MacPherson et al. Supplementary Materials

Deriving a general expression for local adaptation - Local adaptation is most effectively defined as the difference between the expected fitness of individuals tested in their local environment and the expected fitness of individuals in all possible environments [1]. To express this mathematically, let $\overline{W}_{\alpha,\beta}$ be the expected fitness of individuals from population $\alpha$ in environment $\beta$. Local adaptation, $\delta$, is then given by the difference:

$$\delta = E_{\alpha}[\overline{W}_{\alpha,\alpha}] - E_{\alpha,\beta}[\overline{W}_{\alpha,\beta}] \quad (S1)$$

where the notation $E_j[\ast]$ expresses the expectation of $[\ast]$ taken over index $j$. Equation (S1) can be written more insightfully if we assume individual fitness depends on the extent to which an individual’s vector of trait values, $z$, matches the optimal values favored by conditions in environment $\alpha$, $\theta_\alpha$. Specifically, we assume the fitness of individual $i$ from population $\alpha$ in environment $\beta$ is given by:

$$W_{\alpha,\beta}(z_i) = e^{-\gamma \sum_{t=1}^{n} (z_{i,t} - \theta_{t,\beta})^2} \quad (S2)$$

Where $\gamma$ measures the strength of stabilizing selection, and the sum is over the $n$ traits influencing fitness. If we assume that stabilizing selection is relatively weak (i.e. $\gamma \approx 0$) then (S2) can be approximated by the first two terms of its taylor expansion with respect to $\gamma$.

$$W_{\alpha,\beta}(z_i) \approx 1 - \gamma \sum_{t=1}^{n} (z_{i,t} - \theta_{t,\beta})^2 + \mathcal{O}(\gamma^2) \quad (S3)$$

Equation (S3) can now be used to calculate the average finesses in equation (S1). The first of these average finesses $\overline{W}_{\alpha,\alpha}$ is given by:

$$\overline{W}_{\alpha,\alpha} = E_i[W_{\alpha,\alpha}(z_i)] \approx 1 - \gamma \sum_{t=1}^{n} (\overline{z}_{t,\alpha} - \theta_{t,\alpha})^2 + \text{Var}_i[z_{i,t}] + \mathcal{O}(\gamma^2) \quad (S4a)$$

and similarly the second expectation $\overline{W}_{\alpha,\beta}$ is given by:
\[
\begin{align*}
W_{\alpha, \beta} &= E_i[W_{\alpha, \beta}(z_i)] \\
&\approx 1 - \gamma \sum_{t=1}^{n} \left( (\tilde{z}_{t, \alpha} - \theta_{t, \beta})^2 + Var_i[z_{i,t}] \right) + O(y^2) \quad \text{(S4b)}
\end{align*}
\]

Where \(\tilde{z}_{t, \alpha}\) is the average value of trait \(t\) in population \(\alpha\). The notation \(Var_j[*]\) is the variance of \([*]\) with respect to index \(j\). Taking the expectation of (S4a) and (S4b) over \(\alpha\) and \(\beta\) gives the two terms in (S1).

Let \(\tilde{z}_t\) be the global average value of trait \(t\) and \(\tilde{\theta}_t\) the global average phenotypic optima of trait \(t\). Then:

\[
E_{\alpha}[\tilde{z}_{\alpha, t}] \approx 1 - \gamma \sum_{t=1}^{n} \left( \tilde{z}_t^2 + Var_{\alpha}[\tilde{z}_{t, \alpha}] + E_{\alpha}[Var_i[z_{i,t}]] - 2Cov_{\alpha}(\tilde{z}_{t, \alpha}, \theta_{t, \alpha}) + \tilde{\theta}_t^2 + Var_{\alpha}[\theta_{t, \alpha}] \right) + O(y^2)
\]

(S5a)

describes the average fitness of populations in their local environments and:

\[
E_{\alpha, \beta}[\tilde{z}_{\alpha, t}] \approx 1 - \gamma \sum_{t=1}^{n} \left( \tilde{z}_t^2 + Var_{\alpha}[\tilde{z}_{t, \alpha}] + E_{\alpha}[Var_i[z_{i,t}]] - \tilde{\theta}_t^2 + Var_{\beta}[\theta_{t, \beta}] \right) + O(y^2)
\]

(S5b)

describes the average fitness of populations across all possible environments. In (S5), \(Cov_j[*]\) is the covariance of \([*]\) over index \(j\). Taking the difference between (S5a) and (S5b) shows that local adaptation is given by:

\[
\delta \approx 2\gamma \sum_{t=1}^{n} \left( Cov_{\alpha}(\tilde{z}_{t, \alpha}, \theta_{t, \alpha}) \right) + O(y^2)
\]

(S6)

which is equation (2) of the main text.

**Trait Evolution**—The first section of this appendix showed that local adaptation at any particular point in time can be approximated using equation (S6). Equation (S6) suggests that local adaptation should increase with the number of traits under selection simply because the total strength of selection accumulates as traits are added. However, this simple logic holds true only if increasing the number of traits, \(n\), does not systematically reduce the values of \(Cov_{\alpha}(\tilde{z}_{t, \alpha}, \theta_{t, \alpha})\) that ultimately evolve within the metapopulation. We next explore how the number of traits under selection, \(n\), influences the evolution of this important covariance by developing expressions for the change in the vector of population mean phenotypes that occurs within each population. As long as selection is weak, the additive genetic
variance/covariance matrix is fixed over time, and phenotypes are multivariate normally distributed, we can predict the change in the vector of population mean phenotypes which occurs in response to selection within population \( \alpha \) using the multivariate breeder’s equation:

\[
\Delta \bar{z}_{t,\alpha} = G \frac{1}{\bar{W}_{t,\alpha}} \frac{\partial W_{t,\alpha}}{\partial z_{t,\alpha}}
\]

where \( G \) is the additive genetic variance/covariance matrix and \( \bar{W}_{t,\alpha} \) is the population mean fitness within population \( \alpha \).

Substituting (S4a) into (S7) yields the following expression for the mean value of trait \( t \) within population \( \alpha \) after a single bout of selection and mating:

\[
z_{t,\alpha}' \approx z_{t,\alpha} - 2\gamma \sum_{k=1}^{n} \left( z_{k,\alpha} - \theta_{k,\alpha} \right) + \epsilon_t + O(\gamma^2)
\]

where \( \epsilon_t \) is a random deviation in the mean phenotype caused by genetic drift and is drawn from a multivariate normal distribution with mean zero and covariance matrix \( \frac{G}{N} \). To incorporate the impact of gene flow we assume individuals move among populations at rate of \( m \) according to an island model.

Assuming \( m \) is of the same small order as \( \gamma \), the phenotypic mean of trait \( t \) within population \( \alpha \), after a single round of gene flow is:

\[
z_{t,\alpha}'' \approx z_{t,\alpha}' + m (z_t - z_{t,\alpha}) + O(\gamma^2)
\]

Although (S9) can, in principle, be used to predict the crucial quantity \( \text{Cov}_\alpha(\bar{z}_{t,\alpha}, \theta_{t,\alpha}) \) upon which local adaptation depends, this rapidly becomes intractable as the number of populations increases. Previous studies have sidestepped this increasing complexity by addressing phenotypic differences between populations [2, 3] rather than local adaptation as it is commonly measured in empirical studies. Because our goal is to predict values of local adaptation a measured using reciprocal
transplant studies we must confront this challenge directly. In the next section, we will develop a moment based approach which allows us to overcome this practical hurdle.

**Evaluating Local Adaptation at equilibrium** - The key to developing analytical predictions for the evolution of local adaptation within large metapopulations is to recognize that population mean trait values can be described more conveniently as a multivariate frequency distribution. With this realization, it becomes clear that evolution can be tracked by following the statistical moments describing this distribution rather than by following the population mean values within each population [4, 5]. Because equation (S6) shows that one of these statistical moments, $\text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a})$, is the key to quantifying local adaptation, we begin by predicting how this particular statistical moment evolves. Using nothing more than the standard definition of a covariance, it is possible to write down an expression for the value of $\text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a})$ in the next generation:

$$\text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a})'' = E_a[(\bar{z}_{t,a}'' - \bar{z}_t'')(\theta_{t,a} - \bar{\theta}_t)]$$  \hspace{1cm} (S10)

The only two quantities that are time dependent in (S10) are $\bar{z}_{t,a}''$ and $\bar{z}_t''$. The expression for the former was derived above in (S9) and the later can be found by taking the expectation of (S9) over $\alpha$. This leads to the following expression for $\bar{z}_t''$.

$$\bar{z}_t'' = \bar{z}_t - 2\gamma \sum_{k=1}^{n} G_{t,k}(\bar{z}_t - \bar{\theta}_t)$$  \hspace{1cm} (S11)

Substituting (S9) and (S11) into (S10) gives the following expression for the change in $\text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a})$ over a single generation:

$$\Delta \text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a}) = -2\gamma \sum_{k=1}^{n} G_{t,k} \left(\text{Cov}_a(\bar{z}_{k,a}, \theta_{t,a}) - \text{Cov}_a(\theta_{k,a}, \theta_{t,a})\right) - m \text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a})$$ \hspace{1cm} (S12a)

Inspection of this expression reveals the remarkable fact that, at least in the case of weak selection and gene flow, the evolution of local adaptation is completely described by $\text{Cov}_a(\bar{z}_{t,a}, \theta_{t,a})$ and
\[ \text{Note that } \text{Cov}_a(z_{k,\alpha}, \theta_{t,\alpha}) \text{ cannot evolve and thus does not depend on time. Hence, to form a complete description of the evolution of local adaptation requires only (S12a) and the following expression for the change in } \text{Cov}_a(z_{k,\alpha}, \theta_{t,\alpha}): \]

\[ \Delta \text{Cov}_a(z_{t,\alpha}, \theta_{j,\alpha}) = -2\gamma \sum_{k=1}^{n} G_{t,k} \left( \text{Cov}_a(z_{k,\alpha}, \theta_{j,\alpha}) - \text{Cov}_a(\theta_{k,\alpha}, \theta_{j,\alpha}) \right) - m \text{Cov}_a(z_{t,\alpha}, \theta_{j,\alpha}) \] (S12b)

Because equations (S12) depend on no other moments they define a closed system and can thus be used for studying the evolution of local adaptation. The fact that \( \epsilon_t \) is absent from (S12) demonstrates that drift does not influence the evolution of local adaptation, as has been shown previously for a similar model [4]. Predicting local adaptation at evolutionary equilibrium requires evaluating (S6) at the point where the system of equations in (S12) are simultaneously zero. Unfortunately, finding and simplifying this equilibrium expression becomes cumbersome for large numbers of traits without further manipulation.

To simplify the equilibrium expression for local adaptation, we define a matrix, \( \Theta \), as the variance-covariance matrix of optimal trait values across the metapopulation. For any number of traits, \( n \), the expression for local adaptation is complicated by products between elements of the environmental variance-covariance matrix, \( \Theta \), and the genetic variance-covariance matrix, \( G \). Many of these terms can, however, be eliminated by defining new uncorrelated traits, given by the principal components of \( G \). Before performing this coordinate rotation, however, it is important that each of the original traits be measured in equivalent units to prevent distortion. Although in some cases traits will already meet this criteria, in general, some form of standardization, such as conversion to units of standard deviations, will be necessary.
Without risk of distortion we can now perform the coordinate rotation into the principal component space of $G$, which is represented by the spanning set $A$ defined by the eigenvalues of $G$:

$$A = \{e_1, e_2, ..., e_n\} \quad (S13)$$

where $e_i$ is the $i^{th}$ eigenvector of $G$. If we let $G'$ be the representation of $G$ in the principal component basis:

$$G' = A^{-1}G A \quad (S14a)$$

And similarly for the matrix $\Theta$:

$$\Theta' = A^{-1} \Theta A \quad (S14b)$$

It is important to note that the matrix $A$ used in equation (S14) is defined by the eigenvectors of the $G$ matrix not those of the $\Theta$ matrix.

The only other variable in our equilibrium solution for local adaptation which involves units of trait value, and hence must be transformed, is the strength of selection, $\gamma$. Here, our assumption that selection is equivalent on every trait is convenient because it assures that the fitness surface is circular. Since the above basis transformation represents a coordinate rotation without scaling or translation, the strength of selection on the principal components will be equivalent to that on the original traits. With this coordinate rotation the equilibrium expression for local adaptation simplifies to:

$$\delta = 4\gamma^2 \sum_{t=1}^{n} \frac{G'_{t,t} \sigma'_{t,t}}{m + 2\gamma G_{t,t}} \quad (S15)$$

which is equation (4) of the main text.
**Individual Based Simulations** — Although our analytical solution (S15) is quite general, it does rely on some important assumptions. The most important of these are weak selection and a fixed additive genetic variance/covariance matrix. In order to relax these assumptions, and evaluate the robustness of our analytical approximation, we developed and analyzed individual based simulations. These individual based simulations assumed a life cycle consisting of selection, gene flow, and mating/reproduction. In the paragraphs below, we describe the details behind each step of this life cycle.

**Stabilizing selection:**

To simulate selection, we begin by calculating the fitness of individuals using equation (S2) rather than the approximation given by equation (S3). An individual’s fitness represents its probability of surviving to produce offspring. Specifically, selective mortality was simulated by drawing a random number between 0 and 1 for each individual; individuals died and were removed from the population if this number was greater than their fitness but survived and remained within the population otherwise.

**Gene Flow:**

Individuals surviving selection were allowed to move between populations. As in the analytical model, simulations assumed movement among any pair of populations was equally likely and occurred at rate $m$. Gene flow was implemented by drawing a random number between 0 and 1 for each individual; if this number was less than $m$, the individual moved to another population whose identity was determined by drawing a random integer between 1 and the number of populations. For large values of $m$, movement among populations could
significantly alter local population sizes, and, in extreme cases, result in stochastic extinction of some populations, particularly when coupled with strong selection. In those rare cases where this occurred, the simulation was aborted and rerun.

Mating and Reproduction:

The system of mating was particularly important in these simulations since it is in this step that the shape of the $G$ matrix was incorporated. To produce the next generation, parental pairs were drawn at random from within each population with replacement. Each parental pair produced a single offspring whose phenotype was drawn from a multivariate normal distribution with a vector of means equal to the average phenotype of the parents, and a variance covariance matrix given by the desired $G$ matrix. This process continued until an offspring population of a size equal to the size of the parental population before selection was produced. The parental population was then eliminated.

Analysis:

Simulations were run for metapopulations containing 200 demes, each of which contained 400 individuals. The trait optima for each environment were drawn randomly at the beginning of the simulation from a multivariate normal distribution specified by a given variance-covariance matrix centered about 0. Simulations were run to equilibrium with equilibrium identified by plotting the average trait value as a function of time and inspecting the final slope of this curve.

To analyze the accuracy of the analytical prediction, the level of local adaptation at equilibrium was measured in two different ways. First we calculated local adaptation using the
exact definition given by equation (S1). Second, we calculated local adaptation using the
analytical approximation given by equation (S15). To calculate local adaptation using the exact
definition (S1), a reciprocal transplant experiment was simulated where the fitness of all
individuals were measured within all possible environments. In order to test our analytical
approximation, we then calculated local adaptation using the approximate expression (S15).
The use of (S15) required us to calculate the realized $\Theta$ matrix and realized $P$ matrix, which was
used as a proxy for $G$. This use of $P$ results in an additional complication of this measurement
of local adaptation because, in contrast to our analytical model, the simulations do not
explicitly assume that that there is equal variance in each trait. Hence trait value
standardization is necessary; this standardization was performed on the $\Theta$ matrix and $P$ matrix
by dividing the $(t, k)^{th}$ component of each matrix by the phenotypic standard deviation of the
t$^{th}$ trait and the phenotypic standard deviation of the $k^{th}$ trait. Let $\tilde{\Theta}$ and $\tilde{G}$ be the
standardized version of the $\Theta$ and $P$ matrices.

\[
\tilde{\Theta} = \begin{bmatrix}
\frac{\Theta_{11}}{G_{11}} & \cdots & \frac{\Theta_{1n}}{G_{nn}} \\
\frac{G_{11}}{\sqrt{G_{nn}G_{11}}} & \ddots & \frac{G_{nn}}{\sqrt{G_{nn}G_{11}}} \\
\vdots & \ddots & \vdots \\
\frac{\Theta_{1j}}{\sqrt{G_{11}G_{nn}}} & \cdots & \frac{\Theta_{nj}}{\sqrt{G_{nn}G_{11}}}
\end{bmatrix}
\] (S16)

\[
\tilde{G} = \begin{bmatrix}
1 & \cdots & \frac{P_{1n}}{\sqrt{G_{nn}G_{11}}} \\
\frac{G_{11}}{\sqrt{G_{nn}G_{11}}} & \ddots & \frac{G_{nn}}{\sqrt{G_{nn}G_{11}}} \\
\vdots & \ddots & \vdots \\
\frac{P_{1j}}{\sqrt{G_{11}G_{nn}}} & \cdots & 1
\end{bmatrix}
\] (S17)
It is then possible to use the same technique described in equations (S12) through (S14) to generate principal component representations of these two matrices. In order to use the analytical prediction described by equation (S15) it is also necessary to standardize the strength of selection. For a single trait one could simply multiply $\gamma$ by the genetic variance. However, when multiple traits are involved this procedure is complicated by the fact that multiple genetic variances exist. Fortunately, at equilibrium the genetic variances across traits are fairly uniform so standardizing by the average genetic (phenotypic) variance seemed reasonable. This however will introduce small levels of error in our analytical prediction especially when dimensionality is large. However, considering the concurrence between many of the simulations and analytical predictions with high trait dimensionalities this does not seem to present much of a problem.

Simulations were run for strengths of selection ranging from 0.001 to 0.05 and three different correlation regimes; high (+0.9,-0.1), moderate (+0.5,-0.05), and low (+0.1,-0.01). We then compared the value of local adaptation calculated using the exact definition (S1) and the analytical approximation (S15) for between one and eight traits for each parameter combination (Figures S1-S6).

**Estimating dimensionality from reciprocal transplant data** — To estimate dimensionality from published datasets, we adapted the method of Hohenlohe & Arnold [6]. In brief, the method requires a matrix of measurements of fitness from reciprocal transplant experiments, where the matrix is formed by pairwise trials of individuals from source populations tested at different sites (In the original analysis [6], the data were measures of mating success from pairwise mating trials of males and females sampled from the same or different populations. Here are
analogously using the same approach on measures of fitness, estimated from testing individuals from different populations against either their home or a different environment). The method then fits points representing the mean phenotype of each source population and the selective optimum of each site in a $d$-dimensional space, such that the distances between phenotypic means and optima best match the observed fitness data across all cells of the matrix, as follows. The first step is to specify a model of fitness as a function of the distance between the local optimum and the mean phenotype of the source population, and here we analyzed two types of fitness data, requiring two different models. Viability data, in the form of $k$ survivors out of $n$ individuals for each population-site pair, were analyzed with a binomial model, exactly as described by Hohenlohe & Arnold [6]. Briefly, for any pairwise source population and site, the probability of survival in the binomial model is given by the height of a multivariate Gaussian fitness surface, measured at the source population phenotypic mean. The selective optimum of the site is at the peak of the Gaussian surface, which also has no covariance and equal variance across site optima (i.e. uniform stabilizing selection and no correlational selection).

For fitness measurements on a continuous scale (either fecundity or a composite fitness measure), we used a modification of the multivariate Gaussian fitness surface model described above and in Hohenlohe & Arnold [6]. Because scaling and rotation of the space are arbitrary, we scale the space by phenotypic (co)variance within each population. The variance of each site’s fitness surface along each axis was assumed to be $\omega = 10$. Choosing higher or lower values of $\omega$ had a negligible effect on fitting the points or on estimates of dimensionality; essentially this parameter re-scaled the space, but not the points’ relative positions or the likelihood of any
particular arrangement. Fitness at each optimum was taken to be the maximum fitness measured in any cell of the matrix. Given the positions of any site optimum and source population mean phenotype in the space, the expected fitness of an individual from that population tested at that site is calculated from the Gaussian fitness surface. Variance around this expectation was set equal to the square of the mean fitness across all site-population comparisons. These parameter assumptions were based on maximizing the fit of the model to simulated datasets where dimensionality is known. Software to conduct this analysis is available online at (http://webpages.uidaho.edu/hohenlohe/software.html).

The method then fits points in the $d$-dimensional space by maximum likelihood, based on the binomial or Gaussian model of fitness described above [6]. The log likelihood for any particular arrangement of points in $d$-dimensional space is calculated by summing log likelihoods of the data given the distance between the two points for each source population/site pair, allowing us to find the maximum likelihood arrangement of points for any value of $d$ by heuristic hill-climbing algorithms (see Hohenlohe & Arnold [6]). The likelihood for each value of $d$ is used to find the best value of $d$ given the data using information criteria. We calculated corrected AIC (AICc), BIC, and HQC [7]. BIC consistently supported lower dimensionality than the other two measures; here we report results from AICc. We also calculated the effective dimensionality $n_D$ when points representing population mean phenotypes and selective optima are fit in a high-dimensional space (here we used the total number of source populations or sites as the maximum value of $d$, beyond which additional axes do not add to the likelihood). The $n_D$ statistic is calculated as the sum of eigenvalues of the covariance matrix of points, divided by the leading eigenvalue [8].
We gathered data from all studies analyzed by Hereford [9] that met the following criteria: at least 3 source populations and sites, a full reciprocal transplant matrix (i.e. all pairwise fitness measures were available), and sample sizes available. In these 35 datasets (Table S2), fitness measures took the form of either viability (n=18), which we analyzed with a binomial model [6], fecundity, or a composite fitness measure (n=17), which we analyzed with the continuous Gaussian fitness model described above. We calculated local adaptation for each dataset as in Equation (1) of the main text. We tested the correlation between local adaptation and dimensionality (either the AICc estimate of \( d \), or \( n_D \); see Figure S7) across all datasets and within each model type (binomial and Gaussian). We repeated the analysis after log-transforming the fecundity fitness measures, and both correlations (local adaptation with \( d \) and \( n_D \)) remained significant (Figures S10, S11). We also corrected for non-independence of datasets from the same published study or the same reciprocal transplant experiment by using these as random effects factors in a linear mixed model, using the R package lme(). For each, a likelihood ratio test was used to compare models with and without dimensionality as a factor.

The dimensionality method does not take into account which population came from which site; that is, it does not treat “home” or “away” differently in any way. To verify that the dimensionality estimate is not biased by local adaptation, we randomly permuted all 17 continuous-fitness data matrices. This produces a set of matrices for which local adaptation has mean zero. We applied the dimensionality analysis to these datasets and found no correlation between local adaptation and dimensionality. We also found no correlation between local adaptation and dimensionality across many permutations of single empirical matrices as well as randomly generated datasets.
Finally, we tested the dimensionality estimation method against data produced from the simulation approach described above. We simulated datasets in a full factorial design across the following parameter values: $m = 0.01, 0.001; \gamma = 0.001, 0.1; \text{number of traits from 2 to 8}$; and alignment or misalignment between $G$ and Theta as shown in Figure 1, plus the case of no covariance in both matrices. Each simulation included 6 populations tested in six sites in a complete reciprocal transplant experiment, with fitness measured for 100 randomly sampled individuals in each pair. We estimated dimensionality as described above under the continuous fitness model. Effective dimensionality ($n_0$) was significantly correlated with local adaptation across all parameter values ($r^2 = 0.0355; p = 0.0257$). It did not appear to be affected by alignment (mean $nD = 1.981$) versus misalignment (mean $nD = 1.979$) or by other factors.
Table S1: Summary of notation

<table>
<thead>
<tr>
<th>Expression</th>
<th>Equivalent Expression</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>δ</td>
<td>Local adaptation</td>
<td></td>
</tr>
<tr>
<td>α, β</td>
<td>Population/environment indices</td>
<td></td>
</tr>
<tr>
<td>t, k</td>
<td>Trait indices</td>
<td></td>
</tr>
<tr>
<td>i</td>
<td>Individual index</td>
<td></td>
</tr>
<tr>
<td>E_j[*]</td>
<td></td>
<td>Expectation of [+] over index j</td>
</tr>
<tr>
<td>E_i,E_j[*]</td>
<td></td>
<td>Expectation of [+] over index j then index i</td>
</tr>
<tr>
<td>Var_j[*]</td>
<td></td>
<td>Variance in [+] over index j</td>
</tr>
<tr>
<td>Cov_j[*]</td>
<td></td>
<td>Covariance in [+] over index j</td>
</tr>
<tr>
<td>z_{i,t}</td>
<td></td>
<td>The value of individual i's trait t</td>
</tr>
<tr>
<td>z_{t,α}</td>
<td>E_i[z_{i,t}]</td>
<td>Average value of trait t in population α</td>
</tr>
<tr>
<td>z_t</td>
<td>E_α[z_{t,α}]</td>
<td>Global average value of trait t</td>
</tr>
<tr>
<td>θ_{t,α}</td>
<td></td>
<td>Phenotypic optima of trait t in environment α</td>
</tr>
<tr>
<td>θ_t</td>
<td>E_α[θ_{t,α}]</td>
<td>Global average phenotypic optima for trait t</td>
</tr>
<tr>
<td>W_{α,β}(z_i)</td>
<td></td>
<td>Absolute fitness of individual i from population α in environment β</td>
</tr>
<tr>
<td>W_{α,β}</td>
<td>E_i[W_{α,β}(z_i)]</td>
<td>Average fitness of population α in environment β</td>
</tr>
<tr>
<td>G</td>
<td></td>
<td>Genetic Variance/Covariance matrix</td>
</tr>
<tr>
<td>Θ</td>
<td></td>
<td>Variance/Covariance matrix of phenotypic optima across the metapopulation</td>
</tr>
<tr>
<td>G'</td>
<td></td>
<td>Diagonalized (principal component) G</td>
</tr>
<tr>
<td>Θ'</td>
<td></td>
<td>Θ rotated into the principal component space of G</td>
</tr>
</tbody>
</table>
Table S2: Published reciprocal transplant datasets used in estimates of dimensionality.

<table>
<thead>
<tr>
<th>Taxon</th>
<th># populations</th>
<th>Fitness measure</th>
<th>Year</th>
<th>Local adaptation</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Phlox drummondii</em></td>
<td>8</td>
<td>Viability</td>
<td>1980</td>
<td>0.1583</td>
<td>Schmidt &amp; Levin 1985</td>
</tr>
<tr>
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<td>Fecundity</td>
<td>1980</td>
<td>0.1697</td>
<td>Schmidt &amp; Levin 1985</td>
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<tr>
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<td>Composite</td>
<td>1980</td>
<td>0.3415</td>
<td>Schmidt &amp; Levin 1985</td>
</tr>
<tr>
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<td>Viability</td>
<td>1979</td>
<td>0.1231</td>
<td>Schmidt &amp; Levin 1985</td>
</tr>
<tr>
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<td>Fecundity</td>
<td>1979</td>
<td>0.3269</td>
<td>Schmidt &amp; Levin 1985</td>
</tr>
<tr>
<td><em>Phlox drummondii</em></td>
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<td>Composite</td>
<td>1979</td>
<td>0.4458</td>
<td>Schmidt &amp; Levin 1985</td>
</tr>
<tr>
<td><em>Anodontonta piscinalis</em></td>
<td>6</td>
<td>Viability</td>
<td>1990</td>
<td>0.0906</td>
<td>Jokela &amp; Mutikainen 1995</td>
</tr>
<tr>
<td><em>Anodontonta piscinalis</em></td>
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**Figure Legends:**

**Figure S1:** The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about \( \gamma = 0.001 \). Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: \((\rho_G = 0.9, \rho_\Theta = 0.9)\), Row B: \((\rho_G = -0.1, \rho_\Theta = -0.1)\), Row C: \((\rho_G = 0.9, \rho_\Theta = -0.1)\), and Row D: \((\rho_G = -0.1, \rho_\Theta = 0.9)\).

**Figure S2:** The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about \( \gamma = 0.001 \). Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: \((\rho_G = 0.5, \rho_\Theta = 0.5)\), Row B: \((\rho_G = -0.05, \rho_\Theta = -0.05)\), Row C: \((\rho_G = 0.5, \rho_\Theta = -0.05)\), and Row D: \((\rho_G = -0.05, \rho_\Theta = 0.5)\).

**Figure S3:** The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about \( \gamma = 0.001 \). Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: \((\rho_G = 0.1, \rho_\Theta = 0.1)\), Row B: \((\rho_G = -0.01, \rho_\Theta = -0.01)\), Row C: \((\rho_G = 0.1, \rho_\Theta = -0.01)\), and Row D: \((\rho_G = -0.01, \rho_\Theta = 0.1)\).
Figure S4: The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about $\gamma = 0.005$. Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: $(\rho_G = 0.9, \rho_\theta = 0.9)$, Row B: $(\rho_G = -0.1, \rho_\theta = -0.1)$, Row C: $(\rho_G = 0.9, \rho_\theta = -0.1)$, and Row D: $(\rho_G = -0.1, \rho_\theta = 0.9)$.

Figure S5: The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about $\gamma = 0.005$. Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: $(\rho_G = 0.5, \rho_\theta = 0.5)$, Row B: $(\rho_G = -0.05, \rho_\theta = -0.05)$, Row C: $(\rho_G = 0.5, \rho_\theta = -0.05)$, and Row D: $(\rho_G = -0.05, \rho_\theta = 0.5)$.

Figure S6: The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about $\gamma = 0.005$. Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: $(\rho_G = 0.1, \rho_\theta = 0.1)$, Row B: $(\rho_G = -0.01, \rho_\theta = -0.01)$, Row C: $(\rho_G = 0.1, \rho_\theta = -0.01)$, and Row D: $(\rho_G = -0.01, \rho_\theta = 0.1)$. 
**Figure S7:** The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about $\gamma = 0.05$. Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: $(\rho_G = 0.9, \rho_\theta = 0.9)$, Row B: $(\rho_G = -0.1, \rho_\theta = -0.1)$, Row C: $(\rho_G = 0.9, \rho_\theta = -0.1)$, and Row D: $(\rho_G = -0.1, \rho_\theta = 0.9)$.

**Figure S8:** The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about $\gamma = 0.05$. Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: $(\rho_G = 0.5, \rho_\theta = 0.5)$, Row B: $(\rho_G = -0.05, \rho_\theta = -0.05)$, Row C: $(\rho_G = 0.5, \rho_\theta = -0.05)$, and Row D: $(\rho_G = -0.05, \rho_\theta = 0.5)$.

**Figure S9:** The effect of dimensionality on the extent of local adaptation produced in individual based simulations (blue) compared to the predicted analytical values (red). Simulations were run with a 200 deme metapopulation, each deme with 400 individuals, and were run to evolutionary equilibrium. The strength of selection varied stochastically about $\gamma = 0.05$. Traits and optimal values were drawn from multivariate normal distribution with unit variances and the following correlations: Row A: $(\rho_G = 0.1, \rho_\theta = 0.1)$, Row B: $(\rho_G = -0.01, \rho_\theta = -0.01)$, Row C: $(\rho_G = 0.1, \rho_\theta = -0.01)$, and Row D: $(\rho_G = -0.01, \rho_\theta = 0.1)$. 
Figure S10. Correlation ($r = 0.3995; p = 0.0174$) between dimensionality, as estimated by effective
dimensionality $nD$, and local adaptation across 35 published datasets using fitness estimated as viability
(black), fecundity (red), or a composite fitness measure (blue). Symbols indicate different published
studies.

Figure S11. Correlation ($r = 0.3716; p = 0.0280$) between dimensionality, as estimated by corrected AIC,
and local adaptation across 35 published datasets using fitness estimated as viability (black), log-
transformed fecundity (red), or a composite fitness measure (blue). Symbols indicate different published
studies.

Figure S12. Correlation ($r = 0.4072; p = 0.0152$) between dimensionality, as estimated by effective
dimensionality $nD$, and local adaptation across 35 published datasets using fitness estimated as viability
(black), log-transformed fecundity (red), or a composite fitness measure (blue). Symbols indicate
different published studies.
Supplemental References:


