

1 **Supplementary information**

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3 **Title: Properties of ecosystems those are vulnerable during eco-fusion**

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Supplementary Information 1

Explanation of the ecosystem model

1. Outline of the model

In this model, an ecosystem is represented by the following multi-dimensional Lotka-Volterra equation:

$$\frac{dM_i}{dt} = e_i M_i \left(r_i + \sum_{j=1}^n a_{ij} M_j \right), \quad (1)$$

where M_i and M_j are the total biomass of species i and j , respectively; e is the rate of energy exchange; r_i is the intrinsic growth rate of species i ; n is the number of species in the ecosystem; and a_{ij} is the effect of species j on species i . The actual calculation is done by using the Runge-Kutta method. As a result of the calculation, if the total biomass of a species becomes smaller than the individual body size of the species (w : the biomass of one individual of the species), the species becomes extinct. In the initial setting, the value of w is randomly chosen for each species from the interval $[0, 0.003]$, and the initial biomass of a species is set at 0.1.

In the initial state, the model ecosystem consists of 50 animal and 50 plant species. Each of the 100 initial species is a founder of a lineage, which is defined as a group of species derived from a common founder species. Each lineage in the model ecosystem is phylogenetically independent of the others. The value of the intrinsic growth rate (r) of a plant species is randomly chosen from the interval $[0, 2.0]$, reflecting the fact that plant species conduct primary production. Animal species are assumed to have a negative value of r , representing the fact that animal species cannot survive without feeding on other species. The manner of setting r for animal species is mentioned below (section 3).

2. Inter-specific interactions

In the model ecosystem, a predator species feeds on a prey species if the character of the prey meets the feeding preference of the predator. The character of the prey is described by an array of 10 **D** elements, and the feeding preference of the predator is described by an array of 10 **A** elements. Whether a predatory species i feeds on a prey species j is judged by counting the number of **D_j** elements that satisfy the following condition:

$$Ai[k] - Pi < Dj[k] < Ai[k] + Pi, \quad (2)$$

where P_i is the range of feeding preference of species i , and $Ai[k]$ and $Dj[k]$ are the k th elements of **A** of species i and **D** of species j , respectively. If the number of elements of **D_j** satisfying the above condition is larger than a random number chosen from the interval $[0, 10.0]$, then species i can feed on species j ; that is, $a_{ij} > 0$. In the initial setting, the value of a_{ij} is randomly chosen from $[0, 0.2]$, and a_{ji} , which is the effect of species j on species i , is set to $-a_{ij}$.

In the current model, each element of **D** and **A** is randomly chosen from the interval

[0, 100.0]. The range of feeding preference (P) is randomly chosen from the interval [0, 10.0] (the mean value of P is 5). Thereby, the probability that $D_j[k]$ satisfies the above condition is 0.1. In other words, one of the value of D_j is expected to satisfy the condition. Therefore, the probability that species i feeds on species j is 0.1. If the interval for choosing the value of P is narrowed, the connectance in the ecosystems decreases, and the species diversity increases^{1, 2}.

Because predators are usually larger than their prey in natural ecosystems³⁻⁹, this relationship was fixed as a rule in the present model. On the other hand, animal species can feed on plant species regardless of this assumption. In the model, carnivorous plants are not considered. Thus, a_{ij} for plant i cannot be positive.

In the real world, neighboring plant species often hinder each other's growth through competition for light, soil resources, and germination sites, for example. I assumed that plant species tend to hinder each other's growth when they have similar characters. Whether plant species a hinders the growth of plant species b is judged by counting the number of elements of D_b satisfying the following condition:

$$Da[k] - Ca < Db[k] < Da[k] + Ca, \quad (3)$$

where C is the sensitivity to competition and is randomly chosen from the interval [2.0, 10.0], the range of which is determined on the basis of the same concept by which the predator-prey interactions mentioned above were constructed. If the number of elements of D_j satisfying the above condition is larger than a random number chosen from the interval [0, 10.0], then species a hinders the growth of plant species b ($a_{ba} < 0$). Then, the value of a_{ba} is then randomly chosen from [-0.2, 0]. The value of a_{ab} , which is the effect of plant species b on species a , is determined independently of a_{ba} .

Diagonal elements of the interaction matrix a_{ii} represent intra-specific competition coefficients. Generally speaking, plant species with a large intrinsic growth rate (r) produce many seeds, and the seeds are distributed near their parent plant. Consequently, such species suffer from severe intra-specific competition. In this model, plant species with large r values are assumed to suffer from severe intra-specific competition (2). Then, if species i is a plant species, a_{ii} is calculated by the following equation:

$$a_{ii} = -0.3 - \frac{r_i}{4.0} \times 0.7 \quad . \quad (4)$$

3. Intrinsic growth rate and intra-specific competition of animal species

In the model, animal species with larger body sizes have an advantage in that they can feed on a potentially larger number of prey species than can smaller animals. However, they require large amounts of food. To search for prey, they have to move their heavy bodies over long distances. Thus, animal species are assumed to consume large amounts of energy in feeding on other species. In this model, the intrinsic growth rate of animal species is simply defined as follows:

$$r_i = -0.15 - \frac{w_i}{0.03} \times 0.35, \quad (5)$$

This assumption is not always adopted to endothermic animals, but is adopted to ectothermic ones¹⁰. This equation assumes that a large animal species with a body size of 0.03—10 times the upper limit body size of the initial setting—loses half of its biomass in a time step.

Larger animals generally need much food and larger home ranges than do smaller ones¹¹ and, consequently, they experience more severe intra-specific competition than do smaller ones. Then, a_{ii} of animal species is set by the following equation:

$$a_{ii} = -0.15 - \frac{w_i}{0.03} \times 0.35. \quad (6)$$

This equation assumes that the value of a_{ii} of a large animal species with a body size of 0.03 is 0.5.

As frequently seen in such models, constants do not depend on the actual values measured in the real world. The constants in eq. (5) and (6) are arbitrarily set. For simplicity, this model does not incorporate detailed assumptions defining the forms of equations and the intensities of the energy loss (r) and the intra-specific competition (a_{ii}). Therefore, in this model, the simplest form of equations representing the penalty incurred by having a large body size is adopted, and a half of the penalty loading is assigned to r and the other half is assigned to a_{ii} . This is the reason why both equations have the same form. If the absolute value of the first term in the equations is decreased, the loss of biomass of the animal species decreases. As a result, the probability of extinction of the animal species decreases. The second term influences the evolution of body size. If the denominator is increased, larger body size is easily evolved¹².

4. The rate of energy exchange and types of animal species

For their population growth, animal species (i) can use a fraction of the biomass gained via predation. I assumed that an animal species i that has a narrow range of feeding preference (P_i) and consequently feeds on a limited number of prey species can utilize its prey species more effectively than a species with a wide range of feeding preference. Then, the rate of energy exchange, e_i , is defined as K / P_i , where K is a constant. The upper limit of the rate of energy exchange is set to 1.0. There are no data supporting the assumption that e_i is negatively related to P_i . However, the results of simulation without the assumption showed that the ecosystem was filled with generalist predators and herbivores, indicating that the model without the assumption was not compatible with the real world in which many specialist predators and herbivores exist.

In this model, animal species are divided into herbivores (consuming plant species), carnivores (consuming animal species), and omnivores (consuming both animal and plant species). These types of animal species were distinguished not only by their feeding properties but also by the value of K . When omnivores feed on producer species, K is set to 1. When omnivores feed on animals, K is set to 2, because animals are efficient food resources¹⁰. Herbivores and carnivores specialize for feeding on producer species and animals, respectively; K for these types of species is twice that for omnivores.

5. Evolution of model ecosystems

In the model, an ecosystem is evolved via the evolution of species. At every 100 steps, a new species is derived from a randomly chosen species in the model ecosystem. The total biomass of the new species is set to 5% of that of its ancestor species. Variables of the new species are set by adding small values (slight mutations) to those of its ancestor. Values are given for the variables by random numbers drawn from Gaussian distributions with a mean of 0. The standard deviations of the Gaussian distributions are based on the evolutionary rate (E) of the ancestor: E for each element of $\mathbf{A}$ and $\mathbf{D}$, $0.3E$ for P , $0.1E$ for r , $0.1E$ for E , and $0.0003E$ for w . In the initial setting, the value of E is drawn from a Gaussian distribution with mean 1.0 and standard deviation 0.1. These standard deviations are set not to exceed 10% of the maximum of each variable. Gradual evolution is thereby realized in the model.

Inter-specific interactions of the new species are decided by adding slight mutations to those of its ancestor species. When the new species is judged to feed on one of the prey of the ancestor species (using eq. (2)), the coefficient of interaction between the new species and the prey is set by adding the absolute value of a random number to that between the ancestor and the prey. The random number is drawn from a Gaussian distribution, with mean 0 and standard deviation $0.1E$ of the new species. When a new species is judged not to feed on a prey of the ancestor, the coefficient of interaction between them is set by subtracting the absolute value of a Gaussian random number (with mean 0 and standard deviation $0.1E$ of the prey) from the coefficient of interaction between the ancestor and the prey. The coefficient of interaction between the new species and a predator of the ancestor is set in the same manner. Interactions between the new species and other species that are neither predator nor prey of the ancestor are decided by the same manner as in the initial setting.

At every 500 steps in the course of evolution of a mainland model ecosystem, a completely new species invades the ecosystem and establishes a new lineage. Invasions of a plant, omnivore, herbivore, and carnivore occur in that order. Variables and interactions of the new founder species are given in the same manner as in the initial setting.

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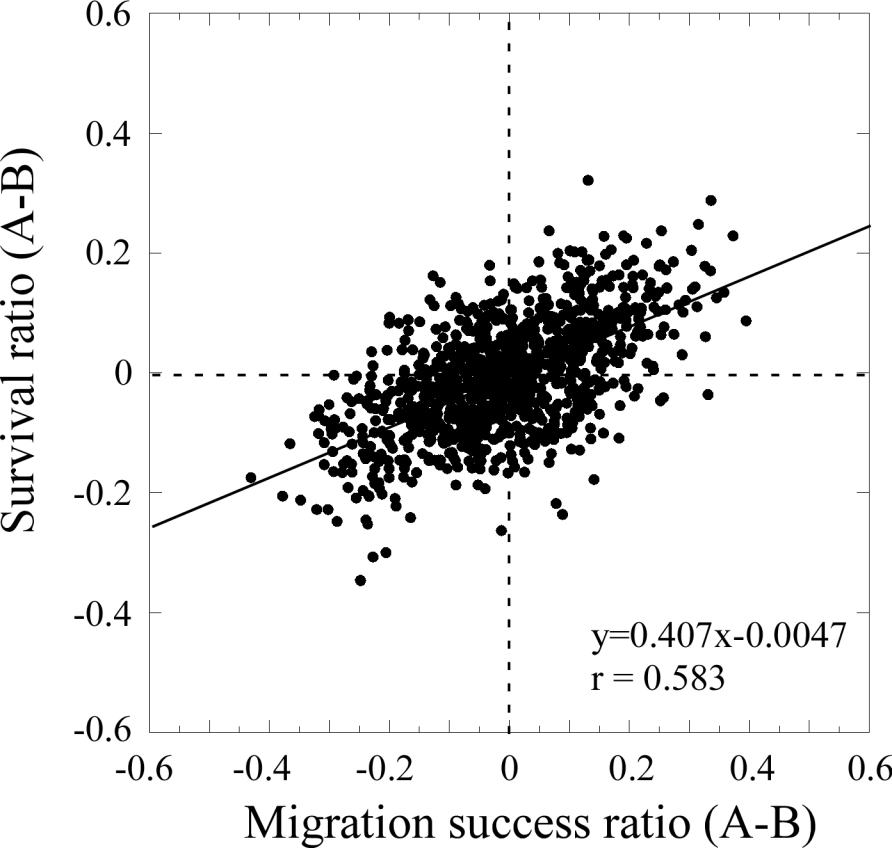
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Supplementary Information 2. Results of simulations with different migration rates

	Migration rate				
	0.005	0.010	0.050	0.100	0.300
Proportion of simulations with asymmetric survival rates	0.312	0.334	0.214	0.294	0.328
Species diversity (ratio of winners to losers)					
Total	0.960	0.938	0.942	0.975	0.934
Animals	0.907	0.874	0.877	0.927	0.873
Plants	1.064	1.063	1.071	1.069	1.054
Omnivores	1.702	1.550	1.807	1.700	1.684
Herbivores	0.754	0.709	0.699	0.777	0.716
Carnivores	1.389	1.579	1.377	1.269	1.152
Food web structure					
% <i>T</i>	0.663	0.677	0.638	0.677	0.668
% <i>I</i>	1.194	1.130	1.177	1.193	1.140
% <i>B</i>	1.108	1.135	1.143	1.100	1.130
% <i>T-I</i>	1.321	1.402	1.268	1.392	1.319
% <i>T-B</i>	0.632	0.633	0.591	0.642	0.650
% <i>I-I</i>	1.948	1.742	2.044	1.778	1.629
% <i>I-B</i>	1.175	1.140	1.196	1.173	1.141
Max. FCL	1.270	1.213	1.301	1.191	1.196
Animal/plant	0.852	0.822	0.819	0.868	0.828

In the main text, we have only presented the results of the simulation with a migration rate of 0.1. Simulations of each migration rate were iterated 500 times. For abbreviations, see the legend of Figure 1.



Supplementary Figure Legend

Figure S1. Relationship between the survival and migration success rates

Each point represents the result of single simulation. The two ecosystems in a given simulation are named A and B. The horizontal axis represents the migration success rate of ecosystem A minus that of ecosystem B (i.e., the difference in the migration success rates between ecosystems A and B). The vertical axis represents the survival rate of ecosystem A minus that of ecosystem B.

Table S1. Comparison of ecosystem properties of the winner, loser, and isolated ecosystems

	Winner	SD	Loser	SD	W/L	U-test	Isolated	SD	W/I	U-test
Species diversity										
Total	115.670	14.606	118.687	14.962	0.975	0.01029	113.044	19.755	1.023	0.043
Animals	73.119	12.837	78.867	12.156	0.927	<0.0001	80.386	16.178	0.910	<0.0001
Plants	42.551	4.582	39.820	4.980	1.069	<0.0001	32.658	5.524	1.303	<0.0001
Omnivores	18.527	10.952	10.898	8.076	1.700	<0.0001	12.534	12.697	1.478	<0.0001
Herbivores	49.796	15.797	64.126	14.666	0.777	<0.0001	66.792	21.917	0.746	<0.0001
Carnivores	4.772	4.664	3.762	3.907	1.269	0.02469	1.060	3.281	4.502	<0.0001
Food web structure										
%T	0.212	0.093	0.314	0.125	0.677	<0.0001	0.432	0.211	0.491	<0.0001
%I	0.417	0.083	0.349	0.117	1.193	<0.0001	0.276	0.195	1.508	<0.0001
%B	0.371	0.043	0.337	0.035	1.100	<0.0001	0.292	0.040	1.272	<0.0001
%T-I	0.095	0.040	0.068	0.036	1.392	<0.0001	0.057	0.051	1.678	<0.0001
%T-B	0.269	0.141	0.418	0.201	0.642	<0.0001	0.567	0.307	0.474	<0.0001
%I-I	0.100	0.059	0.056	0.053	1.778	<0.0001	0.045	0.064	2.211	<0.0001
%I-B	0.537	0.094	0.458	0.146	1.173	<0.0001	0.332	0.224	1.618	<0.0001
Max. FCL	6.371	1.613	5.350	1.732	1.191	<0.0001	4.490	1.979	1.419	<0.0001
Animal/plant	1.731	0.314	1.995	0.303	0.867	<0.0001	2.488	0.450	0.696	<0.0001

Data for the winner and loser ecosystems are based on 294 simulations in type 1 that exhibited asymmetry in survival rate; data for the isolated ecosystems are based on 500 simulations in type 4. Abbreviations: Winner, loser, and isolated represent the mean values of each parameter for the corresponding ecosystems; SD represents the standard deviation; W/L and W/I represent the ratios of winner to loser ecosystems and of winner to isolated ecosystems for each parameter, respectively; U-test represents the significance of the result of Mann-Whitney's U-test. Abbreviations: %T, %I, and %B are the proportions of top species (without predators), intermediate species (with both predators and prey), and basal species (plants); %T-I, %T-B, %I-I, and %I-B represent the proportions of interactions between the two types of species; max. FCL represents the maximum food chain length in an ecosystem; and animal/plant represents the ratio of animal species to plant species.

Table S2. Comparison of ecosystem properties of winner, loser, and isolated ecosystems just before eco-fusion

	Winner	SD	Loser	SD	W/L	U-test	Isolated	SD	W/I	U-test
Animal species										
Biomass	0.317	0.238	0.271	0.213	1.172	<0.0001	0.211	0.173	1.505	<0.0001
Number of predator species	2.141	2.530	1.319	1.865	1.624	<0.0001	1.073	2.018	1.995	<0.0001
Number of prey species	11.134	5.430	11.001	4.922	1.012	0.0598	11.212	5.186	0.993	<0.0001
Number of plant species for grazing	8.992	4.471	9.682	4.387	0.929	<0.0001	10.139	4.229	0.887	<0.0001
Carnivore species										
Biomass	0.248	0.167	0.210	0.148	1.182	<0.0001	0.175	0.175	1.419	<0.0001
Number of predator species	1.350	1.784	1.091	1.559	1.238	0.00103	1.089	1.091	1.240	0.0008546
Number of prey species	10.237	3.930	10.182	4.378	1.005	0.4163	13.192	13.193	0.776	<0.0001
Maximum food chain length	4.151	1.443	3.911	1.316	1.061	<0.0001	4.434	4.427	0.936	0.03953
Omnivore species										
Biomass	0.244	0.178	0.206	0.167	1.184	<0.0001	0.170	0.137	1.439	<0.0001
Number of predator species	1.182	1.685	0.945	1.449	1.251	<0.0001	0.978	1.651	1.208	<0.0001
Number of prey species	5.839	4.351	6.177	5.047	0.945	0.3438	5.769	5.602	1.012	<0.0001
Maximum food chain length	3.884	1.466	3.689	1.317	1.053	<0.0001	3.414	1.244	1.138	<0.0001
Number of plant species for grazing	9.890	4.277	9.530	4.592	1.038	<0.0001	10.249	4.433	0.965	0.0003288
Herbivore species										
Biomass	0.351	0.256	0.285	0.221	1.231	<0.0001	0.219	0.179	1.601	<0.0001
Number of predator species	2.571	2.728	1.395	1.933	1.843	<0.0001	1.091	2.084	2.356	<0.0001
Number of plant species for grazing	9.526	3.767	10.247	3.804	0.930	<0.0001	10.279	4.023	0.927	<0.0001
Plant species										
Biomass	0.640	0.409	0.524	0.357	1.220	<0.0001	0.368	0.269	1.738	<0.0001
Number of herbivore or omnivore species	15.477	6.886	19.061	8.123	0.812	<0.0001	24.956	10.074	0.620	<0.0001
Number of competitors	4.157	2.506	4.317	2.651	0.963	0.0004808	6.463	3.196	0.643	<0.0001

Mean values for the parameters are shown. Data for the winner and loser ecosystems were based on 294 simulations in type 1 that exhibited an asymmetric

250 survival rate; data for isolated ecosystems are based on 500 simulations in type 4. For
251 winner ecosystems, data are based on 21 458 animal species (1408 carnivores, 5400
252 omnivores, and 14 650 herbivores) and 12 512 plant species. For loser ecosystems, data
253 are based on 23 302 animal species (1058 carnivores, 3230 omnivores, and 19 014
254 herbivores) and 11 708 plant species. For the isolated ecosystem, data are based on 40
255 193 animal species (530 carnivores, 6267 omnivores, and 33 396 herbivores) and 16 329
256 plant species.

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Table S3. Changes in the properties of the loser ecosystem after eco-fusion

	Before	SD	After	SD	After/before	<i>U</i> -test
Species diversity						
Total	118.687	14.962	153.259	16.537	1.291	<0.0001
Animals	78.867	12.156	88.204	13.771	1.118	<0.0001
Plants	39.820	4.980	65.054	5.830	1.634	<0.0001
Omnivores	10.898	8.076	16.180	8.948	1.485	<0.0001
Herbivores	64.126	14.666	67.221	13.983	1.048	0.01423
Carnivores	3.762	3.907	4.803	3.801	1.277	<0.0001
Food web structure						
% <i>T</i>	0.314	0.125	0.193	0.080	0.617	<0.0001
% <i>I</i>	0.349	0.117	0.380	0.082	1.087	0.000589
% <i>B</i>	0.337	0.035	0.427	0.038	1.266	<0.0001
% <i>T-I</i>	0.068	0.036	0.067	0.026	0.976	0.7949
% <i>T-B</i>	0.418	0.201	0.290	0.143	0.694	<0.0001
% <i>I-I</i>	0.056	0.053	0.070	0.043	1.240	<0.0001
% <i>I-B</i>	0.458	0.146	0.574	0.104	1.254	<0.0001
Max. FCL	5.350	1.732	6.279	1.618	1.174	<0.0001
Animal/plant	1.995	0.303	1.361	0.210	0.682	<0.0001

Before and after represent the mean values of the ecosystem parameters before and after the eco-fusion, respectively; SD represents the standard deviation; and after/before represents the ratio of the parameter value before eco-fusion to the value after eco-fusion. Abbreviations: %*T*, %*I*, and %*B* are the proportions of top species (without predators), intermediate species (with both predators and prey), and basal species (plants); %*T-I*, %*T-B*, %*I-I*, and %*I-B* represent the proportions of interactions between the two types of species; max. FCL represents the maximum food chain length in an ecosystem; and animal/plant represents the ratio of animal species to plant species.

Table S4. Changes in the properties of species native to loser ecosystems before and after eco-fusion

	Before	SD	After	SD	After/before	<i>U</i> -test
Animal species						
Biomass	0.271	0.213	0.345	0.261	1.276	<0.0001
Number of predator species	1.319	1.865	1.638	1.823	1.242	<0.0001
Number of prey species	11.001	4.922	12.411	5.436	1.128	<0.0001
Maximum food chain length	2.321	0.882	2.368	1.003	1.020	0.1759
Carnivorous species						
Number of prey animals	7.166	5.186	7.221	4.744	1.008	0.1244
Maximum food chain length	3.744	1.320	4.027	1.477	1.076	<0.0001
SD of food chain length	0.442	0.328	0.514	0.349	1.163	<0.0001
Herbivorous species						
Number of plant species for grazing	10.143	3.936	11.100	11.591	1.094	<0.0001
Plant species						
Growth rate	1.514	0.435	1.554	0.400	1.026	0.0265
Biomass	0.524	0.357	0.480	0.327	0.915	<0.0001
Number of herbivores and omnivores	19.061	8.123	16.078	5.834	0.844	0.0095
Number of competitors	4.317	2.651	5.833	2.943	1.351	<0.0001

Before and after represent the mean values of the ecosystem parameters before and after eco-fusion, respectively; SD represents the standard deviation; after/before represents the ratio of the parameter value before eco-fusion to the value after eco-fusion; *U*-test represents the significance of the result of the Mann-Whitney *U*-test. Data for carnivorous species are based on both carnivores and omnivores, and data for herbivorous species are based on both herbivores and omnivores. For the number of species in each category before eco-fusion, see the legend of Table S2. The number of animal species native to loser ecosystems that could survive after eco-fusion was 14 572 (629 carnivores, 2017 omnivores, and 11 926 herbivores), and that of plant species was 7364.

Table S5. Results of eco-fusion in three simulations with different evolutionary histories for the two ecosystems. The control represents the default conditions (type 1 simulation)

Type 2

Ratio of primary production	Control	Low primary production	chi-square value	Significantly different number of wins (chi-square test)
0.3	4	171	159.37	$p < 0.01$
0.4	26	90	35.31	$p < 0.01$
0.5	48	65	2.56	ns
0.6	59	65	0.29	ns
0.7	59	77	2.38	ns
0.8	59	80	3.17	ns
0.9	80	68	0.97	ns

Type 3

Magnitude of fluctuation of primary production	Control	With fluctuation		
0.05	71	80	0.54	ns
0.1	69	87	2.08	ns
0.15	103	68	7.16	$p < 0.01$
0.2	91	62	5.50	$p < 0.05$
0.25	81	58	3.81	ns

Type 4

	Control	Isolated		
Effect of isolation	442	0	442.0	$p < 0.01$

The values represent the number of winner ecosystems in 500 simulations. The upper, middle, and lower parts of this table compare the control ecosystem with three different simulation types: (2) low primary production, (3) fluctuation of primary production, and (4) completely isolated. For simulation type 2, the ratio represents the ratio of primary production in the simulation to that of the control. For simulation type 3, the magnitude of the fluctuation of primary production represents the standard deviation of the fluctuation.

300 Table S6 Number of plant species and clade diversity in the control simulation (type 1)
301 and in the isolated simulation (type 4)
302

	Winner	Loser	Isolated
Mean number of plant species in the simulation	42.551	39.820	32.658
Total number of clades	10535	9506	6453
Number of simulations	294	294	500
Mean number of clades in a simulation	35.833	32.333	12.906
Mean number of species in a clade	1.187	1.232	2.530

303

304 Data for winner and loser ecosystems are based on 294 simulations that exhibited
305 an asymmetric survival rate, whereas data for the isolated ecosystem are based on 500
306 simulations.
307