is the dispersion parameter that the quasibinomial/quasipoisson GLM fitted.

Model fit was formally assessed using R-squared (R2) values. Because the majority of models fitted were poisson or binomial GLMs, a pseudo-R2 value (commonly referred to as McFadden’s R2, but also R2D (Heinzl and Mittlböck, 2003) or ρ2 (Louviere *et al.*, 2000)) was chosen:

R2D = 1 - (residual deviance / null deviance)

as recommended by Cameron and Windmeijer (1996). The values for residual deviance and null deviance are available from the summary() output of the model in R (for the log-likelihood notation, see Heinzl and Mittlböck (2003)). An adjusted pseudo-R2 is also presented, which penalises the model fit metric for the number of parameters included in the model, as proposed by Mittlböck and Waldhör (2000):

R2D, γ = 1 - ((residual deviance + k) / null deviance)

where k = the number of parameters (explanatory variables) fitted in the model. For overdispersed data, a further adjustment was made to penalise for the use of a quasibinomial or quasipoisson family, as suggested by Heinzl and Mittlböck (2003):

R2D, Dγ = 1 - ((residual deviance + k + φ) / null deviance)

where φ = dispersion parameter (given in the summary() output of the quasi-fitted model in R). R2D values in the range of 0.2 to 0.4 are interpreted as indicating a very good model fit (Louviere *et al*., 2000). Simulations by Domencich and McFadden (1975) find this to be equivalent to conventional R2 values of 0.7 to 0.9. For Gaussian-family GLMs (i.e. general linear models), conventional R2 and adjusted R2 values are reported instead.

For the leaf herbivory measurements in UM1, we repeatedly monitored the same plants at each distance point over successive days, so ‘Unique plant ID’ could be included as a random effect in the analysis to control for this non-independence of leaf scores. We therefore attempted to run a sensitivity analysis with Unique\_plant\_ID or Distance included as a random effect which did not change the direction or significance of the Distance:Day interaction. However, we retained the original model without Unique plant ID due to concerns of overfitting with the mixed effects model that included it.

**References**

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