Natural Selection in Variable Environments

Henrique Teotónio

Snigdhadip Dey, Thiago Guzella, Stephen Proulx (UCSB)

ÉCOLE NORMALE SUPÉRIEURE

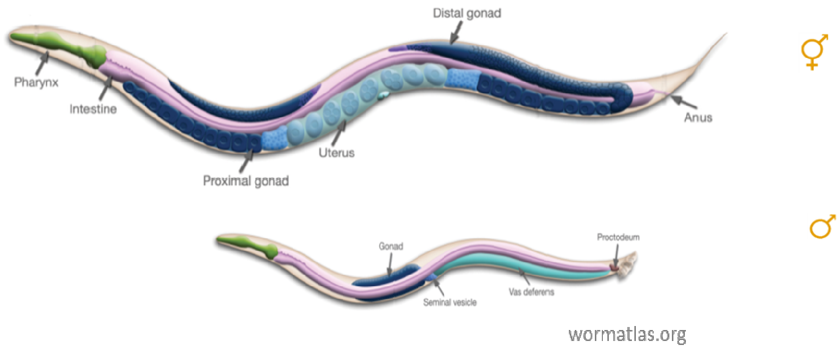
NS in Variable Environments

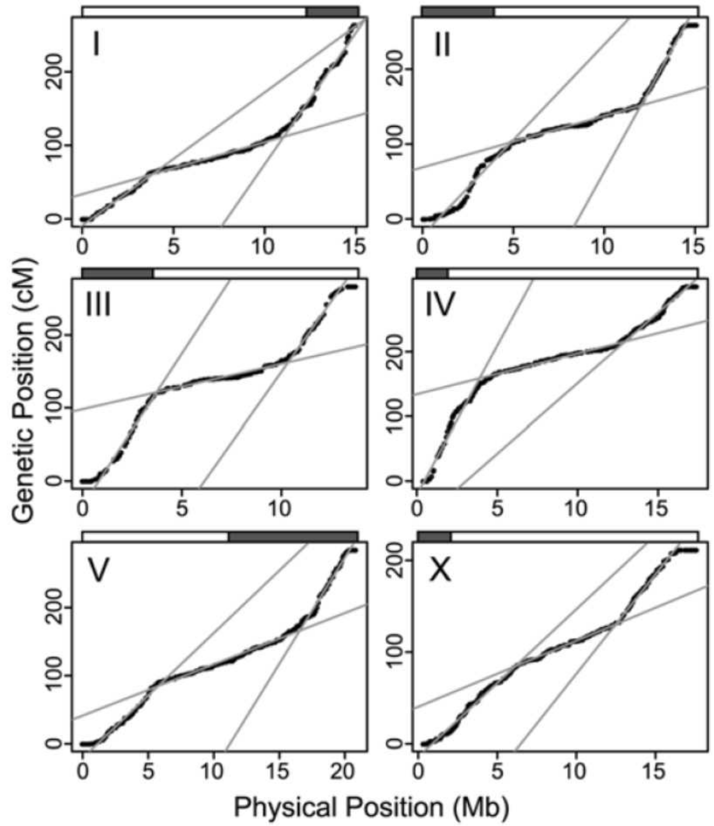
. Temporal versus spatial variation
. Within- versus between-generation variation
. Continuous versus discrete variation
. Rates of environmental change versus environmental fluctuations

. Environmental dimensionality (information, cue reliability)

. Evolution by mutation accummulation
. Evolution from pre-existing genetic diversity
. Evolution from standing genetic variation

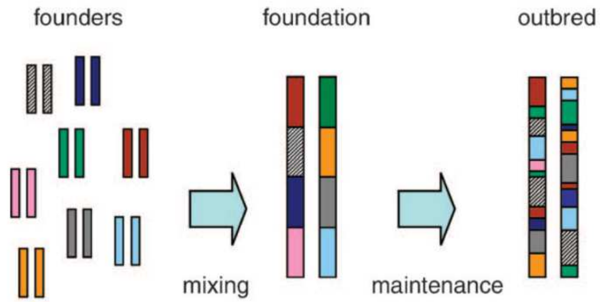
Caenorhabditis elegans

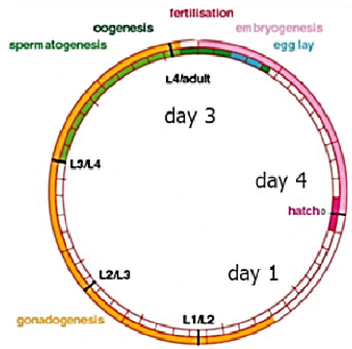




- bacteriofagous androdioecious nematode (ancestral dioecy)
- hermaphrodites can only mate with males: analogous to pollen discounting in angiosperms
- protandrous hermaphrodites (spermatogenesis is followed by oogenesis): self-sperm limited
- sex determination is chromosomal (X0 males; XX hermaphrodites)
- predominant selfing in ephemeral environments (boom and burst dynamics)
- 100 Mb genome size; 1 SNP/kb; recent "whole-genome" sweeps and background selection

C. elegans Experimental Evolution

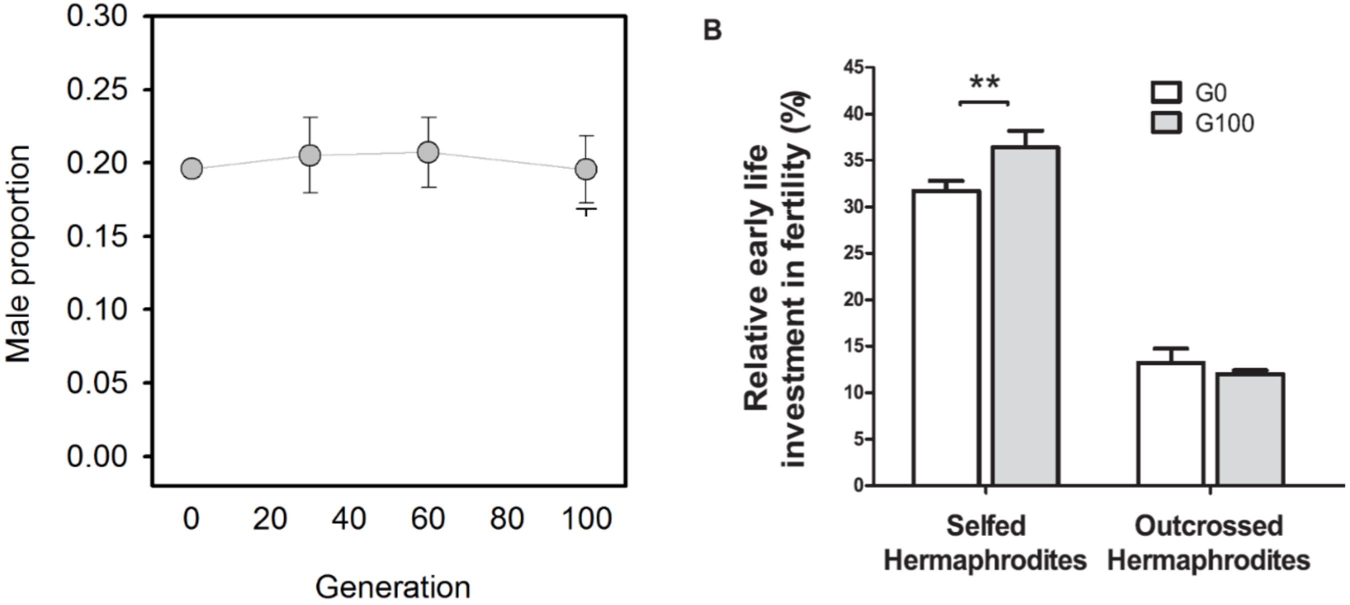




- ancestor population with standing genetic diversity: hybrid from 16 wild isolates
- 4-day discrete non-overlapping generations, constant L1 to adult density of $N=10^4$
- ancestral and derived populations compared in “common garden” assays

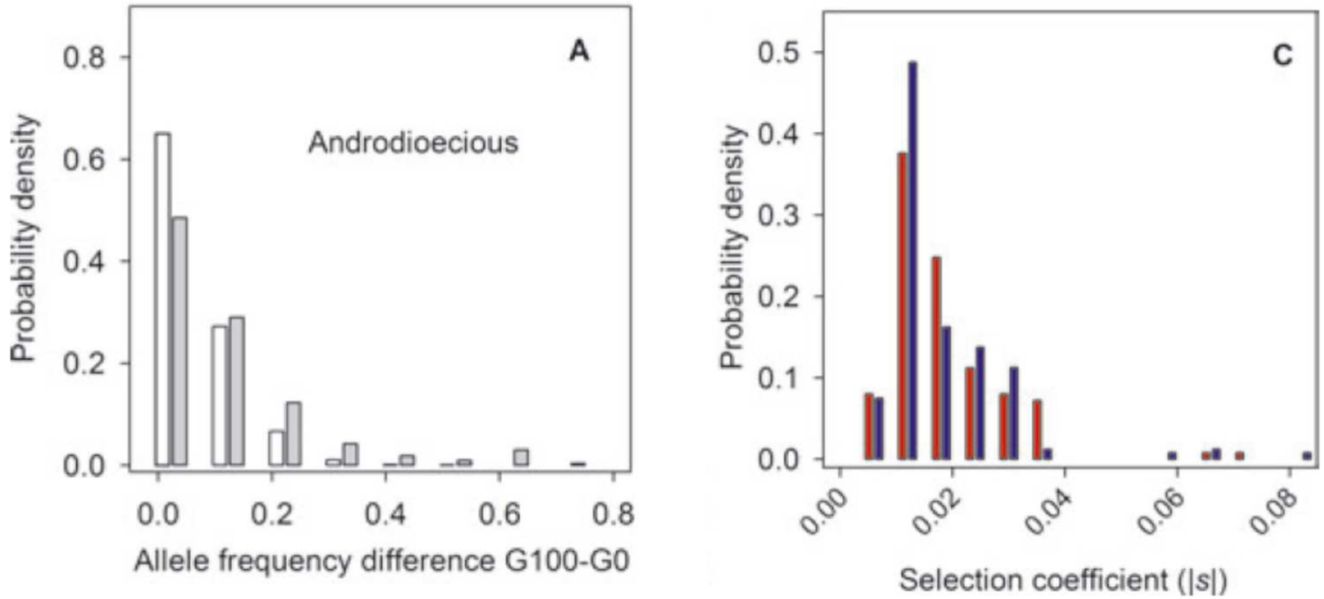
review in Teotónio et al. Genetics (2017)

Domestication to the Lab Environment



Teotónio et al. PlosOne (2012)
Carvalho et al. BMC Evol Biology (2013a,b)
Poullet et al. Evolution (2016)

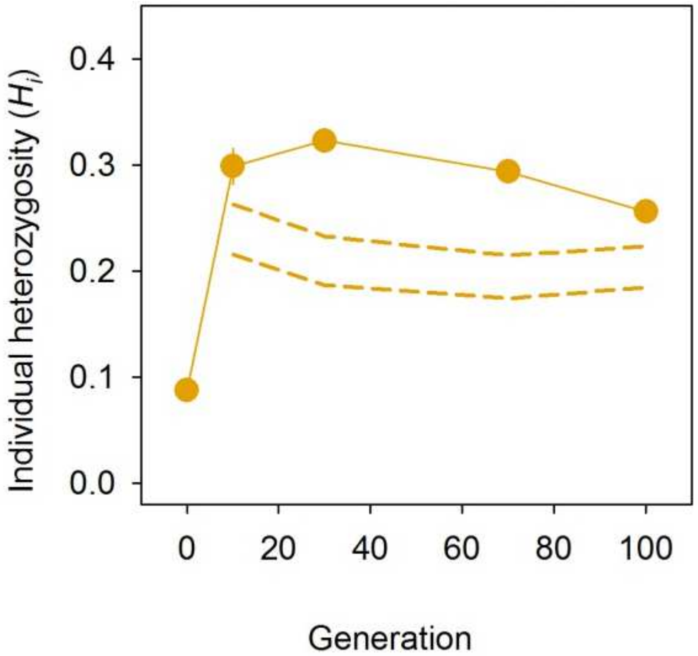
Domestication to the Lab Environment



- ~350 SNPs across 2 chromosomes, ~200k genotypes across 4 time points
- empty bars: expected binomial sampling; filled bars: observed
- 40% differentiated SNPs, 4% extinction_fixation

Chelo and Teotónio Evolution (2013)
Chelo et al. Heredity (2013)

Domestication to the Lab Environment

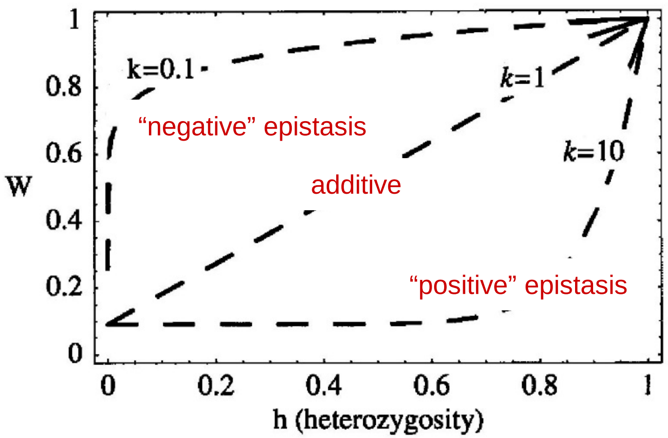


• dashed lines: expected Hi under genetic drift (numerical simulations with imposed/observed demography and expected genetic distances between SNPs; no mutation)

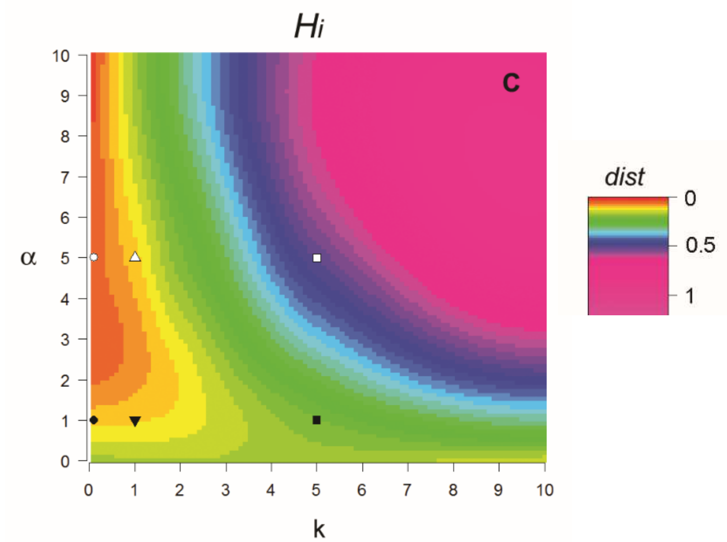
Chelo and Teotónio Evolution (2013)
Chelo et al. Heredity (2013)

Domestication to the Lab Environment

diploid viability = 1 + α Hi ^{k}



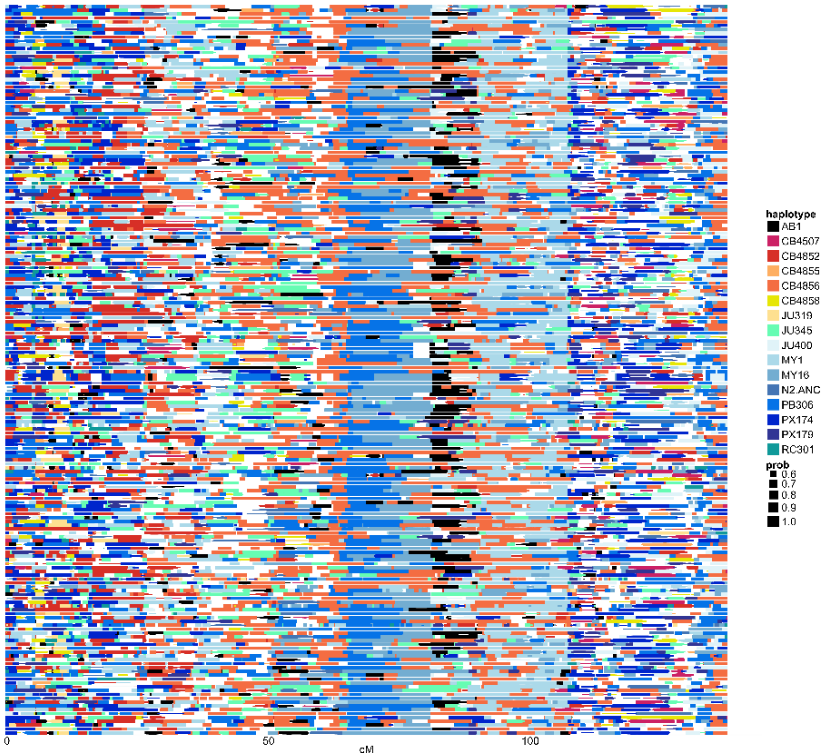
Navarro and Barton (2002)

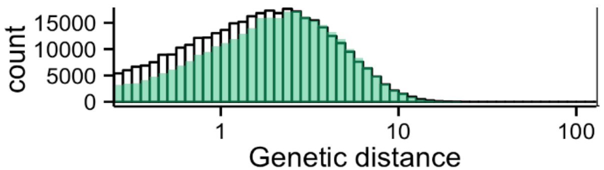


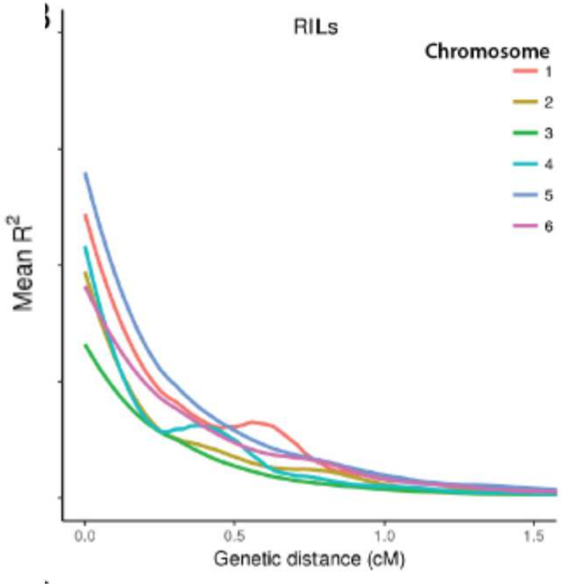
- "ABC" methods on He, Fis, Hi and CV(Hi) support balancing selection during lab domestication
- associative overdominance [w = (1-s)^x * (1-hs)^y] does not fit the data after 30 generations

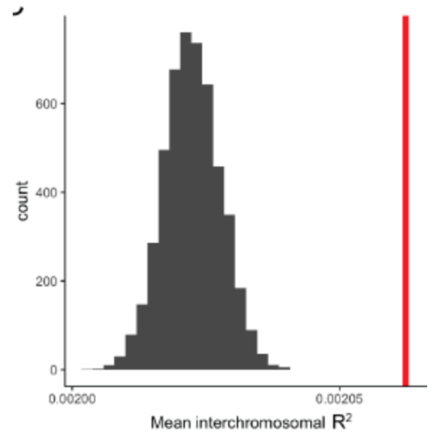
Chelo and Teotónio Evolution (2013)
Chelo et al. Heredity (2013)

Domestication to the Lab Environment



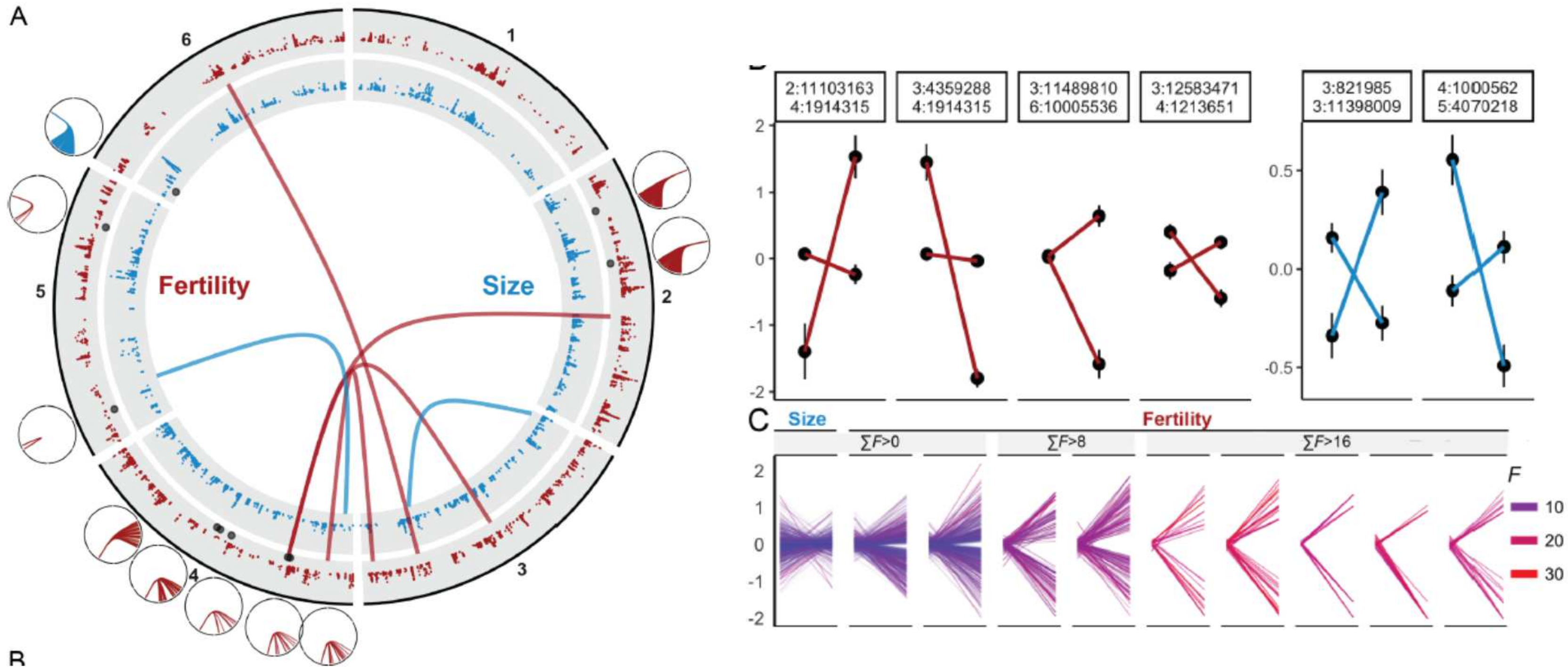






Noble et al. BioRxiv/Genetics (2017)

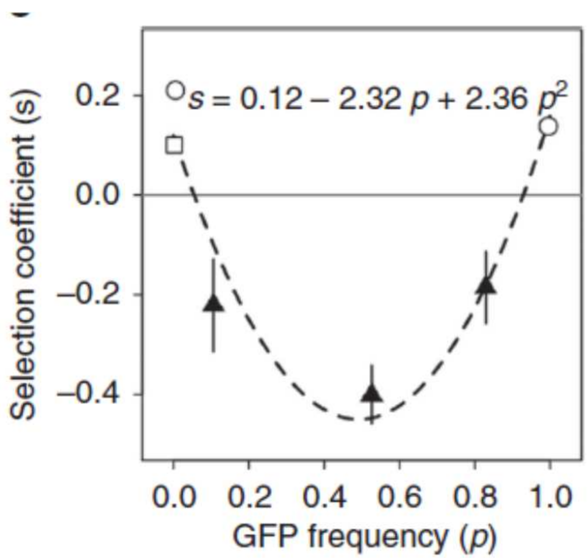
Domestication to the Lab Environment

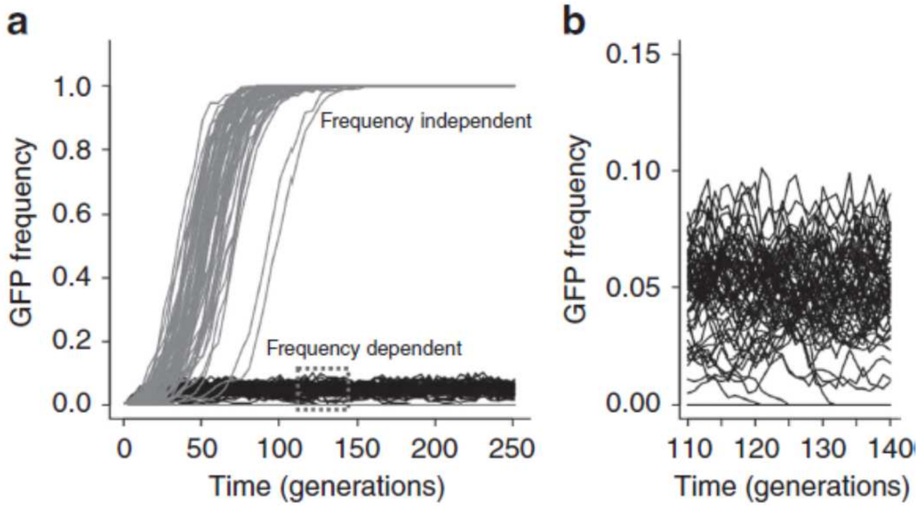


• additive by additive (polygenic) epistasis, without main single locus additive effects

Noble et al. BioRxiv/Genetics (2017)

NS in Constant Environments

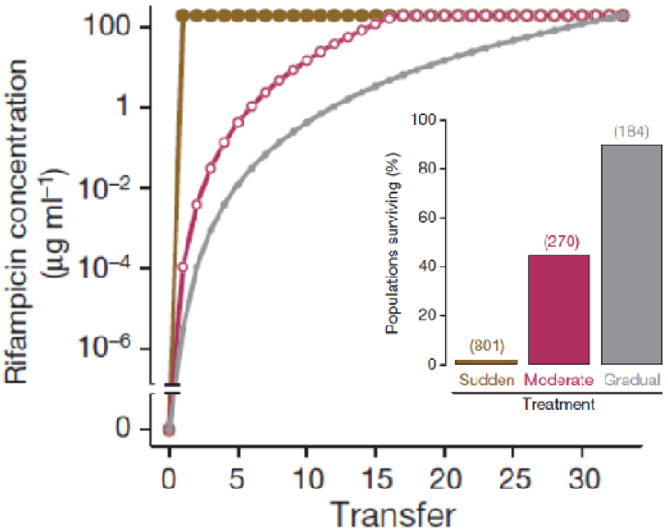


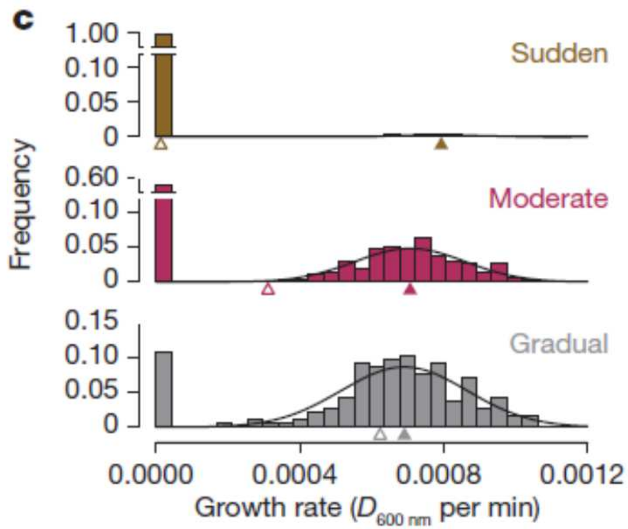


- head-to-head competitions between two inbred lines derived from the domesticated population
- right plots: not only polymorphim can be maintained, but the prob of extinction may increase

Chelo et al. NatComm (2013)

Population genetics and adaptation to changing environments

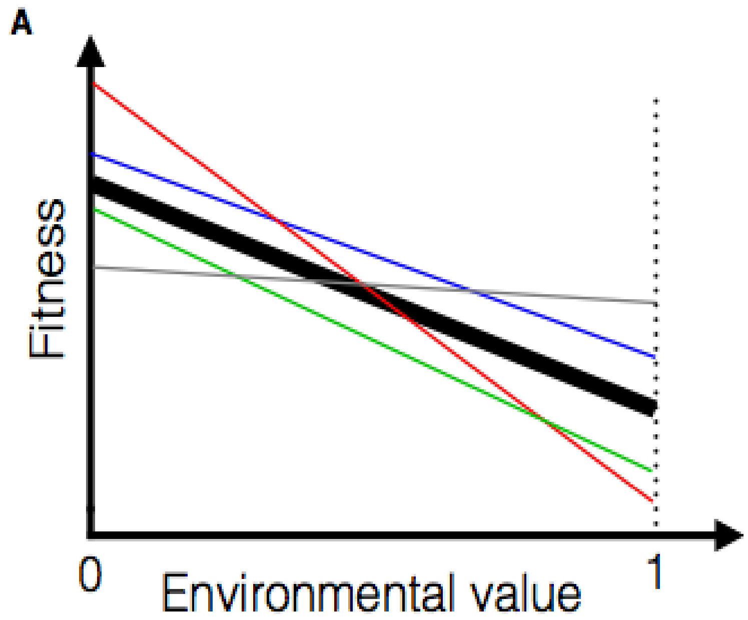




• population survival and adaptation depend on the order of mutation accumulation and time to “explore” the fitness landscape

Lindsey et al. Nature (2013)
see also Gorter et al. AmNat (2015)

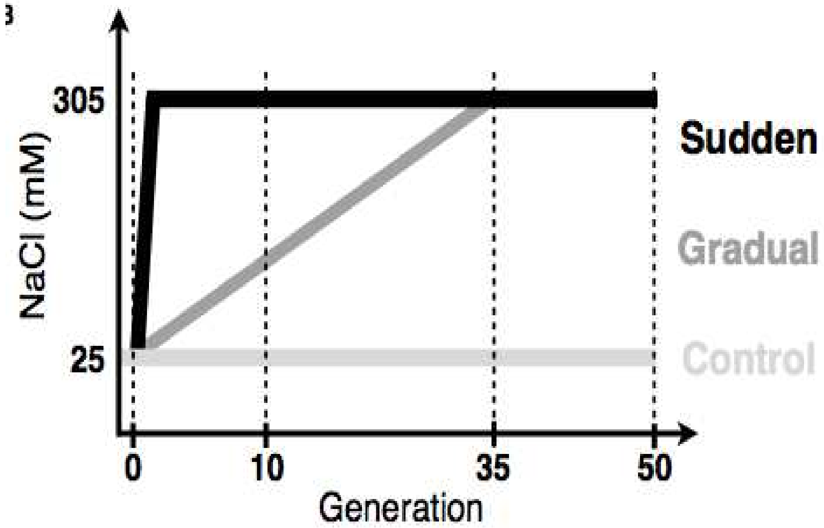
Evolution From Pre-Existing Diversity: Fitness Reaction Norms

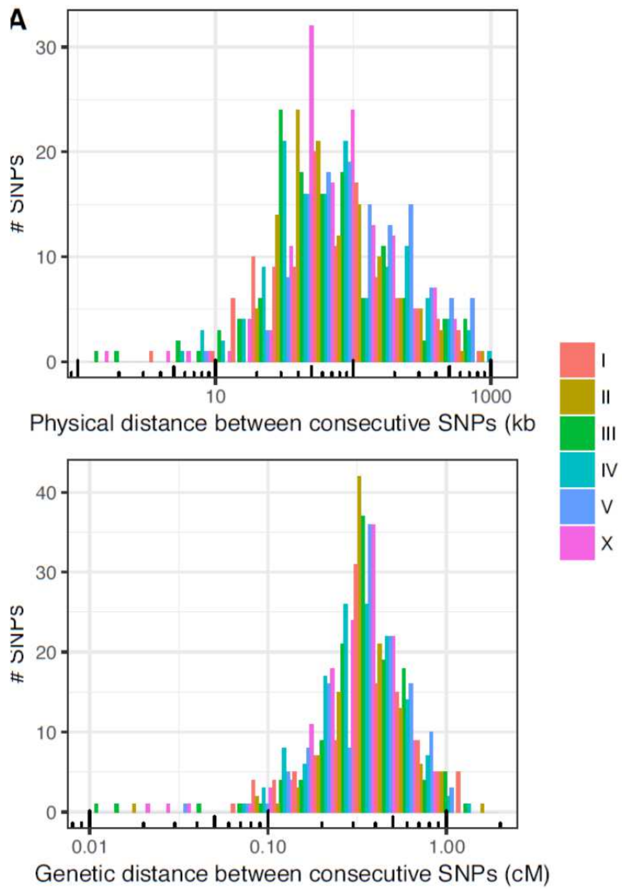


• genetic drift might lead to the loss of the best genotypes in the most extreme environment under slower environmental change

• adaptation can also be compromised the slower the environmental change because similarly fit genotypes can be maintained for longer

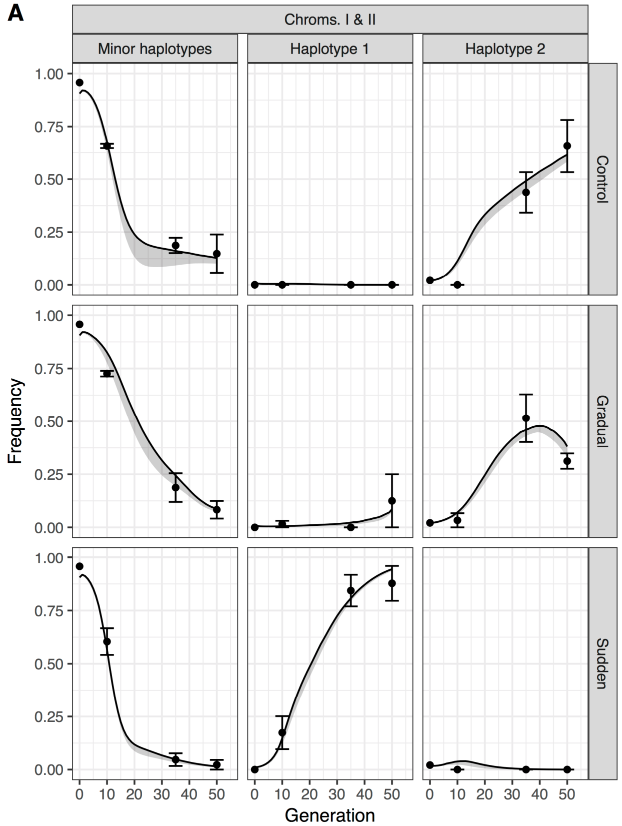
Experimental Evolution Design

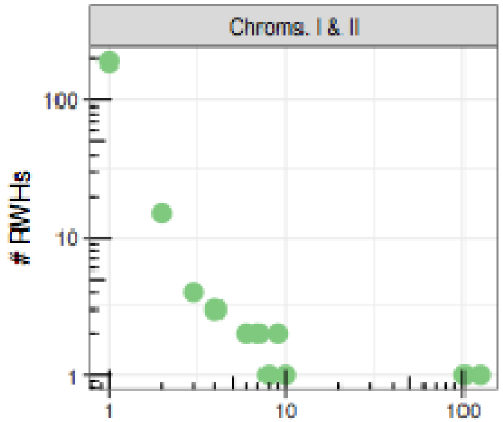




- ancestor population with standing genetic diversity (lab adapted population)
- reproduction exclusively by selfing (genetically-modified to kill males)
- dashed vertical lines indicate sample points for individual genotyping

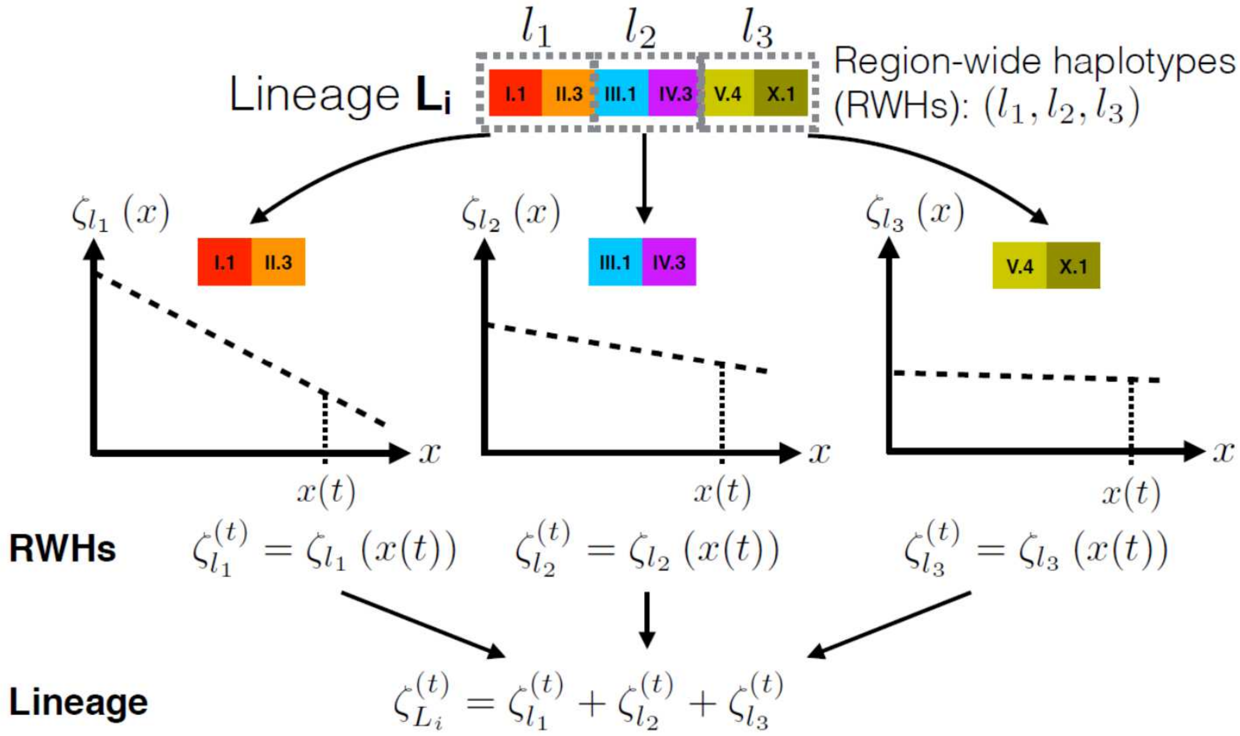
Experimental Population Genetic Dynamics





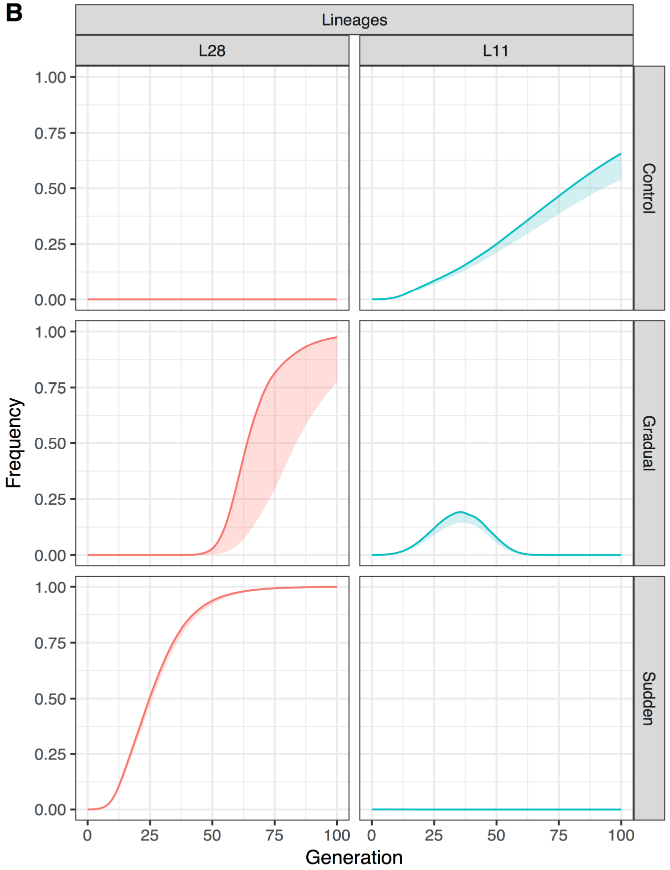
Guzella et al. (submitted)

Inference Model for Lineage ID and Frequency



Guzella et al. (submitted)

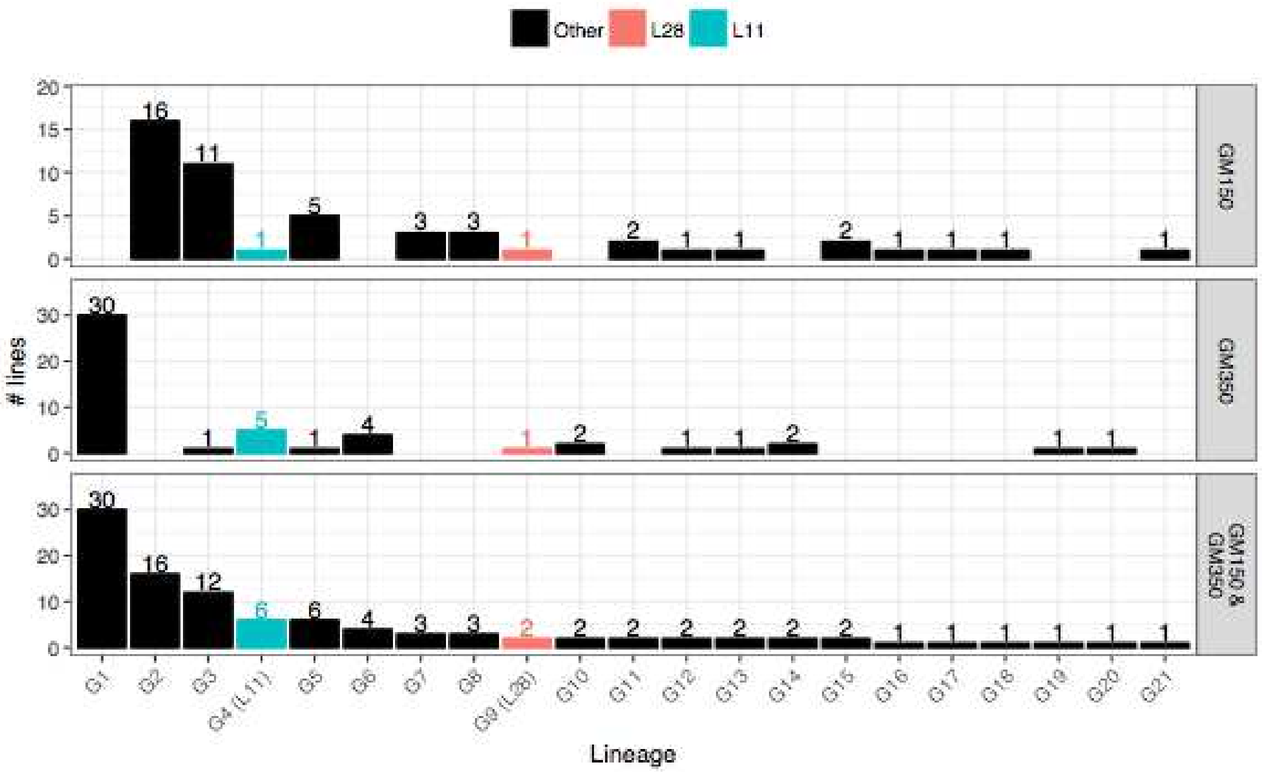
Expected Population Genetic Dynamics



Similar dynamics with linear and quadratic fitness reaction norms

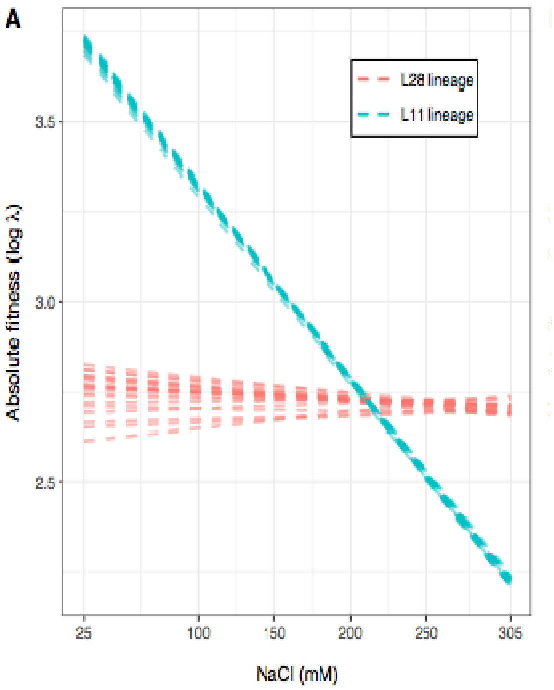
Guzella et al. (submitted)

Identifying the two adaptive lineages



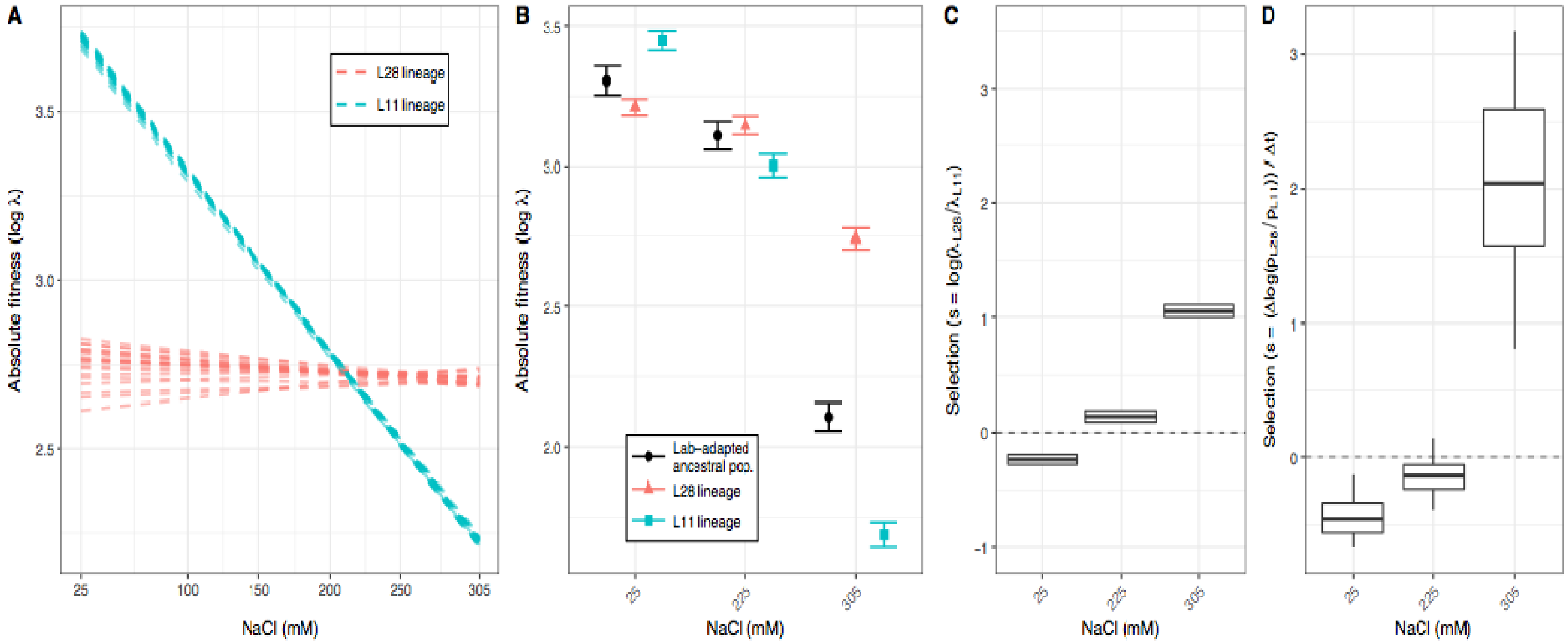
Noble et al. bioRxiv/Genetics (2017)

Expected Fitness Reaction Norms



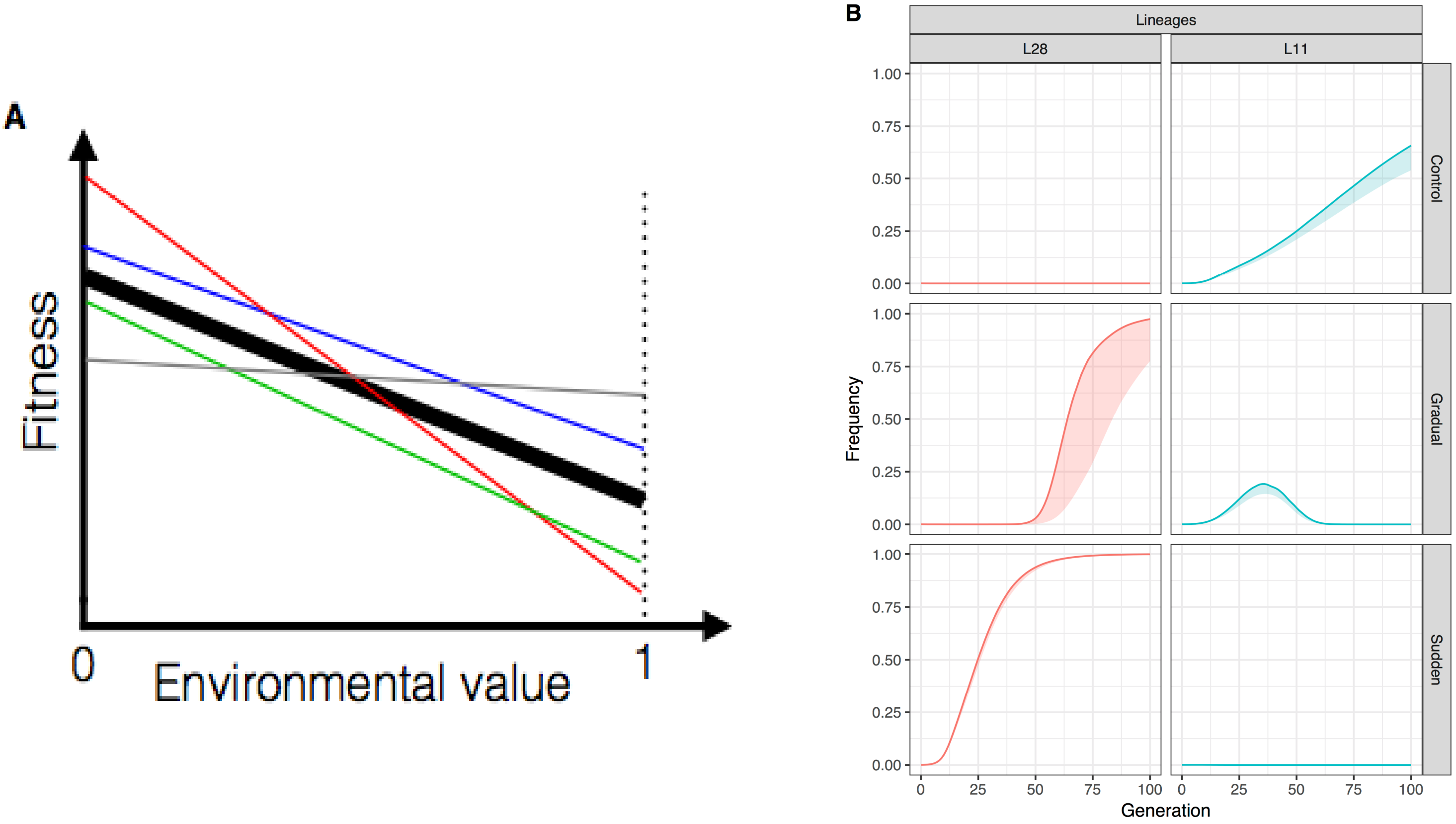
Guzella et al. (submitted)

Expected and Observed Fitness Reaction Norms



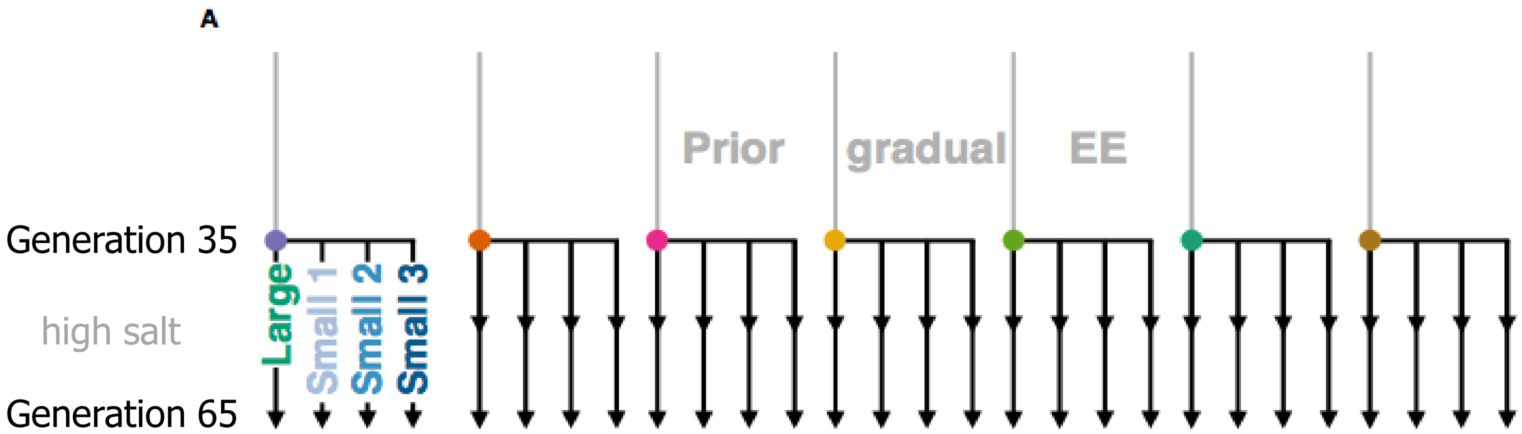
Guzella et al. (submitted)

A Role for Genetic Drift and/or Maintenance of Polymorphim?



Guzella et al. (submitted)

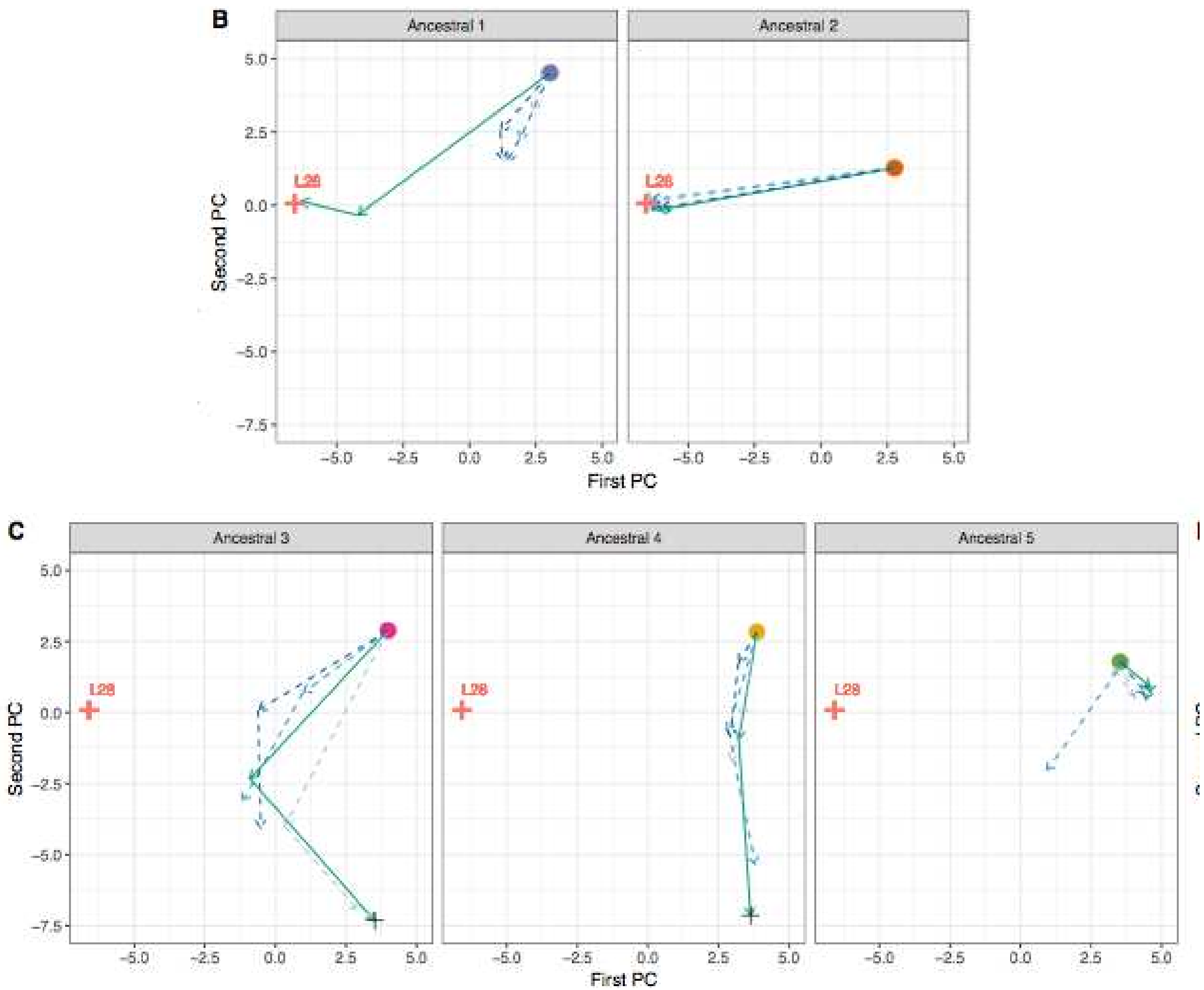
Experimental Evolution Design



- seven gradual populations at G35 revived and high salt evolution repeated
- populations pool-genotyped at G35 and after 15 and 30 generations

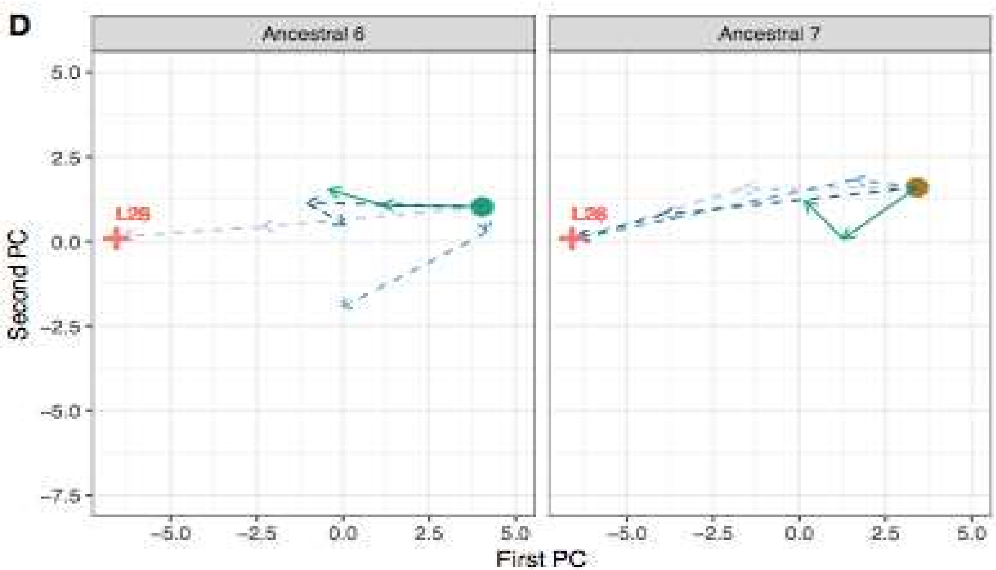
Guzella et al. (submitted)

Founder Effects and Selection Efficiency



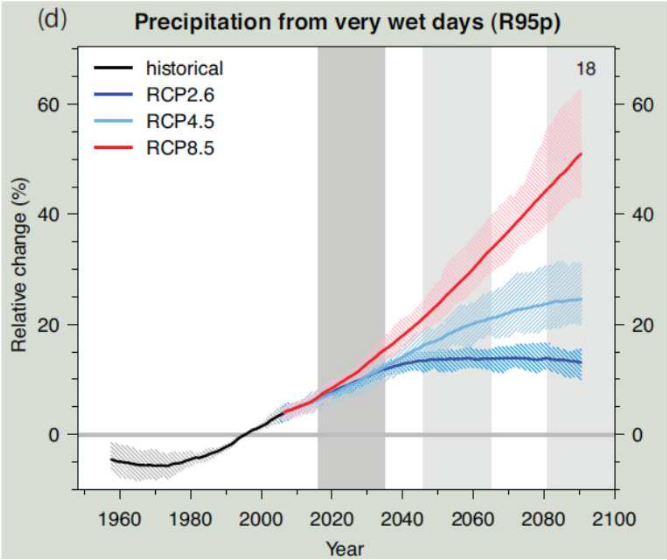
Guzella et al. (submitted)

Founder Effects and Selection Efficiency



Guzella et al. (submitted)

NS in Temporally Fluctuating Environments



Stocker et al. 2013 Intergovernmental Panel on Climate Change

• when individuals have information during development about the environment they will face at reproduction, one expects that the evolution of phenotypic plasticity underlies adaptation

• when this information about environmental change can only be provided by the mother then the selection for maternal effects should underlie adaptation

Maternal Independent Effects

offspring phenotypes do not depend on maternal environment

Consider two discrete phenotypes in two discrete environments;
their geometric mean fitness across all possible environmental regimes can be described by:

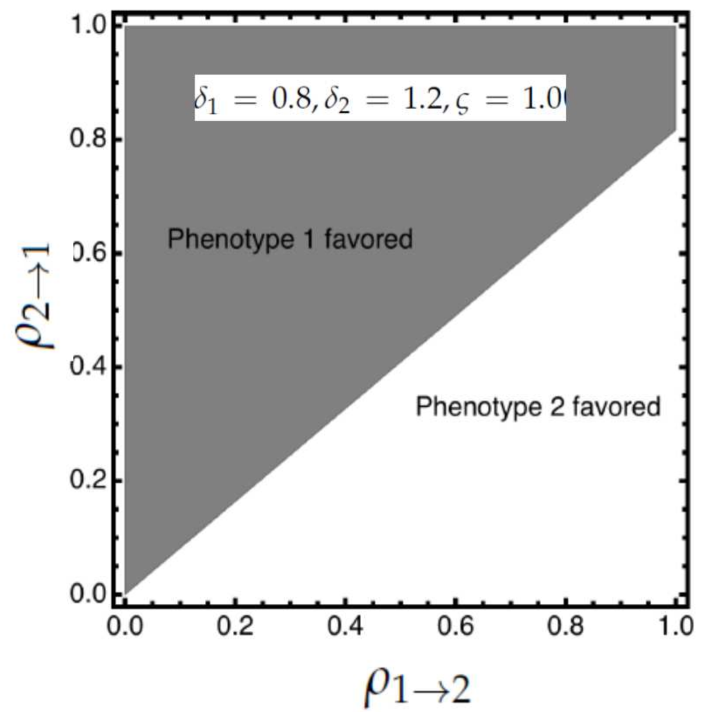
$$\log(\hat{w}_1) = \left(\alpha \log\left(c_1 s_{1,1}\right) + (1-\alpha)\log\left(c_1 s_{2,1}\right)\right)$$
$$\log(\hat{w}_2) = \left(\alpha \log\left(c_2 s_{1,2}\right) + (1-\alpha)\log\left(c_2 s_{2,2}\right)\right)$$

α is the frequency of environment 1
c is the fecundity of phenotype
s is the survivorship of phenotype

Proulx and Teotónio AmNat (2017)

Maternal Independent Effects

offspring phenotypes do not depend on maternal environment



For example, phenotype 2 is favored when:

$$\log(\hat{w}_2) - \log(\hat{w}_1) > 0$$

$$\rho_{2\to1} > -\frac{\rho_{2\to1}\,(\log(\delta_2) + \log(\varsigma))}{\log(\delta_1) + \log(\varsigma)}$$

$\rho_{i\to j}$ is the probability that environment changes from i to j

δ_i is the relative survival of phenotype 2 in environment i

ς is the relative fecundity of phenotype 2

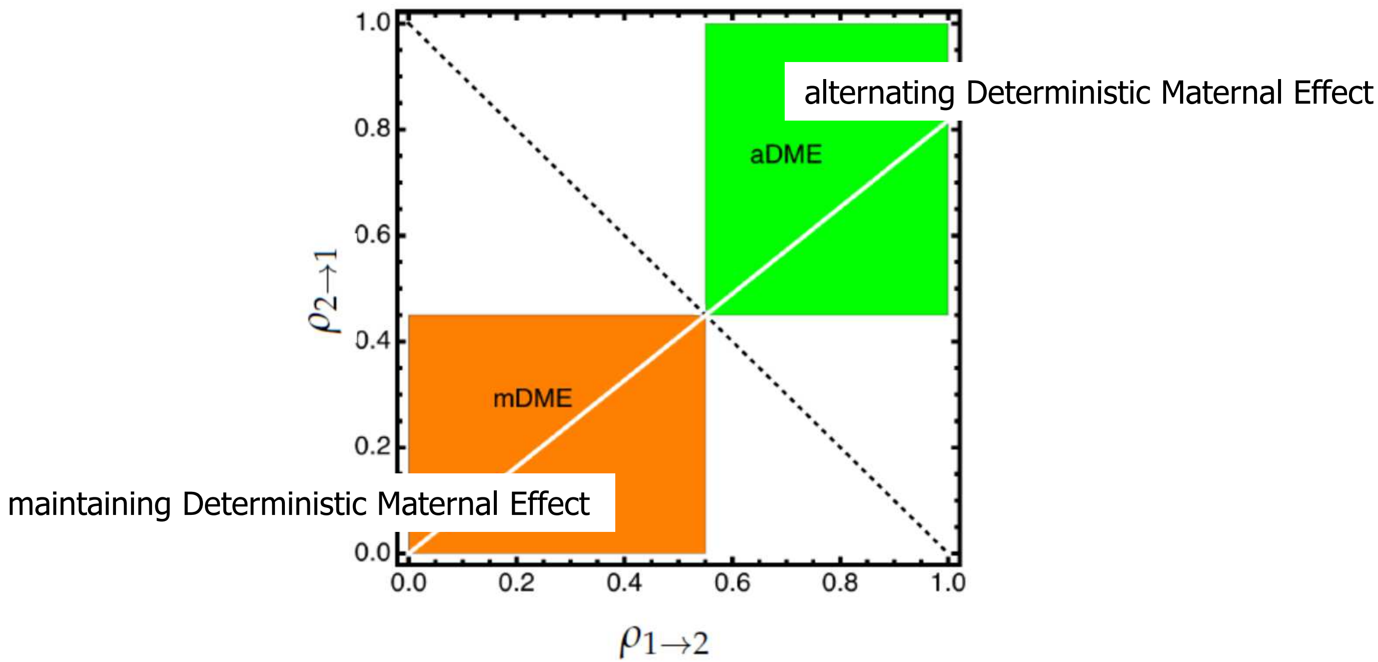
Proulx and Teotónio AmNat (2017)

Deterministic Maternal Effects

offspring phenotypes depend on maternal environment in a consistent manner

$$\log(\hat{w}_{aDME}) = \Big((1-\rho_{1\to 2})\alpha \log(c_2 s_{1,2}) + \rho_{1\to 2}\alpha \log(c_2 s_{2,2}) + \ \dots\Big)$$

$$\log(\hat{w}_{DME}) \ - \ \log(\hat{w}_{MIE}) \ > 0$$



α is the frequency of environment 1

$\rho_{i\to j}$ is the probability that environment changes from *i* to *j*

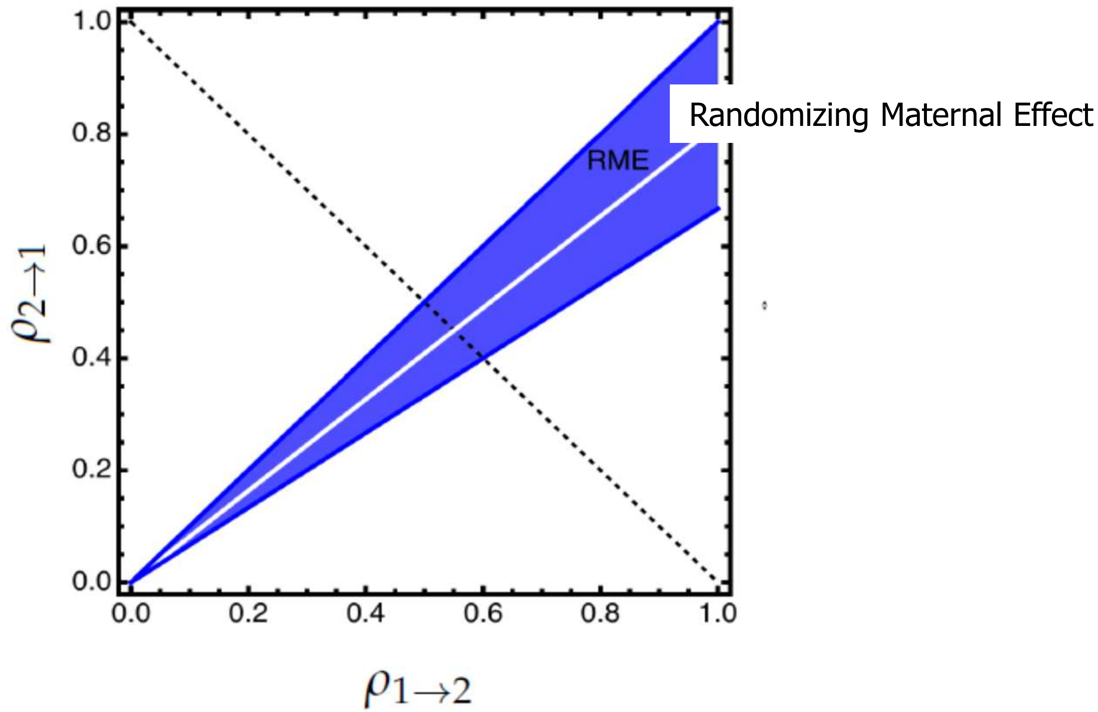
Proulx and Teotónio AmNat (2017)

Randomizing Maternal Effects

mothers randomize offspring phenotypes, but the probability of producing a given phenotype does not depend on maternal environment

$$\log(\hat{w}_{RME}) = \alpha \log\big(\gamma c_1 s_{1,1} + (1-\gamma) c_2 s_{1,2}\big) + \ \ldots$$

$$\log(\hat{w}_{RME}) - \log(\hat{w}_{MIE}) > 0$$

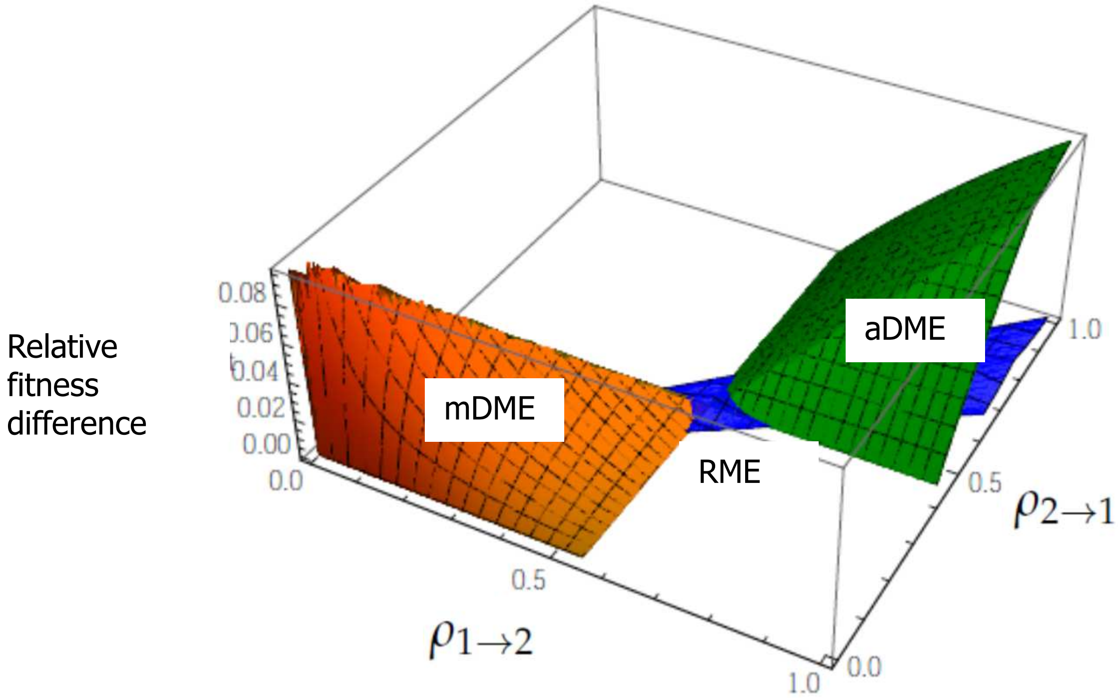


$\rho_{i\to j}$ is the probability that environment changes from *i* to *j*

γ is the probability of producing phenotype 1

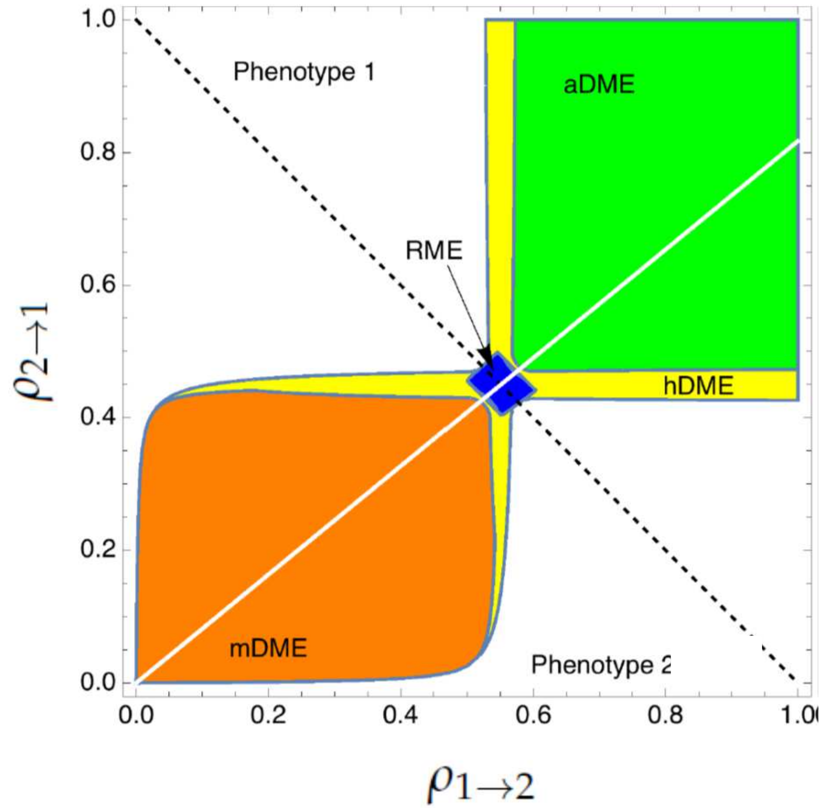
Proulx and Teotónio AmNat (2017)

Deterministic and Randomizing ME Relative Fitness Difference to Maternal Independent Effects



Proulx and Teotónio AmNat (2017)

Selection for Maternal Effects in Fluctuating Environments



Plotted: Fitness difference between maternal effects and maternal independent effects larger than 10^{-3}

hDME: "hybrid deterministic maternal effects", when the probability of randomizing offspring phenotypes depends on the maternal environment

Proulx and Teotónio AmNat (2017)

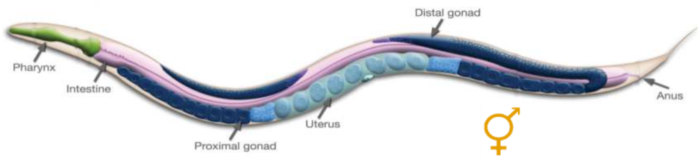
Maternal Effects in *C. elegans*

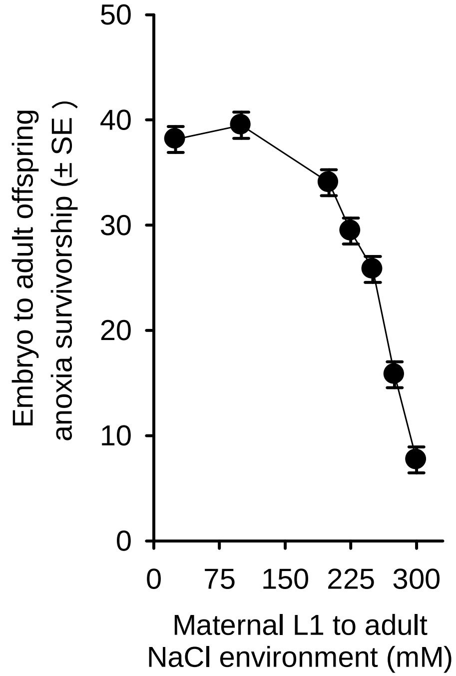
Current Biology *19*, 859–863, May 26, 2009 ©2009 Elsevier Ltd All rights reserved DOI 10.1016/j.cub.2009.03

Adaptive Sugar Provisioning Controls Survival of *C. elegans* Embryos in Adverse Environments

Harold N. Frazier III[1] and Mark B. Roth[2,*]
[1]Molecular and Cellular Biology Graduate Program
University of Washington
Seattle, WA 98195
USA
[2]Basic Science Division
Fred Hutchinson Cancer Research Center
Seattle, WA 98109
USA

embryos are not generally
sure to hyperosmotic con
the salt in a way that mak
We next tested *daf-2(e*
which carry a hypomorph
insulin-like growth factor
engage in OPC and found
adapt their embryos to s
No embryos from OPC e





Dey et al. (not published)

Hermaphrodites challenged with high NaCl concentrations since larval stages have broods with poor survivorship in anoxia

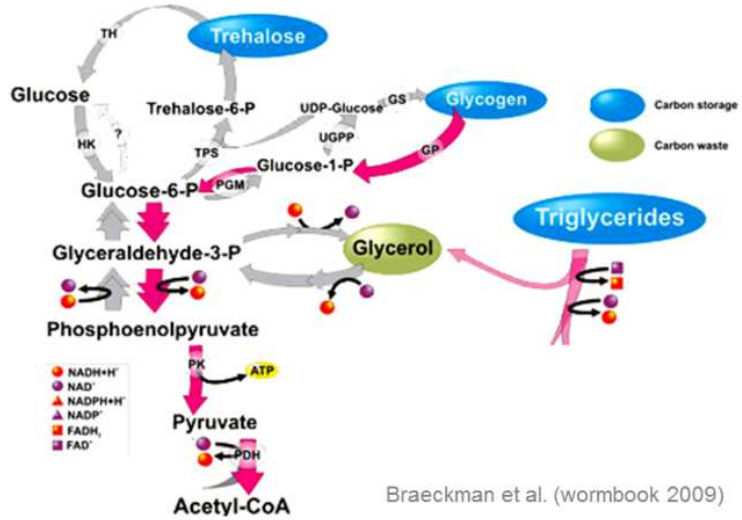
Maternal Effects in *C. elegans*

Current Biology *19*, 859–863, May 26, 2009 DOI 10.1016/j.cub.2009.03

Adaptive Sugar Provisioning Controls Survival of *C. elegans* Embryos in Adverse Environments

Harold N. Frazier III[1] and Mark B. Roth[2,*]
[1]Molecular and Cellular Biology Graduate Program
University of Washington
Seattle, WA 98195
USA
[2]Basic Science Division
Fred Hutchinson Cancer Research Center
Seattle, WA 98109
USA

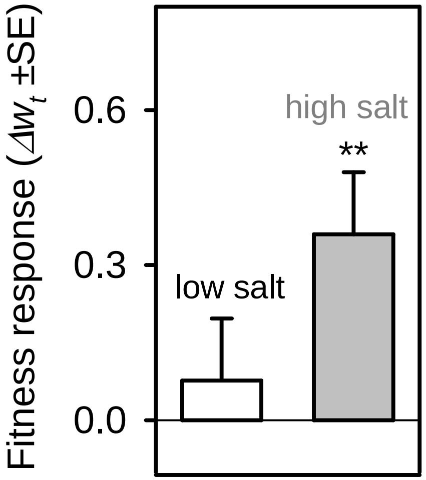
embryos are not generally
sure to hyperosmotic con
the salt in a way that mak
We next tested *daf-2(e*
which carry a hypomorph
insulin-like growth factor
engage in OPC and found
adapt their embryos to s
No embryos from OPC *e*

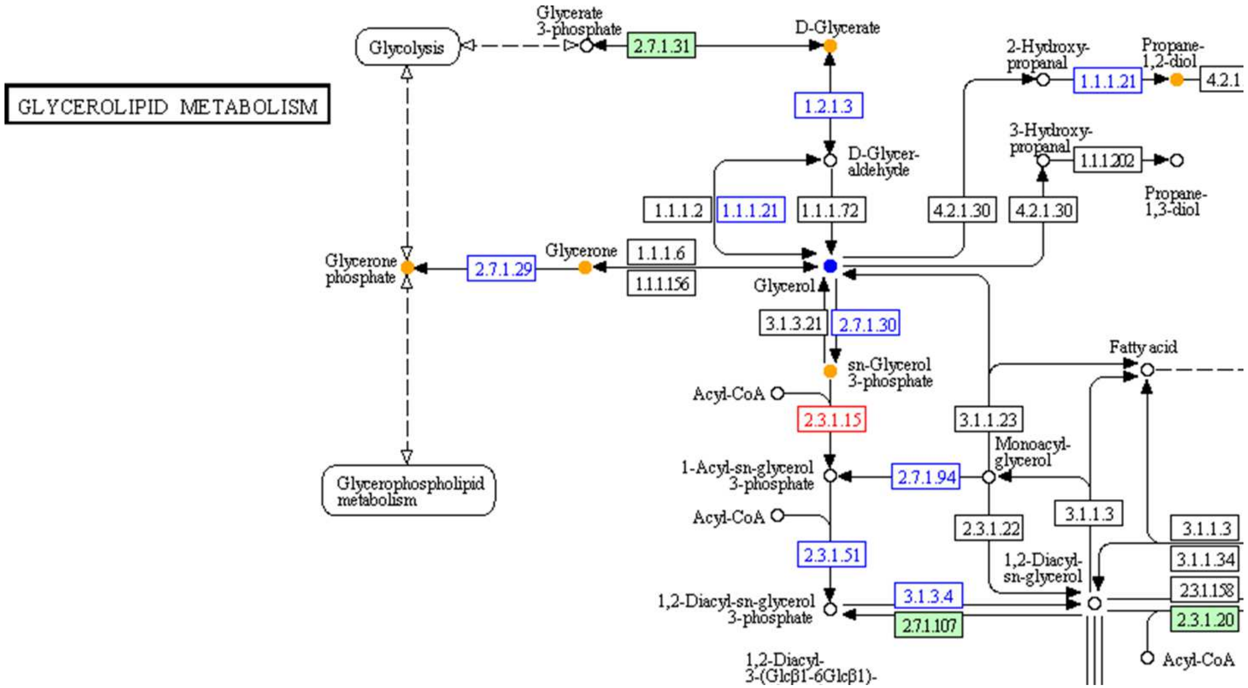


Braeckman et al. (wormbook 2009)

Hermaphrodites trade-off glycerol production necessary for their survival in high salt conditions with glycogen provisioning of their embryos

Adaptation to High Salt Conditions





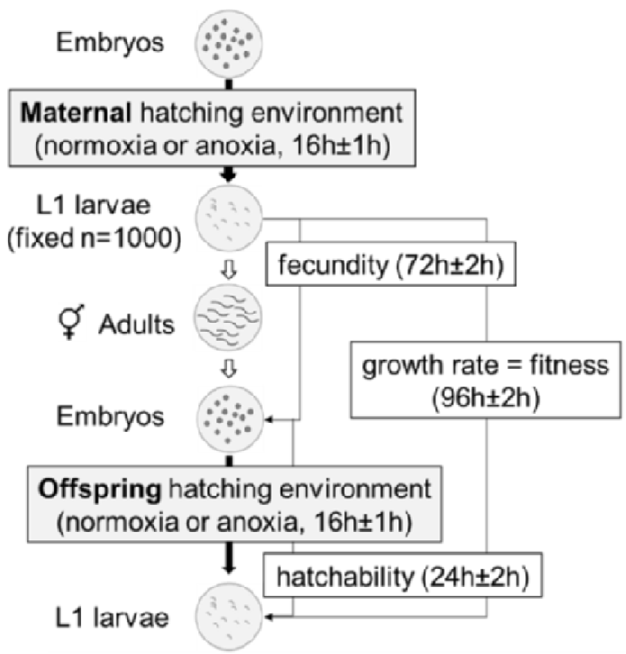
KEGG analysis :

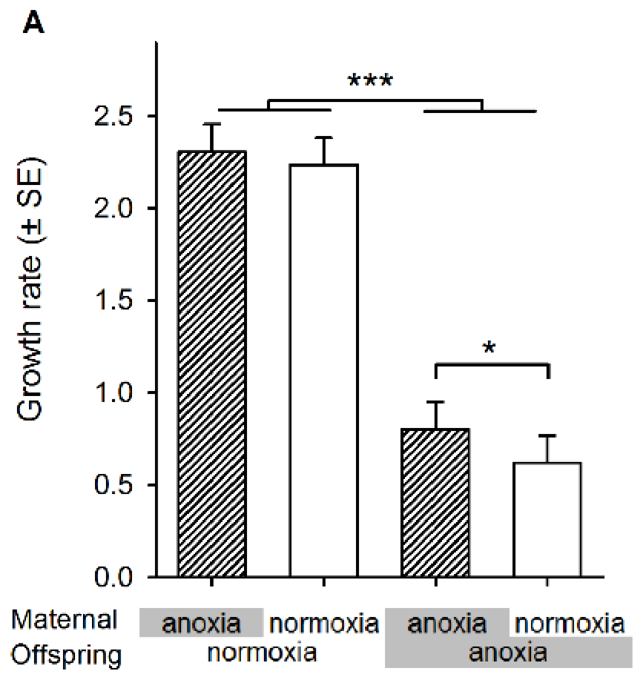
↑ reg ↓ reg no change

Theologidis et al. BMC Biology (2014)
Guzella et al. (not published)

Ancestral Adaptive State

life-cycle and high salt adapted population

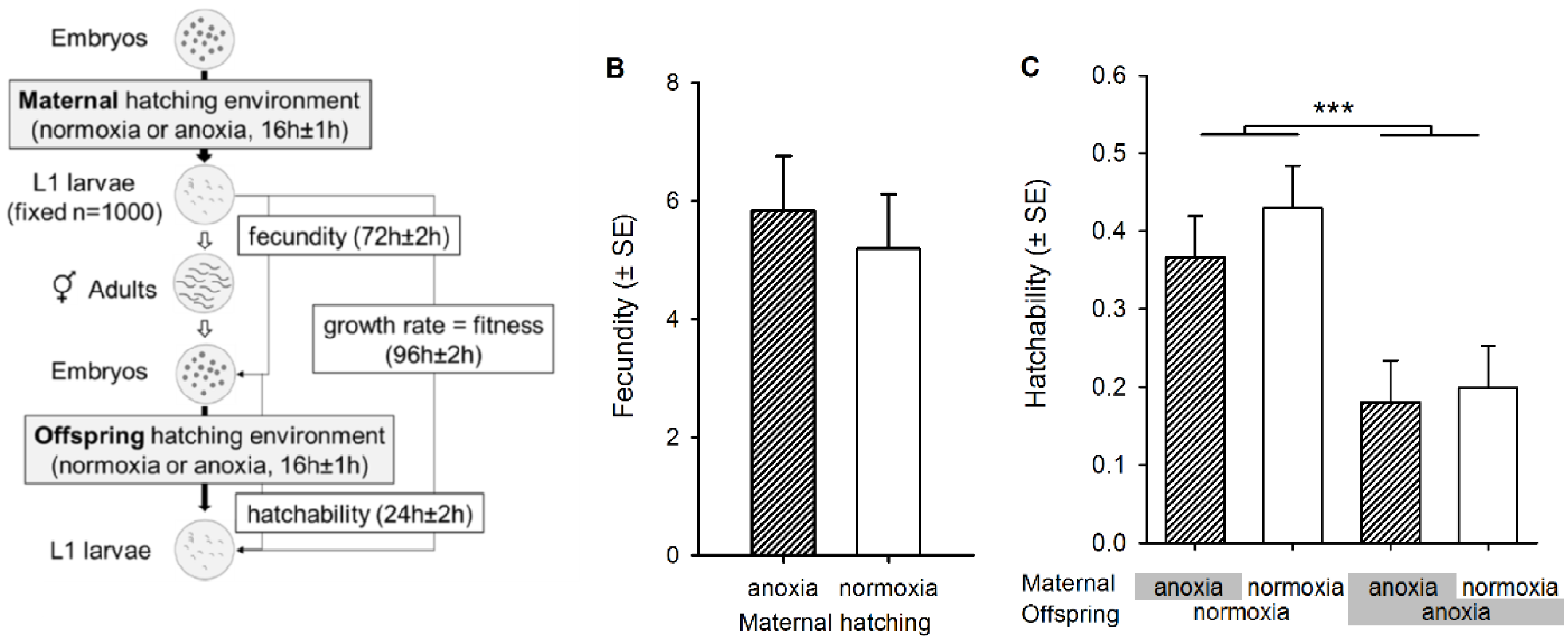




Dey et al. Plos Biology (2016)

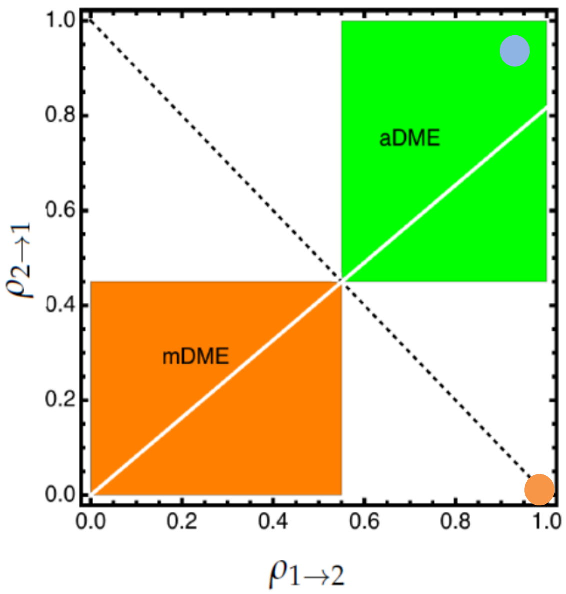
Ancestral Adaptive State

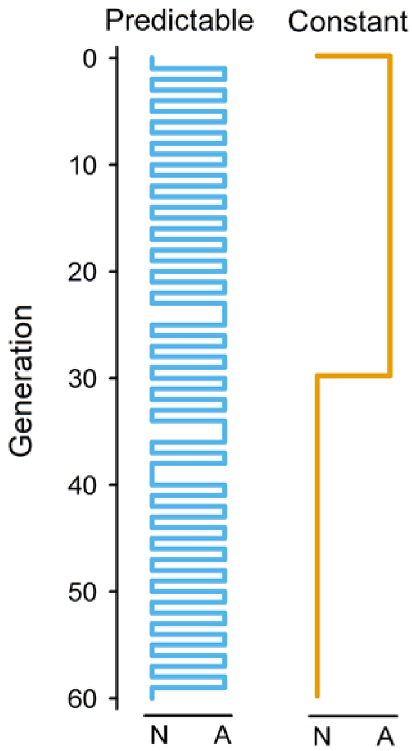
life-cycle and high salt adapted population



Dey et al. Plos Biology (2016)

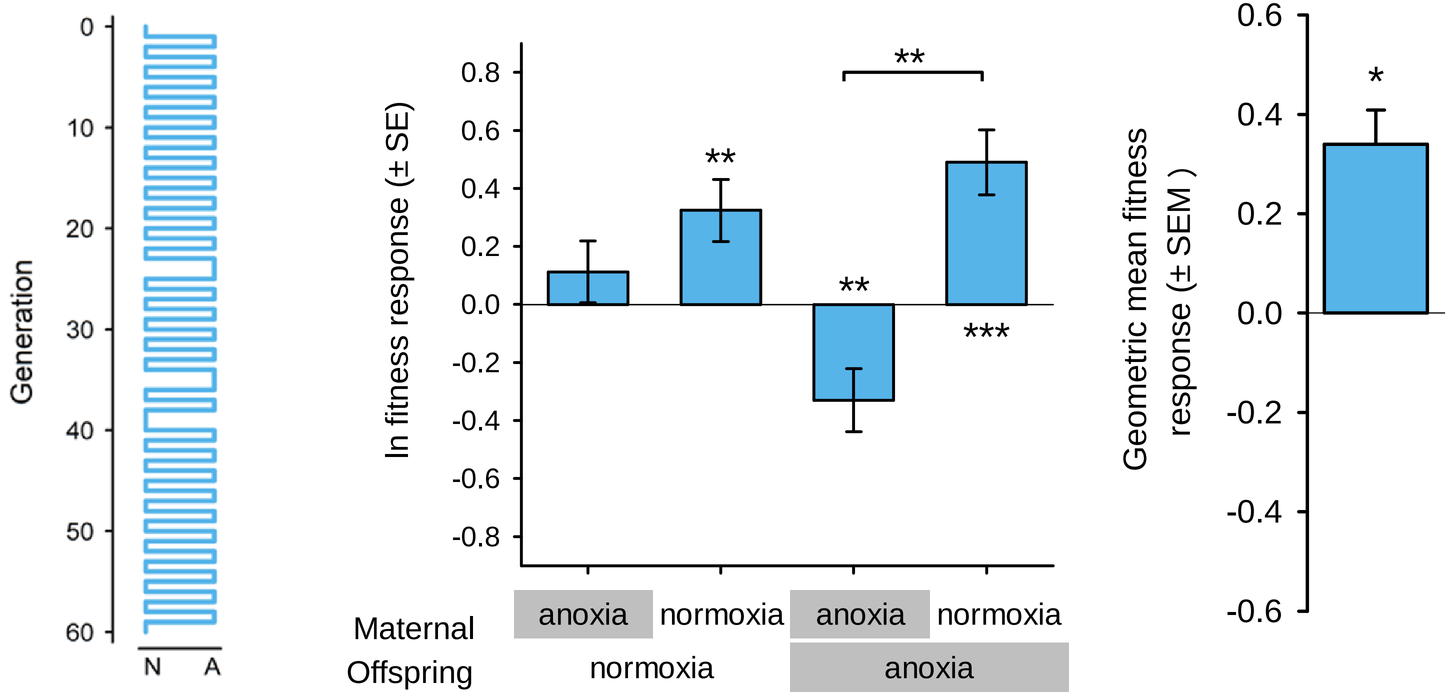
Experimental Evolution in Correlated Environments





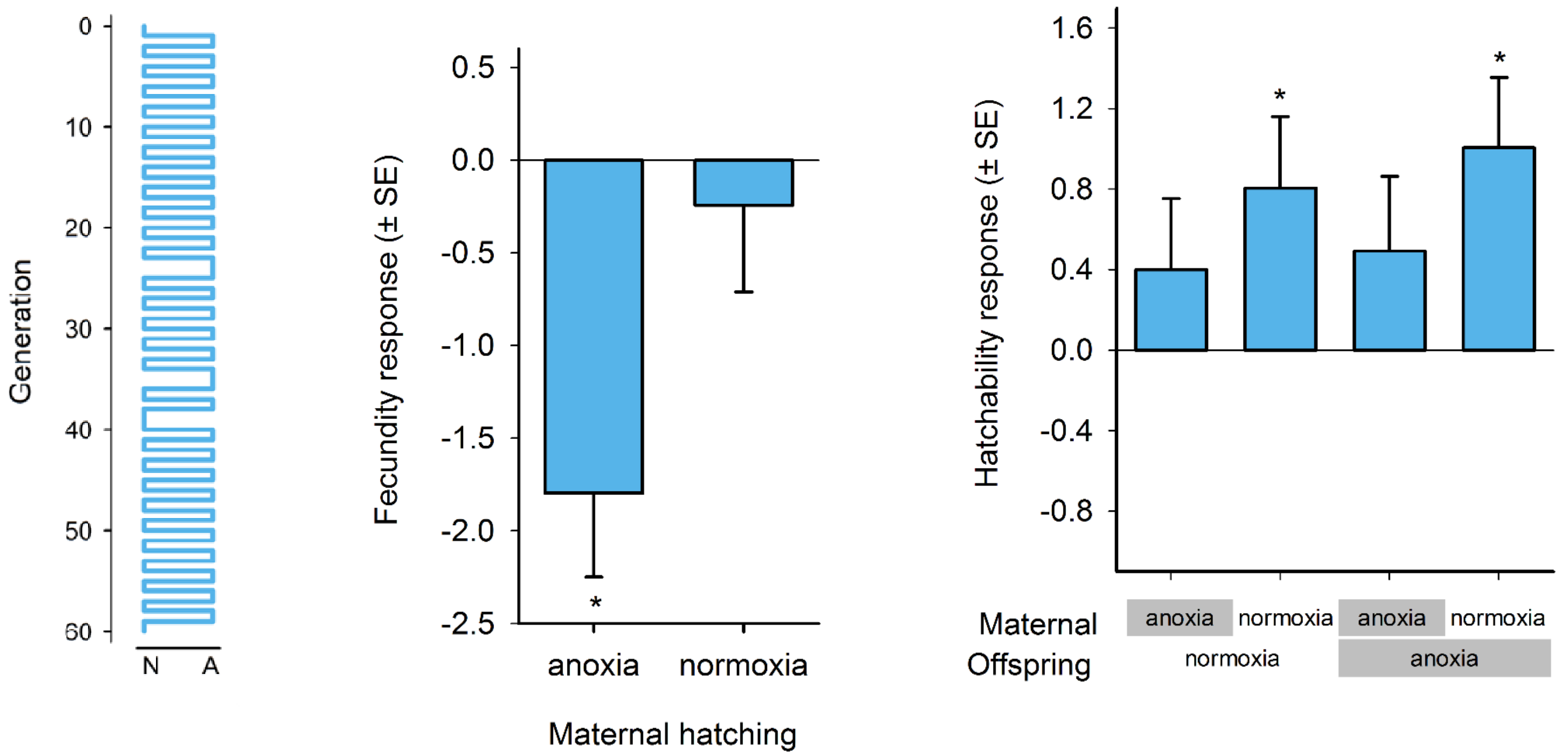
Predictable: probability of changing environments of 0.95 across 60 generations
Constant: probability of changing environments of 0.02 across 60 generations
Both regimes: frequency of anoxia generations of 50%

Adaptation to Predictably Alternating Environments



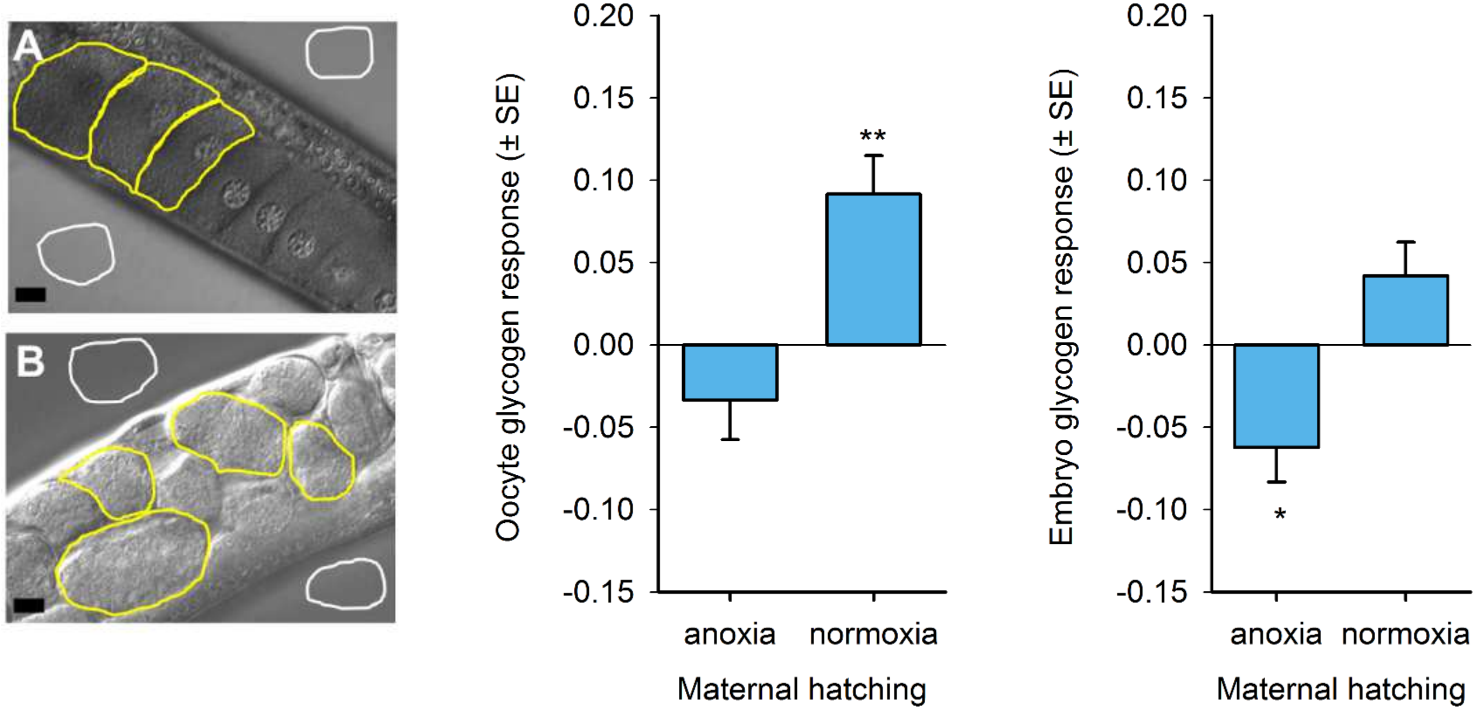
Dey et al. Plos Biology (2016)

Evolution of Deterministic Maternal Effects



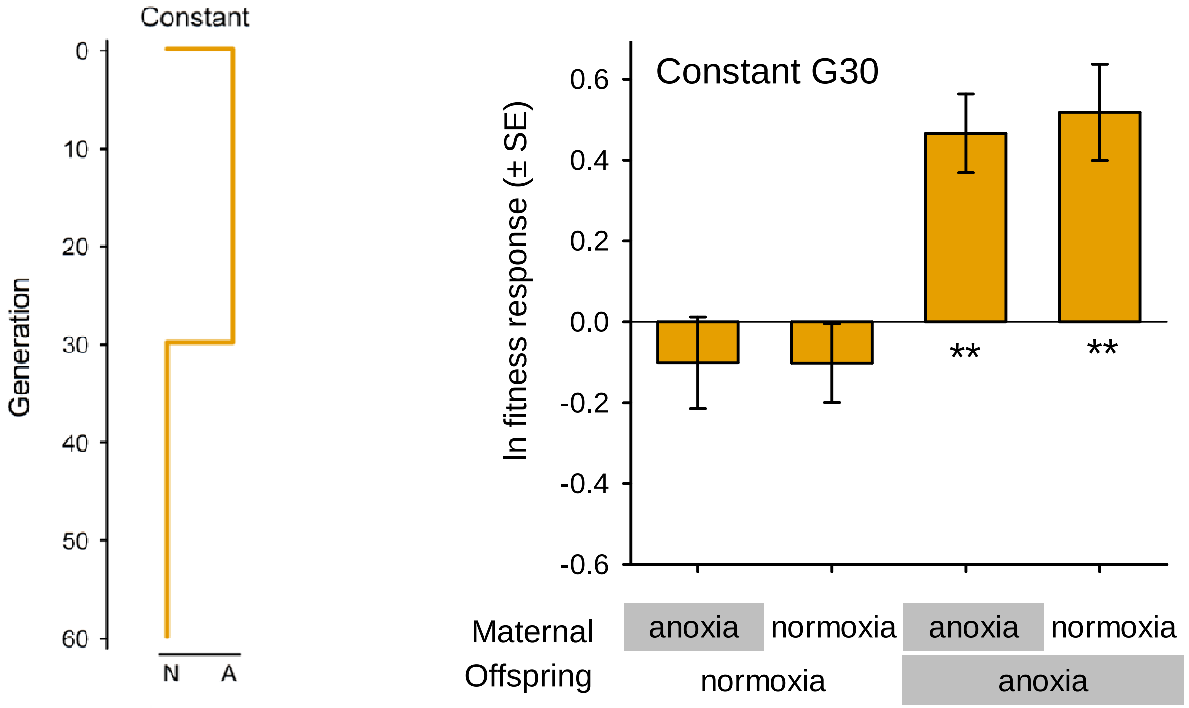
Dey et al. Plos Biology (2016)

Evolution of Glycogen Provisioning



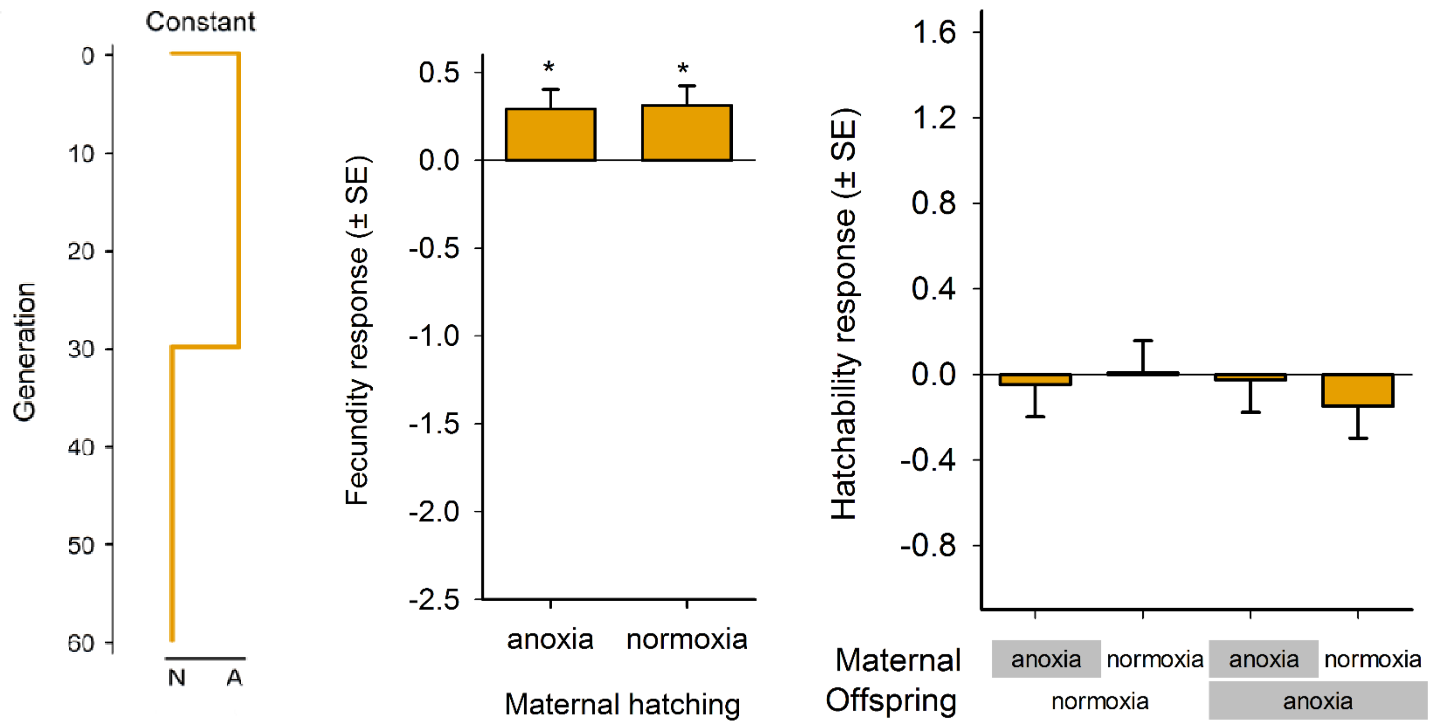
Dey et al. Plos Biology (2016)

Adaptation to (Predictably) Constant Environments



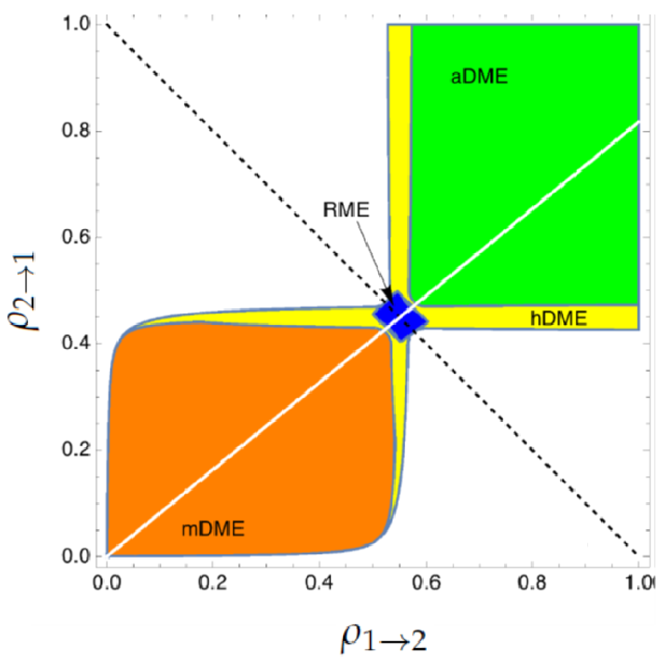
Dey et al. Plos Biology (2016)

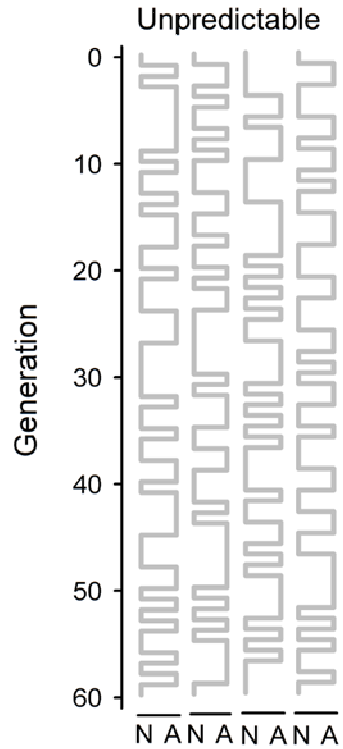
Adaptation to Constant Environments



Dey et al. Plos Biology (2016)

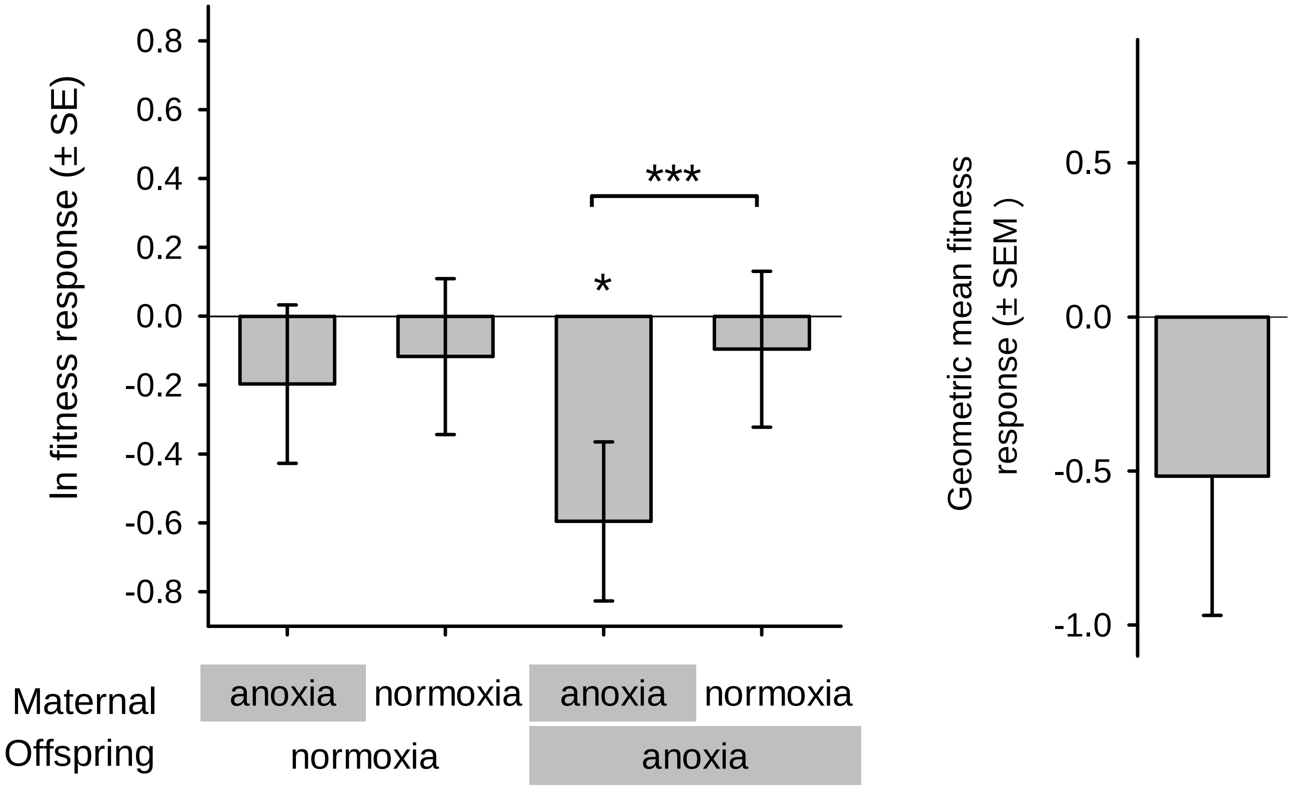
Evolution in Uncorrelated Environments





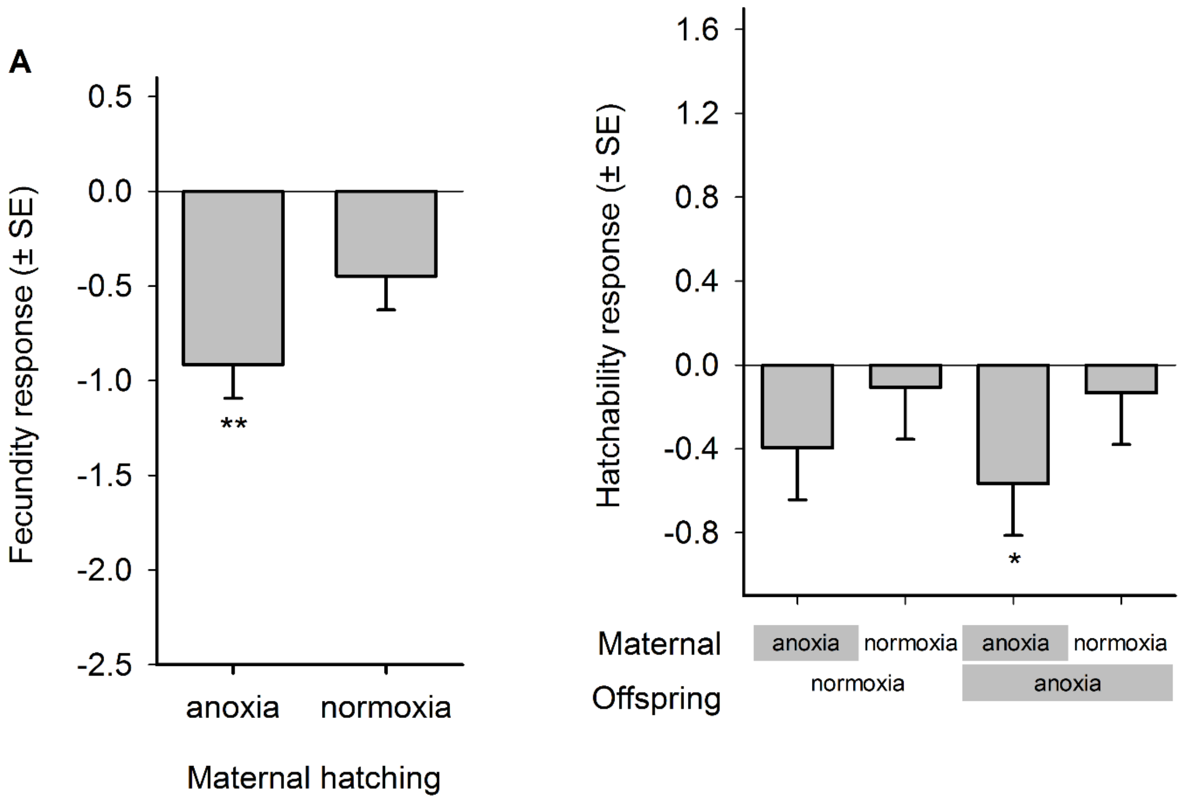
Unpredictable: probability of changing environments of 0.45 across 60 generations as in the other regimes: frequency of anoxia generations of 50%

Adaptation to Unpredictable Environments



Dey et al. Plos Biology (2016)

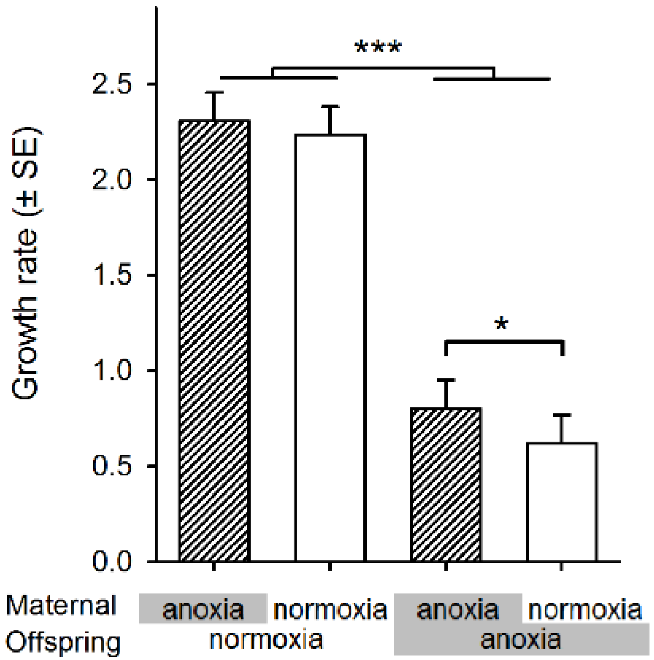
Evolution of Maternal Effects



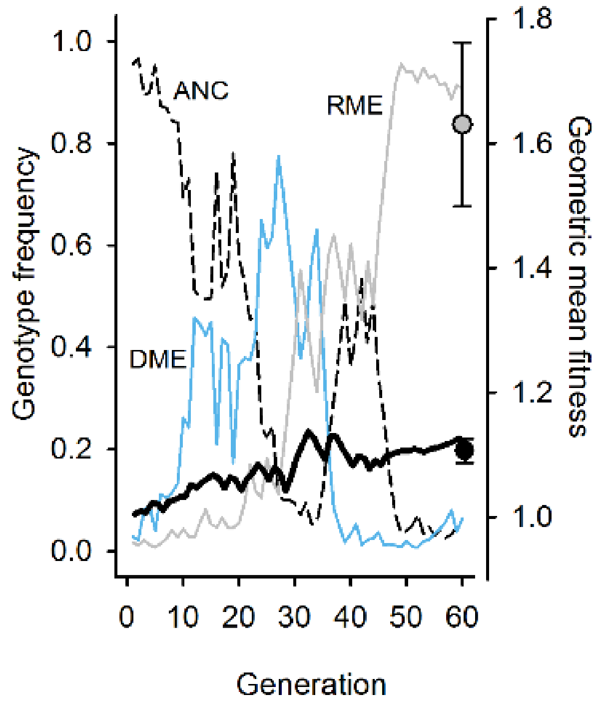
Dey et al. Plos Biology (2016)

Expected Evolution of Randomizing Maternal Effects

Ancestral adaptive state

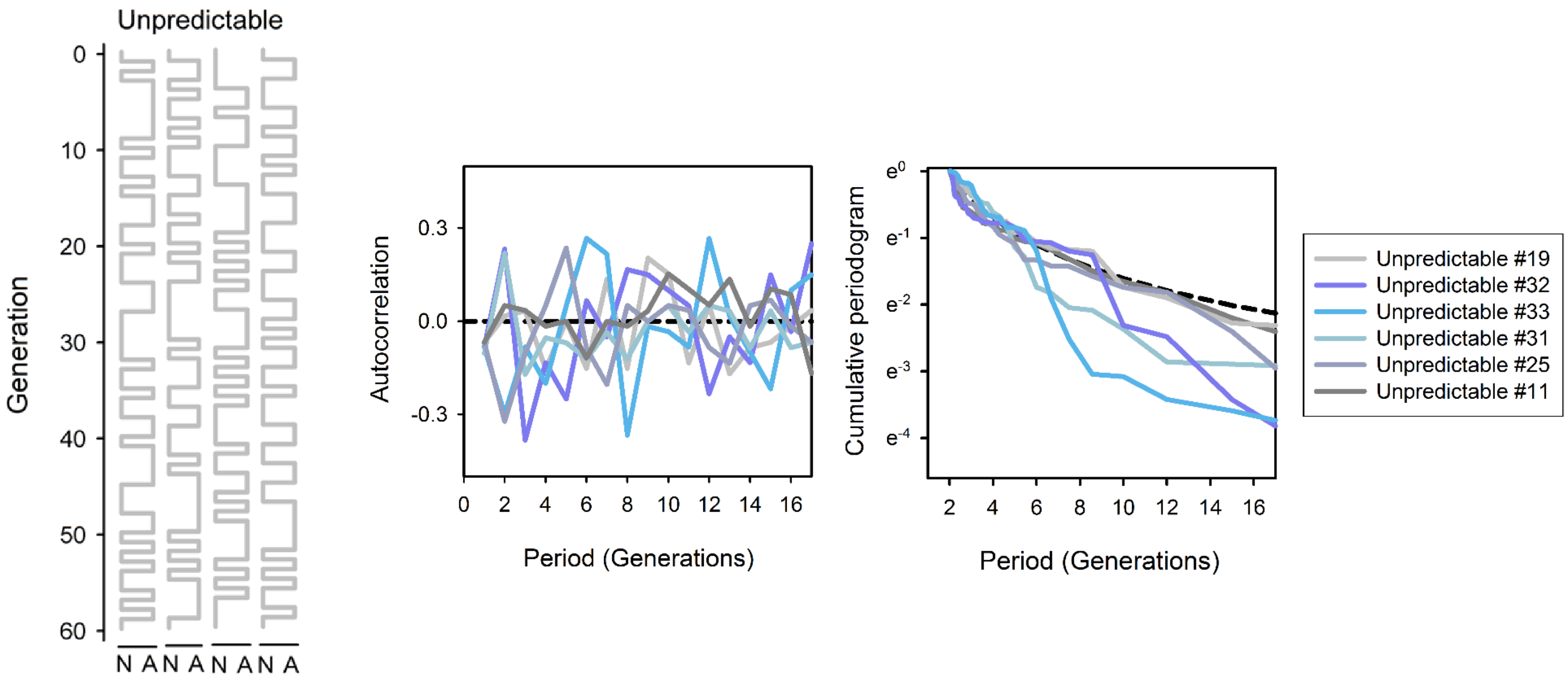


Wright-Fisher numerical simulations under the unpredictable environmental sequences

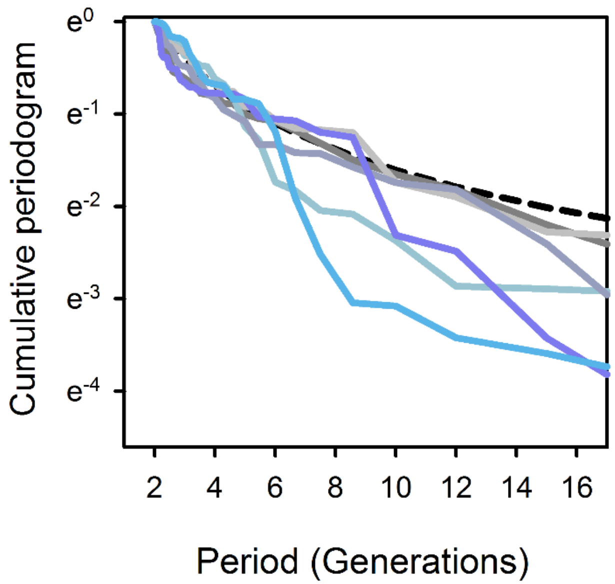


Dey et al. Plos Biology (2016)

Correlated Environmental Sequences

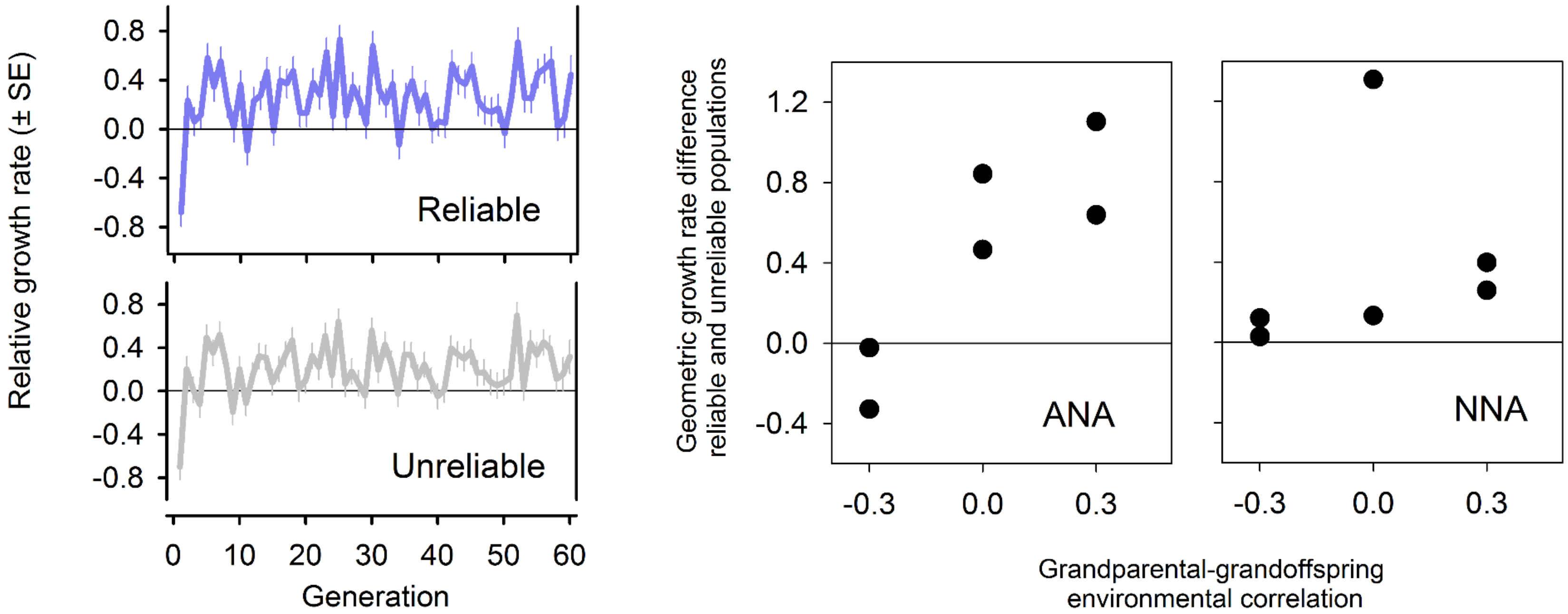


Information and Transgenerational Effects



Unpredictable Reliable: light cue reliably given to mothers during oogenesis whenever their offspring will face anoxia

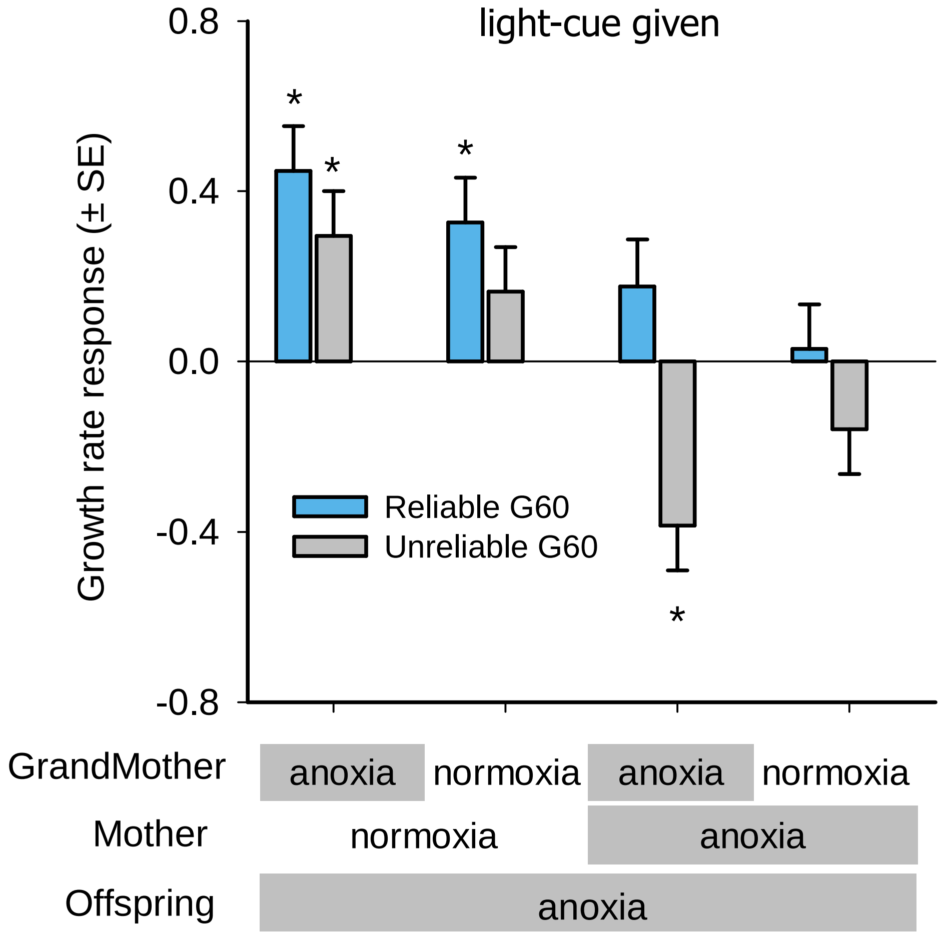
Population Dynamics



?? Grandmothers exposed to anoxia prepare their offspring to perceive the cue in order for them to provision in turn their offspring ??

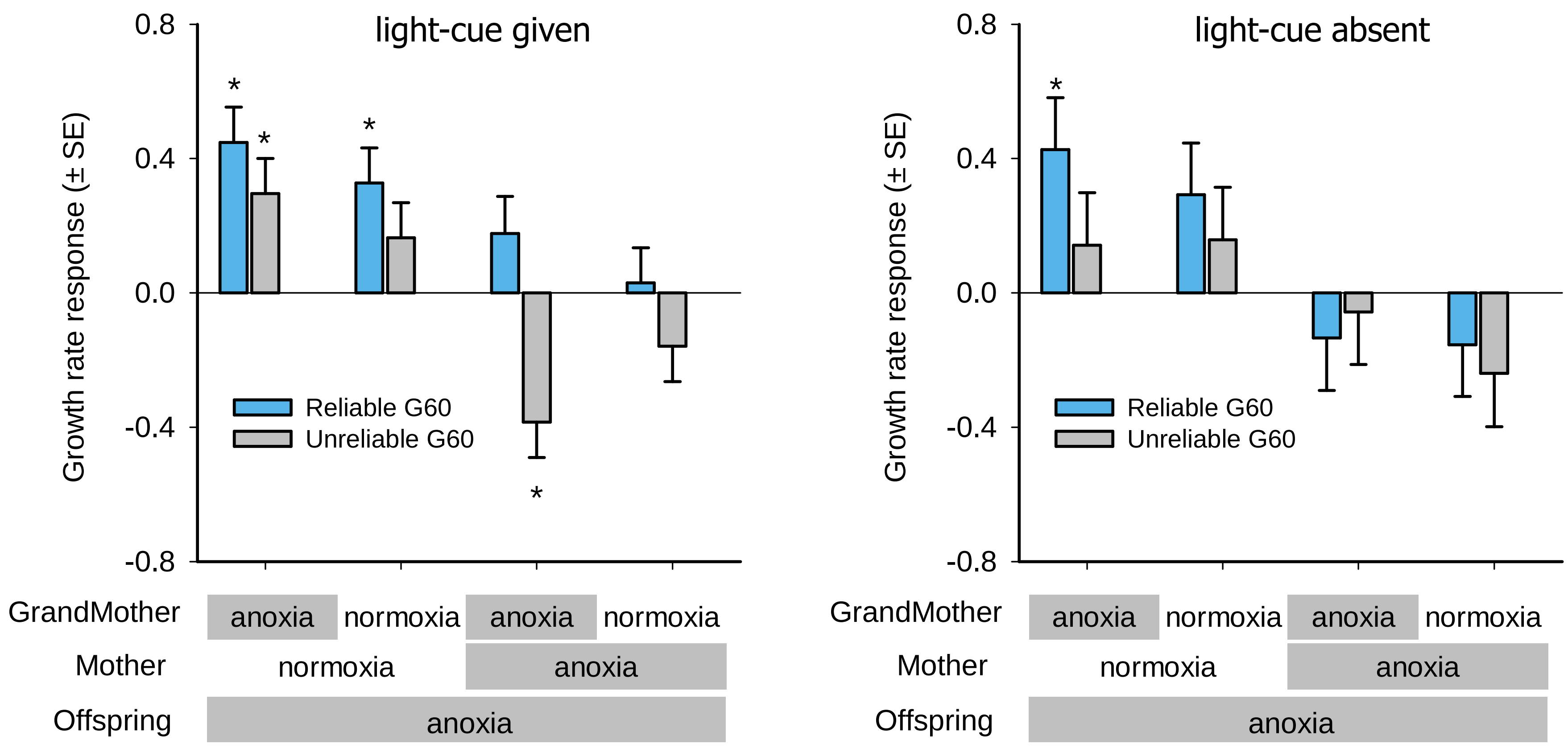
Dey et al. (not published)

Adaptation to Unpredictably Fluctuating Environments?



Dey et al. (not published)

Adaptation to Unpredictably Fluctuating Environments?



Dey et al. (not published)

NS in Variable Environments

. Temporal versus spatial variation
. Within- versus between-generation variation
. Continuous versus discrete variation
. Rates of environmental change versus environmental fluctuations

. Environmental dimensionality (information, cue reliability)

. Evolution by mutation accummulation
. Evolution from pre-existing genetic diversity
. Evolution from standing genetic variation

Collaborators: Christian Braendle (CNRS-Nice), Patrick Phillips (UOregon), Luke Noble and Matt Rockman (NYU), Denis Roze (CNRS-Roscoff), Boris Shraiman (KITP)

Lab Support:

Bruno Afonso, Sara Carvalho, Ivo Chelo, Anna Crist, Hervé Gendrot, Christine Goy, Pablo Ibáñez, Sofia Nunes, Veronica Pereira, Ania Pino, Sara Santos

Funding:

erc ANR NSF

HFSP LABEX MEMO LIFE cnrs

FCT Fundação para a Ciência e a Tecnologia

MINISTÉRIO DA CIÊNCIA, TECNOLOGIA E ENSINO SUPERIOR

Epigenetic Inheritance Model

$$\begin{array}{cc} & \begin{array}{cc} 1 & 2 \end{array} \\ B_i = & \begin{bmatrix} 1-\beta_{i,1} & \beta_{i,1} \\ \beta_{i,2} & 1-\beta_{i,2} \end{bmatrix} \end{array}$$

Matrix determining probability that offspring have phenotype 1 or 2

$$\begin{array}{cc} & \begin{array}{cc} 1 & 2 \end{array} \\ S_i = & \begin{bmatrix} s_{i,1} & 0 \\ 0 & s_{i,2} \end{bmatrix} \end{array}$$

Offspring survivorship in environment *i*

One generation iteration is:

$$N_1 = N_0 S_J B_A$$

Long-run growth of population

For constant reproductive factor: $\lambda = \exp\left[1/T\left(T\log\left[\lambda_{\text{fixed}}\right]\right)\right]$

If per generation multiplier is a random variable then –

$$\lambda = \exp\left[1/T\left(\sum_t \log\left[\lambda_t\right]\right)\right] = \exp\left[\sum_i p_i \log\left[\lambda_i\right]\right]$$

Long-run growth of population : non-scalar

For constant reproductive factor: $$\lambda = \exp\left[1/T\left(T\log\left[\lambda_{\text{fixed}}\right]\right)\right]$$

$$\lambda = \exp\left[1/T\left(\log\left[\begin{bmatrix} n_{1,0} & n_{2,0}\end{bmatrix}\left(B_{E_1}S_{E_1}B_{E_2}S_{E_3}B_{E_3}\ldots\right)\cdot(1,1)\right]\right)\right]$$

For a specific "genotype" that has a pair of B matrices. We can calculate the growth by multiplying together the matrices over time. The lambda that is equivalent to the fixed multiplier is the Lyapunov exponent.