

Details of simulations for figure 2

We simulated evolution of reaction norms in response to a temporally changing environment ε . The environment was binned into 20 discrete categories or environmental units ε_1 to ε_{20} (e.g. temperatures), and the reaction norm was defined by the phenotypic values (character states) expressed at each of the environmental units, for instance z_{10} for environment ε_{10} . Our population-based simulations tracked the mean phenotypes \bar{z}_i expressed in each environment, assuming normal phenotypic distributions within environment, with constant additive genetic variances and covariances, following earlier work [1, 2]. We also assumed for simplicity that the genetic variance is the same in all environments ($G = 1$), and that the additive genetic correlation between trait values expressed in different environments is positive and decreases exponentially with their environmental distance $\Delta\varepsilon$ (that is, $\rho^{|\Delta\varepsilon|}$ with $\rho > 0$). This latter assumption ensures that reaction norms have reasonably smooth shapes, and that character states are more similar between closer environments.

All individuals in the population were assumed to experience the same environment in any generation. In each generation the environment of development was randomly drawn from a mixture of two uniform distributions: one for common environments (ε_1 to ε_{13}) and another for extreme environments (ε_{14} to ε_{20}), with r the odds ratio of frequencies of rare over common environmental units.

Natural selection towards a phenotypic optimum θ was modeled using a Gaussian fitness function with width ω , assumed constant across environments. Selection can only act directly on the expressed trait value, and the fitness of individuals developing in environment ε_i and expressing phenotype z_i in generation t is

$$W_t(z_i) \propto \exp\left(-\frac{(z_i - \theta_{i,t})^2}{2\omega^2}\right).$$

Integrating over the phenotype distribution, the mean fitness is

$$\bar{W}_t(\bar{z}_i) \propto \exp\left(-\frac{S(\bar{z}_i - \theta_{i,t})^2}{2}\right),$$

where $S = 1/(\omega^2 + P)$ (with P the phenotypic variance) is the strength of stabilizing selection. The parameter $\theta_{i,t}$ can be interpreted as the optimum phenotype experienced by individuals developing in environment ε_i at generation t . Note that this optimum may differ from the optimum phenotype occurring in the environment ε_i itself, because the

environment may change between development and selection, or cues may be unreliable [3-6]. To account for partial unpredictability of the environment of selection conditional on the environment of development (or imperfect cue reliability), $\theta_{i,t}$ was drawn from a normal distribution with mean θ_i and variance $\sigma_\theta^2 = \frac{1}{4}$. We considered linear change (with slope $\frac{1}{2}$) of the expected optimum θ_i against the environments of development. Following standard evolutionary quantitative genetics [2, 7], the response by the trait value in each environment ε_j to selection on the trait expressed in environment ε_i in generation t is

$$\Delta\bar{z}_{j,t} = -S(\bar{z}_i - \theta_{i,t}) \rho^{|i-j|} G.$$

Lastly, we accounted for random genetic drift by drawing the vector of mean phenotypes in each environment ε_i in the next generation from a Gaussian distribution with mean $\bar{z}_i + \Delta\bar{z}_i$ and covariance matrix \mathbf{G}/N_e (following [7]), with $N_e = 1000$ the effective population size, and \mathbf{G} the additive genetic (co)variance matrix, with diagonal elements $G_{ii} = G$ and off-diagonal elements $G_{ij} = G\rho^{|i-j|}$.

Simulations were started with the mean phenotype at its conditional optimum for each environment of development, and were run for 20000 generations.

References

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