

Supplementary material: The joint role of
coevolutionary selection and network structure in
shaping trait matching in mutualisms

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Table S1: Values and descriptions of the parameters used to simulate trait evolution.

Parameter	Value	Description
n_{sp}	40, 60, 80, 100	Number of species in simulation
n_A	10, 30, 20, 40, 30, 50, 60	Number of species in guild A
n_B	10, 30, 20, 40, 30, 50, 60	Number of species in guild B
α	0.2	Constant determining the sensitivity of the evolutionary effect to trait matching
$\bar{\Phi}$	0.5	Mean of the normal distribution describing Φ
σ_{Φ}	0.1	Standard deviation of the normal distribution describing Φ
Φ	Drawn from distribution with $\bar{\Phi}$ and σ_{Φ}	Compound parameter proportional to the selection gradient and additive genetic variance
$\bar{m}$	0.10 to 0.95 by 0.05	Mean of the normal distribution describing m
σ_m	0.01	Standard deviation of the normal distribution describing m
m	Drawn from distribution with $\bar{m}$ and σ_m	Strength of mutualistic selection
θ_{min}	0	Lower bound of the uniform distribution describing trait values
θ_{max}	10	Upper bound of the uniform distribution describing trait values
θ	Drawn from distribution with θ_{min} and θ_{max}	Trait value corresponding to the environmental optima
z_{t0}	Drawn from distribution with θ_{min} and θ_{max}	Initial trait value
ϵ	0.000001	Equilibrium was reached when $ Z_i^t - Z_i^{t+1} \leq \epsilon$
t_{max}	10000	Maximum number of simulated generations
n_{sim}	20	Number of simulation replicas performed per network

Table S2: Coordinates of network descriptors on the first two dimensions of the redundancy analysis performed for mutualistic selection ranging from 0.10 to 0.50. Abbreviations indicate the structural descriptor, and are defined as follows: **C**: Connectance, **M**: Modularity, **NM**: Number of modules and **WMD**: Within-module degree.

	RDA1	PC1	Mutualistic Selection
M	-5.14	-30.08	0.10
C	5.02	29.78	0.10
NM	-4.75	-27.41	0.10
MS	2.32	15.43	0.10
MC	2.80	16.03	0.10
WMD	0.86	-7.19	0.10
AMC	2.52	13.53	0.10
M	-6.85	-29.73	0.15
C	6.72	29.44	0.15
N	-6.34	-27.08	0.15
M	3.11	15.31	0.15
M	3.85	15.78	0.15
WMD	1.06	-7.48	0.15
AMC	3.48	13.34	0.15
M	-8.57	-29.26	0.20
C	8.33	29.00	0.20
NM	-7.83	-26.68	0.20
MS	3.71	15.21	0.20
MC	4.78	15.47	0.20
WMD	1.29	-7.86	0.20
AMC	4.13	13.20	0.20
M	-9.30	-29.02	0.25
C	8.98	28.80	0.25
NM	-8.59	-26.44	0.25
MS	3.96	15.16	0.25
MC	5.11	15.34	0.25
WMD	1.40	-8.06	0.25
AMC	4.47	13.11	0.25
M	-9.83	-28.84	0.30
C	9.43	28.65	0.30
NM	-9.09	-26.26	0.30
MS	4.14	15.12	0.30
MC	5.33	15.25	0.30
WMD	1.47	-8.21	0.30
AMC	4.73	13.03	0.30
M	-10.15	-28.73	0.35
C	9.71	28.56	0.35
NM	-9.55	-26.09	0.35
MS	4.31	15.07	0.35
MC	5.43	15.22	0.35
WMD	1.40	-8.27	0.35
AMC	4.84	13.00	0.35
M	-9.82	-28.85	0.40
C	9.37	28.68	0.40
NM	-9.35	-26.16	0.40
MS	4.17	15.09	0.40
MC	5.09	15.37	0.40
WMD	1.35	-8.16	0.40
AMC	4.69	13.05	0.40
M	-9.05	-29.11	0.45
C	8.68	28.90	0.45
NM	-8.75	-26.38	0.45
MS	3.73	15.21	0.45
MC	4.66	15.52	0.45
WMD	1.32	-7.97	0.45
AMC	4.34	13.14	0.45
M	-7.68	-29.52	0.50
C	7.32	29.29	0.50
NM	-7.48	-26.78	0.50
MS	3.05	15.34	0.50
MC	3.71	15.83	0.50
WMD	1.03	-7.58	0.50
AMC	3.67	13.31	0.50

Table S3: Coordinates of network descriptors on the first two dimensions of the redundancy analysis performed for mutualistic selection ranging from 0.55 to 0.95. Abbreviations indicate the structural descriptor, and are defined as follows: **C**: Connectance, **M**: Modularity, **NM**: Number of modules and **WMD**: Within-module degree.

	RDA1	PC1	Mutualistic Selection
M	-5.46	-30.02	0.55
C	5.16	29.76	0.55
NM	-5.64	-27.24	0.55
MS	1.82	15.54	0.55
MC	2.64	16.05	0.55
WMD	1.04	-7.26	0.55
AMC	2.62	13.52	0.55
M	-1.00	-30.51	0.60
C	1.05	30.20	0.60
NM	-1.94	-27.77	0.60
MS	-0.10	15.61	0.60
MC	0.25	16.30	0.60
WMD	0.99	-6.86	0.60
AMC	0.70	13.72	0.60
M	5.53	-30.02	0.65
C	-5.36	29.72	0.65
NM	4.03	-27.56	0.65
MS	-3.16	15.27	0.65
MC	-3.55	15.89	0.65
WMD	1.17	-6.73	0.65
AMC	-1.62	13.71	0.65
M	18.71	-23.77	0.70
C	-18.04	23.83	0.70
NM	15.46	-23.02	0.70
MS	-8.72	13.21	0.70
MC	-10.25	11.91	0.70
WMD	1.88	-8.74	0.70
AMC	-6.19	13.78	0.70
M	-25.30	12.33	0.75
C	23.68	-13.44	0.75
NM	-22.01	12.72	0.75
MS	11.53	-9.43	0.75
MC	13.16	-4.15	0.75
WMD	-2.16	21.02	0.75
AMC	8.60	-20.07	0.75
M	-26.66	-7.61	0.80
C	24.25	9.41	0.80
NM	-24.23	-6.16	0.80
MS	12.19	1.44	0.80
MC	13.12	6.79	0.80
WMD	-1.70	-25.47	0.80
AMC	9.41	21.96	0.80
M	-26.87	-7.47	0.85
C	24.08	9.75	0.85
NM	-24.84	-4.65	0.85
MS	12.37	-3.23	0.85
MC	12.38	11.80	0.85
WMD	-1.61	-24.29	0.85
AMC	9.55	21.34	0.85
M	-26.37	-10.05	0.90
C	22.97	13.13	0.90
NM	-24.70	-6.61	0.90
MS	11.98	-1.23	0.90
MC	11.47	14.07	0.90
WMD	-1.70	-22.06	0.90
AMC	9.23	20.30	0.90
M	-24.58	-16.32	0.95
C	20.54	20.20	0.95
NM	-23.65	-12.16	0.95
MS	11.01	5.40	0.95
MC	9.61	16.49	0.95
WMD	-1.76	-15.20	0.95
AMC	8.34	16.60	0.95

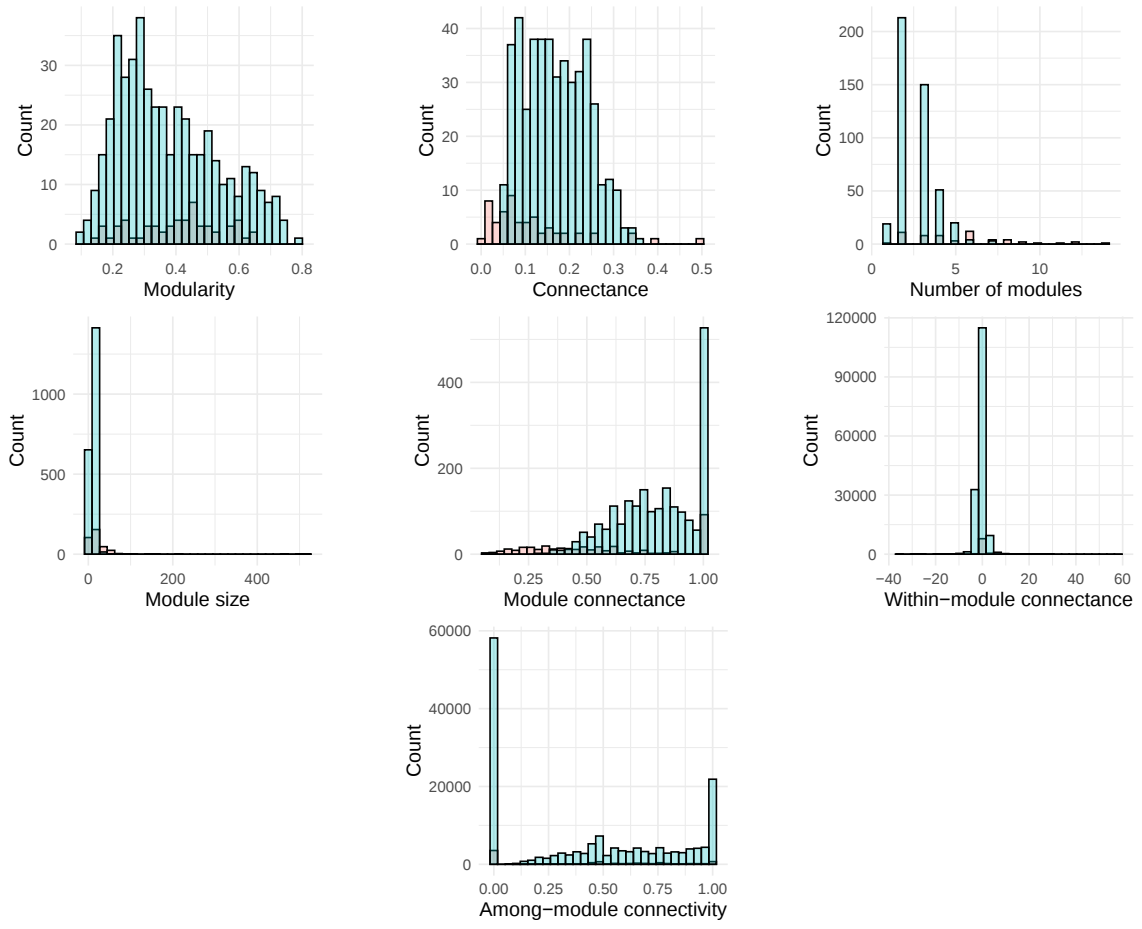


Figure S1: Comparison between real and simulated networks, in terms of the distribution of seven structural descriptors of the networks used to simulate coevolution. Modularity, connectance and number of modules encapsulate the network scale. Module size and module connectance describe the module scale. Within-module degree and among-module connectivity capture species roles. Red bars correspond to properties measured on all pollination and seed dispersal networks available at the web of life repository. Blue bars correspond to properties measured on all the networks built with the niche model.

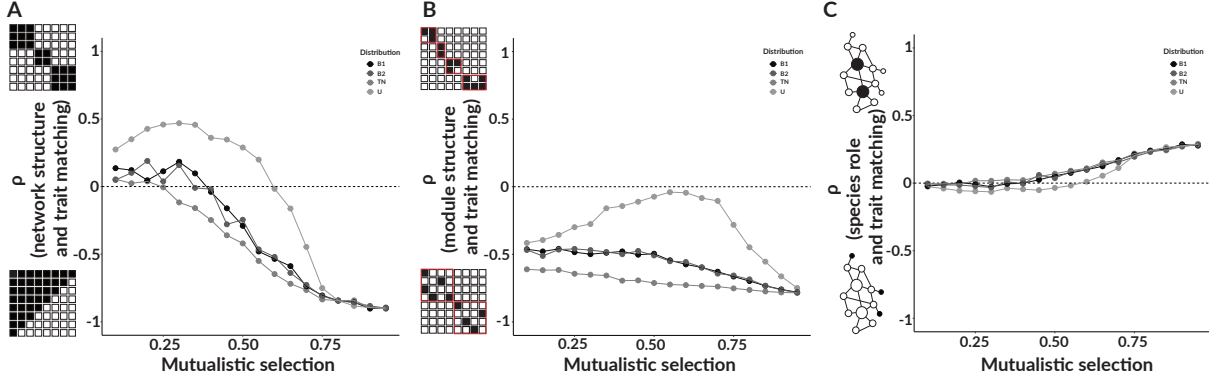


Figure S2: Correlation between network, module and species descriptors with trait matching after simulating coevolution with different Φ values. Across panels, $\rho > 0$ indicates a positive correlation between the PCA scores summarising structural descriptors and trait matching at the corresponding scale. Network PCA scores were negatively associated with connectance, and positively associated with modularity and the number of modules in the network. Module PCA scores were positively associated with module connectance and negatively associated with module size. Species PCA scores were positively associated with within-module degree and among-module connectivity. The colour of dots correspond to different distributions used to sample initial trait values. Abbreviations for distributions are as follows. **B1**: Beta distribution with $\alpha = 2, \beta = 5$, **B2**: Beta distribution with $\alpha = 5, \beta = 2$, **TN**: Truncated normal distribution ranging from 0 to 10 with $\mu = 5, \sigma^2 = 0.1$ and **U**: Uniform distribution ranging from 0 to 10.

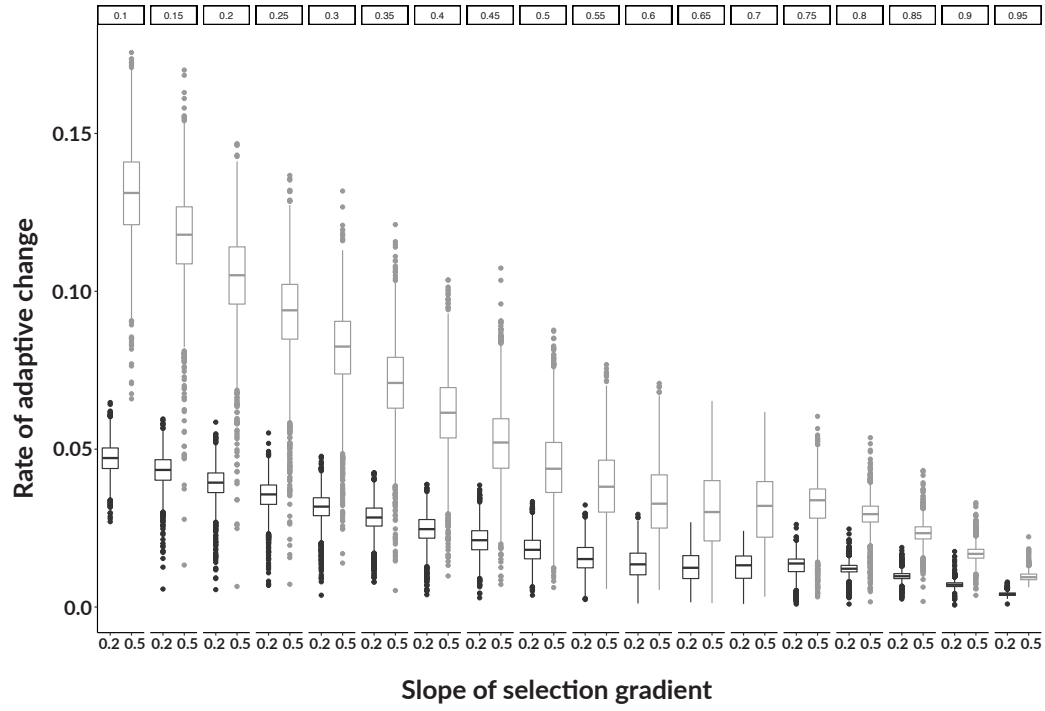


Figure S3: Rate of adaptive change for the coevolution model for two different selection gradients slopes. The slope of the selection gradient controls the rate at which traits change as a result of both environmental and mutualistic selection. This was measured as the mean amount of trait change per species per time step.

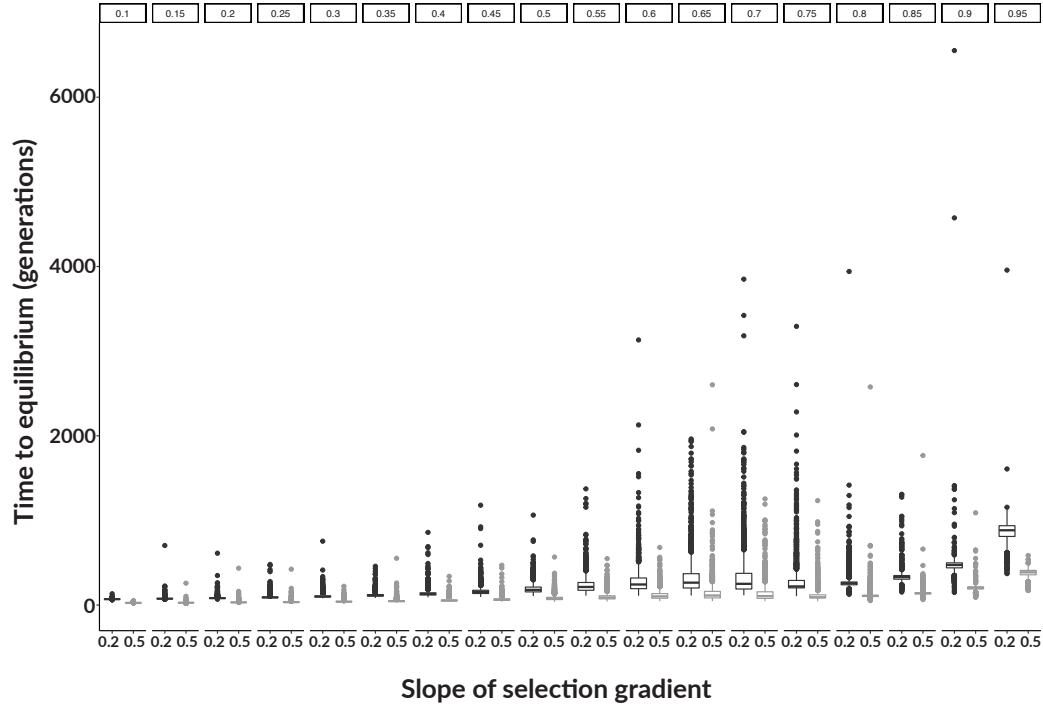


Figure S4: Time required for the coevolution model to reach equilibrium for two different selection gradient slopes. The slope of the selection gradient controls the rate at which traits change as a result of both environmental and mutualistic selection. Results correspond to simulating coevolution for networks of size 40, with an equal number of consumer and resource species.

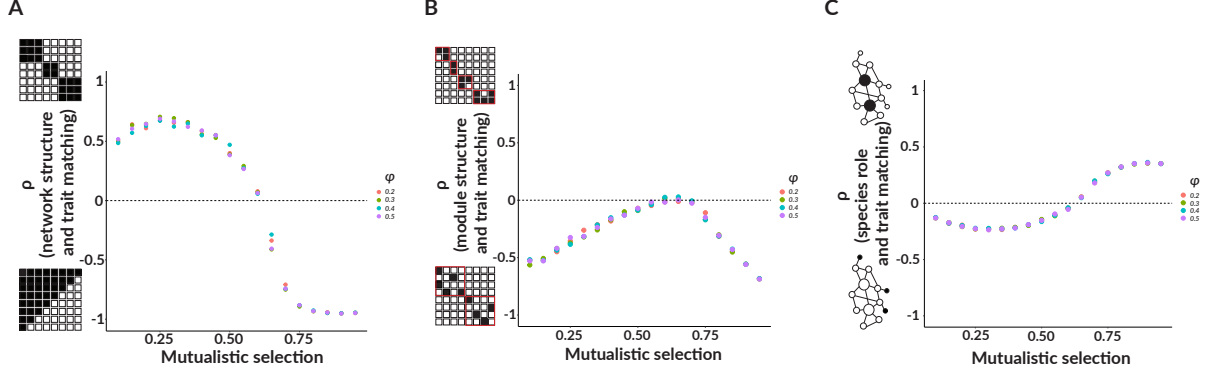


Figure S5: Correlation between network, module and species descriptors with trait matching after simulating coevolution with different selection gradients slopes. Across panels, $\rho > 0$ indicates a positive correlation between the PCA scores summarising structural descriptors and trait matching at the corresponding scale. Network PCA scores were negatively associated with connectance, and positively associated with modularity and the number of modules in the network. Module PCA scores were positively associated with module connectance and negatively associated with module size. Species PCA scores were positively associated with within-module degree and among-module connectivity. The colour of dots correspond to different Φ values used to run the coevolution model.

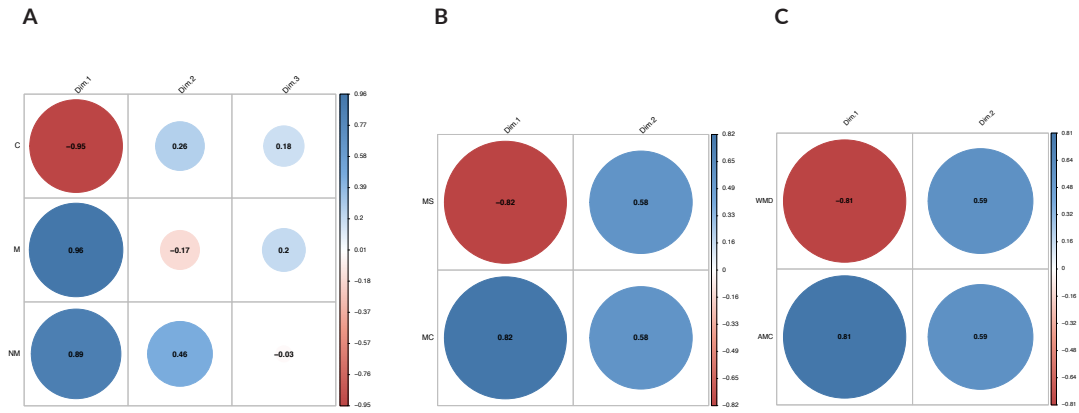


Figure S6: Coordinates of network descriptors on the dimensions of the principal component analysis used to build the *network structure* (A), *module structure* (B), and *species role* axes (C).

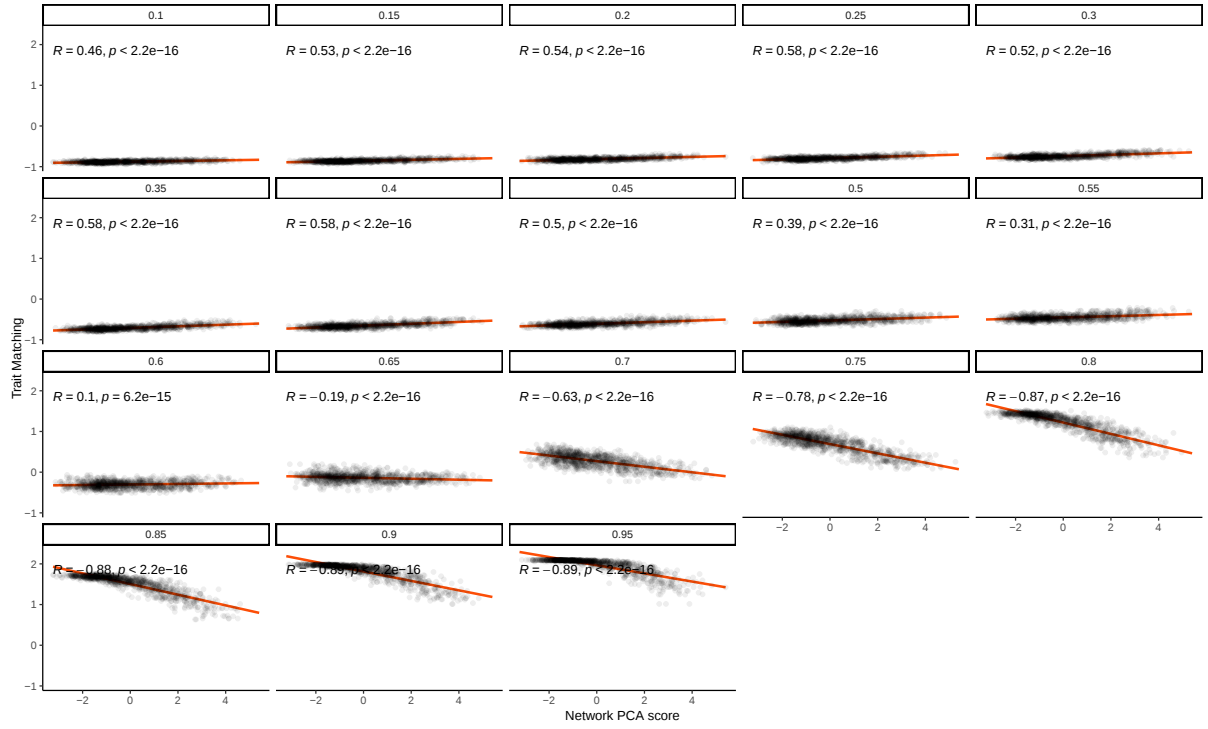


Figure S7: Correlations of network structure with trait matching across a gradient of mutualistic selection for the coevolution scenario. Each point represents a network with a given structure, as determined by a PCA, and a standardised degree of trait matching. The statistic and associated p-value of the Spearman-rank correlation are shown.

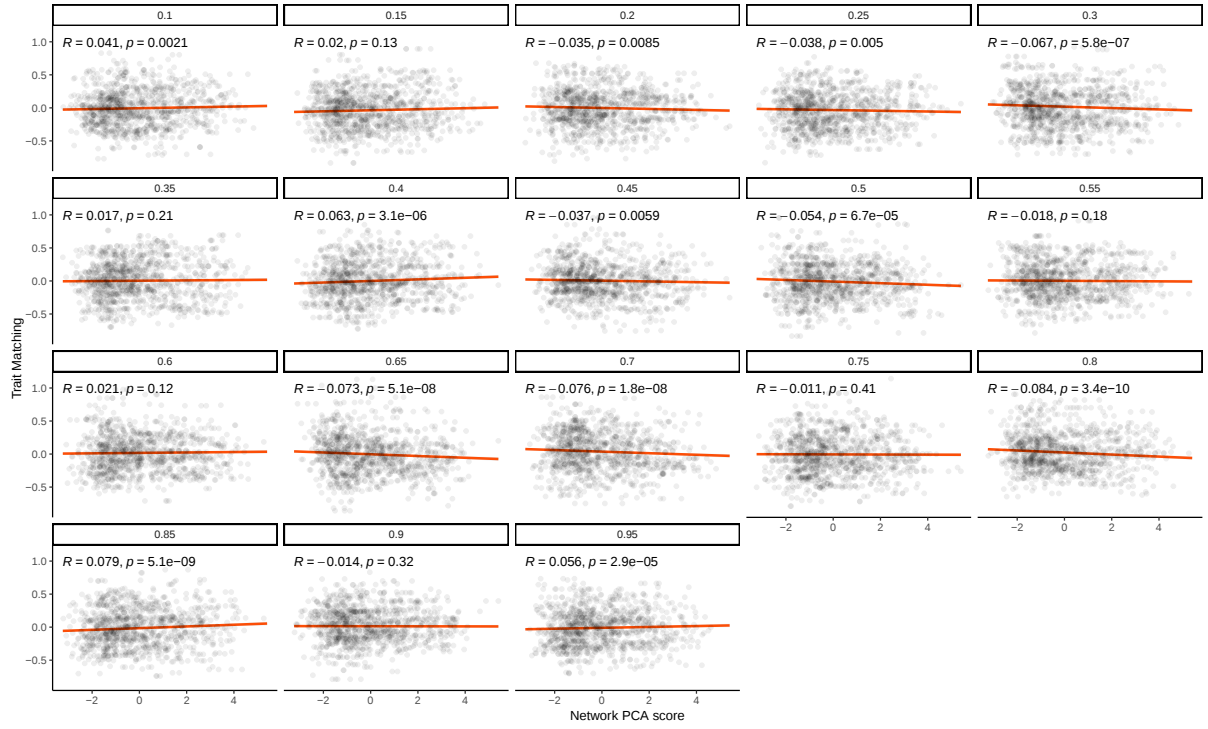


Figure S8: Correlations of network structure with trait matching across a gradient of mutualistic selection for the null coevolution scenario. Each point represents a network with a given structure, as determined by a PCA, and a standardised degree of trait matching. The statistic and associated p-value of the Spearman-rank correlation are shown.

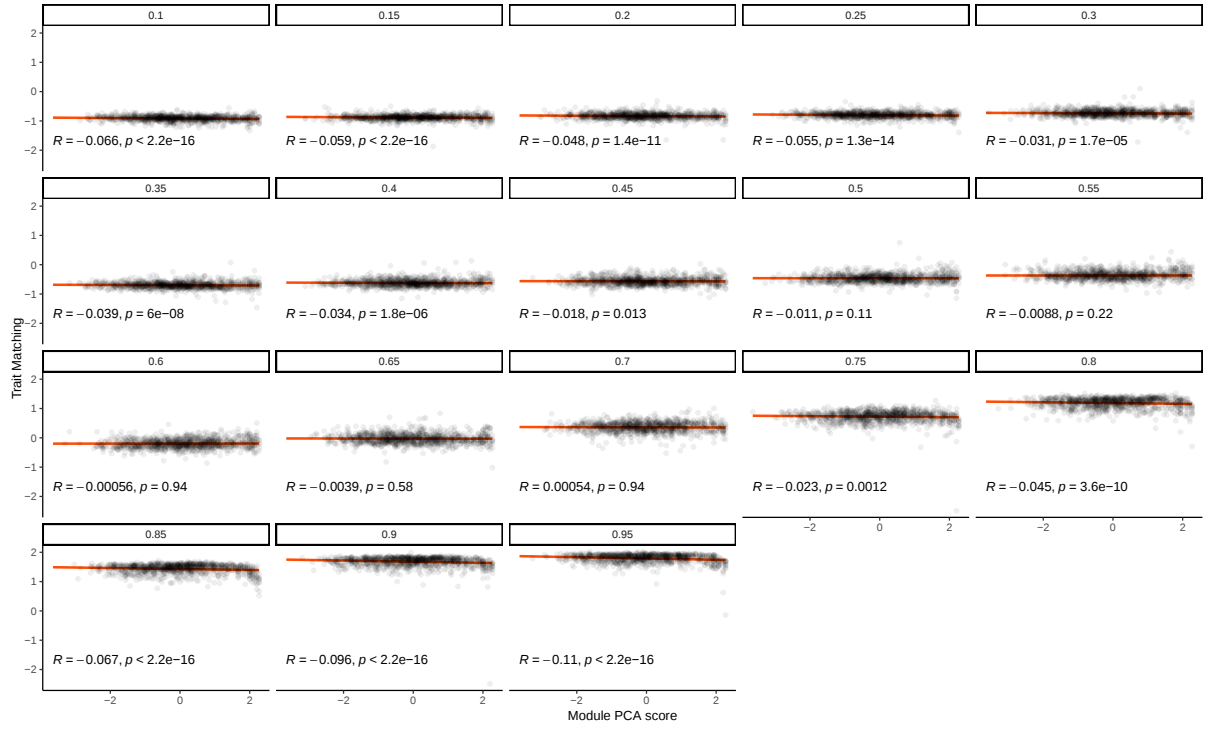


Figure S9: Correlations of module structure with trait matching across a gradient of mutualistic selection for the coevolution scenario. Each point represents a module with a given structure, as determined by a PCA, and a standardised degree of trait matching. The statistic and associated p-value of the Spearman-rank correlation are shown.

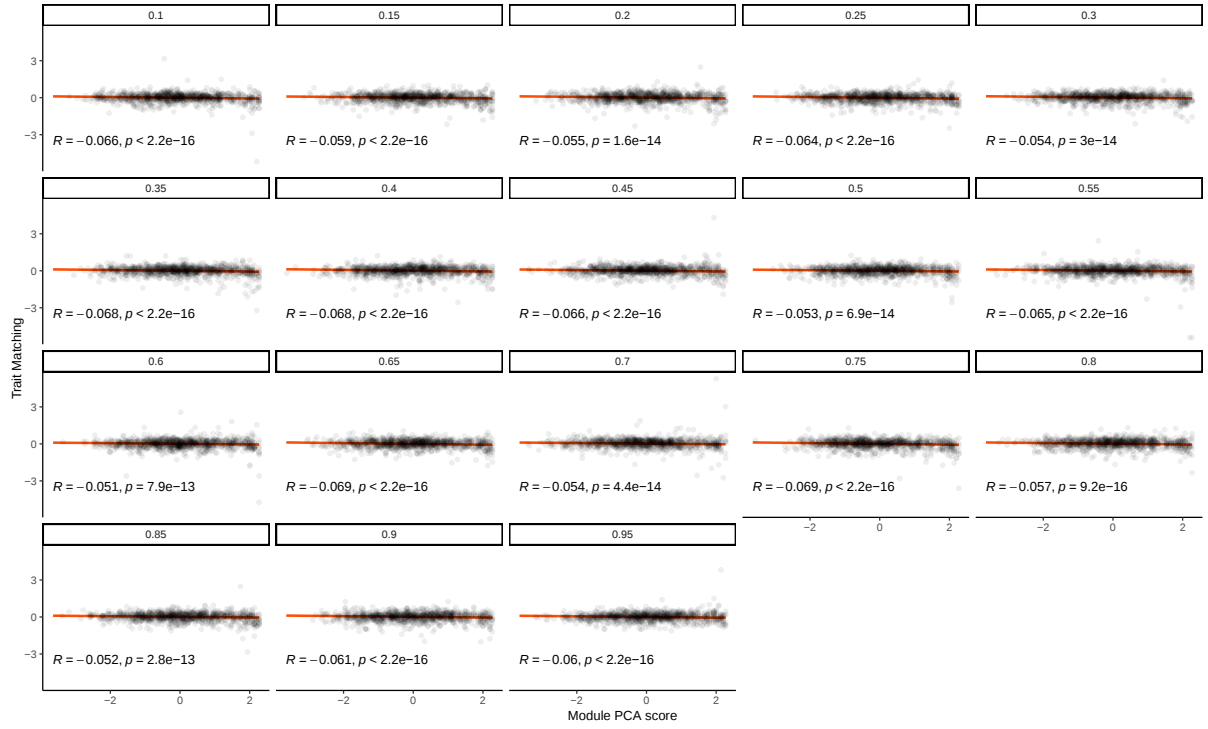


Figure S10: Correlations of module structure with trait matching across a gradient of mutualistic selection for the null scenario. Each point represents a module with a given structure, as determined by a PCA, and a standardised degree of trait matching. The statistic and associated p-value of the Spearman-rank correlation are shown.

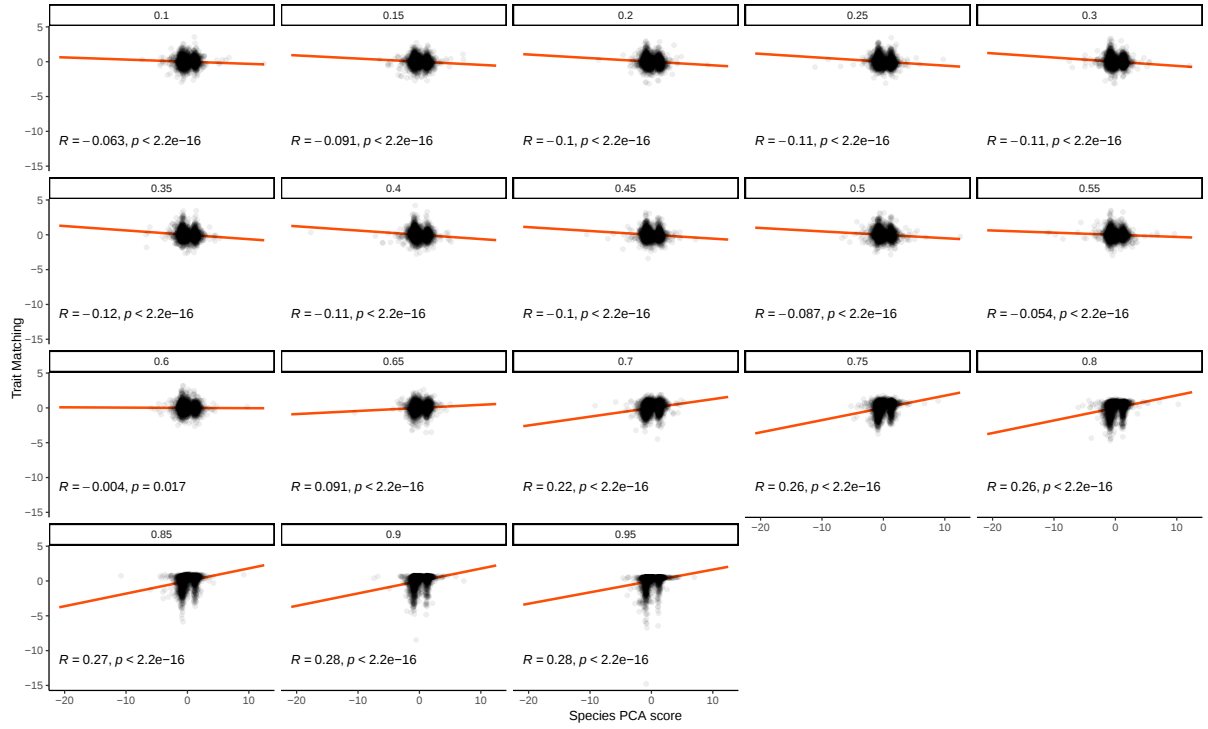


Figure S11: Correlations of species role with trait matching across a gradient of mutualistic selection for the coevolution scenario. Each point represents a species with a given role, as determined by a PCA, and a standardised degree of trait matching. The statistic and associated p-value of the Spearman-rank correlation are shown.

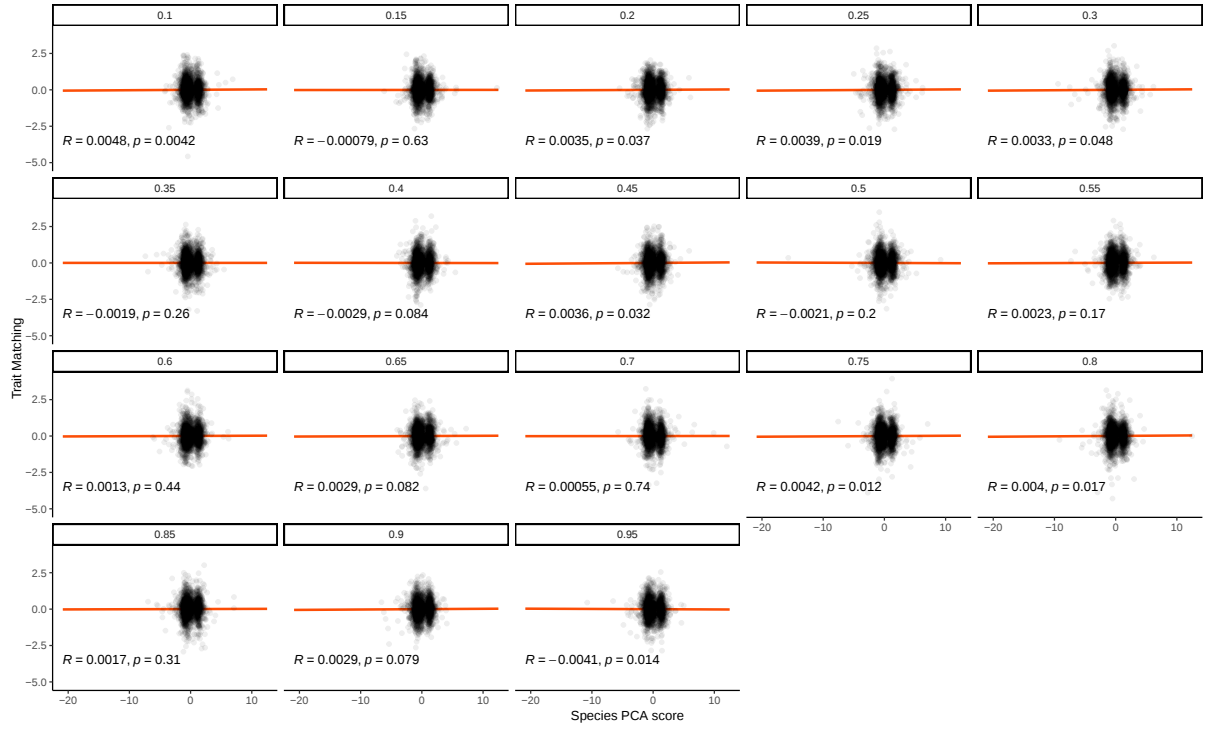


Figure S12: Correlations of species role with trait matching across a gradient of mutualistic selection for the coevolution scenario. Each point represents a species with a given role, as determined by a PCA, and a standardised degree of trait matching. The statistic and associated p-value of the Spearman-rank correlation are shown.

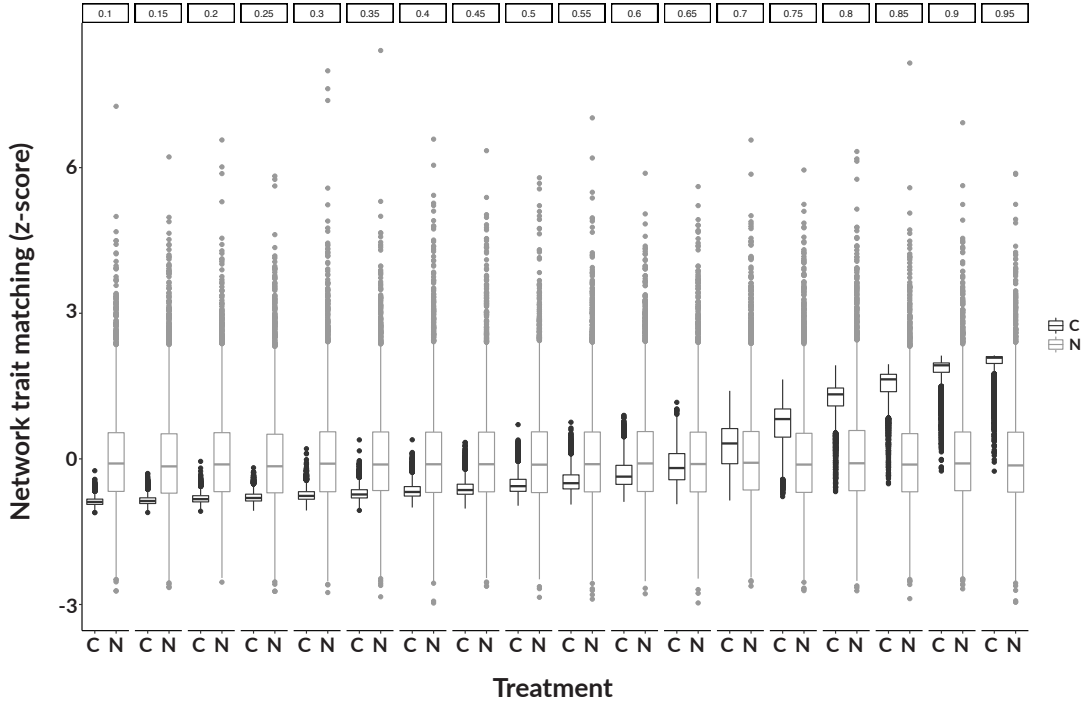


Figure S13: Distribution of network trait matching across a gradient of mutualistic selection. The average degree of trait matching was calculated for each network and standardised by means of a z-score. Black box-plots represent network trait matching after coevolution. Grey points represent the results for the null coevolution scenario, where species traits were fixed to the environmental optima.

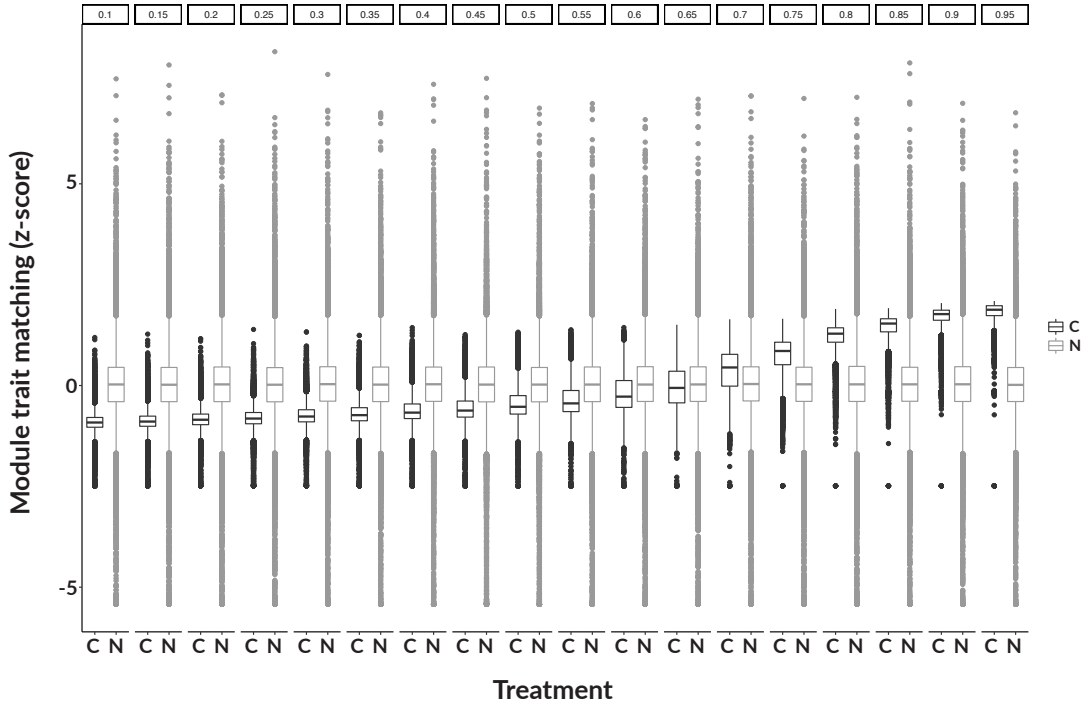


Figure S14: Distribution of module trait matching across a gradient of mutualistic selection. The average degree of trait matching was calculated for each module of each network and standardised by means of a z-score. Black box-plots represent module trait matching after coevolution. Grey points represent the results for the null coevolution scenario, where species traits were fixed to the environmental optima.

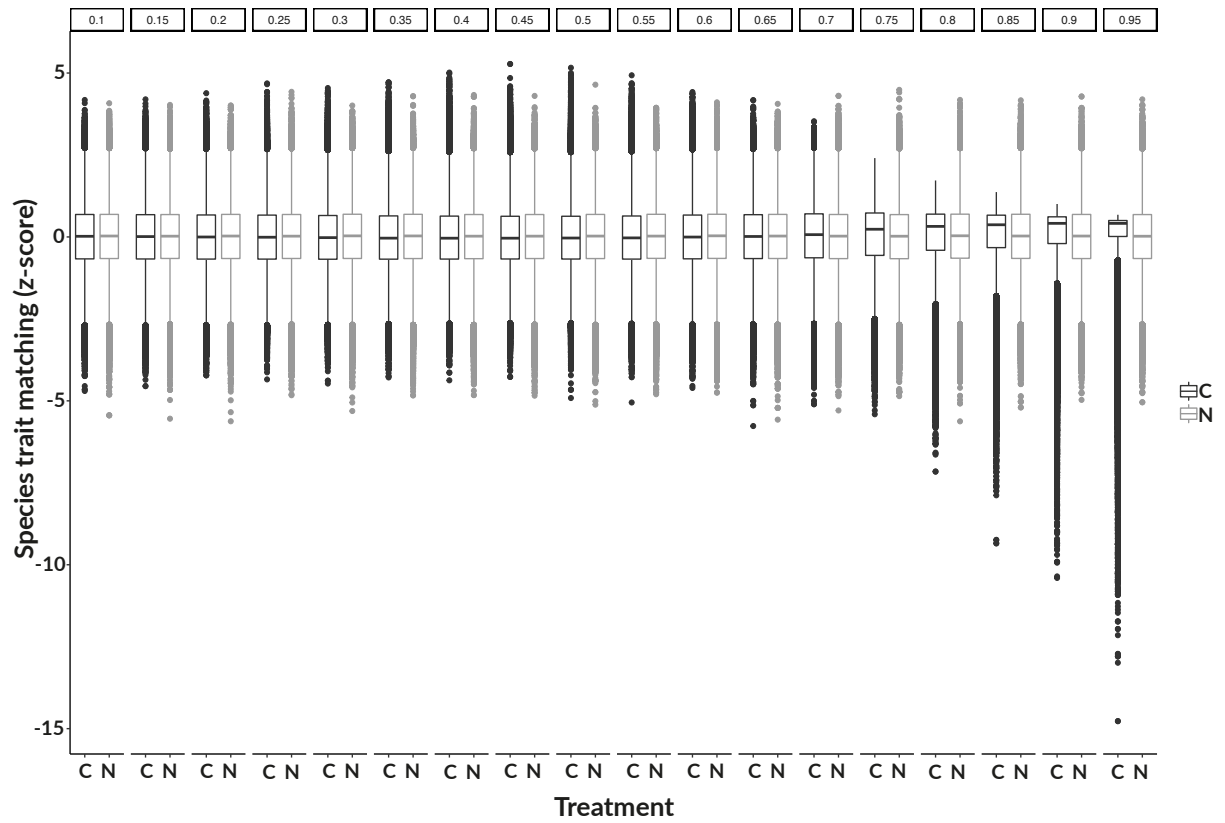


Figure S15: Distribution of species trait matching across a gradient of mutualistic selection. The average degree of trait matching was calculated for each species of each network and standardised by means of a z-score. Black box-plots represent species trait matching after coevolution. Grey points represent the results for the null coevolution scenario, where species traits were fixed to the environmental optima.