

Supplementary materials for “**Fly wing evolution explained by a neutral model with mutational pleiotropy**”

The supplementary materials include:

Legends of supplementary figures

Figures S1-S2

Tables S1-S2

Legends of supplementary figures

Figure S1. Performances of Houle *et al.*'s method and the new method across a range of similarity between M and R , with M and R matrices subject to estimation error. **(a)** Linear regression slope of $\log_{10}(R_{\text{obs}} \text{ variance})$ on $\log_{10}(M_{\text{obs}} \text{ variance})$ estimated by Houle *et al.*'s method (red) and the new method (blue) plotted against that of $\log_{10}(R_w \text{ variance})$ on $\log_{10}(M_{\text{original}} \text{ variance})$ along eigenvectors of M_{original} . **(b)** Pearson's correlation coefficient between $\log_{10}(M_{\text{obs}} \text{ variance})$ and $\log_{10}(R_{\text{obs}} \text{ variance})$ estimated by Houle *et al.*'s method (red) and the new method (blue) plotted against that between $\log_{10}(M_{\text{original}} \text{ variance})$ and $\log_{10}(R_w \text{ variance})$ along eigenvectors of M_{original} . Each data point represents the mean of 100 simulations with the same weight parameter w (see Materials and Methods), and the error bars represent standard deviations.

Figure S2. Performances of Houle *et al.*'s method and the new method when the empirical M matrix is set to be M_{original} and the Drosophilid tree is used to simulate trait evolution (see Materials and Methods). **(a)** Linear regression slope of $\log_{10}(R_{\text{obs}} \text{ variance})$ on $\log_{10}(M_{\text{obs}} \text{ variance})$ estimated by Houle *et al.*'s method (red) and the new method (blue) plotted against that of $\log_{10}(R_w \text{ variance})$ on $\log_{10}(M_{\text{original}} \text{ variance})$ along eigenvectors of M_{original} . **(b)** Pearson's correlation coefficient between $\log_{10}(M_{\text{obs}} \text{ variance})$ and $\log_{10}(R_{\text{obs}} \text{ variance})$ estimated by Houle *et al.*'s method (red) and the new method (blue) plotted against that between $\log_{10}(M_{\text{original}} \text{ variance})$ and $\log_{10}(R_w \text{ variance})$ along eigenvectors of M_{original} . Each data point represents the mean of 50 simulations with the same weight parameter w (see Materials and Methods), and the error bars represent standard deviations.

Figure S1

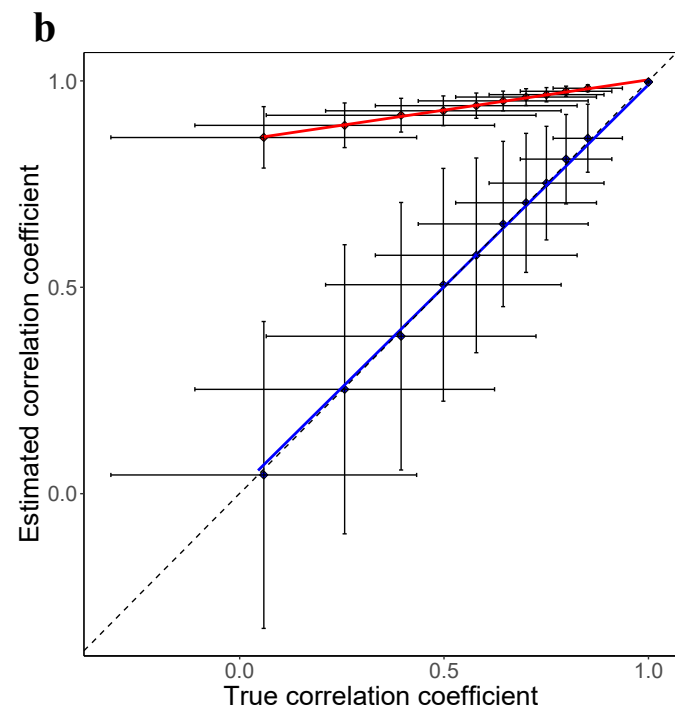
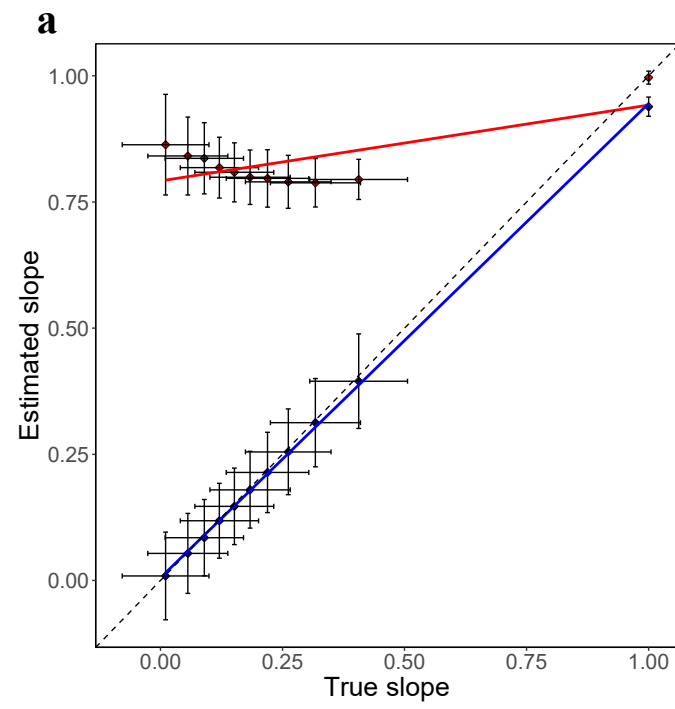
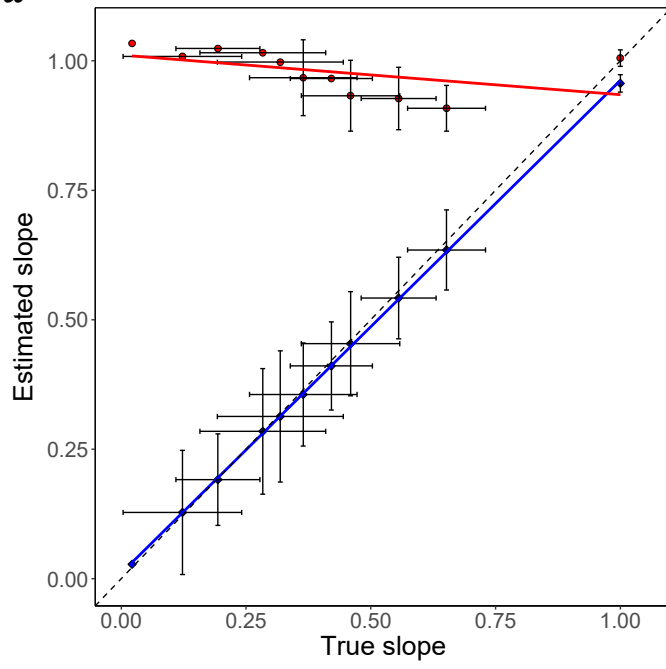


Figure S2

a



b

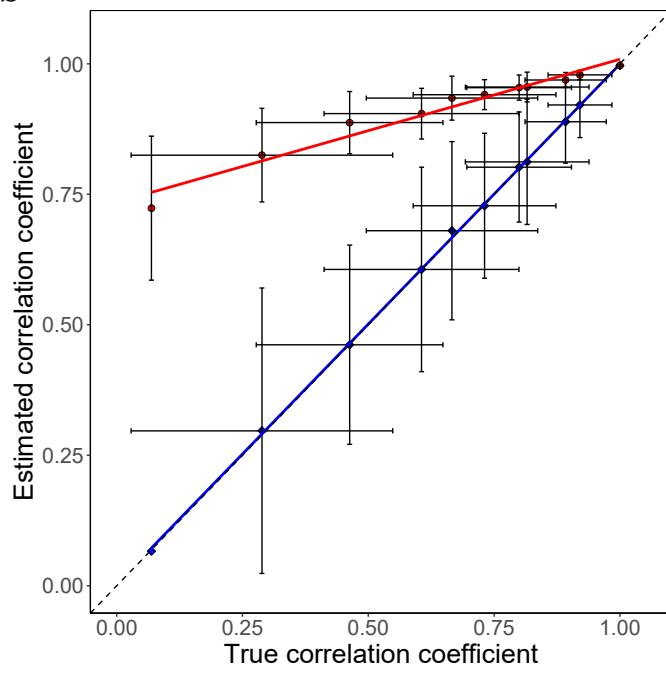


Table S1. Models examined by Houle *et al.* and their predictions regarding evolutionary rate, scaling exponent of evolutionary rate with mutational variance, and phylogenetic signal. Model predictions that are consistent with the corrected observations are marked by asterisks.

Model	Predictions		
	Evolutionary rate	Scaling exponent	Phylogenetic signal
Neutral evolution	High	1	High*
Fluctuating directional selection	High	2	High*
Divergent selection	High	2	Intermediate
Moving optimum			
BM slow	Low*	~0	High*
BM fast	High	~0	High*
White noise	Low*	0	0
OU slow	Low*	~0	Intermediate
OU intermediate	Low*	0-1*	Low
OU fast	Low*	~0	~0
Observations (Houle <i>et al.</i>)	Low	~1	High
Observations (corrected)	Low	0.54	High

Table S2. Patterns of phenotypic evolution observed from computer simulation of non-neutral, orthogonal, focal traits with mutational pleiotropy.

Determinant of M variance	α	Scaling exponent	Median relative divergence*	Median phylogenetic signal
Mutation rate	10^{-4}	0.53	4.37×10^{-5}	0.979
Mutation rate	10^{-3}	0.59	3.97×10^{-5}	0.98
Mutation rate	10^{-2}	0.51	3.77×10^{-5}	0.978
Mutation effect size	10^{-4}	0.51	4.82×10^{-6}	0.968
Mutation effect size	10^{-3}	0.52	4.74×10^{-6}	0.968
Mutation effect size	10^{-2}	0.42	4.74×10^{-6}	0.971

* Ratio of observed divergence (i.e., phenotypic variance across replicate lineages) and expected divergence (i.e., product of mutational variance and time).