Table S1 Chemostats were supplied with a modified version of artificial seawater medium (AN) (1) that induced nitrogen (N) or phosphorus (P) limitation (see Fig. S3) while maintaining similar equilibrium densities of *Synechococcus* (see Fig. S4). We autoclaved a solution containing dissolved Base Salts in 500 mL of Nanopure water. Once cool, we added 0.1-μm sterile-filtered Nutrient Solutions, cyclohexaminde (a eukaryotic inhibitor), the Trace Metals Solution (Table S2), and Vitamin Solution for enrichment and purifications (Table S3). Finally, we brought the mixture to 1 L final volume with autoclaved Nanopure water.

Base Salts	**Mass** ($g\ L^{-1}$)
NaCl	21.61 g
$MgSO_4 \cdot 7H_2O$	7.39 g
$MgCl_2 \cdot 6H_2O$	4.07 g
$CaCl_2 \cdot 2H_2O$	1.47 g
KCl	0.75 g

Nutrient Solutions	**Stock Concentration** ($g\ L^{-1}$)	**Volume** ($mL\ L^{-1}$)	
		N-limited	P-limited
EDTA (disodium salt)	1.00	5.00	
$Na_2CO_3 \cdot H_2O$	3.00	5.00	
$NaHCO_3$	6.10	5.00	
$NaNO_3$	4.00	6.26	12.52
K_2HPO_4	8.40	0.63	0.32
Trace Metals Solution		1.00	
Vitamin Solution		1.00	
Cyclohexamide	50 $mg\ L^{-1}$	100 µL	

Table S2 Recipe for Trace Element Solution used in the modified AN media. All trace metals were dissolved into 1 L of Nanopure water then filter (0.1-μm) sterilized.

Compound	**g L^{-1}**
$ZnSO_4 \cdot 7H_2O$	0.222
$MnCl_2 \cdot 4H_2O$	1.4
$Co(NO_3)_2 \cdot 6H_2O$	0.025
$Na_2MoO_4 \cdot 2H_2O$	0.39
$C_6H_8O_7 \cdot H_2O$	6.25
$C_6H_8FeNO_7$	6.0

Table S3 Recipe for Vitamin Solution used in the modified AN medium, which was used in the medium for enrichment and purification of *Synechococcus* strains in this study. Each compound was prepared as a neat stock (unless otherwise noted) then combined in the volumes listed below to prepare a 100 mL solution. The final solution was filter sterilized (0.1-μm) and stored at -20° C in 50 mL aliquots.

Compound	**Stock Concentration** (g L^{-1})	**Amount per 100 mL**
Inositol		100 mg
Thiamine · HCl		20 mg
Vitamin B_{12}	1.0	0.1 mL
Biotin	0.1	1 mL
Folic Acid	2.0	0.1 mL
p-aminobenzoic acid	2.0	0.5 mL
Niacin (Nicotinic acid)	1.0	10 mL
Ca d-pantothenate	2.0	10 mL
Pyridoxine	1.0	10 mL
Nanopure water		To 100 mL

Table S4 Summary statistics for *Synechococcus* (Syn) and phage in experimental chemostats. Nutrient limitation refers to the nitrogen (N) : phosphorus (P) supply ratio where N-limited chemostats received medium with a 10 : 1 N : P ratio and P-limited chemostats received medium with a 40 : 1 N : P ratio. Each experimental unit was assigned a unique Chemostat ID. Half of the chemostats phage amended with S-RIM8 (Phage Treatment = +) while the remaining chemostats served as no-phage controls (Phage Treatments = -). Equilibrium abundances of *Synechococcus* and phage were estimated as the mean ± SEM of densities over the time series based on methods described in the main text. Mean stability was measured for *Synechococcus* and phage within a chemostat as the inverse of the coefficient of variation of population densities over time.

Type	Nutrient Limitation	Phage Treatment	Mean Density ± SEM				Stability	
			Syn		phage		Syn	phage
Treatment averages	N	+	1.7E+07	± 1.31E+07	2.5E+08	± 1.39E+08	0.75	1.05
	P	+	1.1E+07	± 1.09E+07	2.4E+08	± 9.49E+07	0.59	1.45
	N	-	1.3E+07	± 3.69E+06	·	·	2.05	·
	P	-	1.8E+07	± 9.02E+06	·	·	1.14	·

Type	Nutrient Treatment	Chemostat ID	Phage Treatment	Mean Density ± SEM				Stability	
				Syn		phage		Syn	phage
Phage-amended	N	N2	+	1.8E+07	± 1.21E+07	1.5E+08	± 7.92E+07	0.84	1.11
	N	N3	+	1.6E+07	± 1.00E+07	2.9E+08	± 1.46E+08	0.93	1.16
	N	N5	+	1.7E+07	± 1.65E+07	3.1E+08	± 1.61E+08	0.59	1.12
	P	P2	+	1.3E+07	± 1.43E+07	1.6E+08	± 5.91E+07	0.52	1.58
	P	P4	+	1.1E+07	± 6.66E+06	2.4E+08	± 8.84E+07	0.94	1.59
	P	P5	+	9.4E+06	± 1.04E+07	3.1E+08	± 1.11E+08	0.52	1.63
No-phage Control	N	N1	-	1.3E+07	± 3.69E+06	·	·	2.05	·
	P	P1	-	2.5E+07	± 1.03E+07	·	·	1.43	·
	P	P3	-	9.9E+06	±4.02E+06)	·	·	1.42	·

Table S5 Coevolutionary dynamics in phage-bacteria infection matrices have been inferred from network metrics including modularity and nestedness. We calculated network statistics based on the matrix of infection data resulting from pairwise challenges of phage and *Synechococcus* that were isolated from N- and P-limited chemostats (see Fig S5) using the BiWeb program in Matlab (2), available at https://github.com/tpoisot/BiWeb. Network size is calculated from the number of interactions and reflected the number of strains that were isolated from a chemostat. Connectance, the proportion of possible links between strains, was calculated as the number of interactions divided by network size. Barber's Modularity (Qb) was calculated for each chemostat system using the LP-BRIM algorithm to find the partition that best maximized modularity within a matrix. Nestedness (NODF) is based on overlap and decreasing fill, which returns a value ranging between 0 and 1 (where 1 indicates a perfectly nested structure) and normalizes for matrix size, allowing for differing sizes of matrices to be compared. All calculations were based on 100,000 random Bernoulli simulations as described in the main text.

Treatment	**Chemostat ID**	**Size**	**Connectance**	**Modularity** (Q_b)	**Nestedness** (NODF)
NL	N2	144	0.257	0.162	0.331
	N3	126	0.194	0.197	0.374
	N5	65	0.210	0.168	0.242
PL	P2	253	0.220	0.216	0.387
	P4	180	0.168	0.276	0.266
	P5	95	0.144	0.279	0.224

Figure S1 We tested for nutrient limitation in *Synechococcus* WH7803 that had been acclimated under low (10 : 1) and high (40 : 1) supply ratio of N and P using cellular growth rates. Cells were acclimated semi-continuously under constant light (20 μE m^{-1} s^{-1}) at 25 °C for three serial transfers in either N- or P-limited medium (n = 10). We then inoculated each replicate cell line into fresh medium that doubled the concentration of N (N-limited = 440 μM, P-limited = 880 μM) or P (N-limited = 44 μM, P-limited = 22 μM). Next, we monitored *Synechococcus* population densities for seven days *via* autofluorescence (ex: 550 nm, em: 570 nm) with a Biotek Synergy Mx plate reader (Winooski, VT, USA). With these data, we estimated the maximum growth rate for each culture using a modified Gompertz equation (3) and calculated the percent change in growth rate with additional N or P as compared to the control, which contained no additional N or P. We tested for the effect of nutrient limitation using *t*-tests in the R statistics environment (4). We found that the change in *Synechococcus* growth rate in batch culture significantly increased in response to the addition of limiting resource (N or P) following acclimation to N-limited (N : P = 10 : 1) or P-limited (N : P = 40 : 1) conditions. Data are represented as mean ± SEM (n = 5).

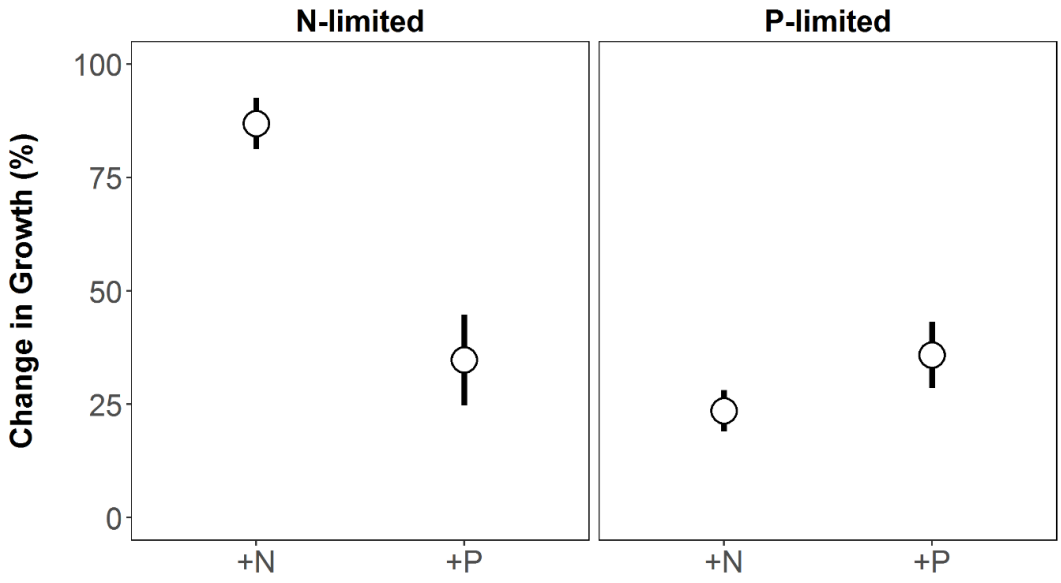


Figure S2 Population dynamics of *Synechococcus* WH7803 in chemostats were relatively stable over time in the absence of phage (*i.e.*, no-phage controls). The N-limited treatment (left) only had one chemostat following the loss of the second control chemostat due to contamination. There were two replicates in the no-phage control P-limited chemostats (data represent mean ± SEM). The grey shaded area corresponds to *Synechococcus* densities prior to phage introduction in the other phage-amended chemostats.

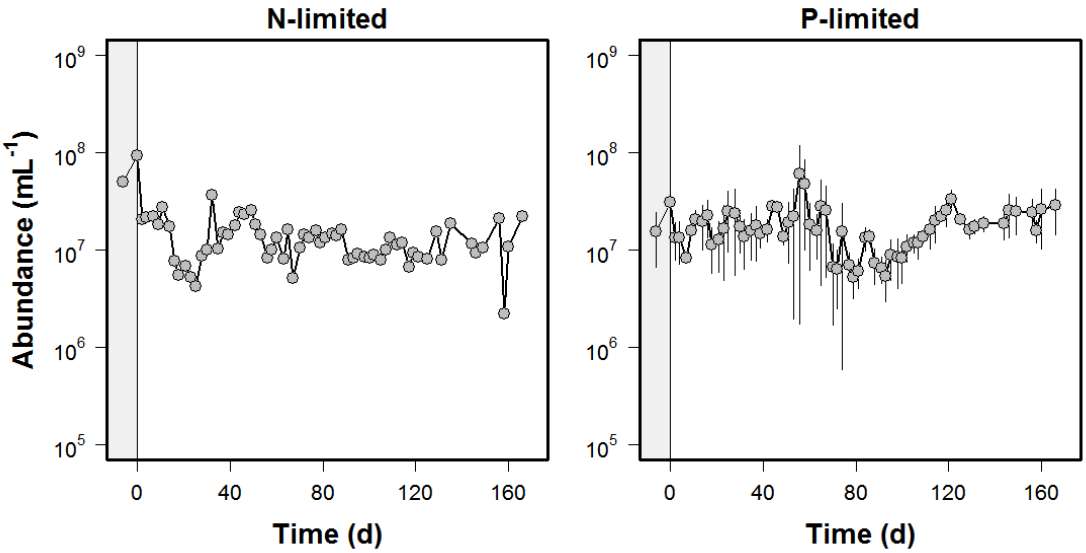


Figure S3 Temporal coherence calculated as the cross-correlation coefficient (CCF) between *Synechococcus* and phage population densities under N- or P-limitation. CCF can range from -1 where host-phage dynamics are out-of-phase to +1 where host-phage dynamics are in-phase. The lag corresponds to the amount of time (days) that the *Synechococcus* and phage densities were shifted when calculating the CCF. Negative time lags suggest that *Synechococcus* densities were correlated with phage densities from the past, while positive lags suggest that phage densities track *Synechococcus* densities from the past. The blue dashed lines in each plot represent the 95% confidence interval after white noise correction.

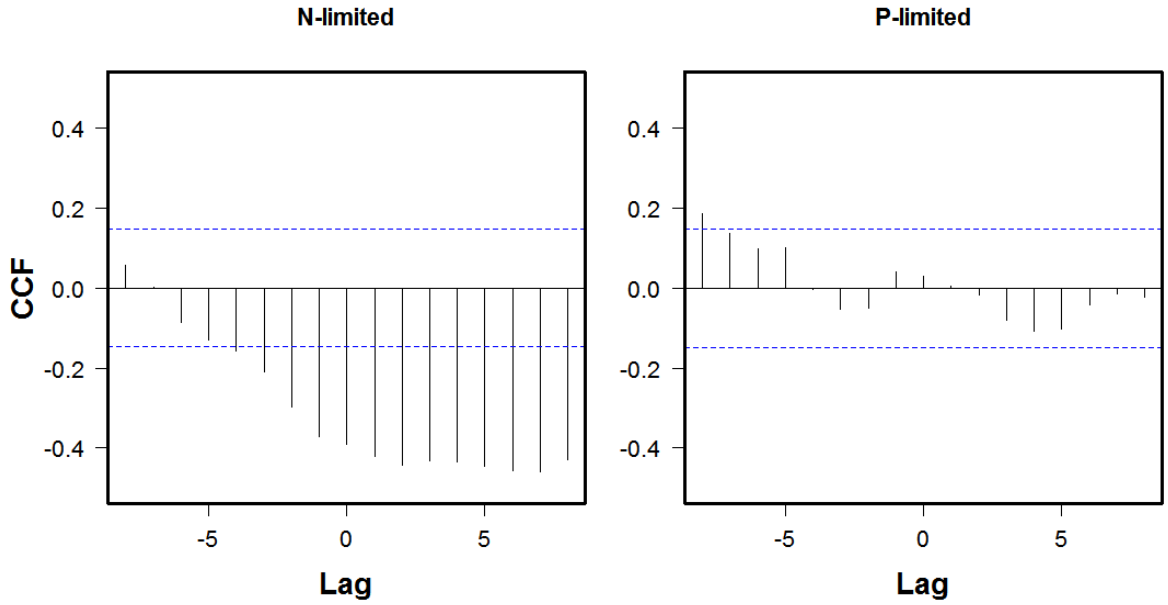
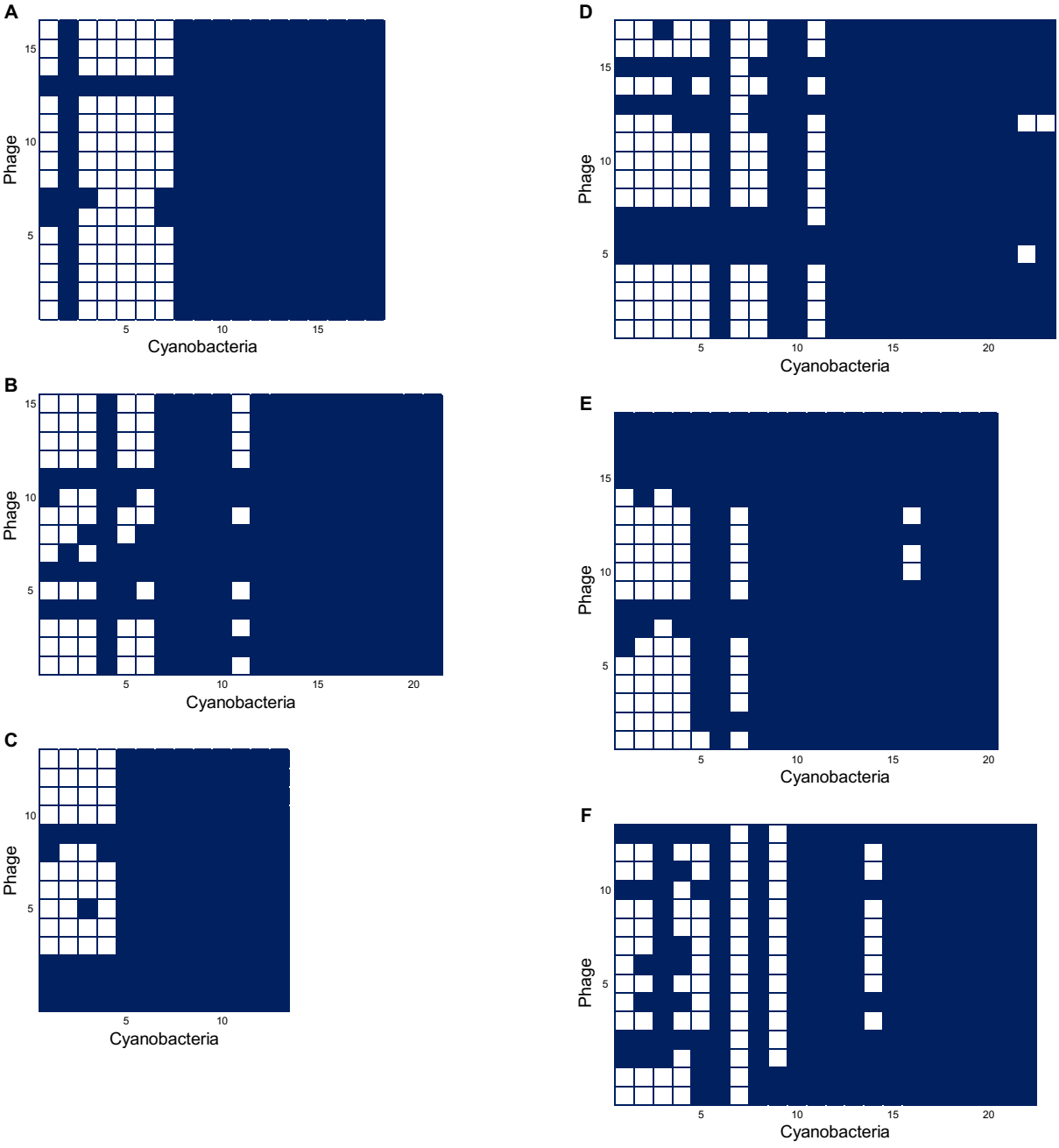


Figure S4 Infection matrices for N-limited (a, b, c) and P-limited (d, e, f) replicate chemostats. Cyanobacteria and phage interactions within a chemostat were quantified using triplicate challenge assays with 3-5 *Synechococcus* and 3-5 phage strains isolated per tested time-point (n = 7). Most of the successful lytic infections between a *Synechococcus* (column) and phage (row) strain were constrained between strains isolated early in the experiment (prior to day 23, white cells). Phage-resistant *Synechococcus* phenotypes appeared quickly within the chemostats and persisted throughout the duration of the experiment (blue cells). Axes correspond to the number of strains within the rows or columns.


A
Phage
Cyanobacteria
B
Phage
Cyanobacteria
C
Phage
Cyanobacteria
D
Phage
Cyanobacteria
E
Phage
Cyanobacteria
F
Phage
Cyanobacteria

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