Electronic supplementary material

Supplementary results

Figure S1. A Venn diagram showing the result of variation partitioning for the contributions of mutation supply rate and diversifying selection for phenotypic richness of the microcosms evolving without immigration. The sample size for this analysis is 8. The response variable, phenotypic richness, is the mean value at every temperature (log-transformed). The explanatory variable mutation supply rate is estimated as the product of mutation rate and effective population size [1]; and effective population size under a batch transfer regime is given by $N_e = N_0\, g$, where N_0 is the initial population size and g is the number of generations during a transfer [2]. Here mean population size at every temperature was used for calculating the effective population sizes. The explanatory variable diversifying selection is a summarization of the fitness values shown in Fig. 3 in the main text; that is, the proportion of phenotypes with significantly positive fitness values at each temperature (0/6, 1/6, 2/6, 4/6, 5/6, 6/6, 6/6 and 6/6 at the eight temperatures from 9-30 ℃). In this diagram, 'M' represents mutation supply rate, and 'S', selection. The fraction jointed explained by 'M' and 'S' ('M∩S') is very large, suggesting a strong collinearity between the two explanatory variables [3, 4]. As the two explanatory variables are both observed variables that co-vary with temperature, a variation partitioning analysis is more appropriate than a general linear model that identifies significant effects.

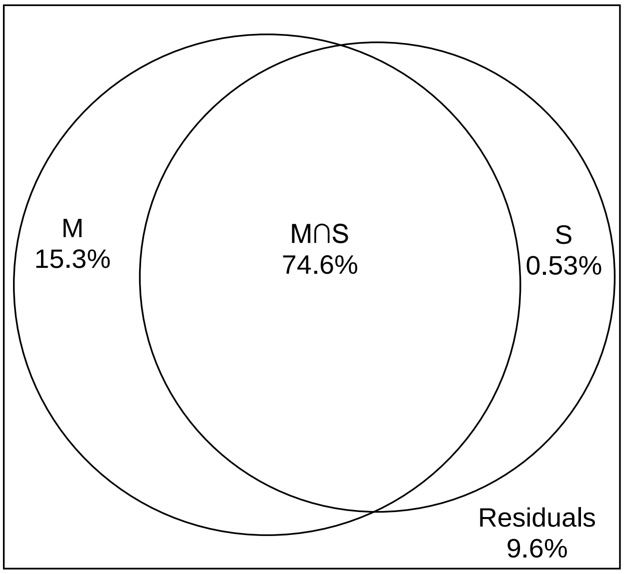

Table S1 Results of two-sample *t* tests for the differences between 'no immigration' and 'with immigration' microcosms (corresponding to Figure 1 in the main text). The sample size for each comparison is 12; however, values of degree of freedom were not constant across the comparisons because of corrections due to non-equal variance in Welch two-sample test. Correction of *P* values for multiple comparisons within each column (for each observed variable) was performed with the Benjamini-Hochberg procedure.

Temperature	Phenotypic richness	Phenotypic diversity	Proportion of SM	Population size
9	$df = 5$	$df = 5$	$df = 5$	$df = 8$
	$t = -2.13$	$t = -1.76$	$t = 2.06$	$t = -1.48$
	$P = 0.0869$	$P = 0.138$	$P = 0.0948$	$P = 0.172$
	$P_{adj} = 0.116$	$P_{adj} = 0.184$	$P_{adj} = 0.126$	$P_{adj} = 0.688$
12	$df = 5$	$df = 5$	$df = 5$	$df = 10$
	$t = -5.00$	$t = -4.22$	$t = 4.75$	$t = -0.407$
	$P = 0.00411$	$P = 0.00837$	$P = 0.00511$	$P = 0.693$
	$P_{adj} = 0.0110$	$P_{adj} = 0.0167$	$P_{adj} = 0.00818$	$P_{adj} = 0.818$
15	$df = 5$	$df = 5$	$df = 5$	$df = 10$
	$t = -9.69$	$t = -14.97$	$t = 25.79$	$t = -0.165$
	$P = 0.000199$	$P = 2.41 \times 10^{-5}$	$P = 1.636 \times 10^{-6}$	$P = 0.872$
	$P_{adj} = 0.00104$	$P_{adj} = 0.000193$	$P_{adj} = 0.0000131$	$P_{adj} = 0.872$
18	$df = 5$	$df = 5$	$df = 5$	$df = 10$
	$t = -9.16$	$t = -4.47$	$t = 5.61$	$t = -1.59$
	$P = 0.00026$	$P = 0.00660$	$P = 0.00248$	$P = 0.144$
	$P_{adj} = 0.00104$	$P_{adj} = 0.0167$	$P_{adj} = 0.00496$	$P_{adj} =0.688$
21	$df = 7$	$df = 6$	$df = 9$	$df = 6$
	$t = -2.83$	$t = -6.87$	$t = 5.89$	$t = 0.382$
	$P = 0.0254$	$P = 0.000395$	$P = 0.000237$	$P = 0.716$
	$P_{adj} = 0.0406$	$P_{adj} = 0.00158$	$P_{adj} = 0.000950$	$P_{adj} = 0.818$
24	$df = 6$	$df = 7$	$df = 7$	$df = 9$
	$t = -4.03$	$t = -2.59$	$t = 4.96$	$t = -0.564$
	$P = 0.00632$	$P = 0.0371$	$P = 0.00182$	$P = 0.587$
	$P_{adj} = 0.0126$	$P_{adj} = 0.0594$	$P_{adj} = 0.00485$	$P_{adj} = 0.818$
27	$df = 10$	$df = 9$	$df = 10$	$df = 9$
	$t = -0.542$	$t = -0.187$	$t = 0.232$	$t = -0.869$
	$P = 0.600$	$P = 0.855$	$P = 0.821$	$P = 0.406$
	$P_{adj} = 0.600$	$P_{adj} = 0.855$	$P_{adj} = 0.821$	$P_{adj} = 0.818$
30	$df = 9$	$df = 10$	$df = 8$	$df = 6$
	$t = 0.613$	$t = 1.33$	$t = 0.490$	$t = 0.809$
	$P = 0.557$	$P = 0.213$	$P = 0.637$	$P = 0.448$
	$P_{adj} = 0.600$	$P_{adj} = 0.243$	$P_{adj} = 0.728$	$P_{adj} = 0.818$

Table S2 Results of one-sample *t* tests for the difference of phenotype fitness from zero (corresponding to Figure 3 in the main text). Correction of *P* values for multiple comparisons within each column (for each genotype) was carried out using the Benjamini-Hochberg procedure.

Temperature	Large SM	Small SM	Large WS	Small WS	Round WS	SM-like WS
9	$t = 0.0850$	$t = -0.984$	$t = -6.05$	$t = -6.67$	$t = 2.48$	$t = 1.92$
	$P = 0.940$	$P = 0.429$	$P = 0.0263$	$P = 0.0218$	$P = 0.132$	$P = 0.195$
	$P_{adj} = 0.940$	$P_{adj} = 0.490$	$P_{adj} = 0.035$	$P_{adj} = 0.0461$	$P_{adj} = 0.151$	$P_{adj} = 0.195$
12	$t = 2.12$	$t = 0.557$	$t = -6.37$	$t = -5.77$	$t = 3.36$	$t = 6.89$
	$P = 0.168$	$P = 0.634$	$P = 0.0238$	$P = 0.0288$	$P = 0.0781$	$P = 0.0205$
	$P_{adj} = 0.192$	$P_{adj} = 0.634$	$P_{adj} = 0.035$	$P_{adj} = 0.0461$	$P_{adj} = 0.104$	$P_{adj} = 0.0273$
15	$t = 2.47$	$t = 2.84$	$t = 2.79$	$t = 2.19$	$t = 8.10$	$t = 4.73$
	$P = 0.132$	$P = 0.105$	$P = 0.108$	$P = 0.161$	$P = 0.0149$	$P = 0.0418$
	$P_{adj} = 0.176$	$P_{adj} = 0.140$	$P_{adj} = 0.108$	$P_{adj} = 0.184$	$P_{adj} = 0.0238$	$P_{adj} = 0.0478$
18	$t = 10.17$	$t = 12.04$	$t = 3.68$	$t = 1.51$	$t = 5.51$	$t = 14.66$
	$P = 0.00953$	$P = 0.00683$	$P = 0.0670$	$P = 0.270$	$P = 0.314$	$P = 0.00462$
	$P_{adj} = 0.0152$	$P_{adj} = 0.0137$	$P_{adj} = 0.0766$	$P_{adj} = 0.270$	$P_{adj} = 0.314$	$P_{adj} = 0.00924$
21	$t = 15.12$	$t = 7.38$	$t = 8.68$	$t = 3.00$	$t = 62.77$	$t = 22.36$
	$P = 0.00431$	$P = 0.0179$	$P = 0.0130$	$P = 0.0952$	$P = 0.000254$	$P = 0.00200$
	$P_{adj} = 0.00862$	$P_{adj} = 0.0286$	$P_{adj} = 0.0260$	$P_{adj} = 0.127$	$P_{adj} = 0.00102$	$P_{adj} = 0.00533$
24	$t = 23.60$	$t = 17.71$	$t = 11.34$	$t = 6.18$	$t = 14.50$	$t = 57.87$
	$P = 0.00179$	$P = 0.00318$	$P = 0.00769$	$P = 0.0252$	$P = 0.00472$	$P = 0.000299$
	$P_{adj} = 0.00739$	$P_{adj} = 0.0127$	$P_{adj} = 0.0205$	$P_{adj} = 0.0461$	$P_{adj} = 0.0126$	$P_{adj} = 0.00239$
27	$t = 18.96$	$t = 13.12$	$t = 42.50$	$t = 24.74$	$t = 11.96$	$t = 10.64$
	$P = 0.00277$	$P = 0.00576$	$P = 0.000553$	$P = 0.00163$	$P = 0.00692$	$P = 0.00872$
	$P_{adj} = 0.00739$	$P_{adj} = 0.0137$	$P_{adj} = 0.00442$	$P_{adj} = 0.00984$	$P_{adj} = 0.0138$	$P_{adj} = 0.0140$
30	$t = 22.41$	$t = 36.0$	$t = 23.79$	$t = 20.12$	$t = 79.42$	$t = 37.18$
	$P = 0.00199$	$P = 0.000771$	$P = 0.00176$	$P = 0.00246$	$P = 0.000159$	$P = 0.000723$
	$P_{adj} = 0.00739$	$P_{adj} = 0.00617$	$P_{adj} = 0.00704$	$P_{adj} = 0.00984$	$P_{adj} = 0.00102$	$P_{adj} = 0.00289$

References

[1] de Visser, J., Zeyl, C.W., Gerrish, P.J., Blanchard, J.L. & Lenski, R.E. 1999 Diminishing returns from mutation supply rate in asexual populations. *Science* **283**, 404-406.
[2] Lenski, R.E., Rose, M.R., Simpson, S.C. & Tadler, S.C. 1991 Long-term experimental evolution in *Escherichia coli*. I. adaptation and divergence during 2,000 generations. *Am. Nat.* **138**, 1315-1341.
[3] Borcard, D., Legendre, P. & Drapeau, P. 1992 Partialling out the spatial component of ecological variation. *Ecology* **73**, 1045-1055. (doi:doi:10.2307/1940179).
[4] Leibold, M.A. & Chase, J.M. 2018 *Metacommunity ecology*. Princeton and Oxford, Princeton University Press.