

Appendix from M. C. Urban, “Maladaptation and Mass Effects in a Metacommunity: Consequences for Species Coexistence” (*Am. Nat.*, vol. 168, no. 1, p. 28)

Simulation Details

The Matlab program used in simulations is available through this link.¹ All model runs were initiated with an equal proportion of individuals assigned to each phenotype and each species within a patch. I used the same potential reproductive rates used in the original mass-effects metacommunity model (N. Mouquet, personal communication; table A1). The Euler approximation was applied to find the equilibrium value for each population’s continuous growth equation ($dt = 0.1$, 20,000 generations), following previous methods (Mouquet and Loreau 2002). This time interval was sufficient to allow models to reach stable values. Model simulations were performed 25 times for each of 11 symmetric migration rates (0–1.0) in Matlab (ver. 13). This was the number of runs used in the original mass-effects metacommunity model; performing additional simulations did not result in significantly different standard deviations among runs. The model also was explored under varying degrees of potential local maladaptation ($\delta = 0, 0.05, 0.10, \text{ and } 0.25$) and with zero and high ($\mu = 1 \times 10^{-2}$) mutation rates. For all simulations, I assessed coexistence as the mean local (alpha diversity) and regional (gamma diversity) species richness. I also evaluated beta (interpatch) diversity as gamma minus alpha diversity (Mouquet and Loreau 2003).

To understand the dynamics underlying model outcomes, I explored species abundance distributions and population-level maladaptation after early (20 generations) community assembly for 25 simulations, assuming low ($a = 0.1$) or intermediate ($a = 0.5$) migration rates. I chose 20 generations because I was interested in the mechanisms underlying equilibrium diversity patterns, because exploratory simulations showed that model outcomes changed relatively little after an initial sorting of species and phenotypes among patches, and because empirical evidence indicates that strong natural selection frequently generates phenotypic divergence after 20 generations (Kinnison and Hendry 2001). For these analyses, I measured relative local maladaptation as the optimal potential reproductive rate for each population minus mean realized reproductive rate weighted by each phenotype’s abundance.

I used the sum of squared deviations and F values calculated from ANOVAs to compare outcomes between the evolutionary and nonevolutionary mass-effects metacommunity models. I entered migration rate into statistical models as a categorical factor rather than assuming a specific relationship between migration and coexistence. In all cases, I tested both the overall difference in species diversity between the evolutionary and original models and the interaction between model type and migration rate.

Mutation

In the mutation submodel $f(\mu)$, I assumed that each phenotype was determined by the sum of four biallelic additive loci coded as 1 or 0 (e.g., Heino and Hanski 2001). Changes in phenotype due to mutation were modeled based on a transition probability matrix weighted by each phenotype’s relative abundance in the population. For example, the probability that phenotype 0 (coded as 0 0 0 0) occurs in the next generation would be equal to the probability of no mutation ($1 - \mu$) to the fourth power times the phenotype’s abundance plus the sum of the probabilities of mutating from phenotypes 4, 3, 2, or 1 into phenotype 0 weighted by their abundances. I assumed equal bidirectional mutation rates among additive and independent loci. Mutation rate was initially set to 1×10^{-5} alterations per locus per time step, but this value also was investigated at 0 and 1×10^{-2} . To scale mutation rate relative to the proportion of individuals in a patch, I assumed a fixed number of 100 individuals per community to maintain consistency with the original mass-effects metacommunity model.

¹ The code has not been peer reviewed, and neither the journal nor the author is able to provide support.

Assuming no mutation did not significantly change patterns of local species richness from the initial model assuming a mutation rate of 1×10^{-5} (model: $F = 0.0$, $df = 1, 363$, $p = .998$; model \times migration: $F = 0.4$, $df = 10, 363$, $p = .931$). Increasing the mutation rate from 0 to 1×10^{-2} generated a statistically different outcome for the interaction term but not for the overall model (model: $F = 0.3$, $df = 1, 363$, $p = .595$; model \times migration: $F = 10.1$, $df = 10, 363$, $p < .00001$). At high mutation rates, local coexistence was diminished at low migration rates ($a = 0.1$) and enhanced at high migration rates ($a = 0.7-0.8$).

Alternative Phenotypic-Trade-Off Models

In addition to the phenotypic-trade-off model explored in the main text, I also evaluated simulations without phenotypic trade-offs (no-trade-off model) and simulations assuming a strong trade-off among divergent patches. In the no-trade-off model, phenotypic rank (and fitness) remained unchanged after emigration. The strong-trade-off model operated in a manner similar to the intermediate-trade-off model, except that all emigrants were assigned to the lowest phenotypic fitness class. Results from the no-trade-off model did not differ from those of the original nongenetic model in diversity-migration relationships ($p > .9$). Moreover, the strong-trade-off model was not quantitatively different from the intermediate-trade-off model analyzed in the main text ($\delta = 0.10$, $p > .2$).

Table A1

Distribution of reproductive rates among species and habitats (N. Mouquet, personal communication)

Species	Habitat																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4
2	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8
3	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6
4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4
5	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2
6	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3
7	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8
8	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2
9	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2
10	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8
11	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4	1.6
12	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2	1.4
13	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1	1.2
14	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4	1
15	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3	.4
16	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2	.3
17	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1	.2
18	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0	.1
19	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5	0
20	0	.1	.2	.3	.4	1	1.2	1.4	1.6	1.8	2	2.2	2.8	3	3.2	3.4	3.6	3.8	4	5