**Supplementary Material**

Demographic model

We used existing demographic data for this species (see Table 1 in Jongejans et al 2008) to construct a baseline annual 4X4 matrix model in R (R Development Core Team 2008).

Seed bank (SB) Small (S) Medium (M) Large (L) (1)



Where: σ1 represents survival of seed in seed bank; σ2 represents survival of small rosettes (S); σ3 denotes survival of medium rosettes (M); σ4 denotes survival of large rosettes (L); γ3 is the growth of establishing seed to M; γ4 is the growth of establishing seed to L; γ32 is the growth of surviving, not-bolting S to M; γ42 is the growth of surviving, not-bolting S to L; γ43 is the growth of surviving, not-bolting M to L; ρ23 represents retrogression of surviving, not bolting M to S; ρ24 represents retrogression of surviving, not bolting L to S; ρ34 represents retrogression of surviving, not bolting L to M. Bolting parameters are given by β2, β3, and β4 (bolting of surviving S, M, and L rosettes respectively). Parameter π2 is the potential seed production by S; π3 is the potential seed production by M; and π4 is the potential seed production by L; while φ represents potential seed escaping from floral herbivory. New seed entering seed bank is given by ν, while ε denotes new seed establishing seedlings and ε1 denotes seed from the seed bank establishing seedlings. Baseline parameters are given in Jongejans et al (2008).

We then modified the model based on the proportional changes of survival (σ2, σ3, σ4), and reproduction (π2, π3, π4) from our experimental results from Zhang and Shea (2012) presented in Table 1.

Dispersal model

We used the mechanistic Wald Analytical Long-distance Dispersal (WALD) model (Katul et al. 2005) to model dispersal of C. nutans. Previous field experiments confirm that this model captures the dispersal of this species very well (Skarpaas and Shea 2007). The model predicts an inverse Gaussian (Wald) distribution of dispersal distances r (Evans et al. 1993):

 (2)

where location parameter **’ and the scale parameter **’ are given by:

 and  (3)

where *H* is the seed release height (mean plant height), *F* is seed terminal settling velocity, *U* is the hourly mean horizontal wind velocity between *H* and the ground, and ** is a turbulent flow parameter which reflects wind variation due to vegetation structure and weather conditions. We modified *H* based on results from the mowing experiment. *F*, *U* and ** were assumed to be the same as in a previous study completed in the same experimental field (Table 1 in Jongejans et al. 2008).

Spread model

We then combined the demographic and dispersal models to model the spatial spread using integrodifference equations (Neubert and Caswell 2000, Shea et al. 2010, Zhang et al. 2011):

H = MA(4)



where A is the demographic matrix model, and signifies the Hadamard product (element by element multiplication), and M is a matrix of the same size as A, which comprises elements containing the moment generating function of the dispersal kernel*k*(*r*) (eqn 6). In our case, the population spread rate converges to a constant speed, *c\**:



 (5)

where *M*(*j*) is the moment generating function of the dispersal kernel. The WALD model is integrated over terminal velocity and seasonal wind conditions to give the seasonal dispersal kernel:

(6)



where *p*(*F*) and *p*(*U*) are the probability density functions of *F* and *U*, respectively, and *p*(*r*) is the WALD model.

For each treatment, we reduced reproduction, survival and plant height relative to the control based on data in Table 1, using experimental treatment means and SEs to estimate the mean and SEs of lambda and c\*. We used the medians of these runs to exclude potential extreme outliers arising from the integrated WALD model. See Jongejans et al. (2008) and Zhang et al. (2011) for further computational details.

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