SUPPLEMENTARY INFORMATION

The hidden costs of living in a transformed habitat: ecological and evolutionary consequences on a tripartite mutualistic system with a keystone mistletoe

Francisco E. Fontúrbel, Michael W. Bruford, Daniela A. Salazar, Jorge Cortés and Caren Vega-Retter

Table S1. Summary of the genetic parameters estimated from the eight microsatellites analyzed for *T. corymbosus* at five sampling sites. n: sample size, N_A: number of alleles, He: expected heterozygosity, Ho: observed heterozygosity. *: significant deviation from the Hardy-Weinberg Equilibrium ($P < 0.05$).

Locus	T1			T2			T3			N1			N2		
	n	Ho/He	N_A	n	Ho/He	N_A	n	Ho/He	N_A	n	Ho/He	N_A	n	Ho/He	N_A
T_29	20	0.150/0.289	2	21	0.762/0.538	3	21	0.524/0.552	4	21	0.619/0.489	3	20	0.500/0.576	3
T_30	15	0.600/0.827*	8	18	0.722/0.762	8	18	0.500/0.769*	12	21	0.524/0.861*	11	18	0.500/0.866*	13
T_36	20	0.600/0.495	2	22	0.591/0.491	2	19	0.316/0.266	2	21	0.429/0.500	2	19	0.474/0.500	2
T_46	19	0.474/0.539	5	19	0.526/0.601	7	21	0.619/0.701	7	21	0.857/0.858	12	18	0.944/0.844	12
T_59	20	0.300/0.625*	3	20	0.600/0.625	4	21	0.286/0.254	3	21	0.667/0.500	3	20	0.700/0.666	5
T_68	19	0.211/0.266	2	22	0.409/0.325	2	21	0.429/0.387	2	21	0.286/0.245	2	18	0.500/0.375	2
T_69	19	0.053/0.051	2	22	0.682/0.505	3	20	0.550/0.501	3	18	0.333/0.494	2	18	0.278/0.323	3
T_76	17	0.353/0.573*	3	18	0.772/0.661	3	19	0.368/0.625*	3	21	0.714/0.663	4	16	0.688/0.678	4

Table S2. Probability of inferred individual ancestry according to STRUCTURE and its correspondence with each sampling site. Red figures correspond to the higher probability of assignment of each individual.

		Inferred clusters				
Individual	Sampling site	1	2	3	4	5
1	T1	0.981	0.016	0.002	0.001	0.000
2	T1	0.780	0.207	0.011	0.001	0.001
3	T1	0.974	0.022	0.003	0.001	0.000
4	T1	0.970	0.023	0.007	0.001	0.000
5	T1	0.969	0.023	0.007	0.001	0.000
6	T1	0.969	0.020	0.010	0.001	0.000
7	T1	0.960	0.032	0.006	0.002	0.000
8	T1	0.978	0.018	0.002	0.001	0.000
9	T1	0.981	0.016	0.002	0.001	0.000
10	T1	0.434	0.560	0.004	0.001	0.000
11	T1	0.691	0.300	0.008	0.001	0.000
12	T1	0.976	0.021	0.002	0.001	0.000
13	T1	0.973	0.024	0.003	0.001	0.000
14	T1	0.921	0.061	0.009	0.008	0.001
15	T1	0.905	0.071	0.009	0.014	0.000
16	T1	0.973	0.023	0.003	0.001	0.000
17	T1	0.966	0.030	0.003	0.001	0.000
18	T1	0.982	0.015	0.002	0.001	0.000

19	T1	0.979	0.018	0.002	0.001	0.000
20	T1	0.963	0.031	0.005	0.001	0.000
21	T2	0.065	0.875	0.019	0.017	0.024
22	T2	0.099	0.835	0.023	0.018	0.026
23	T2	0.066	0.880	0.020	0.014	0.020
24	T2	0.074	0.865	0.023	0.016	0.022
25	T2	0.080	0.837	0.017	0.016	0.049
26	T2	0.089	0.832	0.021	0.025	0.033
27	T2	0.098	0.841	0.020	0.014	0.026
28	T2	0.094	0.852	0.018	0.013	0.023
29	T2	0.082	0.858	0.022	0.015	0.023
30	T2	0.084	0.848	0.021	0.022	0.025
31	T2	0.106	0.829	0.021	0.020	0.025
32	T2	0.072	0.871	0.018	0.014	0.025
33	T2	0.072	0.864	0.019	0.014	0.032
34	T2	0.082	0.859	0.021	0.014	0.025
35	T2	0.075	0.857	0.018	0.021	0.029
36	T2	0.077	0.860	0.022	0.016	0.025
37	T2	0.093	0.850	0.019	0.017	0.022
38	T2	0.107	0.814	0.017	0.024	0.038
39	T2	0.086	0.847	0.023	0.020	0.024
40	T2	0.072	0.871	0.018	0.015	0.025
41	T2	0.080	0.860	0.022	0.015	0.023

42	T2	0.088	0.845	0.019	0.014	0.033
43	T3	0.017	0.037	0.919	0.010	0.016
44	T3	0.031	0.035	0.902	0.011	0.021
45	T3	0.017	0.054	0.892	0.014	0.023
46	T3	0.020	0.048	0.902	0.011	0.019
47	T3	0.021	0.040	0.911	0.010	0.018
48	T3	0.019	0.050	0.897	0.014	0.021
49	T3	0.021	0.043	0.905	0.012	0.020
50	T3	0.023	0.042	0.897	0.016	0.022
51	T3	0.028	0.040	0.888	0.021	0.023
52	T3	0.020	0.038	0.912	0.011	0.020
53	T3	0.016	0.048	0.909	0.010	0.017
54	T3	0.018	0.054	0.888	0.011	0.029
55	T3	0.020	0.035	0.904	0.014	0.027
56	T3	0.019	0.045	0.897	0.014	0.025
57	T3	0.021	0.037	0.915	0.010	0.017
58	T3	0.025	0.050	0.882	0.011	0.031
59	T3	0.033	0.044	0.871	0.011	0.041
60	T3	0.017	0.040	0.913	0.010	0.020
61	T3	0.019	0.041	0.908	0.011	0.021
62	T3	0.026	0.038	0.906	0.011	0.019
63	T3	0.021	0.050	0.898	0.012	0.019
64	N1	0.017	0.009	0.013	0.943	0.018

65	N1	0.028	0.013	0.018	0.925	0.015
66	N1	0.019	0.009	0.014	0.944	0.013
67	N1	0.018	0.016	0.016	0.933	0.016
68	N1	0.023	0.013	0.013	0.938	0.014
69	N1	0.028	0.010	0.017	0.931	0.015
70	N1	0.024	0.010	0.020	0.928	0.017
71	N1	0.018	0.010	0.015	0.943	0.014
72	N1	0.020	0.013	0.014	0.939	0.014
73	N1	0.020	0.010	0.016	0.937	0.016
74	N1	0.017	0.010	0.015	0.943	0.015
75	N1	0.026	0.020	0.027	0.911	0.016
76	N1	0.019	0.009	0.015	0.942	0.014
77	N1	0.021	0.012	0.020	0.930	0.017
78	N1	0.017	0.010	0.015	0.944	0.014
79	N1	0.018	0.009	0.013	0.946	0.013
80	N1	0.020	0.010	0.014	0.943	0.013
81	N1	0.018	0.011	0.017	0.939	0.014
82	N1	0.019	0.010	0.015	0.942	0.014
83	N1	0.019	0.010	0.015	0.942	0.014
84	N1	0.017	0.010	0.017	0.943	0.014
85	N2	0.056	0.015	0.015	0.020	0.894
86	N2	0.058	0.012	0.010	0.015	0.905
87	N2	0.061	0.025	0.015	0.013	0.885

88	N2	0.035	0.025	0.010	0.014	0.916
89	N2	0.039	0.014	0.012	0.025	0.911
90	N2	0.036	0.012	0.012	0.014	0.926
91	N2	0.054	0.013	0.013	0.023	0.897
92	N2	0.051	0.015	0.017	0.022	0.894
93	N2	0.069	0.015	0.013	0.043	0.859
94	N2	0.045	0.012	0.010	0.014	0.919
95	N2	0.038	0.013	0.013	0.017	0.919
96	N2	0.052	0.019	0.029	0.019	0.881
97	N2	0.039	0.011	0.016	0.024	0.911
98	N2	0.047	0.015	0.015	0.022	0.902
99	N2	0.047	0.011	0.011	0.014	0.918
100	N2	0.042	0.018	0.013	0.015	0.912
101	N2	0.043	0.014	0.011	0.013	0.919
102	N2	0.046	0.013	0.012	0.018	0.911
103	N2	0.035	0.017	0.018	0.019	0.911
104	N2	0.039	0.020	0.025	0.019	0.897

Table S3. Population assignment for each individual and its correspondence with the sampling sites, based on the results of GENELAND. Geographic coordinates of each plant (in decimal degrees) are also shown.

Individual	Sampling site	Longitute	Latitude	Assigned population
1	T1	-73.649	-39.966	T1
2	T1	-73.649	-39.966	T1
3	T1	-73.649	-39.966	T1
4	T1	-73.649	-39.967	T1
5	T1	-73.649	-39.967	T1
6	T1	-73.649	-39.967	T1
7	T1	-73.649	-39.967	T1
8	T1	-73.648	-39.968	T1
9	T1	-73.647	-39.968	T1
10	T1	-73.645	-39.964	T2
11	T1	-73.645	-39.964	T2
12	T1	-73.647	-39.968	T1
13	T1	-73.648	-39.968	T1
14	T1	-73.649	-39.967	T1
15	T1	-73.648	-39.968	T1
16	T1	-73.649	-39.967	T1
17	T1	-73.649	-39.967	T1
18	T1	-73.648	-39.968	T1

19	T1	-73.648	-39.968	T1
20	T1	-73.649	-39.967	T1
21	T2	-73.652	-39.974	T2
22	T2	-73.652	-39.974	T2
23	T2	-73.652	-39.974	T2
24	T2	-73.652	-39.974	T2
25	T2	-73.652	-39.974	T2
26	T2	-73.652	-39.974	T2
27	T2	-73.652	-39.974	T2
28	T2	-73.652	-39.974	T2
29	T2	-73.652	-39.975	T2
30	T2	-73.652	-39.975	T2
31	T2	-73.652	-39.975	T2
32	T2	-73.652	-39.975	T2
33	T2	-73.652	-39.974	T2
34	T2	-73.652	-39.975	T2
35	T2	-73.652	-39.974	T2
36	T2	-73.652	-39.975	T2
37	T2	-73.652	-39.975	T2
38	T2	-73.652	-39.975	T2
39	T2	-73.652	-39.974	T2
40	T2	-73.652	-39.975	T2
41	T2	-73.652	-39.975	T2

42	T2	-73.653	-39.975	T2
43	T3	-73.651	-39.981	T3
44	T3	-73.651	-39.981	T3
45	T3	-73.651	-39.981	T3
46	T3	-73.651	-39.981	T3
47	T3	-73.651	-39.981	T3
48	T3	-73.651	-39.981	T3
49	T3	-73.652	-39.981	T3
50	T3	-73.653	-39.982	T3
51	T3	-73.653	-39.982	T3
52	T3	-73.653	-39.982	T3
53	T3	-73.653	-39.982	T3
54	T3	-73.653	-39.983	T3
55	T3	-73.653	-39.985	T3
56	T3	-73.653	-39.982	T3
57	T3	-73.652	-39.981	T3
58	T3	-73.653	-39.982	T3
59	T3	-73.653	-39.983	T3
60	T3	-73.652	-39.981	T3
61	T3	-73.652	-39.981	T3
62	T3	-73.651	-39.981	T3
63	T3	-73.652	-39.981	T3
64	N1	-73.676	-40.005	N1

65	N1	-73.676	-40.005	N1
66	N1	-73.676	-40.005	N1
67	N1	-73.676	-40.005	N1
68	N1	-73.676	-40.005	N1
69	N1	-73.675	-40.007	N1
70	N1	-73.675	-40.007	N1
71	N1	-73.675	-40.007	N1
72	N1	-73.675	-40.007	N1
73	N1	-73.675	-40.007	N1
74	N1	-73.674	-40.009	N1
75	N1	-73.675	-40.007	N1
76	N1	-73.676	-40.005	N1
77	N1	-73.675	-40.007	N1
78	N1	-73.676	-40.005	N1
79	N1	-73.676	-40.005	N1
80	N1	-73.676	-40.006	N1
81	N1	-73.675	-40.007	N1
82	N1	-73.676	-40.005	N1
83	N1	-73.676	-40.005	N1
84	N1	-73.675	-40.007	N1
85	N2	-73.630	-39.980	N2
86	N2	-73.631	-39.980	N2
87	N2	-73.608	-39.984	N2

88	N2	-73.596	-39.992	N2
89	N2	-73.596	-39.992	N2
90	N2	-73.596	-39.993	N2
91	N2	-73.562	-40.000	N2
92	N2	-73.570	-39.995	T1
93	N2	-73.564	-40.005	N2
94	N2	-73.596	-39.993	N2
95	N2	-73.595	-39.993	N2
96	N2	-73.596	-39.992	N2
97	N2	-73.596	-39.992	N2
98	N2	-73.629	-39.981	N2
99	N2	-73.629	-39.981	N2
100	N2	-73.630	-39.980	N2
101	N2	-73.621	-39.982	N2
102	N2	-73.621	-39.982	N2
103	N2	-73.602	-39.989	N2
104	N2	-73.602	-39.989	N2

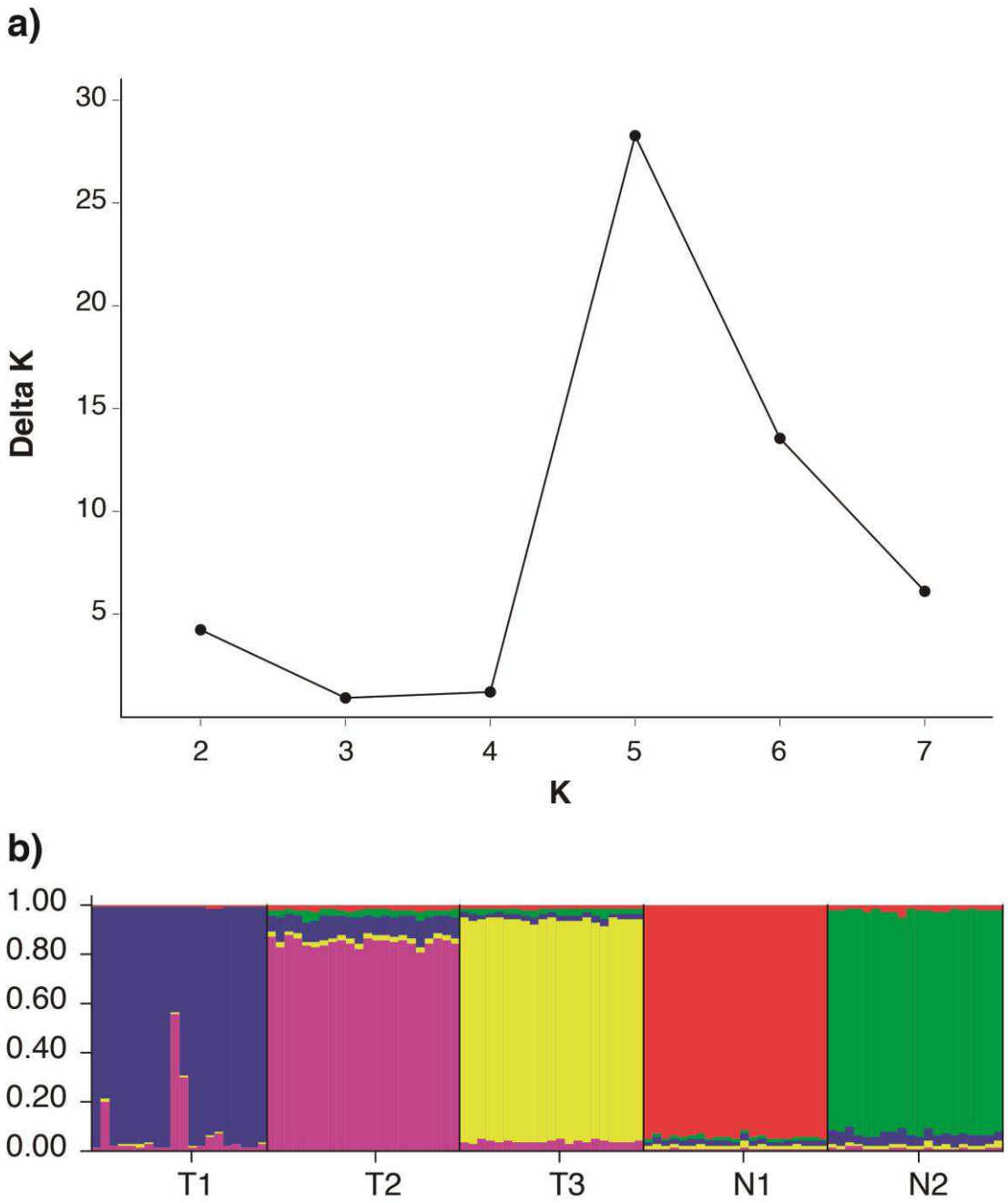

Figure S1. (a) Structure Harvester plot showing the modal value of K = 5 for the ΔK method and (b) Results of the STRUCTURE software based on the five sampling sites and the resulting K = 5 clusters. Each bar represents an individual.

Table S4. Estimates of (a) number of alleles, (b) genetic diversity and (c) allelic richness for each sampled population. Values are presented for each locus and the sampling site mean.

(a) Number of alleles					
Locus	T1	T2	T3	N1	N2
T_29	2	3	4	3	3
T_30	8	8	12	11	13
T_36	2	2	2	2	2
T_46	5	7	7	12	12
T_59	3	4	3	3	5
T_68	2	2	2	2	2
T_69	2	3	3	2	3
T_76	3	3	3	4	4
Mean	3.375	4.000	4.500	4.875	5.500
(b) Genetic diversity					
T_29	0.300	0.548	0.567	0.498	0.593
T_30	0.864	0.786	0.799	0.890	0.902
T_36	0.505	0.500	0.272	0.514	0.515
T_46	0.556	0.620	0.720	0.880	0.866
T_59	0.650	0.642	0.260	0.508	0.683
T_68	0.275	0.331	0.395	0.250	0.382
T_69	0.053	0.513	0.513	0.513	0.333

T_76	0.597	0.678	0.649	0.679	0.700
Mean	0.475	0.577	0.522	0.592	0.622

(c) Allelic richness

T_29	2.000	2.923	3.638	2.923	3.000
T_30	8.000	7.756	11.190	10.102	11.806
T_36	2.000	2.000	2.000	2.000	2.000
T_46	4.710	6.289	6.333	10.413	10.971
T_59	3.000	3.998	2.919	2.714	4.928
T_68	2.000	2.000	2.000	2.000	2.000
T_69	1.789	2.904	2.942	2.000	2.833
T_76	2.999	3.000	3.000	3.981	3.998
Mean	3.312	3.859	4.253	4.517	5.192

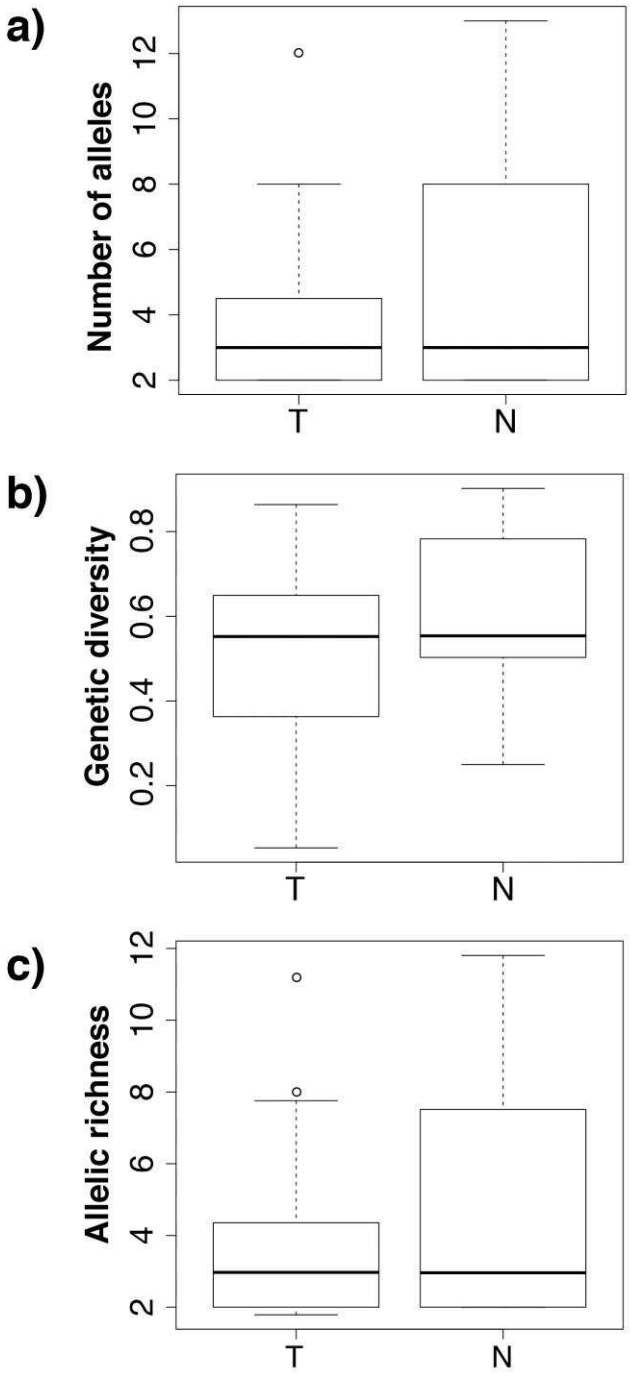

Figure S2. Comparison of (a) number of alleles, (b) genetic diversity and (c) allelic richness between native (N) and transformed (T) habitats.

Table S5. Number of private alleles per locus, with respect to the number of alleles (N_A) present.

Locus	Total N_A	Number of alleles present only in T1, T2 and/or T3	Number of alleles present only in N1 and/or N2
T_29	4	1	0
T_30	26	5	9
T_36	2	0	0
T_46	20	3	7
T_59	6	0	2
T_68	2	0	0
T_69	4	1	1
T_76	5	0	2

Table S6. Relatedness estimates (r_{xy}) and its statistical significance (P-value) for each sampling site.

Sampling site	r_{xy}	P-value
T1	-0.096	0.721
T2	-0.058	0.058
T3	-0.098	0.145
N1	-0.051	0.139
N2	-0.113	0.884
All individuals	-0.014	0.190

Table S7. Spatial association between the number of visits of *Tristerix corymbosus* pollinator (*Sephanoides sephaniodes*) and seed disperser (*Dromiciops gliroides*) mutualists at different time periods (see main text for details). The spatial association index (X_p) and its significance were calculated using the SADIE approach in SADIEShell v 2.0. Bold numbers represent significant associations (after applying a sequential Bonferroni correction for multiple comparisons).

Habitat	Interaction	Period	Resource level	X_p	P-value
Native	Pollination	March	*T. corymbosus* flowers	0.271	0.209
			Neighborhood flowers	-0.418	0.935
			All flowers	0.254	0.229
		August	*T. corymbosus* flowers	0.537	**0.039**
			Neighborhood flowers	0.118	0.364
			All flowers	0.526	**0.042**
	Seed dispersal	November	*T. corymbosus* fruits	-0.776	0.998
			Neighborhood fruits	0.714	**0.007**
			All fruits	-0.516	0.955
		January	*T. corymbosus* fruits	No *D. gliroides* visits	
			Neighborhood fruits	No *D. gliroides* visits	
			All fruits	No *D. gliroides* visits	
Transformed	Pollination	March	*T. corymbosus* flowers	-0.547	0.959
			Neighborhood flowers	Too few flower data	
			All flowers	-0.547	0.959

	August	*T. corymbosus* flowers	-0.299	0.815
		Neighborhood flowers	Too few flower data	
		All flowers	-0.299	0.815
Seed dispersal	November	*T. corymbosus* fruits	0.172	0.327
		Neighborhood fruits	-0.241	0.773
		All fruits	-0.128	0.642
	January	*T. corymbosus* fruits	0.611	**0.011**
		Neighborhood fruits	-0.611	0.985
		All fruits	0.008	0.480

Table S8. Current migration rate (m) estimated for *T. corymbosus* populations in the VCR. Each value represents the mean of five different runs. Bold values represent self-recruitment within each population.

From / To	T1	T2	T3	N1	N2
T1	**0.921**	0.043	0.052	0.019	0.088
T2	0.016	**0.731**	0.037	0.016	0.019
T3	0.027	0.185	**0.867**	0.035	0.048
N1	0.015	0.015	0.016	**0.916**	0.020
N2	0.020	0.027	0.029	0.014	**0.824**
Population with the greatest contribution	T3	T3	T1	T3	T1
Population with the least contribution	N1	N1	N1	N2	T2