Appendix B: Technical details of the metacommunity model.

This appendix describes the technical details of the meta-community model, the Bayesian estimation, and the model evaluation. In particular, we here describe the dispersal and the population dynamic components, whereas for the observational model, we refer to the main text. An overview of the model structure is given in Fig. B1.

1. The diffusion model

When constructing the population dynamic model, we use two quantities to characterize the movement process: Of these, $\mathcal{R}_{lj}^{(i)}$ is the probability that an individual of species *i* initially in tree *l* will visit tree *j* before it dies. $T_j^{(i)}$ is the time that an individual of species *i* currently in tree *j* will spend in tree *j* before it dies. These two quantities can be calculated analytically from the diffusion model (Ovaskainen and Cornell 2003, Zheng et al. 2007). This model accounts for the spatial configuration of the whole landscape, since the movement of an individual is generally affected not only by the focal patches (including the distance between them) but also by the other trees it encounters.

While we account for the full landscape structure in the population dynamic model, for the dispersal experiments we only consider the source area and one target tree at a time. This solution is justified by the distribution of target trees in the dispersal experiments, where these trees were small and far away from each other.

Since species are assumed to be independent, we drop the species index (i) in the subscript and let $\boldsymbol{\mathcal{R}}$ be the matrix of dimension $n_T \times n_T$ with element $\mathcal{R}_{lj}$ and $\boldsymbol{T}$ be the matrix with element T_{lj}. The T_j is given by the diagonal element T_{jj}, and $\mathcal{R}_{lj} = T_{lj}/T_{jj}$. Thus we will focus on the calculation of the matrix $\boldsymbol{T}$.

Let D_l, k_l, and α_l be the diffusion coefficient, relative habitat preference, and dispersal ability in patch $l = 1, \dots, n_T$, respectively, and D_m, k_m, and α_m for the surrounding matrix. We define two matrices $\boldsymbol{Z}$ with element Z_{lj} and $\boldsymbol{W}$ with element W_{lj} as follows

$$Z_{lj} = \left[(1 - \delta_{lj}) \frac{K_0(\alpha_m d_{lj})}{K_0(\alpha_m r_l)} + \delta_{lj} \right],$$

$$W_{lj} = Z_{lj}\frac{K_0(\alpha_m r_j)I_1(\alpha_j r_j)}{K_1(\alpha_m r_j)I_0(\alpha_j r_j)},$$

where $\delta_{lj} = 1$ if $l = j$ and 0 otherwise, r_j is the radius of patch j, d_{lj} is the distance between patch l and patch j, and K_ν and I_ν are the modified Bessel functions of the first and the second kind, respectively. Let $\boldsymbol{\Lambda}(x_j)$ be the diagonal matrix with j^{th} diagonal element x_j. According to Appendix A of Zheng et al. (2007), it holds that

$$\begin{aligned}\boldsymbol{T} &= \left[\boldsymbol{\Lambda}\left(\frac{D_j k_j \alpha_j\, I_1(\alpha_j r_j)}{D_m k_m I_0(\alpha_j r_j)}\right) + \boldsymbol{\Lambda}\left(\frac{\alpha_m\, K_1(\alpha_m r_j)}{K_0(\alpha_m r_j)}\right)\boldsymbol{Z}^{-1}\right]^{-1} \boldsymbol{\Lambda}\left(\frac{k_j\, I_1(\alpha_j r_j)}{D_m k_m \alpha_j I_0(\alpha_j r_j)}\right) \\ &= \left[\boldsymbol{\Lambda}(D_j k_j \alpha_j) + D_m k_m \alpha_m \boldsymbol{W}^{-1}\right]^{-1} \boldsymbol{\Lambda}\left(\frac{k_j}{\alpha_j}\right).\end{aligned}$$

If $D_j = D_m = D$, $k_j = k$, $k_m = 1$, $\alpha_j = \alpha_m = \alpha$ for $j = 1, \ldots n_T$, and by definition $\alpha = \sqrt{m/D}$ where m is the death rate, thus we have

$$\boldsymbol{T} = \frac{1}{m}\left[\boldsymbol{\delta} + \frac{1}{k}\boldsymbol{W}^{-1}\right]^{-1}$$

where $\boldsymbol{\delta}$ is an identity matrix with dimension $n_T \times n_T$.

We use tildes to distinguish the quantities in the dispersal experiments from those in the observations in the island Wattkast. We calculate $\widetilde{\mathrm{R}}_{\mathrm{sj}}^{(\mathrm{i})}$ and $\widetilde{\mathrm{T}}_{\mathrm{j}}^{(\mathrm{i})}$ for the two dispersal experiments, where the effects of landscape configuration are ignored. It then holds that

$$\tilde{R}_{sj}^{(i)} = \frac{K_0(\alpha^{(i)} d_{Sj})}{K_0(\alpha^{(i)} r_S)},$$

$$\tilde{T}_j^{(i)} = \frac{1}{m}\left[1 + \frac{1}{k}\frac{K_1(\alpha^{(i)} r_j) I_0(\alpha^{(i)} r_j)}{K_0(\alpha^{(i)} r_j) I_1(\alpha^{(i)} r_j)}\right]^{-1}.$$

2. The process model

Assuming the number of larvae is large and the larval survival probability is small, $n_{ij}(t)$ can be approximated by a Poisson distribution

$$n_{ij}(t)|a_{ij}(t-1), E_{ij}(t) \sim \text{Poisson}\left[\sum_l a^*_{il}(t-1)p_{il}(t-1)\mathcal{R}^{(i)}_{lj}\right], \qquad \text{(Eq. B.1)}$$

where $a^*_{ij}(t-1) = a_{ij}(t-1)\,[1 - E_{ij}(t-1)]$ and $E_{ij}(t-1)$ is the indicator for the extinction experiment. The summation is over all the trees on the island, and the $X|Y$ denotes that the random variable X is conditional on Y. The dependencies on the process parameters, such as the larval surviving probabilities $\mathrm{p_{il}(t-1)}$ and dispersal parameters α_i and k_i are shown explicitly neither here nor in the followings.

The total amount of time $q_{ij}(t)$ spent in tree *j* by all females visiting the tree is gamma distributed

$$q_{ij}(t)|n_{ij}(t) \sim \text{Gamma}\left[n_{ij}(t), T^{(i)}_j\right], \qquad \text{(Eq. B.2)}$$

where $n_{ij}(t)$ is the shape parameter, and $T^{(i)}_j = \mathcal{T}^{(i)}_j/m_i$ the scale parameter. The number $e_{ij}(t)$ of laid eggs by a mated female in tree *j* in year *t* is Poisson distributed

$$e_{ij}(t)|q_{ij}(t) \sim \text{Poisson}\left[\frac{q_{ij}(t)}{\tau^*_i}\right]. \qquad \text{(Eq. B.3)}$$

The number $a_{ij}(t)$ of 1st instar larva in tree *j* in year *t* is binomially distributed

$$a_{ij}(t)|e_{ij}(t) \sim \text{Binomial}\left[e_{ij}(t), s_i\right]. \qquad \text{(Eq. B.4)}$$

Integrating over $n_{ij}(t)$, $q_{ij}(t)$, $e_{ij}(t)$ in the Eqs. A.1–A.4, we obtain the following year-to-year transition probability for the state variable $a_{ij}(t)$.

$$p\left(a_{ij}(t)|\boldsymbol{a}(t-1)\right) = \begin{cases} e^{-[1-\varphi_{ij}\lambda_{ij}(t-1)]} & a_{ij}(t) = 0 \\ e^{-\lambda_{ij}(t-1)}\lambda_{ij}(t-1)\varphi_{ij}\left(1-\varphi_{ij}\right)\ {}_1F_1\left(1+a_{ij}(t), 2, \lambda_{ij}(t-1)\varphi_{ij}\right) & a_{ij}(t) > 0 \end{cases},$$

(Eq. B.5)

where ${}_1F_1$ is a confluent hypergeometric function (Weisstein 2014), $\lambda_{ij}(t-1) = \sum_l a_{il}(t-1)[1 - E_{ij}(t-1)]p_{il}(t-1)\mathcal{R}_{lj}^{(i)}$, and $\varphi_{ij} = 1/\left(1 + \mathcal{T}_j^{(i)} f_i\right)$. Here $\mathcal{R}_{lj}^{(i)}$ and $\mathcal{T}_j^{(i)}$ can be calculated according to the diffusion model in the previous section.

Similarly, we build the process model for two dispersal experiments, and use tildes to distinguish the corresponding quantities. Let X denote the study site of the dispersal experiment, X=I corresponding to Inkoo and X=H to Hakoinen. Corresponding to Eq. (A.1), we have

$$\tilde{n}_{ij}^{(X)} \sim \text{Poisson}\left[h_{is}^{(X)} \tilde{R}_{sj}^{(i)}\right] \qquad \text{(Eq. B.6)}$$

where only the contribution of source tree S in the center of the experiment is included. Similarly corresponding to Eqs. (A.2–A.4),

$$\tilde{q}_{ij}^{(X)} | \tilde{n}_{ij}^{(X)} \sim \text{Gamma}\left[\tilde{n}_{ij}^{(X)}, \tilde{T}_j^{(i)}\right], \qquad \text{(Eq. B.7)}$$

$$\tilde{e}_{ij}^{(X)} | \tilde{q}_{ij}^{(X)} \sim \text{Poisson}\left[\frac{\tilde{q}_{ij}^{(X)}}{\tau_i^*}\right], \qquad \text{(Eq. B.8)}$$

$$\tilde{a}_{ij}^{(X)} | \tilde{e}_{ij}^{(X)} \sim \text{Binomial}\left[\tilde{e}_{ij}^{(X)}, s_i\right]. \qquad \text{(Eq. B.9)}$$

Integrating over $\tilde{n}_{ij}^{(X)}$, $\tilde{q}_{ij}^{(X)}$, $\tilde{e}_{ij}^{(X)}$ in the Eqs. A.6–A.9, we obtain

$$p\left(\tilde{a}_{ij}^{(X)} | h_{is}^{(X)}\right) = \begin{cases} e^{-[1-\tilde{\varphi}_{ij}\tilde{\lambda}_{ij}]} & \tilde{a}_{ij}^{(X)} = 0 \\ e^{-\tilde{\lambda}_{ij}} \tilde{\lambda}_{ij} \tilde{\varphi}_{ij} \left[1 - \tilde{\varphi}_{ij}\right] {}_1F_1\left(1 + \tilde{a}_{ij}^{(X)}, 2, \tilde{\lambda}_{ij}\tilde{\varphi}_{ij}\right) & \tilde{a}_{ij}^{(X)} > 0 \end{cases} \qquad \text{(Eq. B.10)}$$

where $\tilde{\lambda}_{ij} = h_{is}^{(X)} \tilde{\mathcal{R}}_{sj}^{(i)}$, and $\tilde{\varphi}_{ij} = 1/(1 + \tilde{\mathcal{T}}_j^{(i)} f_i)$ with $\tilde{\mathcal{T}}_j^{(i)} = \tilde{T}_j^{(i)} m_i$.

3. Bayesian estimation

The meta-community model parameters consist of $\sigma_p, \boldsymbol{\mu}_D, \boldsymbol{\Sigma}_D, \mu_i^{\mathrm{p}}, \varepsilon_{t,i}^{p}, \mathrm{k_i}, \alpha_i, \mathrm{f_i}, \gamma_i, L_j, h_{is}^{(I)}, h_{is}^{(H)}$, $a_{ij}(t)$, where $i = 1, \ldots, n_S$, $j = 1, \ldots, n_P$, and $t = 1, \ldots, n_T$. We estimate parameters by Gibbs sampling. We denote by $AM(d)$ the adaptive Metropolis algorithm for sampling d dimensional parameters (Haario et al. 2001, Ovaskainen et al. 2008). In the $AM(d)$ algorithm, the proposal

distribution is the d dimensional normal distribution with the mean being the current value. If $d = 1$ the variance is adjusted to give the acceptance rate ~0.44 in the adaptive phase, and otherwise (when $d > 1$) the scale of covariance matrix is adjusted to give the acceptance rate ~0.234 (Gelman et al. 2003). The covariance matrix is calculated based on the historical samplings in the adaptive phase. After the adaptive phase (initial 2000 iterations), the variance-covariance matrix is fixed.

In the Gibbs sampler, the full conditional posterior distributions are extracted from the directed acyclic graph (Fig. B1) by considering only the edges involving the focal parameters (Gilks et al. 1996). The model parameters are divided into blocks, and each block is updated by the $AM(d)$ algorithm if the direct sampling approach is not available or complicated. The following updates are the basic part of the Gibbs sampler.

- Update $\boldsymbol{\mu}_D$ by the $AM(4)$ algorithm.
- Update L_j independently for $j = 1..n_P$ by the $AM(1)$ algorithm.
- Update γ_i independently for $i = 1..n_S$ by the $AM(1)$ algorithm.
- Update $\boldsymbol{\varepsilon}_i^D$ independently for $i = 1..n_S$ by the $AM(4)$ algorithm, where by definition $\boldsymbol{\varepsilon}_i^D = \left(\log(\mathrm{k_i}), \log\left(\frac{1}{\alpha_\mathrm{i}}\right), \mathrm{f_i}, \mu_\mathrm{i}^\mathrm{p}\right) - \boldsymbol{\mu}_D$.
- Update $\left(h_{is}^{(I)}, h_{is}^{(H)}\right)$ independently for $i = 1..n_S$ by the $AM(2)$ algorithm.
- Update $\varepsilon_{t,i}^p$ independently for $t = 1..n_T - 1$ and $i = 1..n_S$ by the $AM(1)$ algorithm.
- Update $1/\sigma_p$ by the Gamma distribution
- Update $\boldsymbol{\Sigma}_D^{-1}$ by the Wishart Distribution
- Update $a_{ij}(t)$ independently for $i = 1, \dots, n_S,\ j = 1, \dots, n_P,\ t = 1, \dots, n_T$ by the $AM(1)$ algorithm.
- Update $\left(a_{ij}(1), a_{ij}(2), ..\right)$ independently for $i = 1..n_S$ and $j = 1..n_P$ by the $AM(n_Y)$ algorithm.

In addition, the following updates are performed to improve the mixing of MCMC.

- Update $\left(\boldsymbol{\varepsilon}_i^D, h_{is}^{(I)}, h_{is}^{(H)}, \gamma_i\right)$ independently for $i = 1..n_S$ by the $AM(7)$ algorithm.
- Update $\left((\boldsymbol{\varepsilon}_1^D)_c, (\boldsymbol{\varepsilon}_2^D)_c .. \left(\boldsymbol{\varepsilon}_{n_S}^D\right)_c\right)$ independently for $c = 1..4$ by proposing $\Delta\left((\boldsymbol{\varepsilon}_1^D)_c, (\boldsymbol{\varepsilon}_2^D)_c .. \left(\boldsymbol{\varepsilon}_{n_S}^D\right)_c\right)$, where Δ follows the proposal normal distribution with mean 0 and variance adjusted to give the acceptance rate ~0.44. This scale transformation is a generalized Gibbs sampler and the Jacobian factor is $|\Delta|^{n_S-1}$ (Liu and Sabatti 2000).
- Update $(\gamma_1, \gamma_2 .. \gamma_{n_S})$ by proposing $(\gamma_1, \gamma_2 .. \gamma_{n_S}) + \Delta$, where Δ follows the normal distribution with mean 0 and variance adjusted to give the acceptance rate ~0.44.
- Update $\left(\varepsilon_{t,1}^p, \varepsilon_{t,2}^p .. \varepsilon_{t,n_S}^p\right)$ independently for $t = 1..n_T - 1$ by proposing $\left(\varepsilon_{t,1}^p, \varepsilon_{t,2}^p .. \varepsilon_{t,n_S}^p\right) + \Delta$, where Δ follows the normal distribution with mean 0 and variance adjusted to give the acceptance rate ~0.44.
- Update $\left(\varepsilon_{1,i}^p, \varepsilon_{2,i}^p .. \varepsilon_{n_T-1,i}^p\right)$ independently $i = 2..n_S$ by proposing $\left(\varepsilon_{1,i}^p, \varepsilon_{2,i}^p .. \varepsilon_{n_T-1,i}^p\right) + \Delta$, where Δ follows the normal distribution with mean 0 and variance adjusted to give the acceptance rate ~0.44.
- Conditional on $\left(\log(\mathrm{k_i}), \log\left(\frac{1}{\alpha_\mathrm{i}}\right), \mathrm{f_i}, \mu_\mathrm{i}^\mathrm{p}\right)$ $(i = 1..n_S)$ update $\boldsymbol{\mu}_D$ by the posterior multi-normal distribution. Afterwards $\boldsymbol{\varepsilon}_i^D$ is set.
- Conditional on $\delta_{t,i} = \left(\boldsymbol{\varepsilon}_i^D\right)_4 + \varepsilon_{t,i}^p$ $(t = 1..n_P - 1)$ update $\left(\boldsymbol{\varepsilon}_i^D\right)_4$ independently for $i = 1..n_S$ by the $AM(1)$ algorithm. Afterwards $\varepsilon_{t,i}^p$ is set.
- Conditional on $\epsilon_{t,i} = (\boldsymbol{\mu}_D)_4 + \varepsilon_{t,i}^p$ $(i = 1..n_S,\ t = 1..n_T - 1)$ update $(\boldsymbol{\mu}_D)_4$ by the $AM(1)$ algorithm. Afterwards $\varepsilon_{t,i}^p$ is set.
- Conditional on $\delta_{t,i} = \left(\boldsymbol{\varepsilon}_i^D\right)_4 + \varepsilon_{t,i}^p$ $(t = 1..n_T - 1)$ update $\left(\boldsymbol{\varepsilon}_i^D\right)_3$ and $\left(\boldsymbol{\varepsilon}_i^D\right)_4$ independently for $i = 1..n_S$ by the $AM(2)$ algorithm. Afterwards $\varepsilon_{t,i}^p$ is set.
- Conditional on $\epsilon_{t,i} = (\boldsymbol{\mu}_D)_4 + \varepsilon_{t,i}^p$ $(i = 1..n_S,\ t = 1..n_T - 1)$ update $(\boldsymbol{\mu}_D)_3$ and $(\boldsymbol{\mu}_D)_4$ by the $AM(2)$ algorithm. Afterwards $\varepsilon_{t,i}^p$ is set.

- Conditional on $\delta_{t,i} = \left(\boldsymbol{\varepsilon}_i^p\right)_4 + \varepsilon_{t,i}^p$ $(t = 1..n_T - 1)$ update $\boldsymbol{\varepsilon}_i^p$ independently for $i = 1..n_S$ by the $AM(4)$ algorithm. Afterwards $\varepsilon_{t,i}^p$ is set.
- Conditional on $\epsilon_{t,i} = (\boldsymbol{\mu}_D)_4 + \varepsilon_{t,i}^p$ $(i = 1..n_S,\ t = 1..n_T - 1)$ update $\boldsymbol{\mu}_D$ by the $AM(4)$ algorithm. Afterwards $\varepsilon_{t,i}^p$ is set.

The MCMC chain was run for more than 8000 iterations. We took every second generation for the last 4000 iterations resulting in a total of 2000 samples.

4. Priors for Bayesian analysis

We assigned for $a_{ij}(1)$ a geometric prior distribution with mean $\gamma_i \mu_j^L$, where γ_i denotes the mean number of larvae of species i per leaf; $\ln(\gamma_i)$ was assumed to be normally distributed with mean $\ln(\gamma_i^{(0)})$ and variance 1, where the expected value $\gamma_i^{(0)}$ was measured from an independent data set (Table A1).

For $\ln(h_{ij}^{(X)})$ $(X = I, H$ and $i = 1, \ldots, n_S)$, we assumed a normal distribution with mean $\ln(10)$ and variance 1. For the mean vector $\boldsymbol{\mu}$ we assumed a multivariate normal prior with mean $\ln(200)$, $\ln(200)$, $\ln(10)$, $\mathrm{Log}(0.1)$ for the components 1, 2, 3 and 4, respectively, variance 100 for each component, and zero covariance for pairs of components. For the variance-covariance matrix $\boldsymbol{\Sigma}$ we assigned the scaled inverse–Wishart prior distribution with 6 degrees of freedom and identity scale matrix, and the gamma distribution with shape 2 and scale 1 for σ_p^2.

5. Model validation

We first tested the validity of the parameter estimation scheme by fitting the model to simulated data generated by the model. The estimation procedure was able to identify the parameter values used to generate the data, as shown by a close match between estimated and true parameter values: the posterior medians were unbiased estimates of the true values, and 95% credibility intervals contained the true parameter values in ca. 95% of the cases (Fig. B2). We then fitted the model to the real data,

and evaluated the model performance by predictive posterior simulations, showing that the model was able to reproduce key structural aspects of the data both at the levels of individual species (Fig. B3) and the entire community (Fig. B4). This comparison suggests that the structural model assumptions are compatible with the data.

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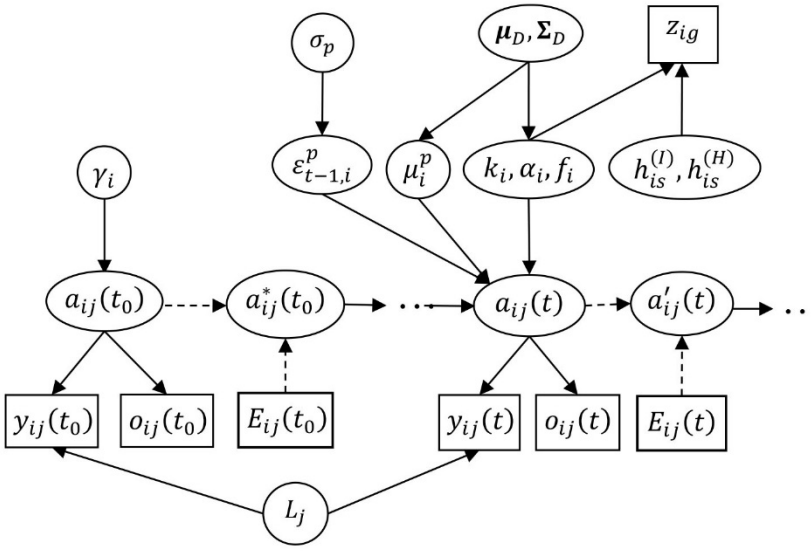

Symbols	Explanations
Data	
$y_{ij}(t)$	Measured abundance of 1st instar larvae of species i on tree j in year t from 20 randomly chosen shoots
$o_{ij}(t)$	Measured occurrence of species i on tree j in year t
$E_{ij}(t)$	Indicator of extinction experiments for species i on tree j in year t, $E_{ij}(t) = 1$ if all individuals of species i are removed from tree j, and equals to 0 otherwise.
z_{ig}	Measured abundance of 1st instar larvae of species i on tree (or group of trees) g during dispersal experiments
Parameters	
$a_{ij}(t)$	Abundance of 1st instar larvae of species i on tree j in year t. And $a^*_{ij}(t) = a_{ij}(t)\,[1 - E_{ij}(t)]$, the abundance after extinction experiment.
$h^{(X)}_{is}$	Number of mated females of species i that emigrated from the source tree S in the dispersal experiment in Inkoo (X=I) and in Hakoinen (X=H)
L_j	Total number of leaves on tree j
γ_i	Expected number of 1st instar larvae of species i per leaf at the initial year.
k_i	Preference of species i staying in a tree
α_i	Dispersal ability of species i, $\alpha_i = \sqrt{D_i/m_i}$ and $1/\alpha_i$ denotes the average dispersal distance (in meter) in the lifetime of species i. Here D_i is the diffusion coefficient and m_i is the mortality rate of adult species i.
f_i	$f_i = s_i/(\tau_i m_i)$ where τ_i denotes the mean amount of time required for adult species i to oviposit one egg, s_i the probability that an egg of species i survives into a 1st instar larva.
$\mu^p_i, \varepsilon^p_{t,i}$	Mean and residual defined by $\text{logit}\, p_{ij}(t) = \mu^p_i + \varepsilon^p_{t,i}$, where $p_{ij}(t)$ is the survival probability of 1st instar larva of species i into newly born adults at year $t+1$.
σ_p	Standard deviation of $\varepsilon^p_{t,i}$.
$\boldsymbol{\mu}_D, \boldsymbol{\Sigma}_D$	Mean and covariance of species properties $\left(\ln k_i, \ln\frac{1}{\alpha_i}, \ln f_i, \mu^p_i\right)$

FIG. B1. Probabilistic structure of the model illustrated as a directed acyclic graph (DAG). Solid arrows denote probabilistic dependencies, dashed arrows deterministic dependencies. Rectangles refer to observed data, and circles to unknown quantities to be estimated. An explanation of data and specific parameters are shown below the DAG.

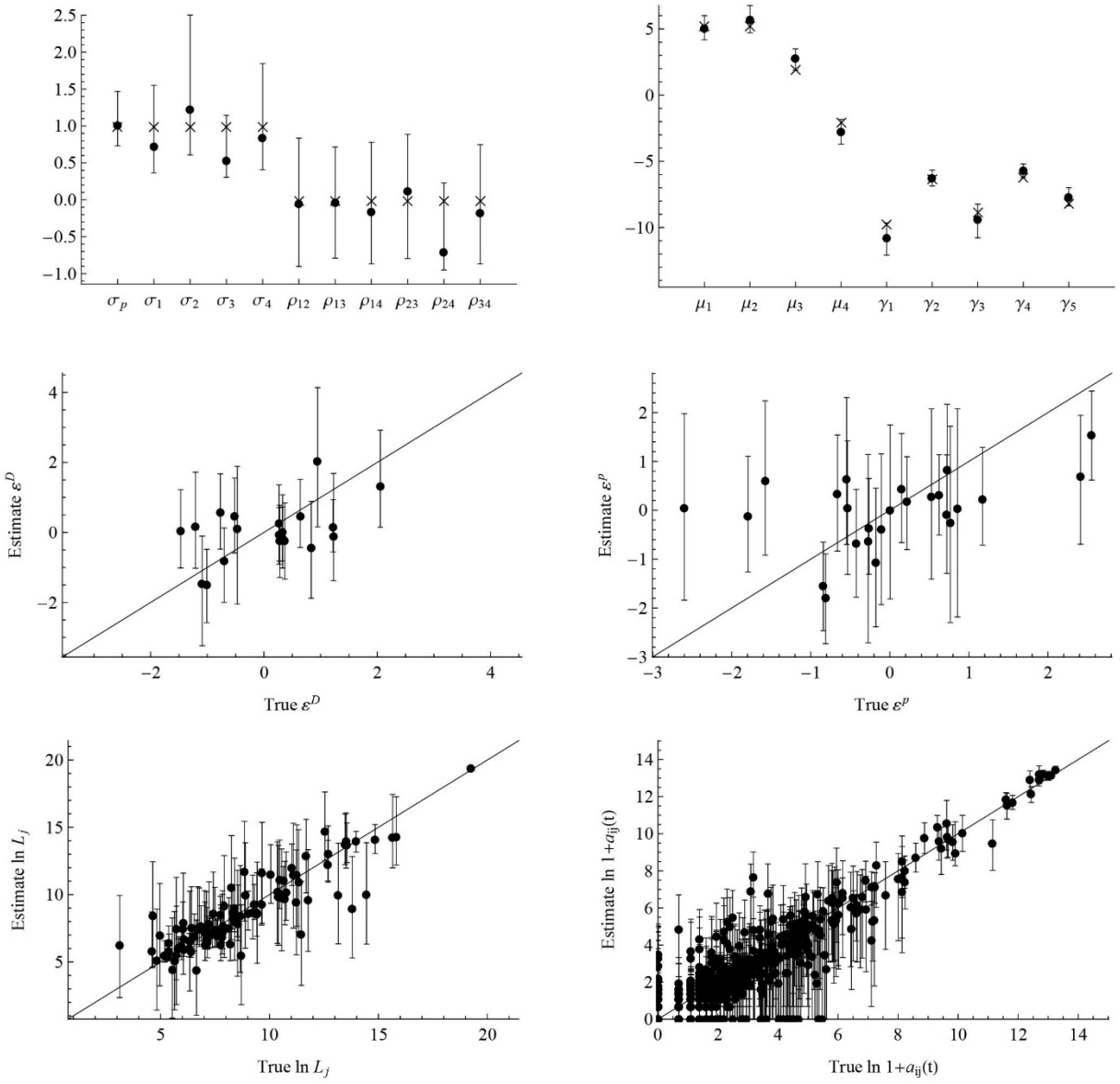

FIG. B2. Model validation by simulating data for five species (Acal, Acur, Afoe, Amit, and Apseas; for the abbreviations used, see Table A1). True parameter values used in simulating data are shown as the crosses in the first row panels, and on the x-axis in the other panels. Posterior medians and 95% central intervals are denoted by the black dots and the error bars, respectively. The solid black line denotes the line $y = x$.

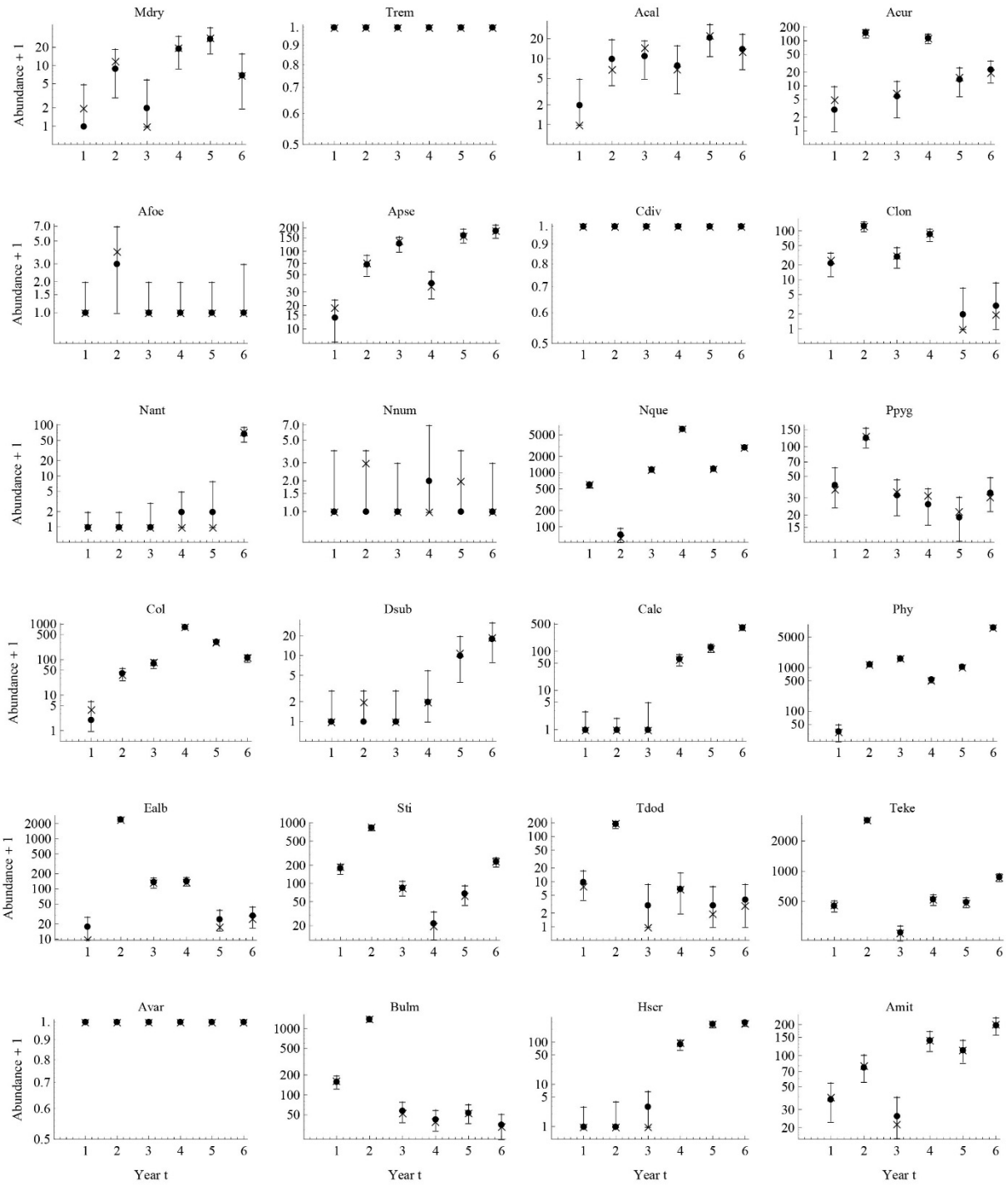

FIG. B3. Posterior predictive distributions of responses at the level of individual species. Shown are abundances for each species in each year (t = 1 refers to year 2003). The crosses refer to true abundances; the black dots refer to median values, the error bars to the corresponding 95% central posterior intervals.

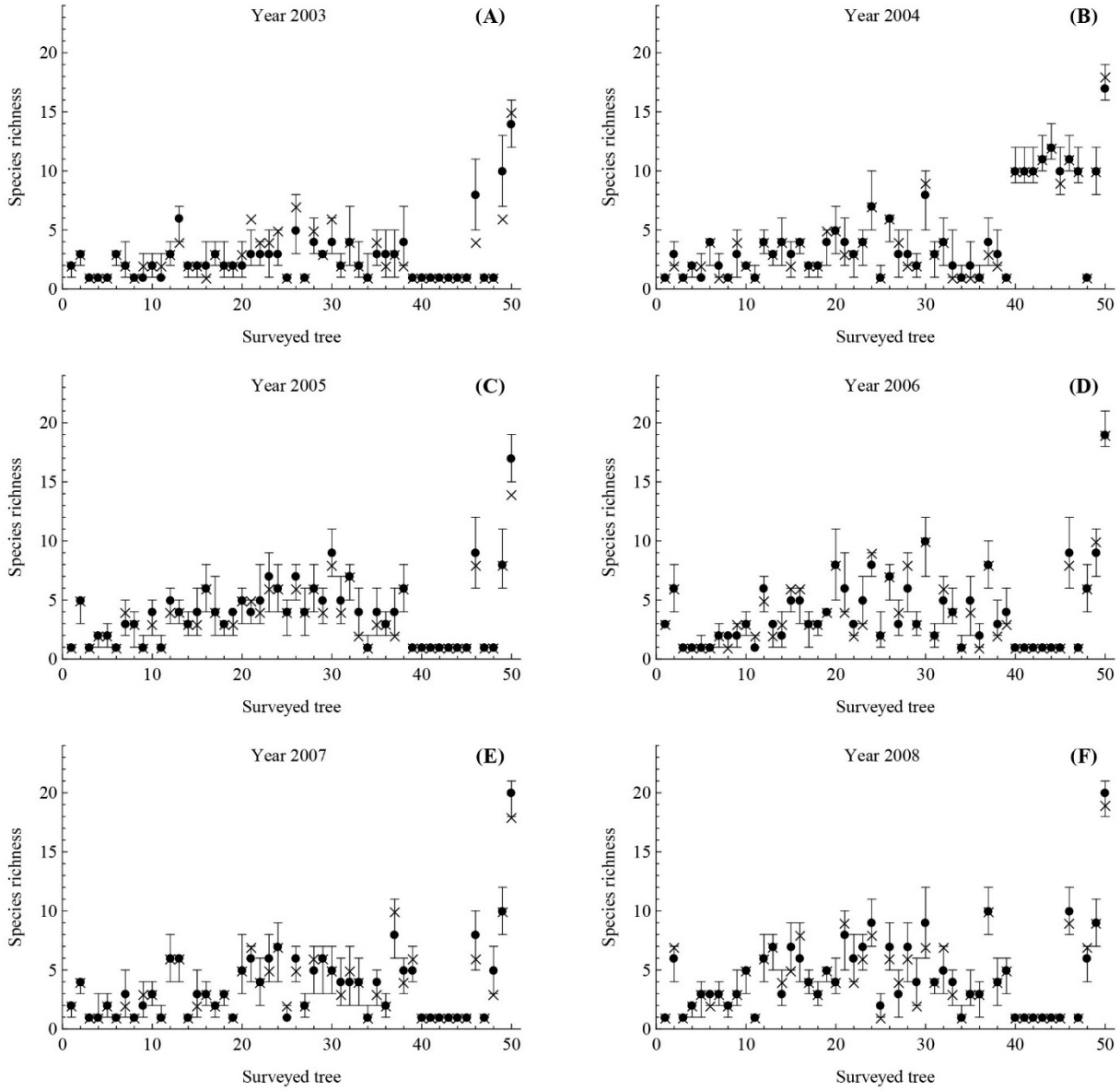

FIG. B4. Posterior predictive distributions of emergent properties at the level of the entire community. Shown is species richness (number of species) for 50 surveyed trees (as obtained by merging some of 88 individual trees surveyed in years 2003–2008; see text for details). The black dots refer to median values, the error bars to the corresponding 95% central posterior intervals. Empirically observed richness values are shown as crosses. Predictive richness was obtained by binomial sampling from the estimated posterior abundances.

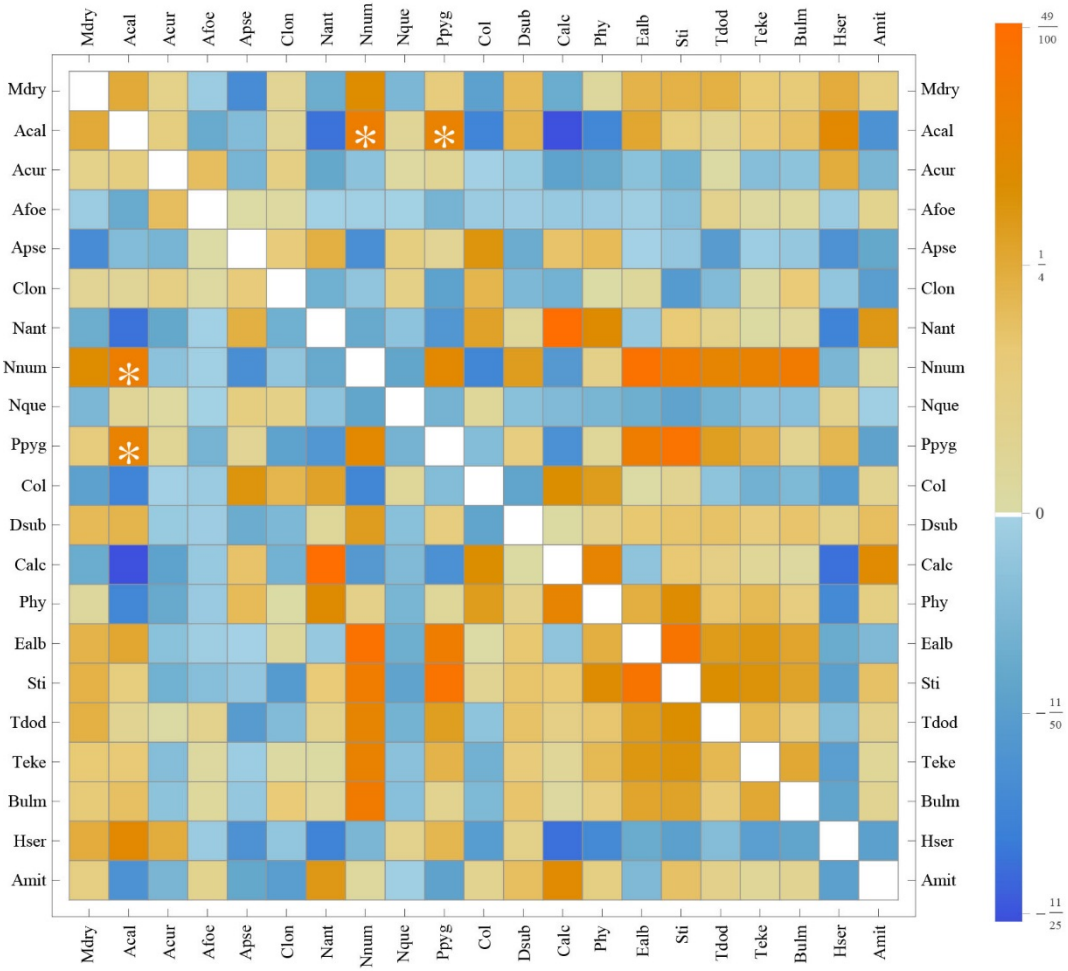

FIG. B5. Median posterior interspecific correlation coefficients for residual species-specific abundances. Red refers to the positive correlations and blue to negative correlations. The color identifies the strength of the correlation: the darker the color, the larger is the absolute correlation value. Pairs of species for which the posterior probability of the correlation being positive (or negative, which was not the case in these data) was greater than 0.9 are labeled with stars. For an explanation of species-specific abbreviations, see Table A1.