SUPPLEMENTARY DATA

Appendix S1. Spatial size structure

To detect spatial autocorrelation in DBH, we calculate the spatial semivariance for DBH for every pair of trees (ie. a variogram cloud), where the estimator of the semivariance for a given pair of trees $\{j,k\}$ is

$$\gamma(d_{jk}) = \frac{1}{2}(x_j - x_k)^2$$

Where d_{jk} is the distance between tree j and tree k, and x_j, x_k are the DBH of trees j and k. We fit a LOESS curve to describe the trend of semivariance over distance: $\gamma(d_{jk})$ is modelled as a smooth function of d_{jk}. We compared the fitted curve against a null distribution generated by bootstrapping DBH and refitting a LOESS to the semivariance for each bootstrapped dataset.

We use a Gaussian correlation function to capture spatial autocorrelation in the location and dispersion regressions. Between tree j and any other tree k, the covariance among mean seed viability of fruit (θ), and among log dispersions (ln ψ) is

$$cov(\theta_j, \theta_k) = \tau^2 \exp\left\{-\left(\frac{d_{jk}}{\delta}\right)^2\right\}, j \neq k$$

$$cov(\ln \psi_j, \ln \psi_k) = \omega^2 \exp\left\{-\left(\frac{d_{jk}}{\delta}\right)^2\right\}, j \neq k$$

where d_{jk} is the distance in meters between two trees and δ controls the decay of spatial correlation over distance (δ is the distance at which the correlation equals approximately 0.35). We use vague priors for the hyperparameters; $\delta \sim U(0, 500)$, $\chi \sim U(-1, 1)$, $\beta \sim N(0, 10^3)$, $\rho \sim N(0, 10^3)$, $\omega \sim iG(10^{-2}, 10^{-2})$, $\tau \sim iG(10^{-2}, 10^{-2})$. We use $iG(shape, rate)$ to notate the inverse Gamma distribution, $U(lower, upper)$ to notate the uniform distribution, and $N(mean, variance)$ to notate the normal distribution.

Appendix S2. Results of spatial autocorrelation in the models

The spatial correlation of mean seed viability among trees was restricted to a relatively small scale: the range parameter δ had an expectation of 10.7 (0.95 CI: 0.5, 29.2). The eigenvectors of the expected spatial variance-covariance matrix indicate that a group of four closely clustered trees drives the spatial correlation (coordinates [225, 250] in Figure 1). These trees are tightly clustered and have relatively high mean seed viabilities.

Appendix S3. Total seed production analyses

We fit a separate model to determine the degree of correlation between the total number of seeds and the proportion of viable seeds. We model the total number of seeds n_{ij} as a Poisson-distributed random variable with fruit-specific rate λ_{ij}, and the number of viable seeds y_{ij} as binomial with probability ϕ_{ij}:

$$n_{ij} \sim Po(\lambda_{ij})$$

$$y_{ij} \sim Bi(\phi_{ij})$$

where ln λ_{ij} and logit ϕ_{ij} are multivariate normal with tree-specific means and tree-specific correlation c_j. We treat the inverse hyperbolic tangent of these correlations as random normal (following Fisher 1915, Schisterman *et al.* 2003) centred at a population-level correlation, with variance σ^2:

$$\tanh^{-1} c_j \sim N(\tanh^{-1} c_{pop}, \sigma^2)$$

this transformation allows partial pooling of tree-level correlations into a population level estimate. We give c_{pop} a flat uniform prior $c_{pop} \sim U\,(-1, 1)$, and σ^2 a vague inverse-Gamma prior $\sigma^2 \sim iG(10^{-2}, 10^{-2})$.

To assess the relationship between total seed production and the covariates, we fit a separate hierarchical regression model where we treat total seed production for the ith fruit in the jth tree as a Poisson-lognormal random variable with rate λ and tree-specific dispersion σ_j. We treat $\log(\lambda)$ as a linear function of the covariates used for the seed viability model and regression coefficients beta, and allow for spatial autocorrelation among trees as described for the seed viability model. We estimate separate dispersion parameters σ_j for each tree, assuming a vague inverse-Gamma (0.01, 0.01) prior. We use vague N (0, 100) priors on beta.

JAGS code for all of these models is available from the second author by request

Table S1. Count of seeds per mother tree of *M. affinis*. For each mother, we report the mean total number of seeds per fruit (*Total number of seeds*) and the mean number of viable seeds per fruit (*Viable number of seeds*), the minimum number of seeds and viable seeds per fruit (*Lower*), the maximum number of seeds and viable seeds per fruit (*Upper*) and the standard deviation (*SD*).

	Total number of seeds				Viable number of seeds			
Mother tree	Mean	Lower	Upper	SD	Mean	Lower	Upper	SD
88381	42.81	31	57	5.88	23.90	3	47	13.74
188258	49.62	34	59	5.61	37.54	4	55	13.52
242033	48.75	39	56	4.52	41.00	35	52	4.55
275170	38.68	25	49	5.14	28.58	10	46	8.79
403736	52.11	34	65	8.13	40.50	6	60	16.06
408992	63.24	37	78	10.48	30.76	13	45	10.16
411329	27.13	0	39	9.56	7.00	0	38	11.78
449025	34.75	22	53	7.70	15.80	3	40	9.68
508100	45.67	12	62	10.54	33.78	4	48	12.58
519147	38.67	18	50	7.82	31.48	8	43	10.67
523111	37.26	22	46	5.57	18.74	5	34	10.26

523289	26.67	20	30	3.14	18.38	8	30	7.03
602301	42.17	34	52	4.85	30.39	14	50	10.92
611235	49.77	35	62	6.95	27.36	9	44	10.35
629156	40.36	34	55	4.93	13.64	1	45	13.84
629210	43.43	31	63	8.60	25.71	7	39	7.98
701488	39.65	31	53	5.57	23.65	3	36	11.56
709226	70.39	51	89	8.80	66.09	35	85	10.57
717111	28.58	14	38	5.42	17.42	3	30	8.79
810197	57.95	48	67	5.18	44.90	8	61	16.69
Overall	44.06	0	89	12.98	29.27	0	85	17.11

Table S2. Summary of posterior distributions of regression coefficients from the seed viability models using the mean nearest neighbour distance (mean distance to the 10 nearest neighbours) instead of the coefficient of variation (CV) of nearest neighbour distances. The siring success model was not run with nearest neighbour distance, as nearest neighbour distance was collinear with mother-father distance. All covariates are scaled, hence the 'mean effect' corresponds to the expected change in the linear predictor of the response (on the scale given in the brackets), with a change of 1 standard deviation in the covariate.

Parameter	Covariate	Mean Effect	0.95 C.I.	Hypothesis	Pr(Hypothesis)	Odds
Mean seed viability across trees [logit scale]						
β_0	intercept	0.80	(0.24, 1.31)			
β_{dbh}	DBH*	-0.48	(-1.09, 0.09)	$\beta_{dbh} > 0$	0.052	0.05
β_{nn10}	neighbour distance*	-0.50	(-1.12, 0.01)	$\beta_{nn10} < 0$	0.975	38.5
β_{nkin}	local kinship*	-0.16	(-0.93, 0.59)	$\beta_{nkin} < 0$	0.682	2.1
$\beta_{nn10:nkin}$	interaction of neighbour distance*, local kinship*	0.27	(-0.43, 1.01)	$\beta_{nn10:nkin} > 0$	0.786	3.6
Within-tree variance in seed viability [log scale]						
ρ_0	intercept	0.65	(0.27, 1.01)			

ρ_{dbh}	DBH*	-0.04	(-0.46, 0.37)	$\rho_{dbh} < 0$	0.582	1.4
ρ_{nn10}	neighbour distance*	0.34	(-0.07, 0.76)	$\rho_{nn10} > 0$	0.957	22.3
ρ_{nkin}	local kinship*	0.58	(0.07, 1.11)	$\rho_{nkin} > 0$	0.981	52.5
$\rho_{nn10:nkin}$	interaction of neighbour distance*, local kinship*	-0.45	(-0.96, 0.05)	$\rho_{nn10:nkin} < 0$	0.962	25.3

*Of the mother.

Table S3. Average pollen dispersal in the *M. affinis* population in the 50 ha Barro Colorado Island plot. The average dispersal distance and its standard deviation were calculating using the fractional paternity model by Hadfield *et al.* (2006) (see Material and Methods for a more detailed explanation). For each parameter, we report their posterior average, the 2.5 and 97.5 % credibility intervals.

| Parameter	Posterior Average	0.95 C.I.
Average dispersal distance	231. 38	(219.28, 244.01)
Standard deviation dispersal distance	165.08	(154.85, 174.73)

Table S4. Comparison between mother trees used in the seed viability models and the entire reproductive population of *M. affinis* within the BCI plot. NND_10 represents the mean distance to the ten nearest neighbours and DBH refers to diameter at breast height. We report the number of reproductive trees (N), mean, minimum and maximum values (min. and max.), and standard deviation (SD) for NND_10 and DBH.

|	NND_10 (m)	DBH (mm)

|	N	mean	min.	max.	SD	mean	min.	max.	SD
Seed viability models	20	93.0	16.1	421.8	88.6	42.2	10	78	19.2
Entire population	124	67.2	16.1	421.8	62.2	38.9	10	92	20.3
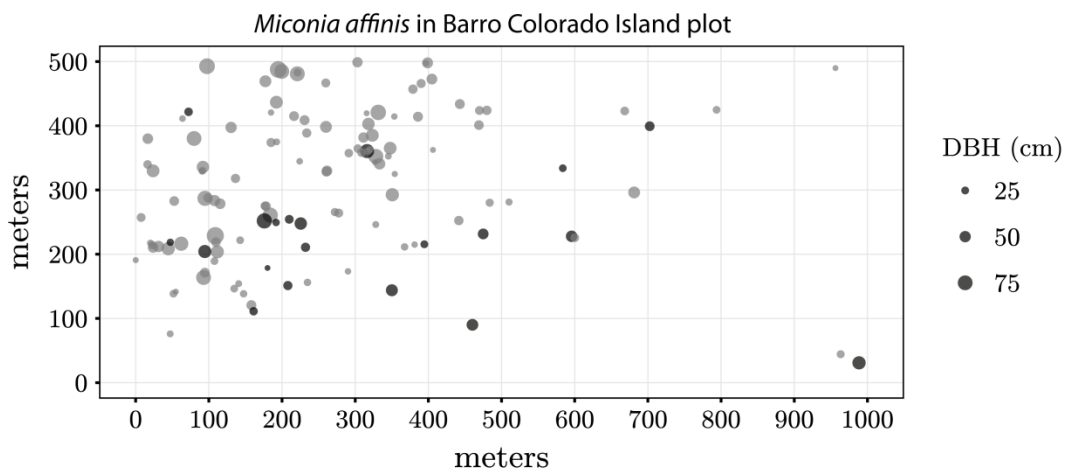
Figure S1. Map with the spatial location of the 124 *M. affinis* reproductive trees in the 50-ha Barro Colorado Island plot (Panama). Each reproductive tree is represented with a dot whose size is proportional to its diameter at the breast height (DBH). The 20 mothers for which we collected fruits are represented with dark grey dots and the remaining trees with light grey dots.
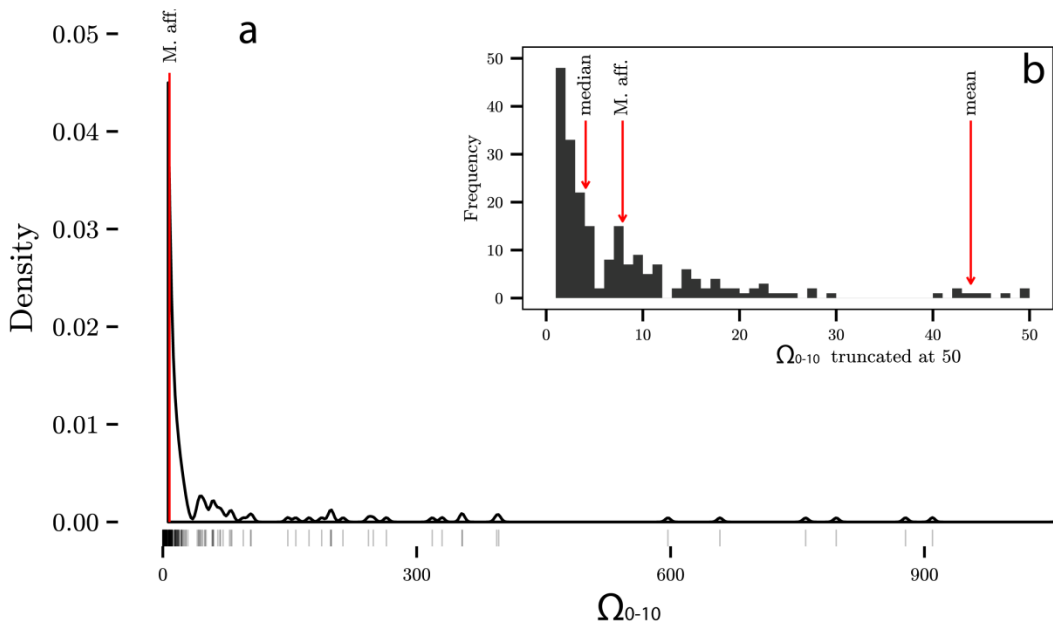
Figure S2. (a) Smoothed density estimate of the spatial aggregation index $\Omega_{0\text{-}10}$ by Condit et al.

(2000) across all 312 species in the 2010 census of BCI. The red bar indicates the $\Omega_{0\text{-}10}$ found for

M. affinis. (b) Inset: histogram showing frequency distribution of of $\Omega_{0\text{-}10}$ from 0 to 50,

representing the bulk of the species (N = 256). *M. affinis'* $\Omega_{0\text{-}10}$ is compared to the median and

mean for all tree species in the plot exhibiting $\Omega_{0\text{-}10} \leq 50$. Short vertical lines at the bottom of the

figure represent the observed number of species for each value of $\Omega_{0\text{-}10}$.
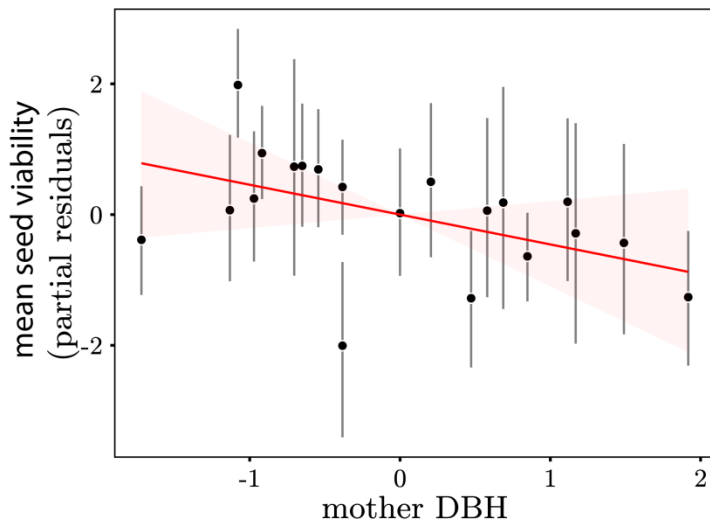
Figure S3. Relationship between the partial residuals of the proportion of viable seeds per tree and the mother DBH. Mother DBH is scaled, with positive and negative values representing trees with DBH above and below the population mean DBH respectively. The mean seed viabilities per tree are indicated with black points and the 95 % credibility interval around each mean is indicated with the grey lines. The fitted relationship and 95 % credibility interval are shown by the red line and red shaded area, respectively.
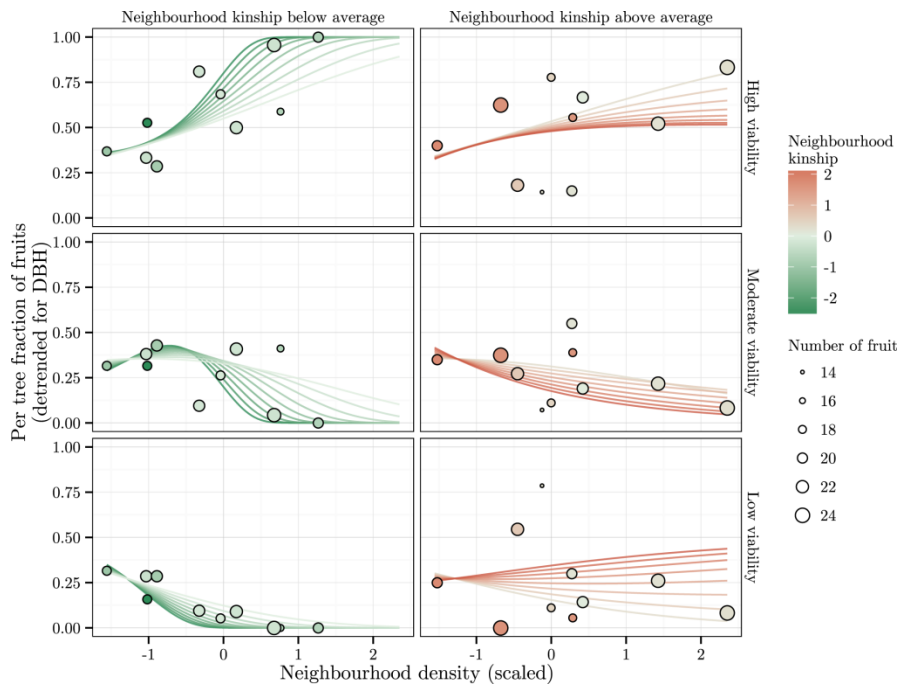
Figure S4. The fraction of fruit on the tree within three quality categories based on seed viability (vertical panels, including low viability with 0-33.3% viable seeds; medium viability with 33.3-66.6% viable seeds; high viability with 66.6-100% viable seeds), plotted against neighborhood density. The left series of panels shows trees that occurred in neighbourhoods with below-average kinship; the right series of panels shows trees that occurred in neighbourhoods with

above-average kinship. The lines show the fitted value from the seed viability model, for various

neighbourhood kinship values. In both points and lines, the color indicates the average

neighbourhood kinship. The data were detrended for the effect of DBH on seed viability.