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Appendix from I. M. Smallegange et al., "Correlative Changes in Life-History Variables in Response to Environmental Change in a Model Organism"

(Am. Nat., vol. 183, no. 6, p. 784)

Data Collection, Character-Demography Functions, and Additional Analyses

In the first section we describe the methods for the additional data collection on the life history of the bulb mite, *Rhizoglyphus robini*. In the second section we give the parameter values of all character-demography functions that comprise the good- and bad-environment integral projection models (IPMs). What follows next are eight figures: figure A1 displays the fitted Gompertz function, figure A2 displays the survivorship function of mites of all juvenile life stages in the bad environment, figure A3 displays the stationary stage distribution, figures A4 and A5 display additional results on the deterministic elasticity analysis, and figure A6 displays additional results on the stochastic elasticity analysis. Figures A7 and A8 display the same correlations as in figures 3 and 4 of the main text but with adult survival rate in the bad environment set equal to that of juveniles in the bad environment ($y = 0.96657$).

Additional Data Collection

Data on juvenile growth and survival were additionally collected. To this end, 9 females from the yeast stock cultures and 1 female from the filter paper stock cultures were isolated into individual tubes. Stock cultures are kept at Imperial College London and are maintained as detailed in Smallegange (2011*a*). After isolating the females, they were photographed using a Lumenera Infinity 3.1 camera connected to a Meiji EMZ-8TRD (× 10–45) stereomicroscope to measure body length (without mouthparts) to the nearest 0.1 μm using Infinity Analyze Imaging Software (Lumenera, Ottawa, Ontario). Over a period of 5 days, 1–10 eggs were collected from each female each day and put into individual tubes. A total of 53 eggs were collected from females on the yeast diet and put into individual tubes with ad lib. access to yeast. A total of 49 eggs were collected from females on the filter paper diet and put into individual tubes with ad lib. access to filter paper. Tubes were kept in an unlit incubator at 24°C and >70% relative humidity. Each day, until maturation, each individual was photographed and its size measured. On the yeast diet, 17 individuals died before reaching maturity. Because the sex and morph of mites can only be assessed after maturation, of the 17 individuals that died we randomly assigned 8 mites as females and 9 as males to calculate juvenile survival rates (see below) (the sex-ratio for mites at birth and at maturation is 1 : 1; Gerson et al. 1983). On a yeast diet, 72% of males emerge as a fighter and 28% as a scrambler (Smallegange 2011*b*). Of the 9 mites that were categorized as male we randomly assigned 6 as fighters and 3 as scramblers. Randomly assigning sex and male morph to these juveniles assumes that the survival rates do not differ between the sexes and male morphs. Indeed, daily survival rates of males of different morph and females are very similar (Smallegange and Coulson 2011; J. A. Deere and I. M. Smallegange, unpublished data). On the filter paper diet, 36 individuals died before reaching maturity. As before, we randomly assigned 18 mites as females and 18 as males to calculate juvenile survival rates. On a filter paper diet, 90% of males emerge as a scrambler and 10% as a fighter (Smallegange 2011*b*). Therefore we randomly assigned 2 males as fighters and 16 as scramblers. To calculate juvenile growth and stage transition rates (see "Parameterizing the Character-Demography Functions" in the main text) we only used observations of females that had matured successfully.

Parameter Values of Character-Demography Functions

Survival and transition rates were generalized linear mixed models (GLMMs) with a binomial error structure; fertility rate and the growth kernel were GLMMs with a Gaussian error structure; and the inheritance kernel was fitted using GLMs with a Gaussian error structure. The functions are listed below for the life stages eggs (E), larvae (L), protonymphs (P), tritonymphs (T), and adults (A). In the functions below, B denotes body length (μm) and sample size n is given in between brackets for each fitted function. When an individual moves to the next life stage, its mean growth rate and variance in growth rate is determined by the functions of the next life stage and not the previous life stage. See main text for details on how these parameters are used to construct the IPMs and the matrix approximations of it. Note that mite identity was included in the statistical analyses (except in the inheritance function) but was not modeled within the IPMs.

Survival Rates for the Good Environment (*Fraction per Day*)

E: $y = 0.999$ ($n = 110$); L: $y = 0.948$ ($n = 58$); P: $y = 0.999$ ($n = 38$); T: $y = 0.999$ ($n = 152$); A: $y = 1/[1 + 1/(e^{26.05-0.542B+0.0000318B^2})]$ ($n = 1{,}103$).

Survival Rates for the Bad Environment (*Fraction per Day*)

E: 0.96657 ($n = 642$); L: 0.96657 ($n = 642$); P: 0.96657 ($n = 642$); T: 0.96657 ($n = 642$); A: $y = 1/[1 + 1/(e^{-58.03+0.2982B-0.0003532B^2})]$ ($n = 437$).

Life Stage Transition Rates for the Good Environment (*Fraction per Day*)

E→L: $y = 1/[1 + 1/(e^{-0.9089 + 0.00415B})]$ ($n = 80$); L→P: $y = 1/[1 + 1/(e^{-3.10686 + 0.0170B})]$ ($n = 48$); P→T: $y = 1/[1 + 1/(e^{-4.100 + 0.0126B})]$ ($n = 37$); T→A: $y = 1/[1 + 1/(e^{-8.006 + 0.015B})]$ ($n = 150$).

Life Stage Transition Rates for the Bad Environment (*Fraction per Day*)

E→L: $y = 1/[1 + 1/(e^{2.635-0.018B})]$($n = 42$); L→P: $y = 1/[1 + 1/(e^{-2.679 + 0.009B})]$ ($n = 59$); P→T: $y = 1/[1 + 1/(e^{-9.654 + 0.030B})]$ ($n = 37$); T→A: $y = 1/[1 + 1/(e^{-5.146 + 0.011B})]$ ($n = 163$).

Reproduction Rate for the Good Environment (*Number per Day*)

$$y = 0.5(-213.3 + 0.510B - 0.000274B^2) \ (n = 701).$$

Reproduction Rate for the Bad Environment (*Number per Day*)

$$y = 0.5 \times 2.159 \ (n = 82).$$

Mean Growth Rates for the Good Environment (*When Staying in the Same Life Stage;* μm)

E: $y = L$ ($n = 59$); L: $y = 97.721 + 0.817B$ ($n = 24$); P: $y = 197.340 + 0.684B$ ($n = 29$); T: $y = 90.035 + 1.062B$ ($n = 118$); A: $y = 589.570 + 0.342B$ ($n = 422$).

Variance in Growth Rates for the Good Environment (*When Staying in the Same Life Stage;* μm^2)

E: $y = 10$ ($n = 59$); L: $y = -3{,}025.416 + 14.951B$ ($n = 24$); P: $y = -3{,}659.040 + 15.480B$ ($n = 29$); T: $y = 9{,}506.022 - 10.915B$ ($n = 118$); A: $y = 1{,}427.351 - 0.683B$ ($n = 422$).

Mean Growth Rates for the Bad Environment (*When Staying in the Same Life Stage;* μm)

E: $y = B$ ($n = 53$); L: $y = 93.116 + 0.638B$ ($n = 17$); P: $y = 93.257 + 0.733B$ ($n = 11$); T: $y = 61.124 + 0.817B$ ($n = 101$); A: $y = -248.1 + 2.475B - 0.00203B^2$ ($n = 97$).

Variance in Growth Rates for the Bad Environment (*When Staying in the Same Life Stage;* μm^2)

E: $y = 10$ ($n = 53$); L: $y = -192.031 + 2.918B$ ($n = 17$); P: $y = 1{,}300.248 - 3.067B$($n = 11$); T: $y = 1{,}731.488 - 2.809B$($n = 101$); A: $y = -1{,}970.0 + 10.57B - 0.01241B^2$($n = 97$).

Inheritance Function (*Mean Offspring-Mother Difference*) *for the Good Environment* (μm)

$$y = 166.279 \ (n = 208).$$

Variance around Inheritance Function for the Good Environment (μm^2)

$$y = 196.430 \ (n = 208).$$

Inheritance Function (*Mean Offspring-Mother Difference*) *for the Bad Environment* (μm)

$$y = 167.083 \ (n = 110).$$

Variance around Inheritance Function for the Bad Environment (μm^2)

$$y = 158.290 \ (n = 110).$$

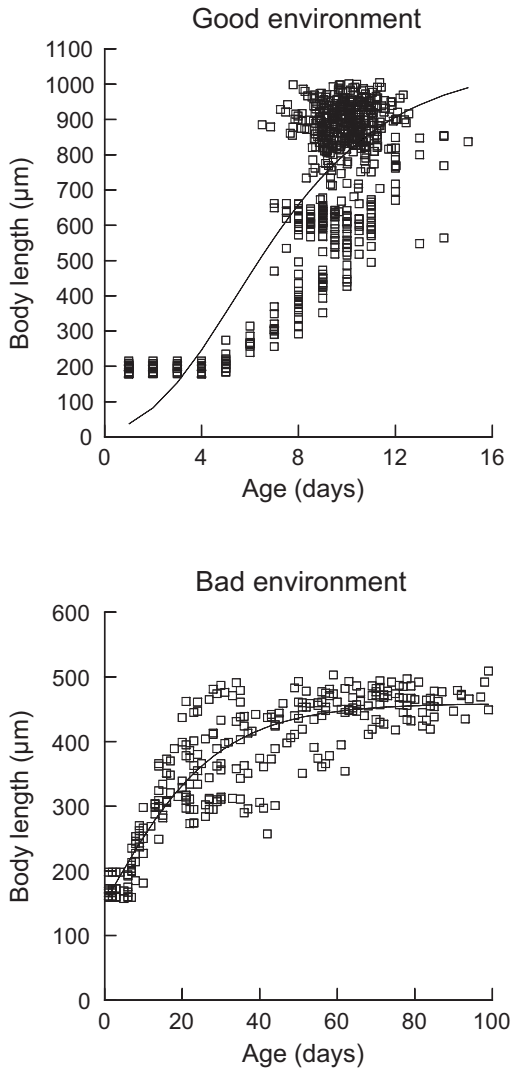

Figure A1: Gompertz function (black lines) fitted against data on the growth of females raised in the good environment (*top*) and bad environment (*bottom*).

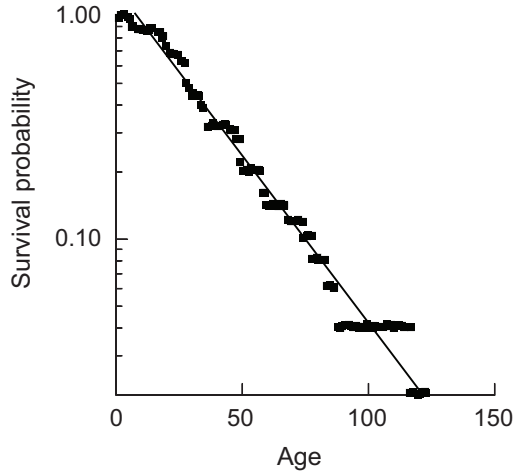

Figure A2: Survivorship function of female mites in the bad environment (filter paper diet). Note the log scale on the *Y*-axis. A slight jitter was added to display overlapping data points.

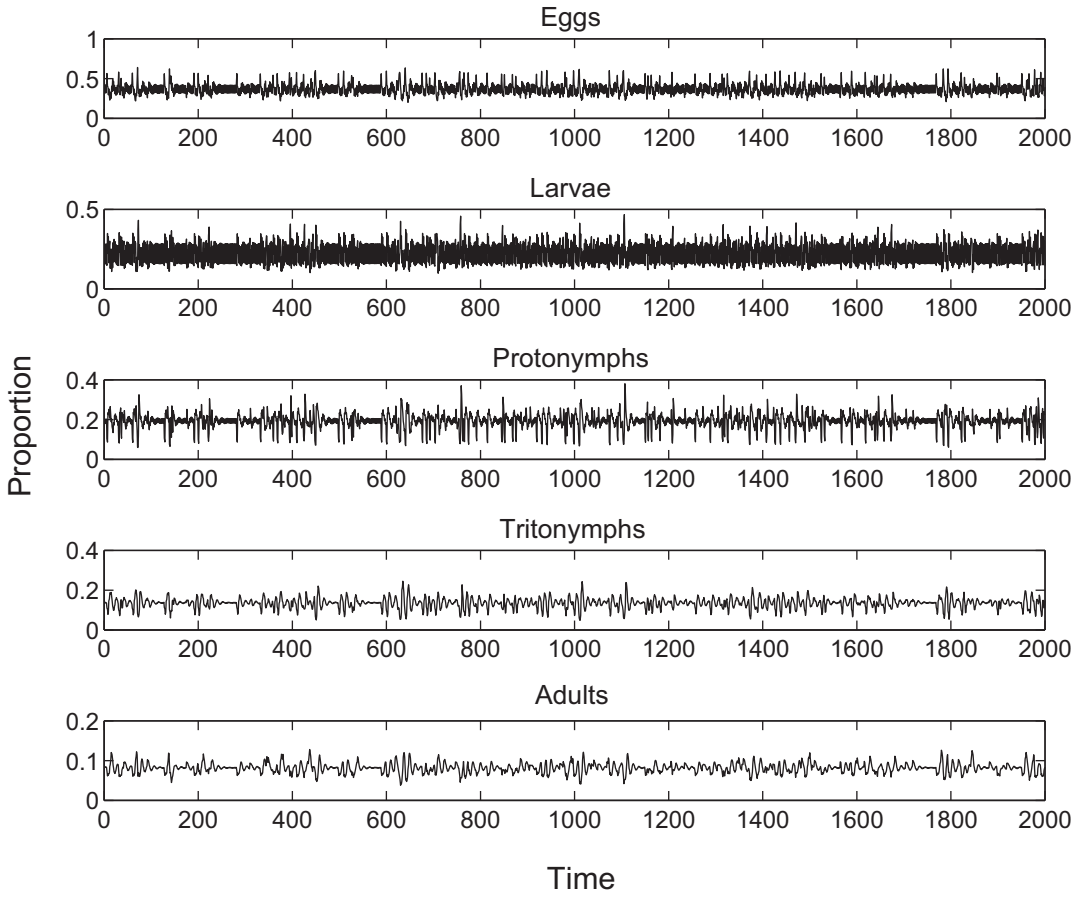

Figure A3: Time series plots of a Markov Chain of length 2,000 showing the stationary time series of the stage distribution for $p = q = 0.9$.

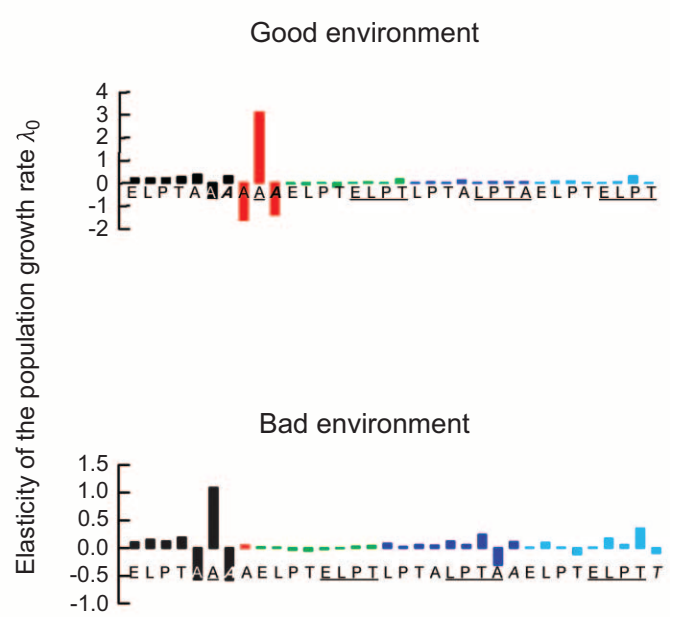

Figure A4: The elasticity of the population growth rate λ_0 to perturbation of intercepts (normal letters), linear coefficients (underscored letters) and quadratic coefficients (bold italic letters) of the character survival (black bars), fertility (red bars), transition rates (green bars), mean growth rate when staying in the same life stage (blue bars), and mean growth rate when growing into the next life stage (indigo bars) functions. Perturbations of the functions describing variation around the body length growth rate when staying in the same life stage and when growing into the next life stage, the inheritance function, and the function describing variation around the inheritance function were very small and are given in figure A5. The elasticity of λ_0 is calculated by multiplying each function parameter by 1.001 using the character-demography functions estimated for mites in the good environment (yeast diet; *top*) and bad environment (filter paper diet; *bottom*). In the case of negative parameter values, perturbations resulted in a further decrease of values, which is why some elasticities are negative. Letters under the bars denote the different life stages: eggs (E), larvae (L), protonymphs (P), tritonymphs (T), and adults (A).

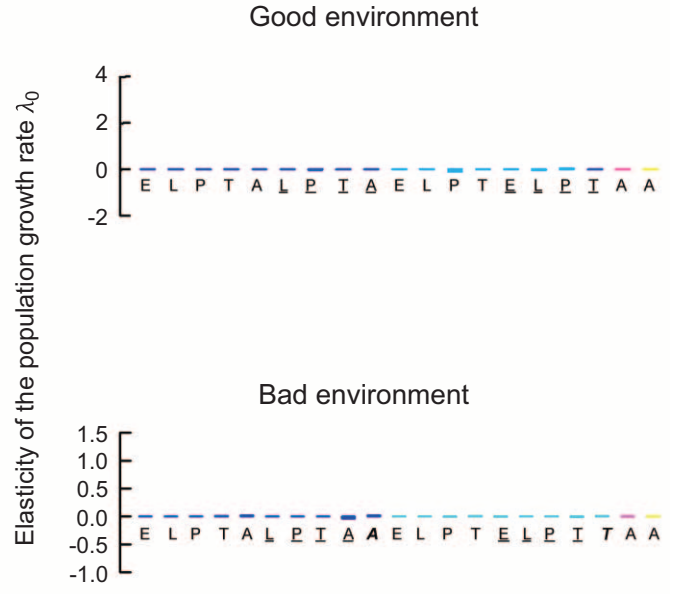

Figure A5: The elasticity of the population growth rate λ_0 to perturbation of intercepts (normal letters), linear coefficients (underscored letters) and quadratic coefficients (bold italic letters) of the functions describing variation around the body length growth rate when staying

in the same life stage (blue bars) and when growing into the next life stage (indigo bars), the inheritance function (pink bars), and the function describing variation around the inheritance function (yellow bars). Elasticities are calculated using the character-demography functions estimated for mites in the good environment (yeast diet; *top*) and bad environment (filter paper diet; *bottom*). In the case of negative parameter values, perturbations resulted in a further decrease of values, which is why some elasticities are negative. Letters under the bars denote the different life stages: eggs (E), larvae (L), protonymphs (P), tritonymphs (T), and adults (A). Note that the scale on the *Y*-axes is the same as in figure A4.

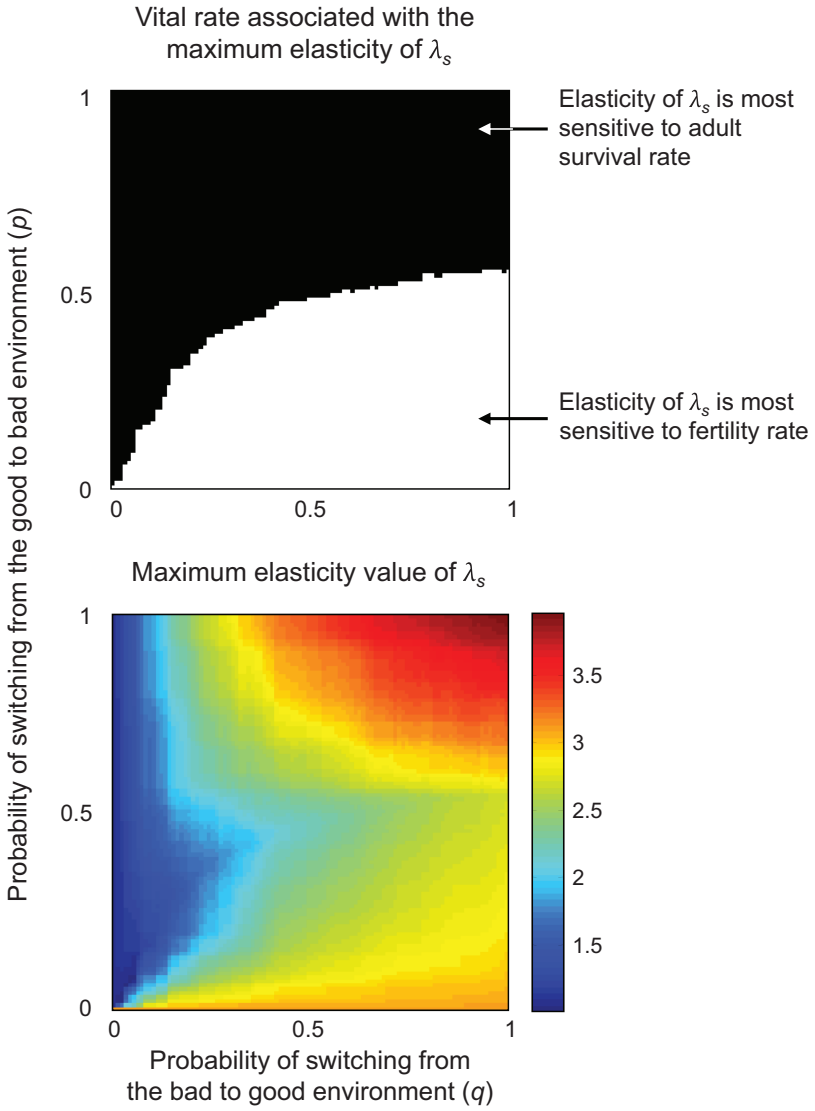

Figure A6: Stochastic elasticity analysis of λ_s. *Top*, panel shows which vital rate λ_s is most sensitive to depending on the probability of switching from the good to bad environment p and the probability of switching from the bad to good environment q. Rate λ_s is either most elastic to adult survival rate (black region; linear coefficient of adult survival rate of both IPMs) or fertility rate (white region; linear coefficient of fertility rate of the good-environment IPM and intercept of fertility rate of the bad-environment IPM). *Bottom*, panel shows for each value of p and q the elasticity values associated with the vital rate that λ_s is most elastic to.

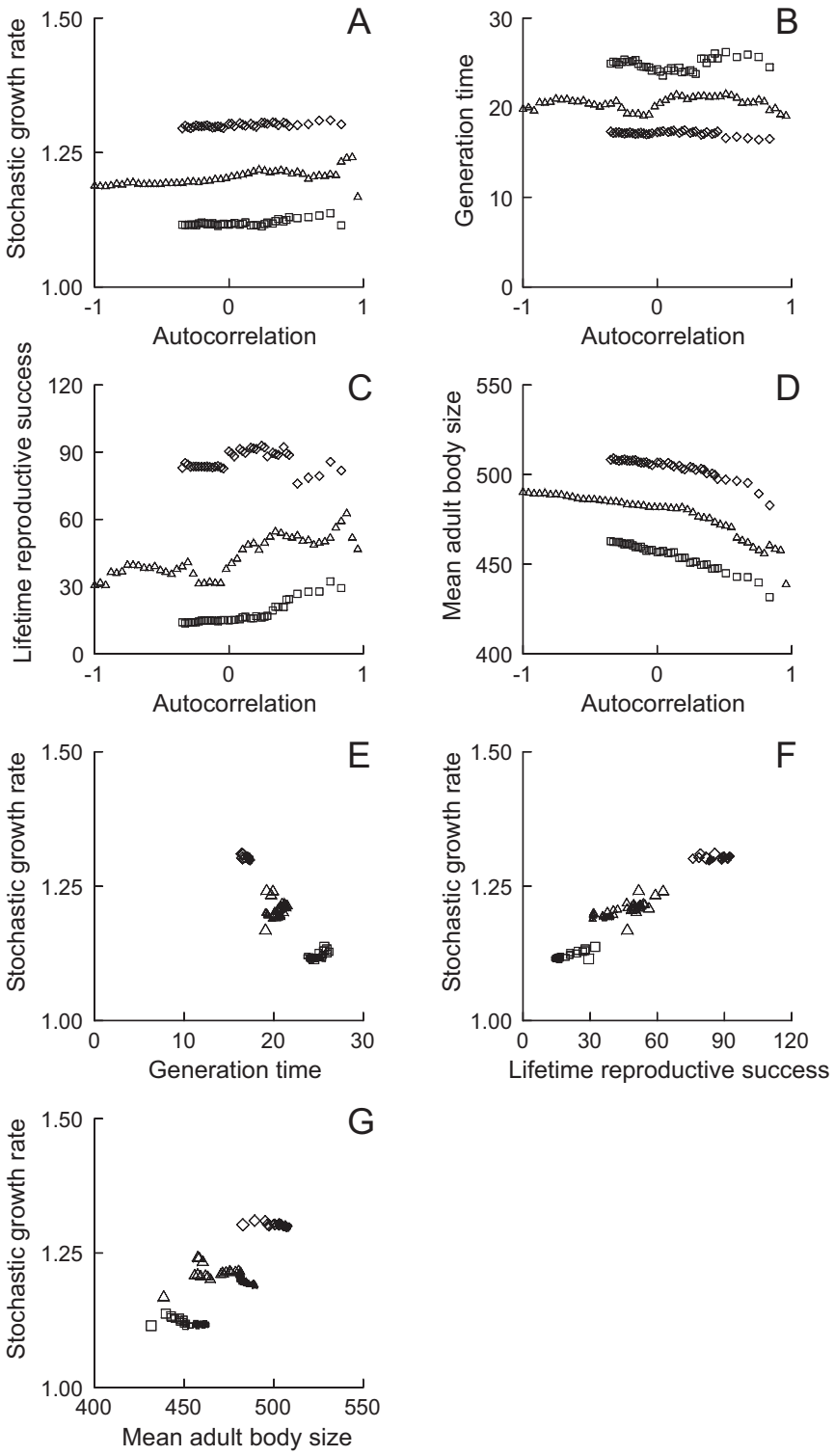

Figure A7: The same figure as figure 3 in the main text but with adult survival rate in the bad environment set equal to the juvenile survival rates ($y = 0.96657$). Shown are the stochastic growth rate λ_s (*A*), generation time (days; *B*), lifetime reproductive success (number of eggs produced; *C*), and mean adult body size (μm; *D*) as a function of the autocorrelation ρ of environmental regimes and the stochastic growth rate in relation to generation time (*E*), lifetime reproductive success (*F*), and mean adult body size (*G*). Symbols indicate three values of *f*, the good-environment frequency: 0.25 (squares), 0.50 (triangles), and 0.75 (diamonds). In *E–G*, the size of the symbols increases with increasing autocorrelation (ρ) in the environmental regimes: small symbols denote blue noise (negative ρ), intermediately sized symbols denote white noise ($\rho = 0$), and large symbols denote red noise (positive ρ).

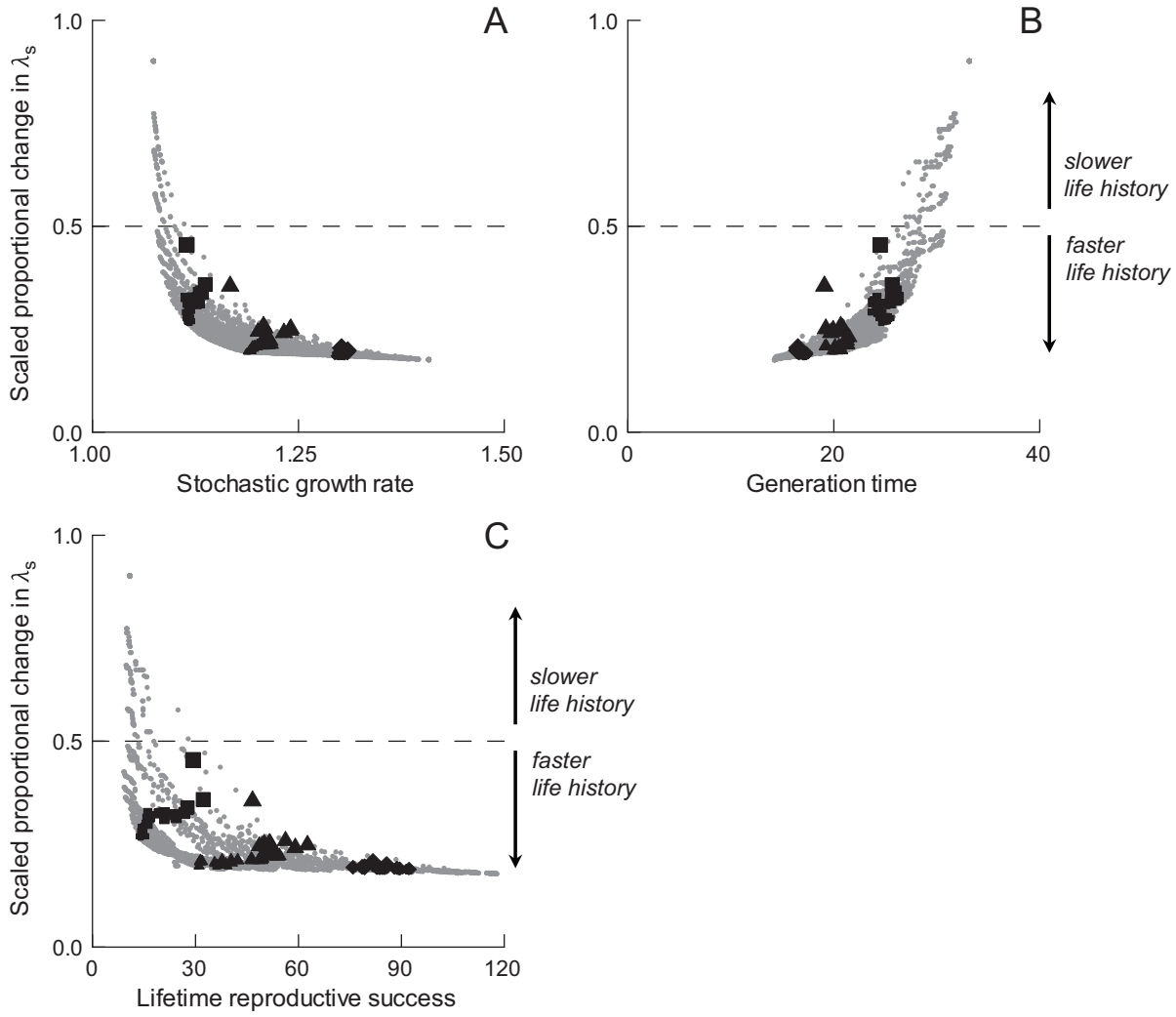

Figure A8: The same figure as figure 4 in the main text but with adult survival rate in the bad environment set equal to the juvenile survival rates ($y = 0.96657$). Shown are the scaled elasticity λ_s to perturbation of adult survival rate as a function of stochastic growth rate (*A*), generation time (*B*), and lifetime reproductive success (*C*). The black symbols represent three values of *f*, the good-environment frequency: 0.25 (squares), 0.50 (triangles), and 0.75 (diamonds). The size of these symbols increases with increasing autocorrelation (ρ) in the environmental regimes: small symbols denote blue noise, intermediately sized symbols denote white noise, and large symbols denote red noise. The horizontal dashed lines denote where the scaled elasticity of λ_s equals 0.5: values above this line correspond to a slow life history, and values below this line correspond to a fast life history.

Literature Cited Only in the Appendix

Caswell, H. 2001. Matrix population models: construction, analysis, and interpretation. Sinauer, Sunderland, MA.

Gerson, U., S. Capua, and D. Thorens. 1983. Life history and life tables of *Rhizoglyphus robini* Claparède (Acari: Astigmata: Acaridae). Acarologia 24:439–448.