Supplementary Material for "Dispersal syndrome and landscape fragmentation in the salt-marsh specialist spider *Erigone longipalpis*"

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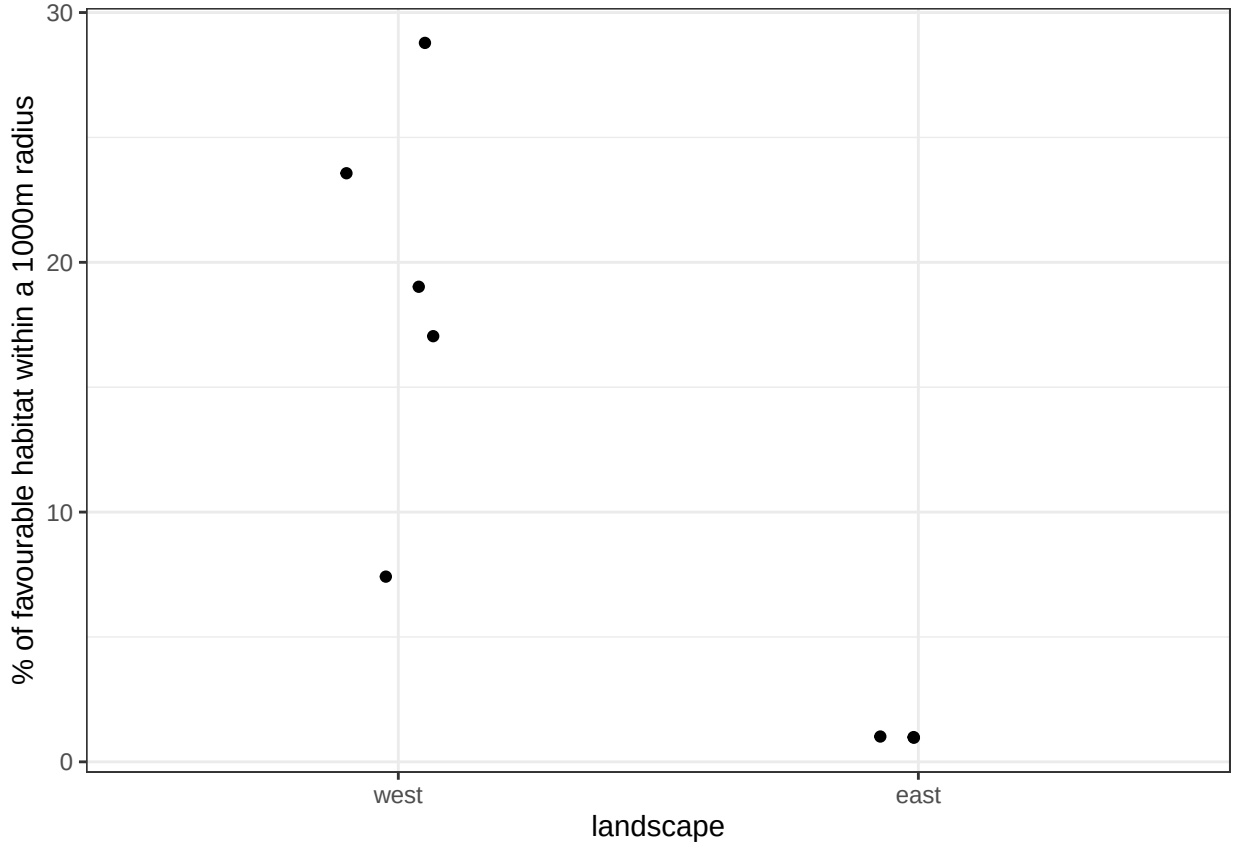
Supplementary Material 1. Difference in habitat availability between the two focal "landscapes"



Supplementary Figure S1.1. Proportion of land and sea cover occupied by favourable habitat (i.e. *Puccinellia maritima*-dominated lawns) within a 1000m radius of each sampling site, as a function of landscape.

Supplementary Material 2. Relationship between the numbers of lab-born spiders and wild-caught spiders sourced from a patch

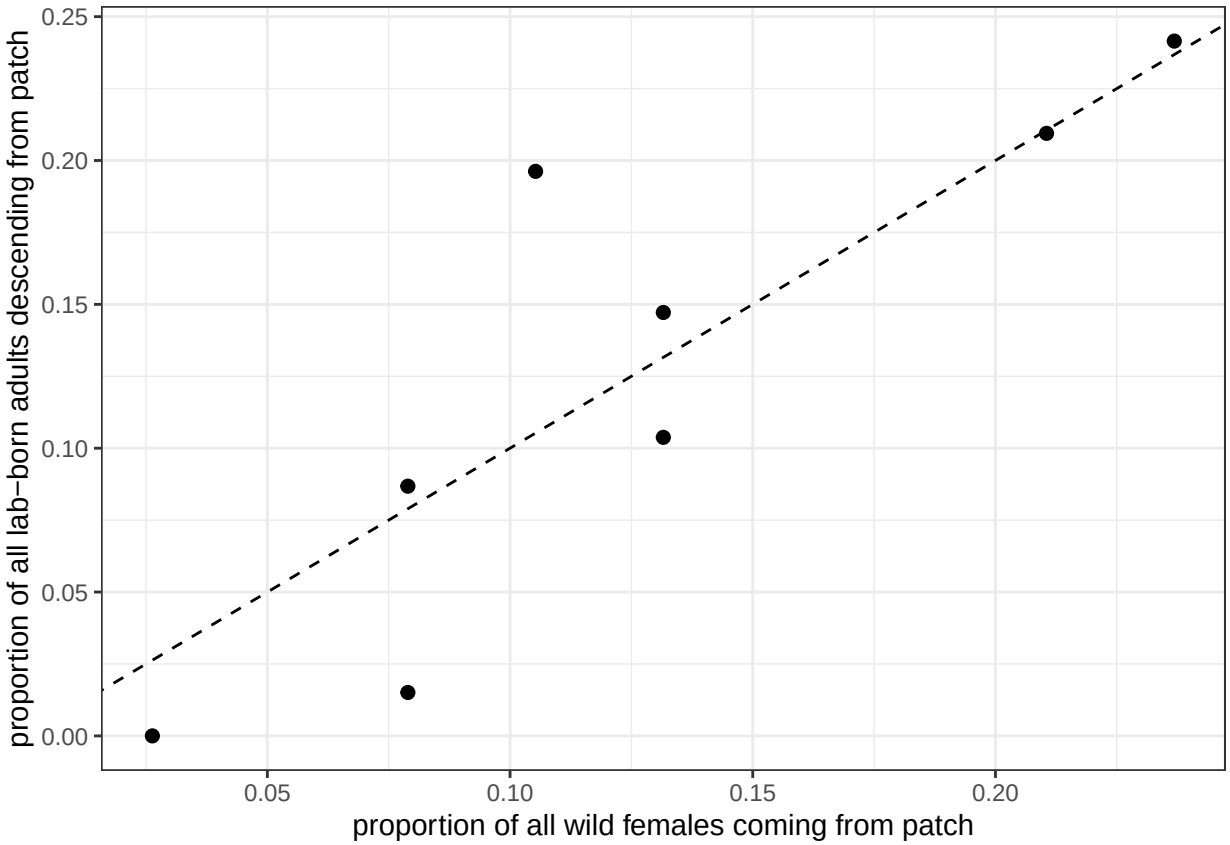


Figure S2.1. Relationship between the relative number of female spiders caught in a patch and the corresponding number of lab-born adults kept. The dashed line corresponds to y = x. Note that the same pattern is found whether the variable on the y-axis is "all adult spiders in the lab" or only the female ones.

Supplementary Material 3. Detailed description of statistical models

Spider abundance

The number of spiders N_p caught in patch p was analysed using the following model:

$$N_p \sim \text{Poisson}(\lambda_{[N]} \times t_p),$$

$$\log(\lambda_{[N]}) = \beta_{0[N]} + \beta_{1[N]} \times x_p,$$

with t_p being an offset corresponding to the patch-specific sampling effort (in person-hours), and x_p a binary variable denoting the landscape to which the patch p belongs (0: the western, more continuous landscape; 1: the eastern, more fragmented landscape). We used weakly informative priors as suggested by , namely Normal$(0, 1)$ for both the intercept β_0 and the landscape effect β_1.

Spider phenotype

Let $M_{i,p}$, $D_{i,p}$, $F_{i,p}$, $L_{i,p}$ be the *recorded* ages at maturity, dispersal propensity (number of rappelling attempts), fecundity and adult longevity of individual i whose (grand)mother was caught in patch p. In addition, let $S_{i,p,o}$ be the observation/measure o of individual i's body size (here cephalothorax width), *after* standardisation to mean 0 and SD 1. Then we can assume these traits are distributed as follows:

$$
\begin{aligned}
S_{i,p,o} &\sim \text{Normal}(\mu_{i,p}, \sigma_r), \\
M_{i,p} &\sim \text{Poisson}(\lambda_{[M]i,p}), \\
D_{i,p} &\sim \text{Poisson}(\lambda_{[D]i,p}), \\
F_{i,p} &\sim \text{Poisson}(\lambda_{[F]i,p} \times d_{i,p}),
\end{aligned}
$$

where $d_{i,p}$ is an offset based on the number of potential egg-laying days this individual was observed, and

$$
\begin{aligned}
L_{i,p}|C_{i,p} = 0 &\sim \text{Poisson}(\lambda_{[L]i,p}), \\
L_{i,p}|C_{i,p} = 1 &\sim \text{Poisson-CCDF}(\lambda_{[L]i,p}),
\end{aligned}
$$

where $C_{i,p}$ is a censoring indicator = 0 if natural death was recorded during the experiment, or = 1 if individuals outlived the experiment or died accidentally.

The models for the corresponding μ and λ are all pretty similar to each other:

$$
\begin{aligned}
\mu_{i,p} &= \beta_{0[S]} + \beta_{1[S]} \times x_p + \alpha_{[S]p} + \gamma_{[S]i}, \\
\log(\lambda_{[M]i,p}) &= \beta_{0[M]} + \beta_{1[M]} \times x_p + \beta_{2[M]} \times y_{[M]p} + \alpha_{[M]p} + \gamma_{[M]i}, \\
\log(\lambda_{[D]i,p}) &= \beta_{0[D]} + \beta_{1[D]} \times x_p + \alpha_{[D]p} + \gamma_{[D]i}, \\
\log(\lambda_{[F]i,p}) &= \beta_{0[F]} + \beta_{1[F]} \times x_p + \alpha_{[F]p} + \gamma_{[F]i}, \\
\log(\lambda_{[L]i,p}) &= \beta_{0[L]} + \beta_{1[L]} \times x_p + \beta_{2[L]} \times y_{[L]p} + \alpha_{[L]p} + \gamma_{[L]i},
\end{aligned}
$$

with y a binary variable denoting whether the time-to-event response (time to maturity or longevity) is based on records with gaps (i.e. maturity recorded after a week-end) and thus potentially biased. The random effects of patch of origin and individual identity are denoted by α and γ respectively. These random effects are distributed as follows:

$$
\begin{aligned}
\alpha_{[S]p} &\sim \text{Normal}(0, \sigma_{\alpha[S]}), \\
\alpha_{[M]p} &\sim \text{Normal}(0, \sigma_{\alpha[M]}), \\
\alpha_{[D]p} &\sim \text{Normal}(0, \sigma_{\alpha[D]}), \\
\alpha_{[F]p} &\sim \text{Normal}(0, \sigma_{\alpha[F]}), \\
\alpha_{[L]p} &\sim \text{Normal}(0, \sigma_{\alpha[L]}),
\end{aligned}
$$

$$
\begin{bmatrix} \gamma_{[S]i} \\ \gamma_{[M]i} \\ \gamma_{[D]i} \\ \gamma_{[F]i} \\ \gamma_{[L]i} \end{bmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \mathbf{\Omega} \right),
$$

where $\boldsymbol{\Omega}$ is the individual-level covariance matrix, which can be decomposed into its constituent standard deviations and correlation matrix $\boldsymbol{R}$ as follows:

$$\boldsymbol{\Omega} = \begin{bmatrix} \sigma_{\gamma[S]} & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\gamma[M]} & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\gamma[D]} & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\gamma[F]} & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\gamma[L]} \end{bmatrix} \boldsymbol{R} \begin{bmatrix} \sigma_{\gamma[S]} & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\gamma[M]} & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\gamma[D]} & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\gamma[F]} & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\gamma[L]} \end{bmatrix}.$$

Priors for fixed effects β are the same as in the abundance model (Normal$(0, 1)$) except for the intercepts of the time to maturity and longevity submodels. For these, priors were shifted to Normal$(3.4, 1)$ based on knowledge that typical development times and adult longevity in *Erigone* are on the order of 30 days (i.e. $\simeq \exp(3.4)$) . We used Half $-$ Normal$(0, 1)$ priors for all standard deviations σ (including the residual SD σ_r for the size submodel), and a LKJCorr(3) prior for the correlation matrix R of individual-level random effects. Note that our LKJ prior is narrower than the one used in McElreath (2021)(LKJCorr(2)); in effect this penalizes against strong correlations (i.e. against our hypotheses of interest) unless support from the data is substantial.

Splitting among- and within-family correlations

In a second time, we refitted the above model, this time splitting the individual-level variation into its within- and among-family components. The model is largely as above, with two exceptions:

- first, individuals i are not only indexed by their patch of origin p, but also by their mother m (so the dispersal propensity $D_{i,p}$ is now written $D_{i,m,p}$)
- second, the individual-level random effects γ, and the corresponding covariance, are decomposed into a sum of family-level random effects η and the remaining within-family individual effects ν as follows:

$$\begin{aligned} \gamma_{[S]i,m,p} &= \eta_{[S]m,p} + \nu_{[S]i,m,p}, \\ \gamma_{[M]i,m,p} &= \eta_{[M]m,p} + \nu_{[M]i,m,p}, \\ \gamma_{[D]i,m,p} &= \eta_{[D]m,p} + \nu_{[D]i,m,p}, \\ \gamma_{[F]i,m,p} &= \eta_{[F]m,p} + \nu_{[F]i,m,p}, \\ \gamma_{[L]i,m,p} &= \eta_{[L]m,p} + \nu_{[L]i,m,p}, \end{aligned}$$

$$\begin{bmatrix} \eta_{[S]i} \\ \eta_{[M]i} \\ \eta_{[D]i} \\ \eta_{[F]i} \\ \eta_{[L]i} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \boldsymbol{\Omega_\eta} \right),$$

$$\boldsymbol{\Omega_\eta} = \begin{bmatrix} \sigma_{\eta[S]} & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\eta[M]} & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\eta[D]} & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\eta[F]} & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\eta[L]} \end{bmatrix} \boldsymbol{R_\eta} \begin{bmatrix} \sigma_{\eta[S]} & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\eta[M]} & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\eta[D]} & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\eta[F]} & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\eta[L]} \end{bmatrix},$$

$$\begin{bmatrix} \nu_{[S]i} \\ \nu_{[M]i} \\ \nu_{[D]i} \\ \nu_{[F]i} \\ \nu_{[L]i} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \boldsymbol{\Omega_\nu} \right),$$

$$\boldsymbol{\Omega_\nu} = \begin{bmatrix} \sigma_{\nu[S]} & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\nu[M]} & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\nu[D]} & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\nu[F]} & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\nu[L]} \end{bmatrix} \boldsymbol{R_\nu} \begin{bmatrix} \sigma_{\nu[S]} & 0 & 0 & 0 & 0 \\ 0 & \sigma_{\nu[M]} & 0 & 0 & 0 \\ 0 & 0 & \sigma_{\nu[D]} & 0 & 0 \\ 0 & 0 & 0 & \sigma_{\nu[F]} & 0 \\ 0 & 0 & 0 & 0 & \sigma_{\nu[L]} \end{bmatrix}.$$

Supplementary Material 4. Effect of landscape of origin on abundance, revisited

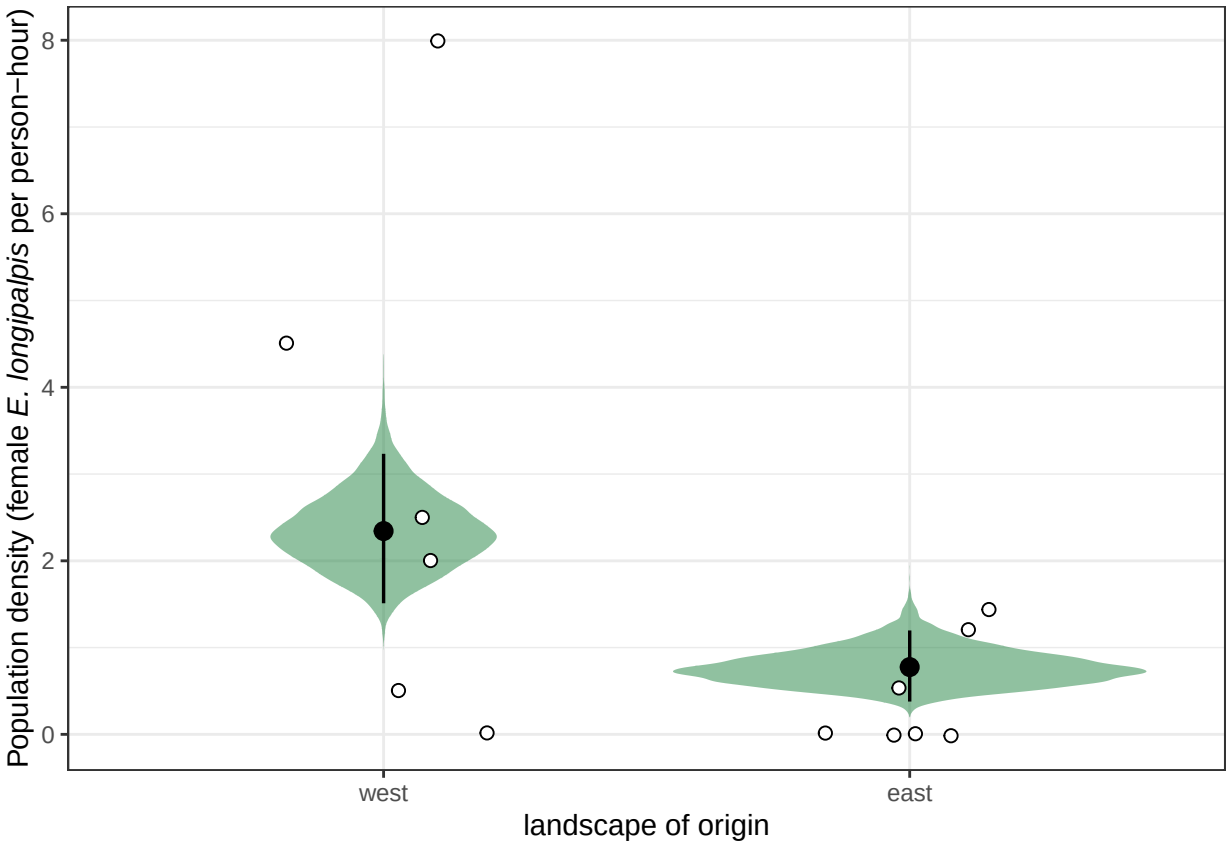


Figure S4.1. Effect of landscape of origin on the number of spiders found per patch (weighted by sampling effort). White dots corresponding to observed data are shown alongside model posteriors.Contrary to main text **Fig. 2**, all visited patches are included here, even those where *Puccinellia maritima* is not dominant.

Supplementary Material 5. Effect of landscape of origin on phenotypic traits, revisited

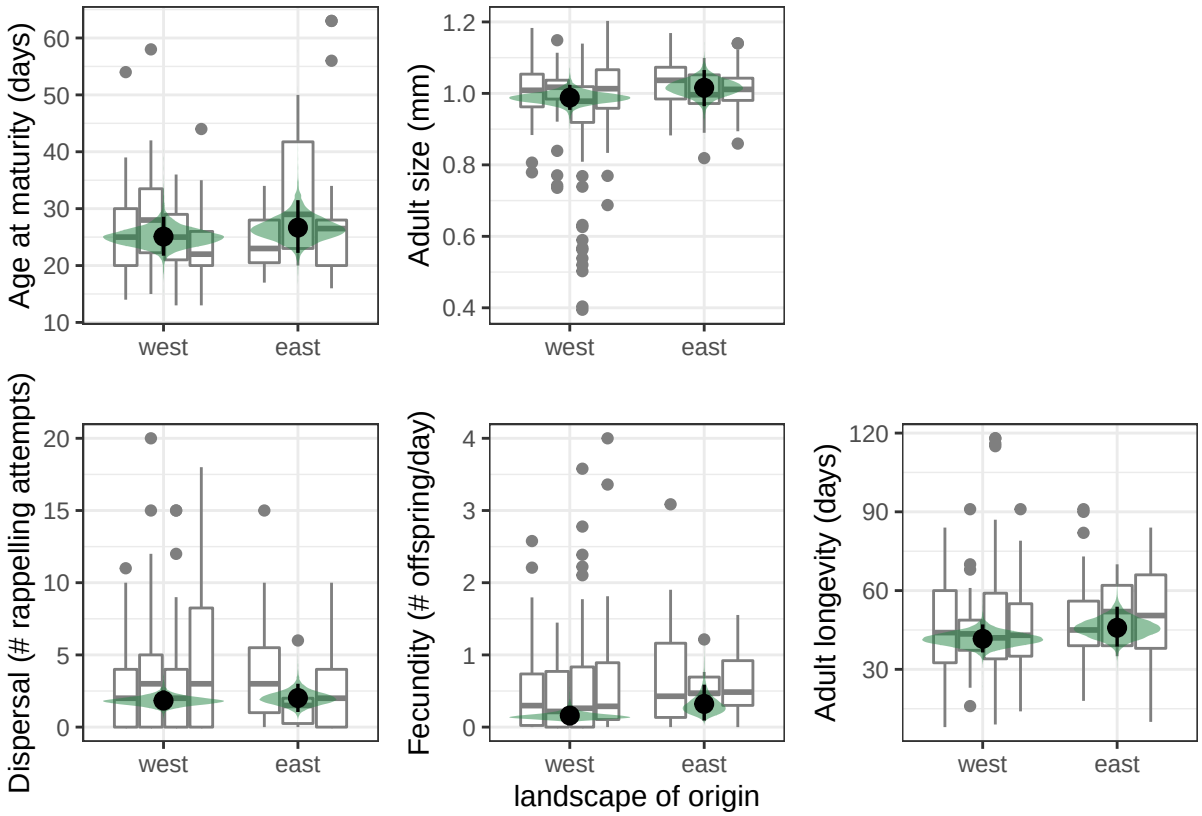


Figure S5.1. Phenotypic traits of lab-born spiders as a function of landscape of origin. Observed data are displayed as boxplots (one boxplot per patch of origin), alongside model posteriors. Predictions are based on the model where individual trait co-variance **is** partitioned between among- and within-family components; see main text **Fig. 3** for a similar figure based on the model where individual-level variation is **not* partitioned.

Supplementary Material 6: overall within-patch, individual-level correlations among traits, based on the "split variance" model

Supplementary Table S6.1. Means and 95% Higher Posterior Density intervals for the overall individual-level correlations among traits, based on the model where individual-level (co-)variance is split into among- and within-family levels (compare with **Table 1a** in the main text, which is based on the model where individual-level variation is **not** split into its among- and within-family components).

	Time to maturity	Body size	Dispersal	Fecundity
Body size	-0.36 [-0.52; -0.20]			
Dispersal	-0.28 [-0.45; -0.09]	0.12 [-0.02; 0.24]		
Fecundity	-0.28 [-0.46; -0.10]	0.27 [0.11; 0.43]	0.14 [0.02; 0.28]	
Adult longevity	0.01 [-0.16; 0.19]	-0.23 [-0.36; -0.09]	0.11 [-0.03; 0.26]	-0.05 [-0.21; 0.11]