Experimental Evolution & The Evolution of Genetic Architecture

Patrick C. Phillips

Institute for Ecology and Evolution

University of Oregon

pphil@uoregon.edu

@granex

Evolutionary Quantitative Genetics

$$\Delta\bar{z} = G\beta$$

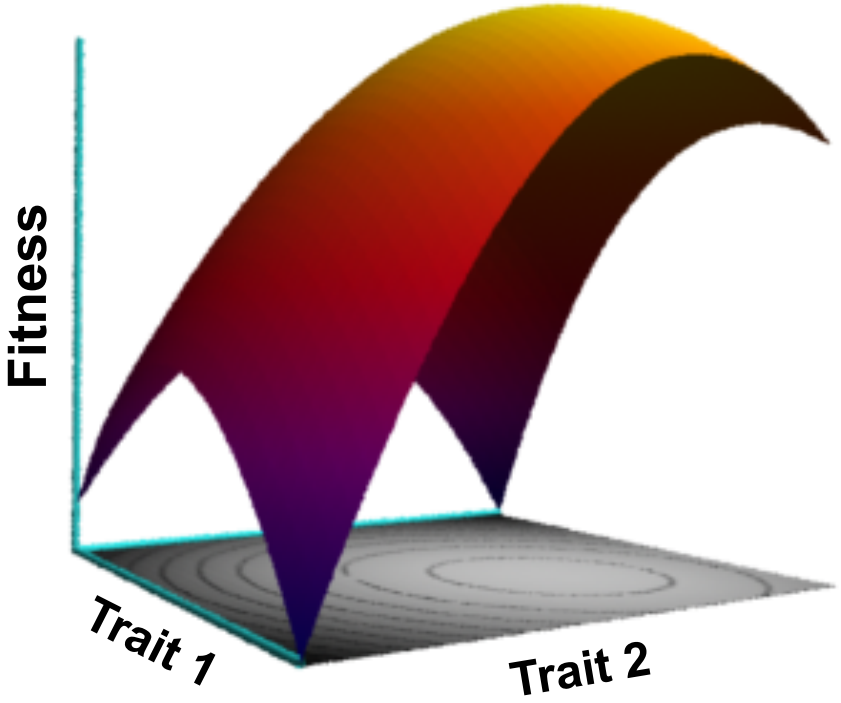
Phenotypic Change

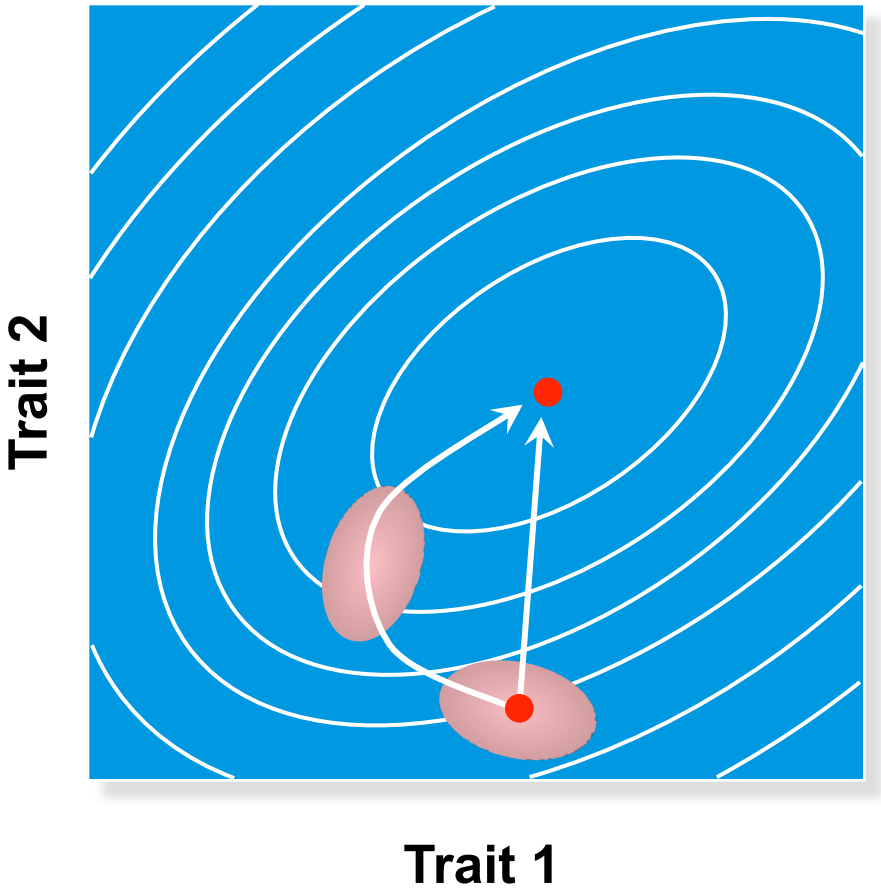
Natural Selection

Genetic Variance and Covariance

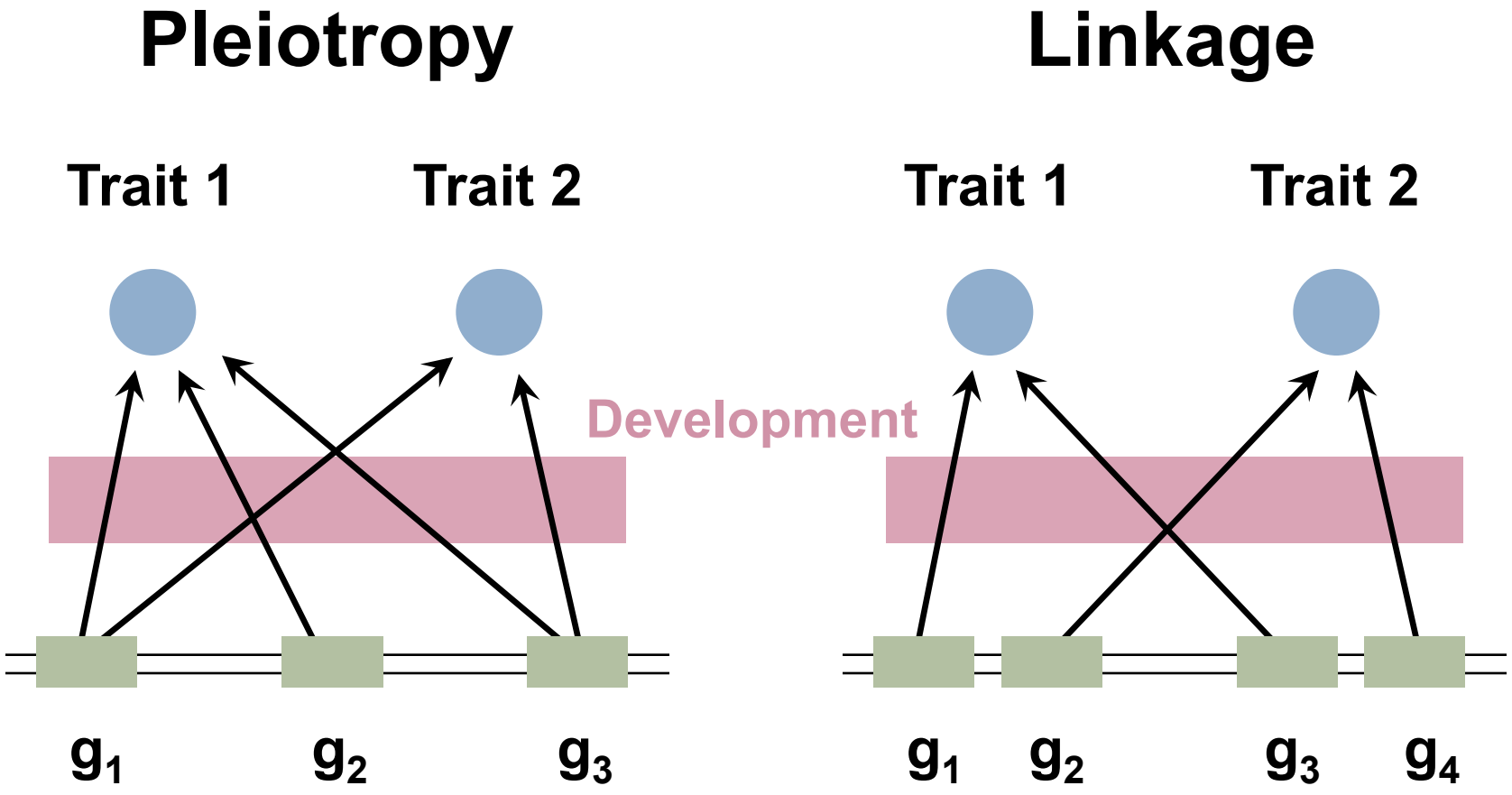
Russ Lande

Evolutionary impact of genetic correlations





Evolution of genetic architecture

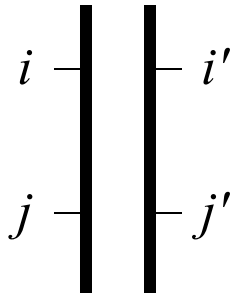


Genetics of genetic covariances

$$\mathbf{G} = 2\sum_{i=1}^{n}\sum_{j=1}^{n}(\mathbf{C}_{ij} + \mathbf{C}'_{ij})$$

Covariance between gametes

Covariance within a gamete



Genetics of genetic covariances

Effects single loci on multiple traits (for locus i):

$$\mathbf{C}_{ii} = \mathrm{E}\left[\begin{pmatrix} (x_{i1}-\bar{x}_{i1})^2 & (x_{i1}-\bar{x}_{i1})(x_{i2}-\bar{x}_{i2}) \\ (x_{i1}-\bar{x}_{i1})(x_{i2}-\bar{x}_{i2}) & (x_{i2}-\bar{x}_{i2})^2 \end{pmatrix}\right] = \begin{pmatrix} \sigma^2_{i1} & \sigma_{i1i2} \\ \sigma_{i1i2} & \sigma^2_{i2} \end{pmatrix}$$

Additive genetic variance

Covariance from pleiotropy

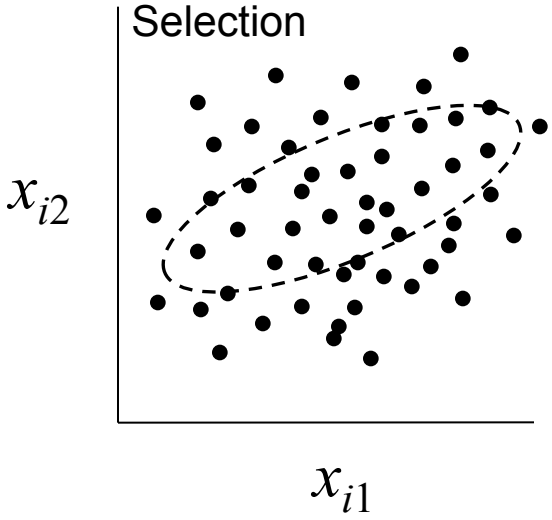
Effects pairs of loci on multiple traits (for loci i and j):

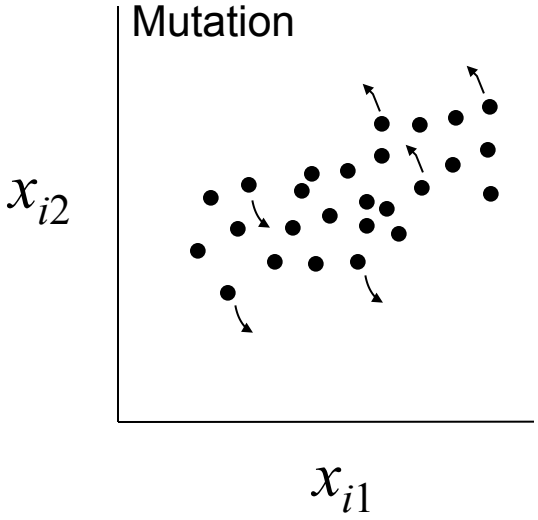
$$\mathbf{C}_{ij} = \mathrm{E}\left[\begin{pmatrix} (x_{i1}-\bar{x}_{i1})(x_{j1}-\bar{x}_{j1}) & (x_{i1}-\bar{x}_{i1})(x_{j2}-\bar{x}_{j2}) \\ (x_{i2}-\bar{x}_{i2})(x_{j1}-\bar{x}_{j1}) & (x_{i2}-\bar{x}_{i2})(x_{j2}-\bar{x}_{j2}) \end{pmatrix}\right] = \begin{pmatrix} \sigma_{i1j1} & \sigma_{i1j2} \\ \sigma_{i2j1} & \sigma_{i2j2} \end{pmatrix}$$

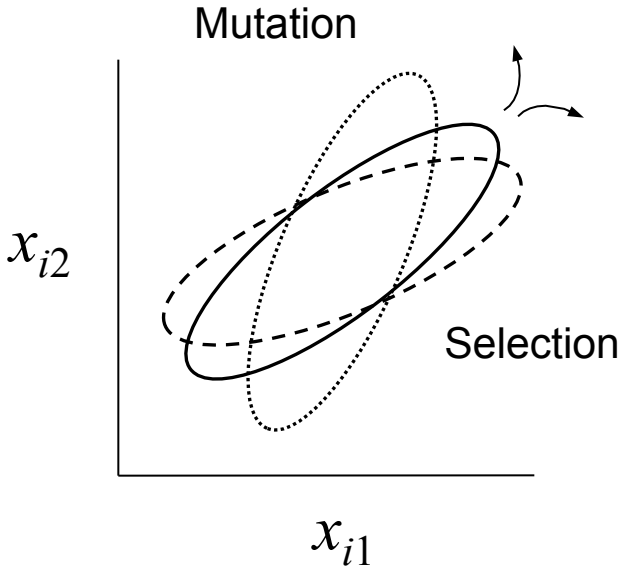
Linkage on variation, single trait

Linkage on covariance between traits

Evolution of the G matrix

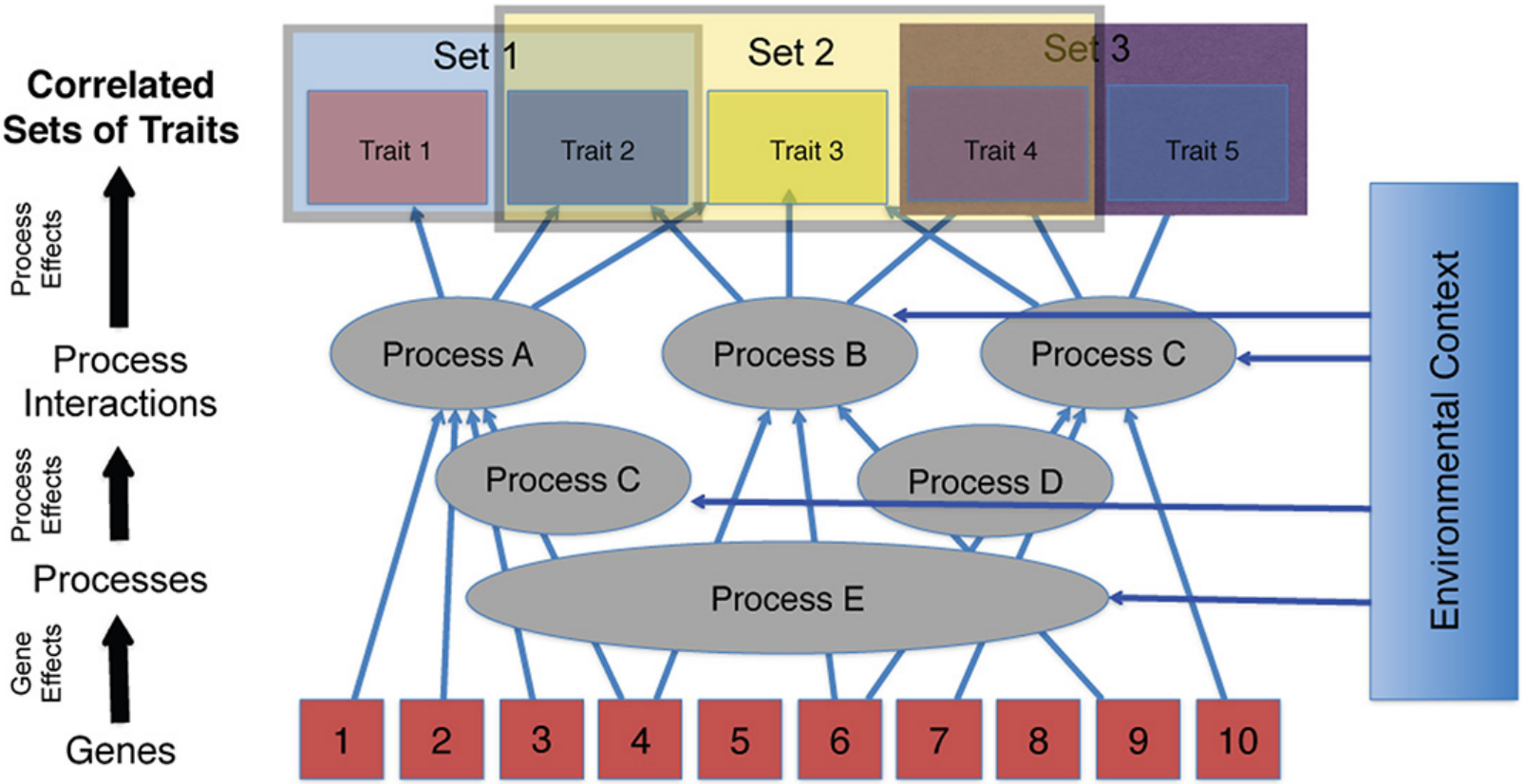






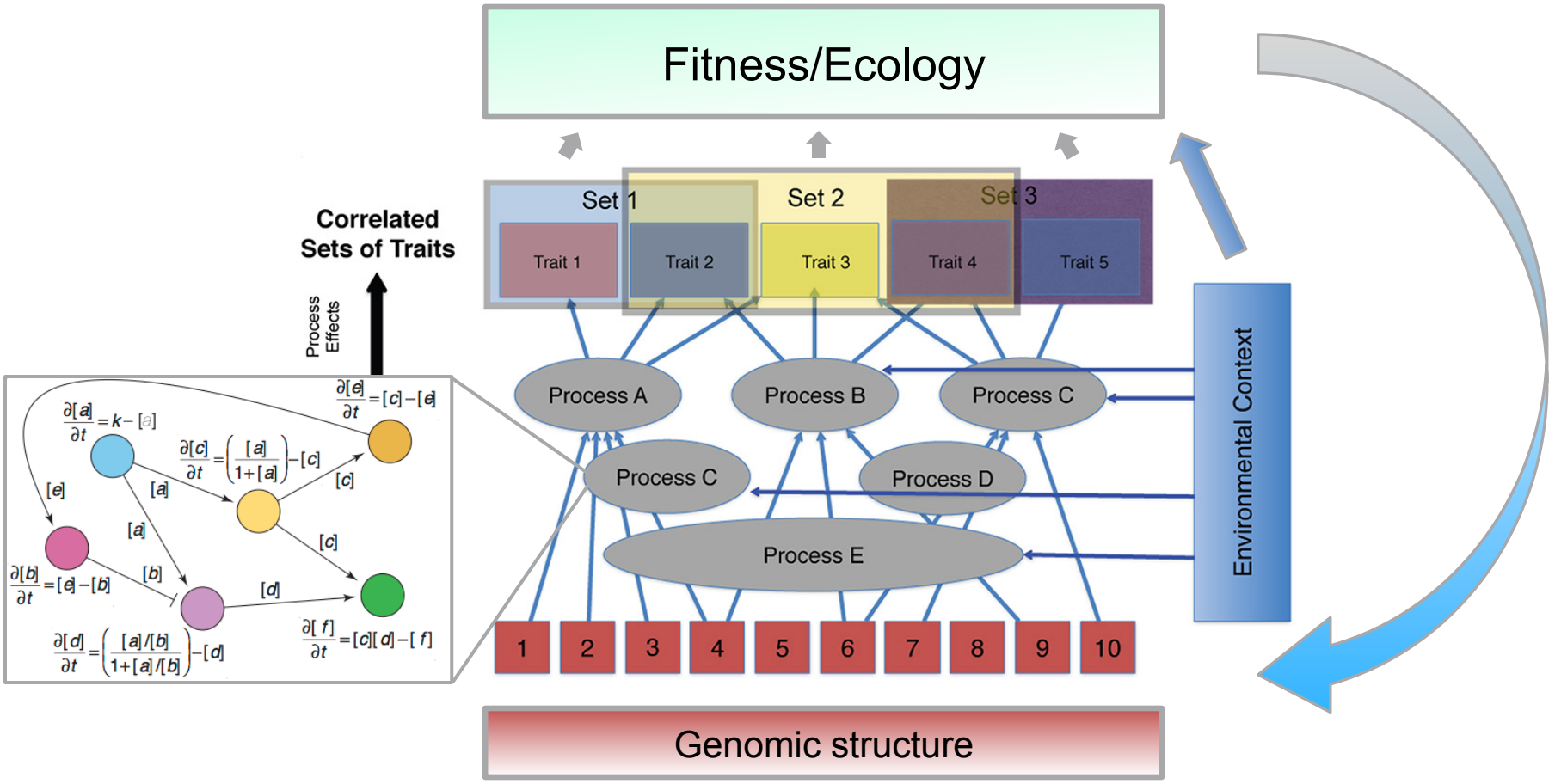
Pleiotropy is a property of alleles not loci

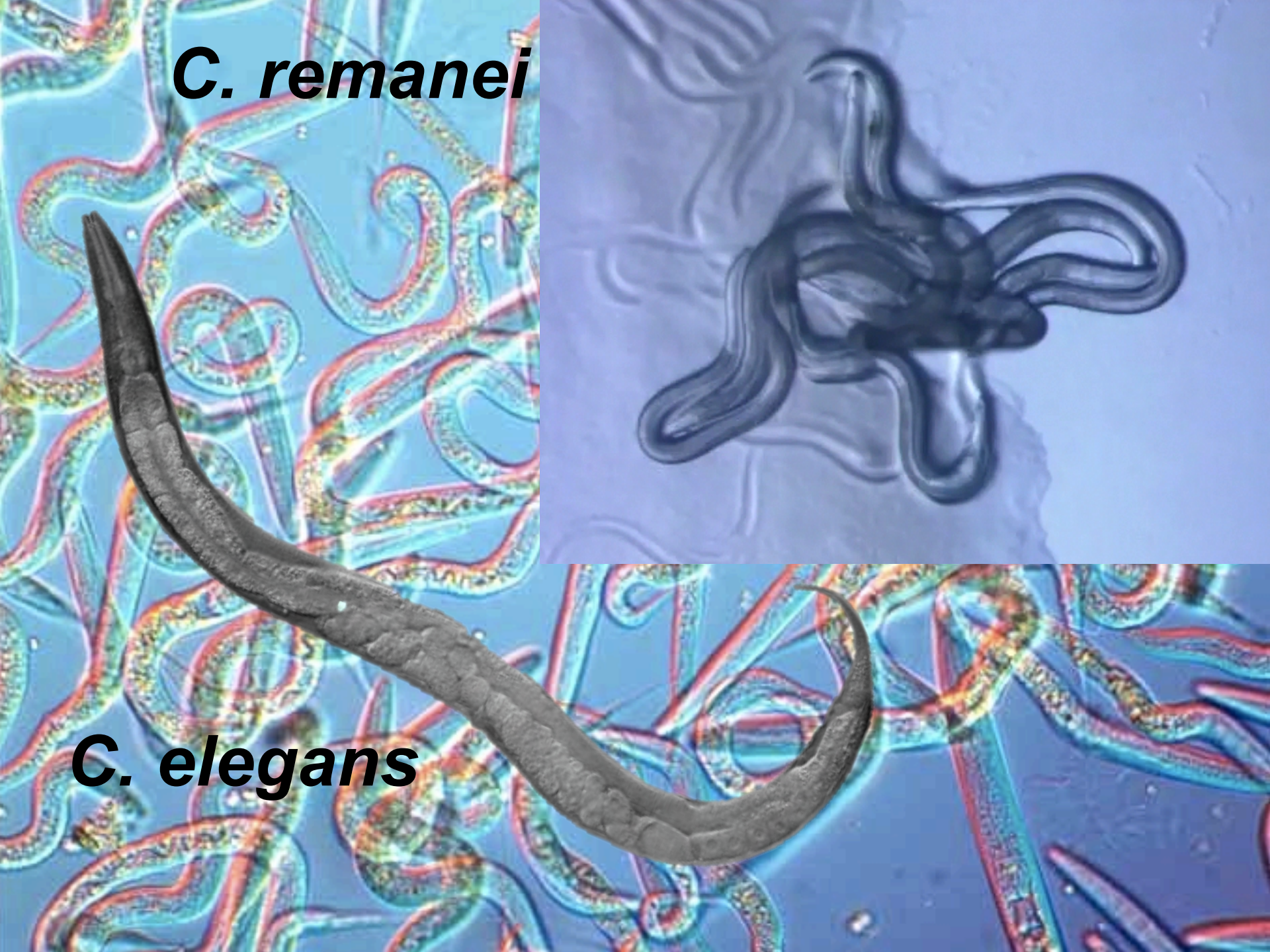
Systems biology



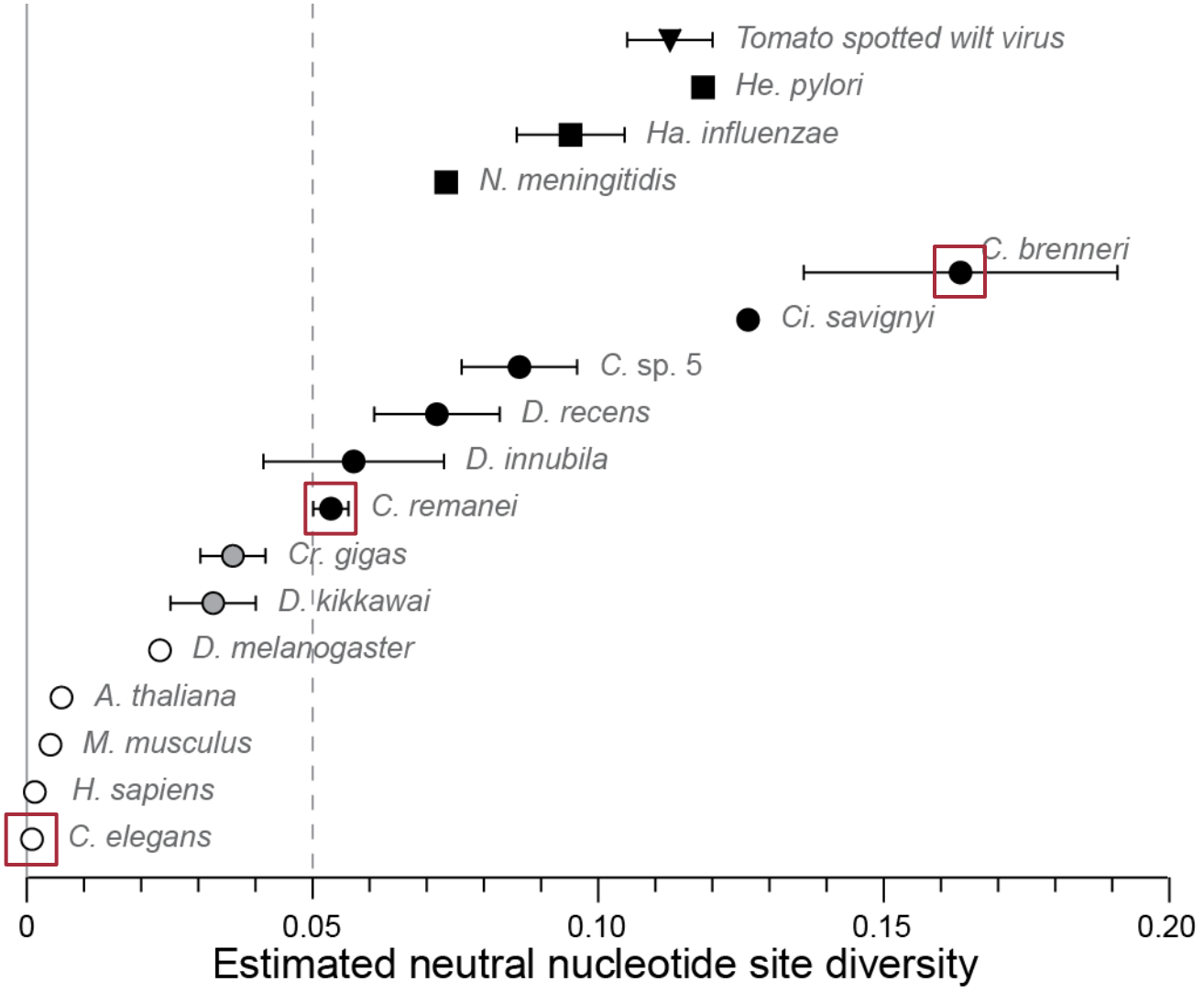
Halligrimsson et al. 2014 PLoS Genetics

Evolutionary systems biology



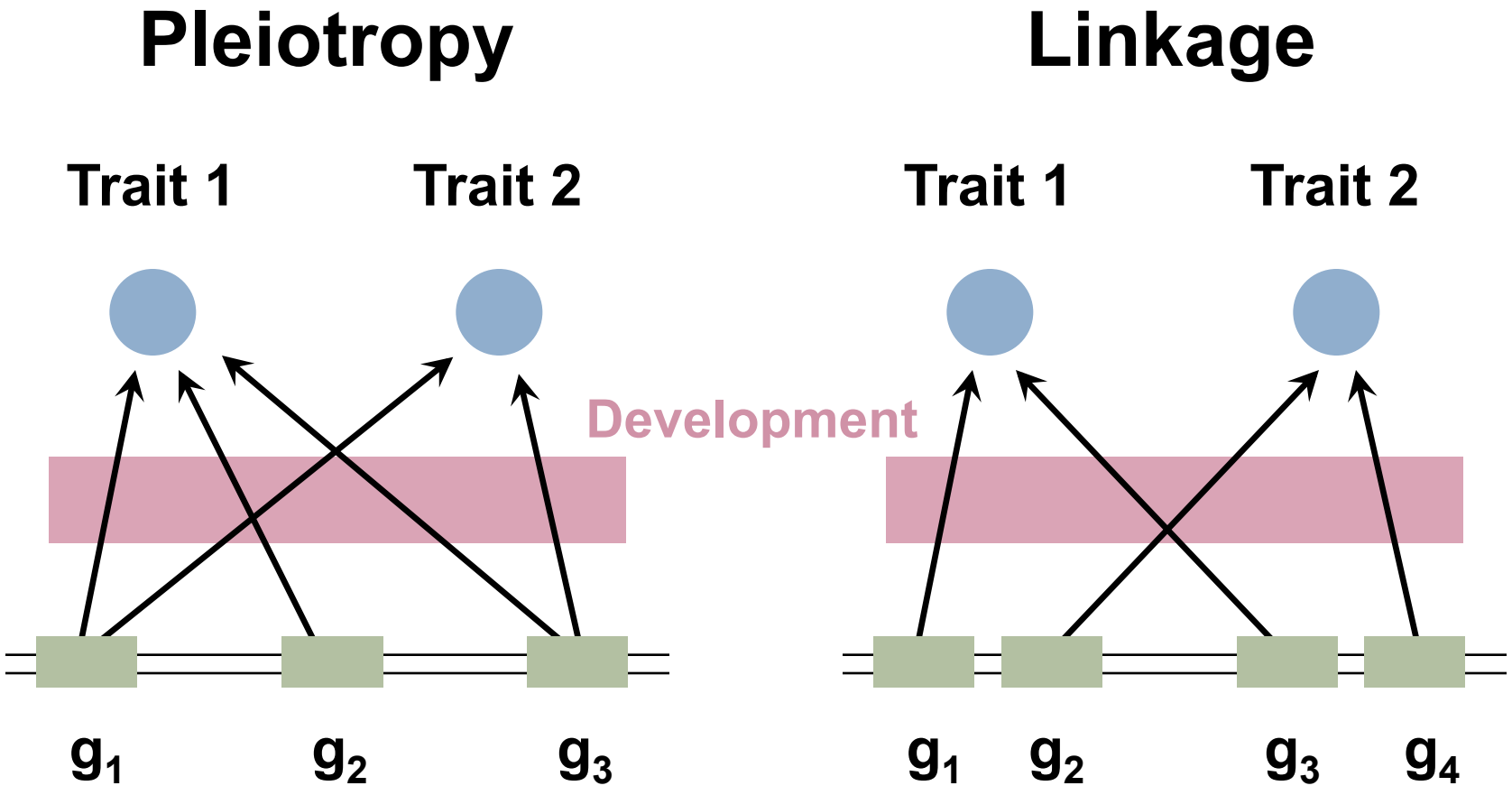

C. remanei
C. elegans

Hyper-diversity in nematodes

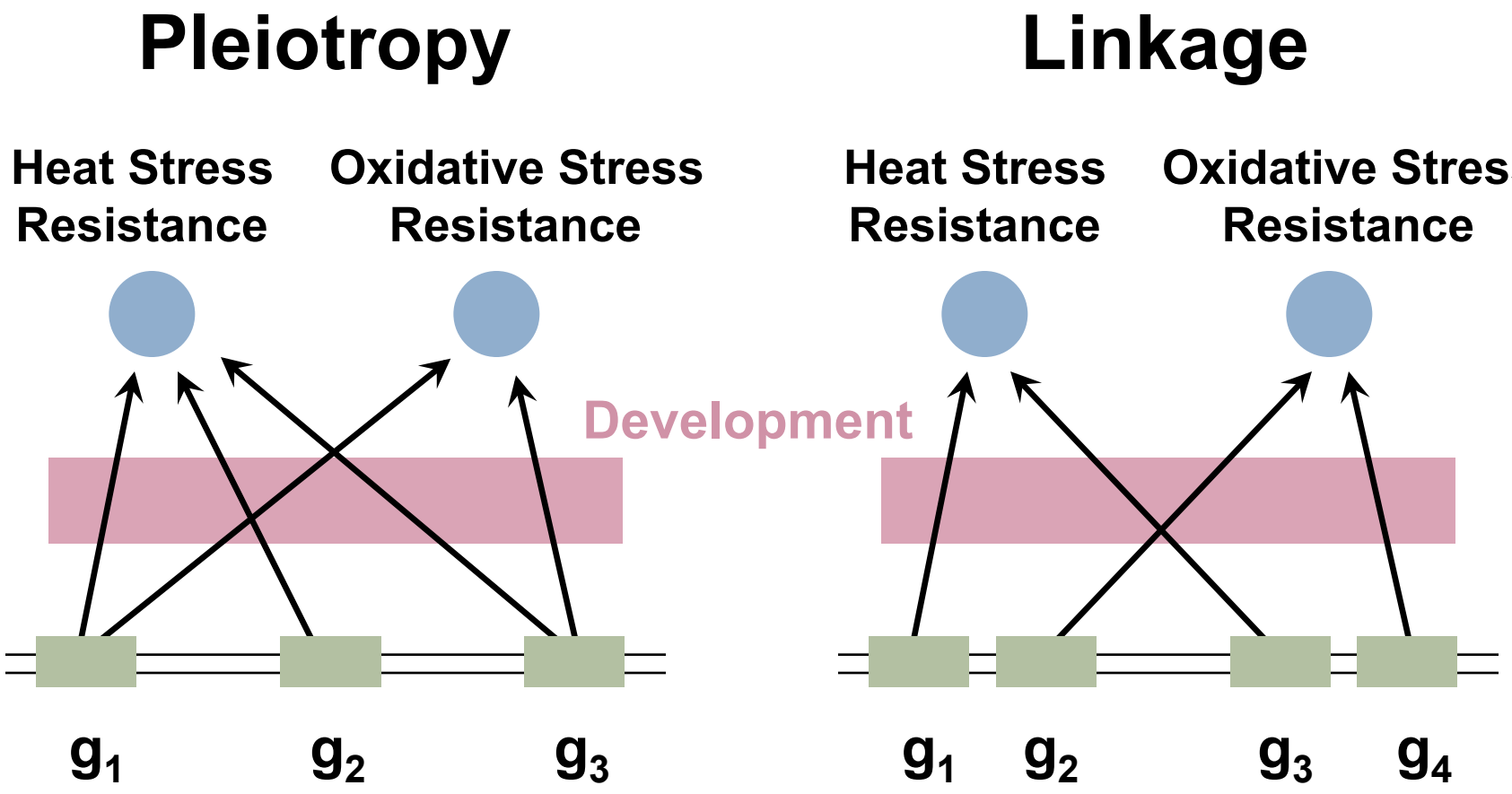


Cutter et al. 2013 Mol Ecol

Evolution of genetic architecture



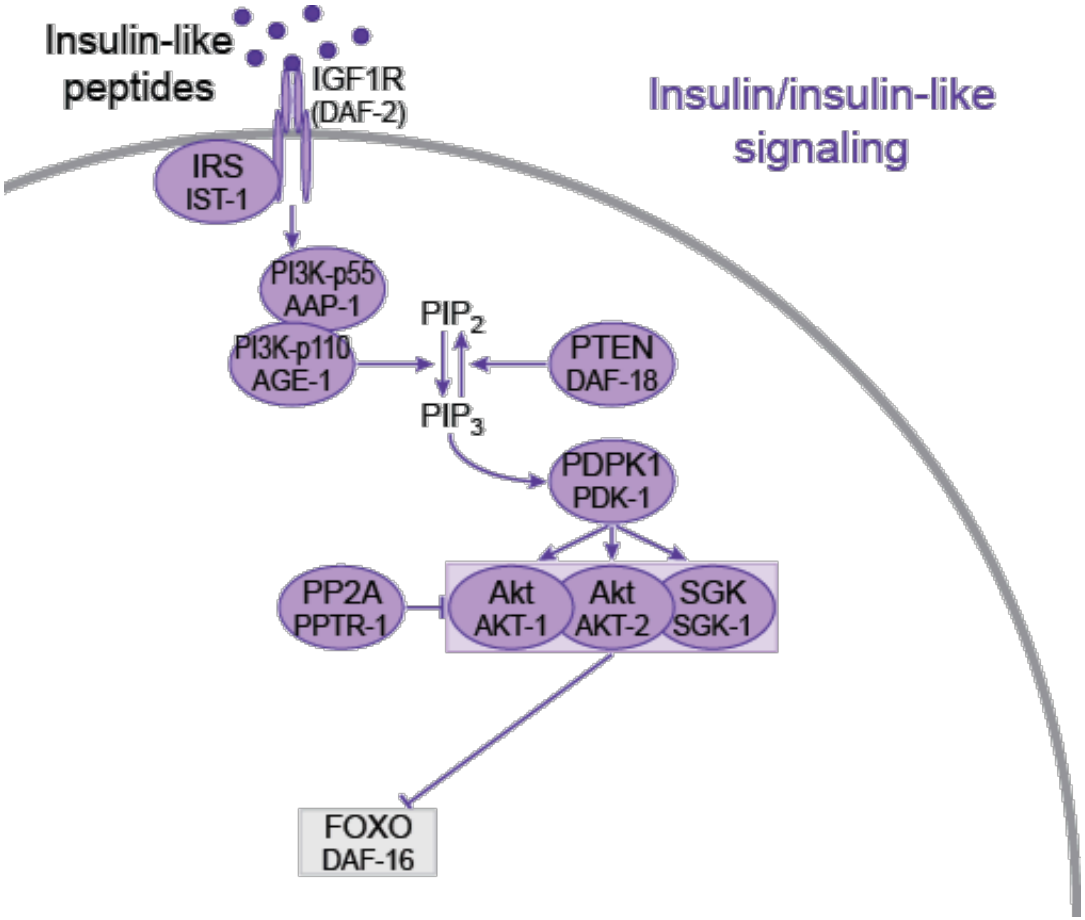
Evolution of genetic architecture



Themes

- Sufficiency of quantitative genetics theory

Stress response pathways



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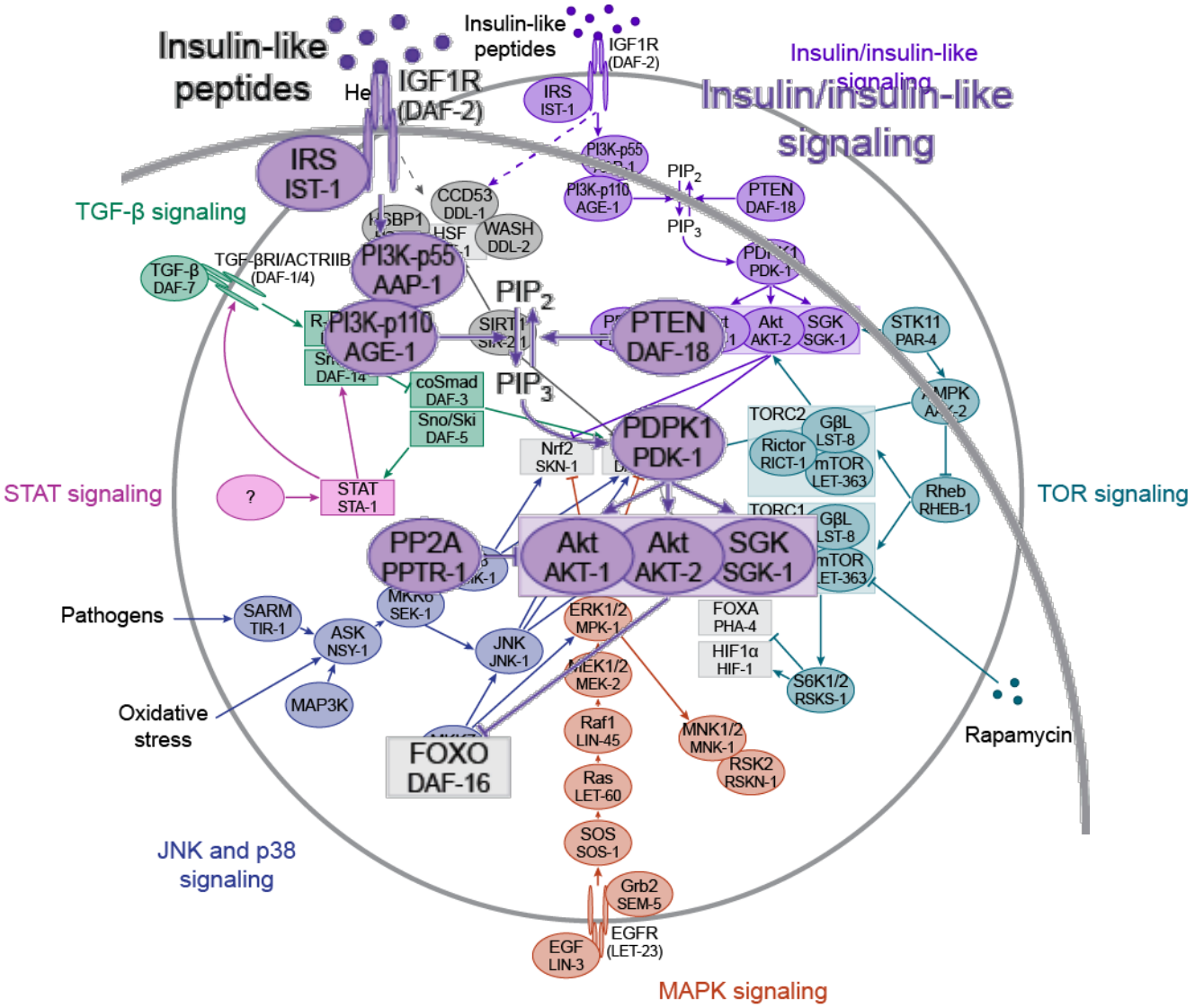

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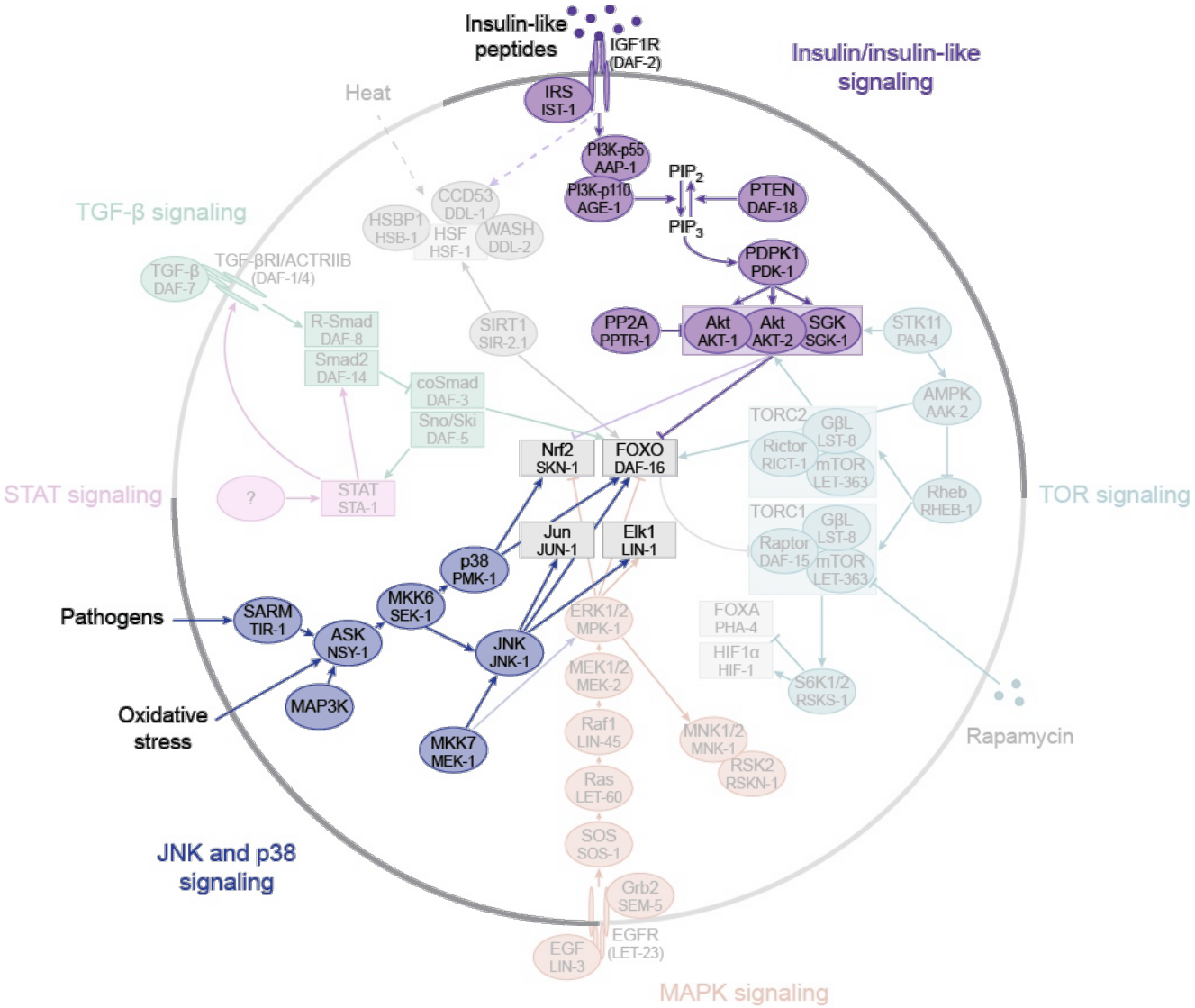
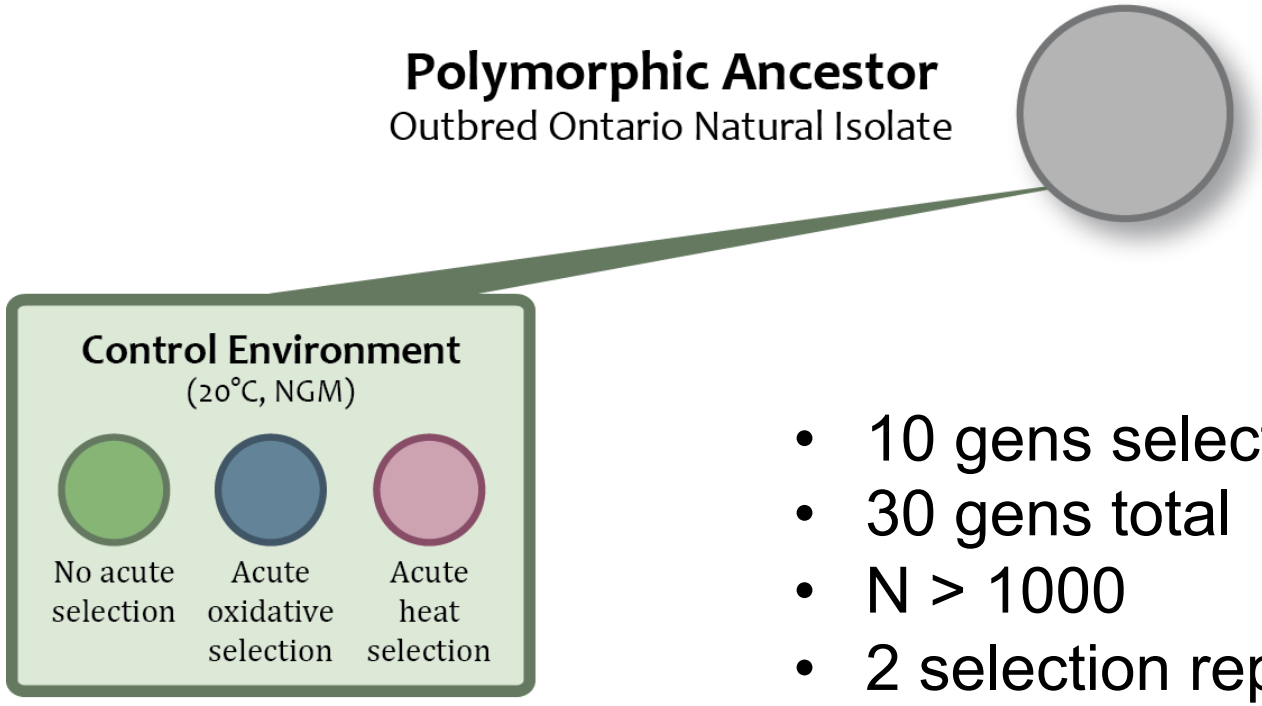


Themes

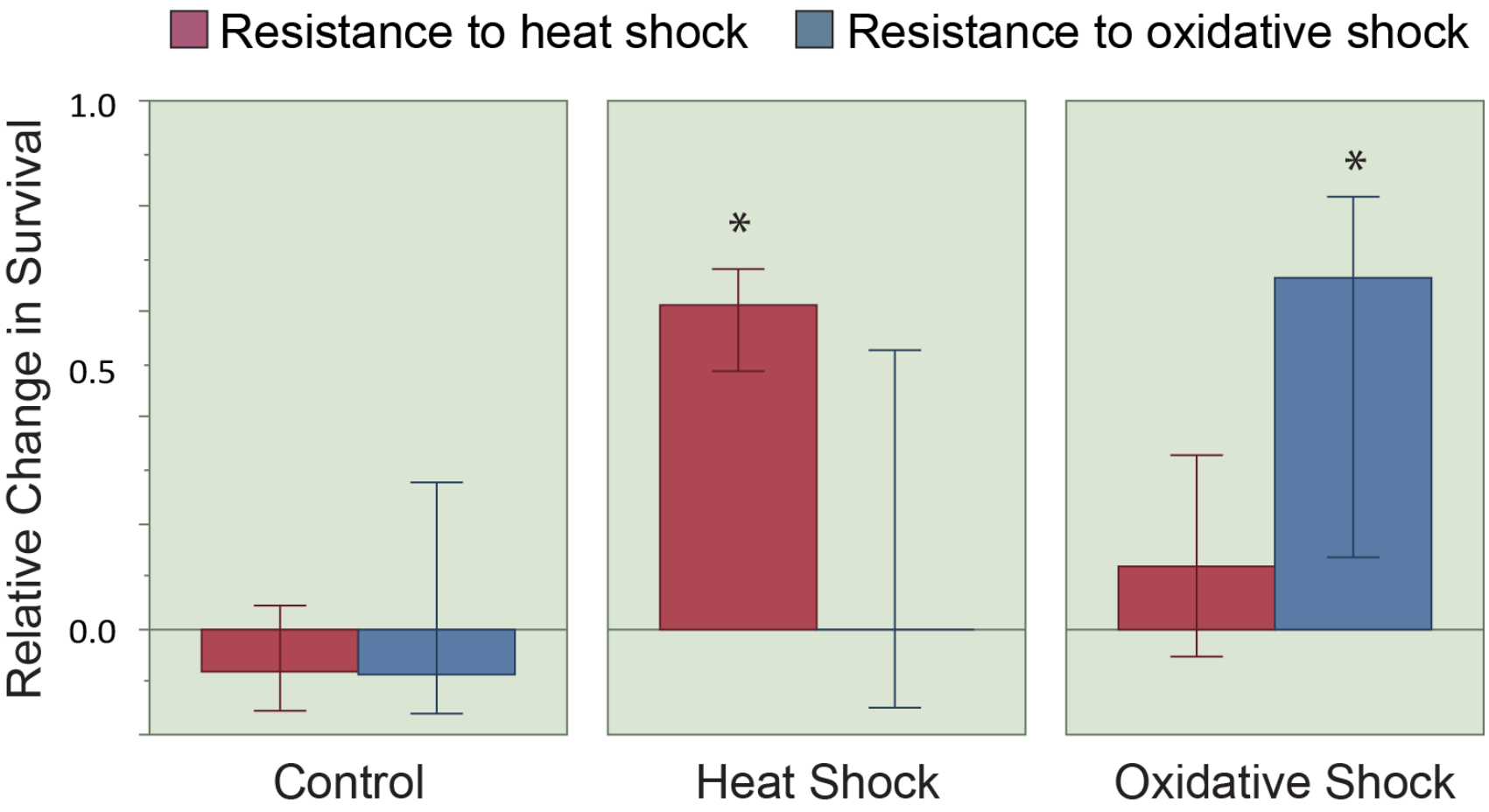
- Sufficiency of quantitative genetics theory
- Experimental evolution as a closed inferential system

Selection for stress resistance

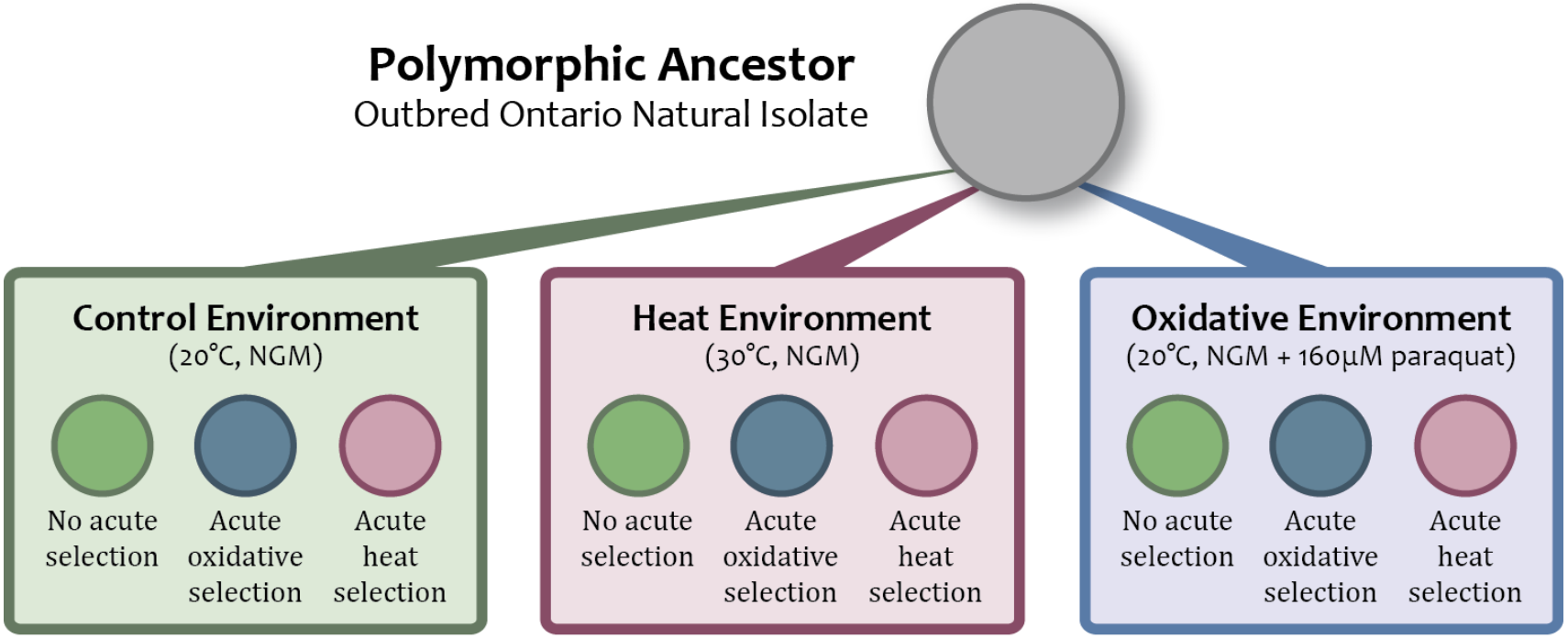


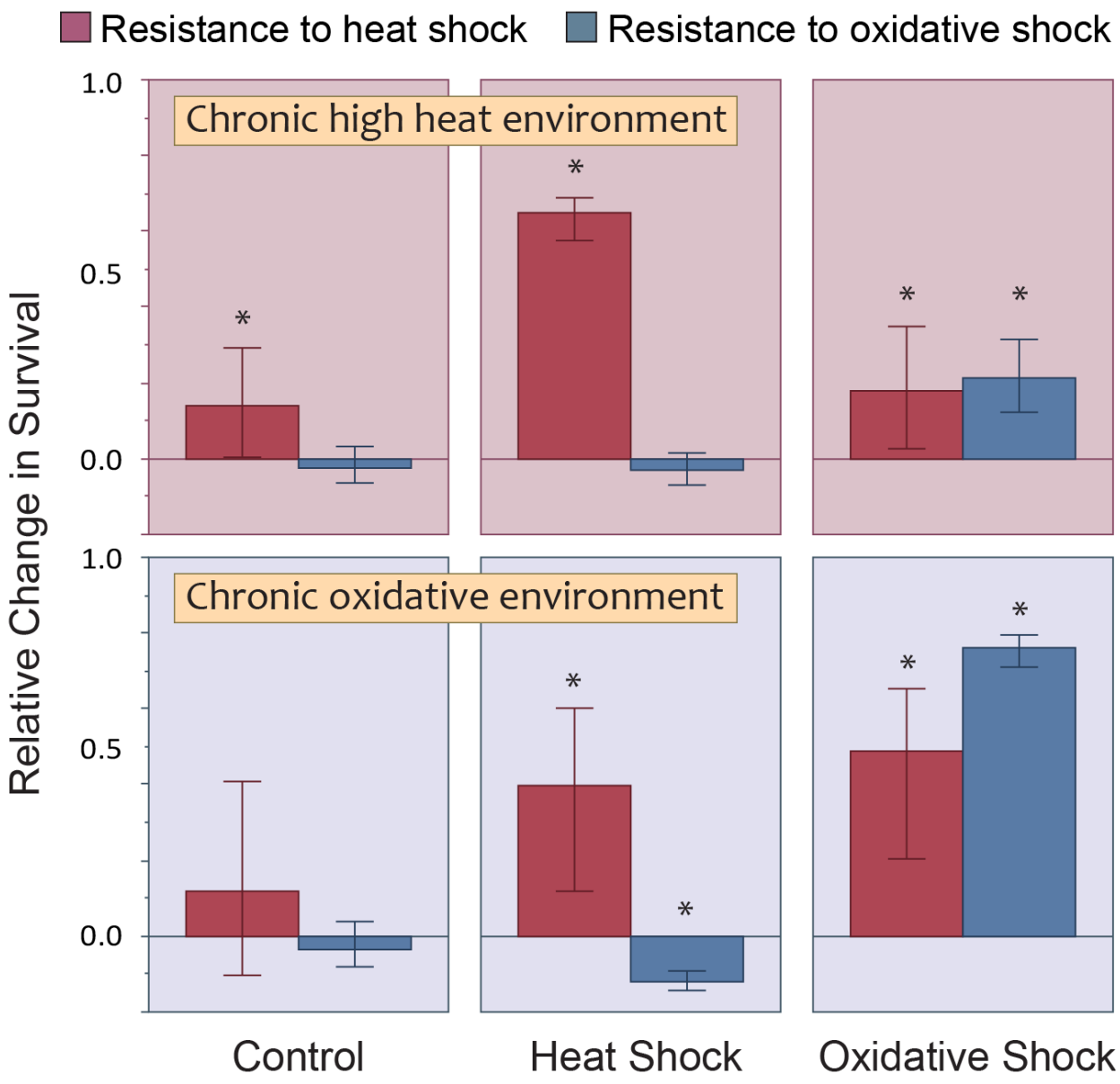
- 10 gens selection
- 30 gens total
- N > 1000
- 2 selection replicates
- 100,000's individuals assayed

Correlated responses to selection



Selection for stress resistance




Resistance to heat shock
Resistance to oxidative shock
Chronic high heat environment
Chronic oxidative environment
Relative Change in Survival
1.0
0.5
0.0
1.0
0.5
0.0
*
*
*
*
*
*
*
*
Control
Heat Shock
Oxidative Shock

Patterns of genetic correlation

- Usually no pleiotropy for segregating variation for heat and oxidative shock resistance
- Correlated responses to selection depend on environmental context
- Correlated responses can be asymmetrical and in opposite directions

Hidden selection or variation?

"Cryptic Genetic (co)Variation"

$$\Delta\bar{z}_1 = G_{11}\beta_1 + G_{12}\beta_2$$
$$\Delta\bar{z}_2 = G_{12}\beta_1 + G_{22}\beta_2$$

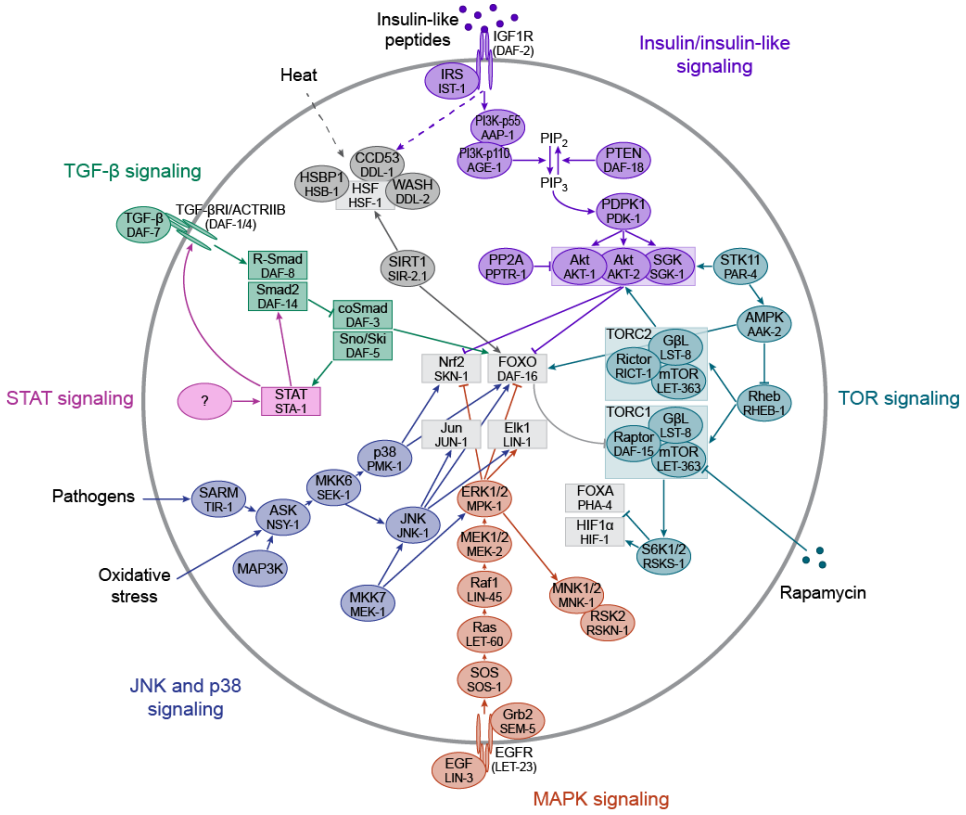
Rapidly evolving **G**

"Cryptic Selection"

$$\Delta\bar{z}_1 = G_{11}\beta_1 + G_{12}\beta_2 + G_{13}\beta_3$$
$$\Delta\bar{z}_2 = G_{12}\beta_1 + G_{22}\beta_2 + G_{23}\beta_3$$

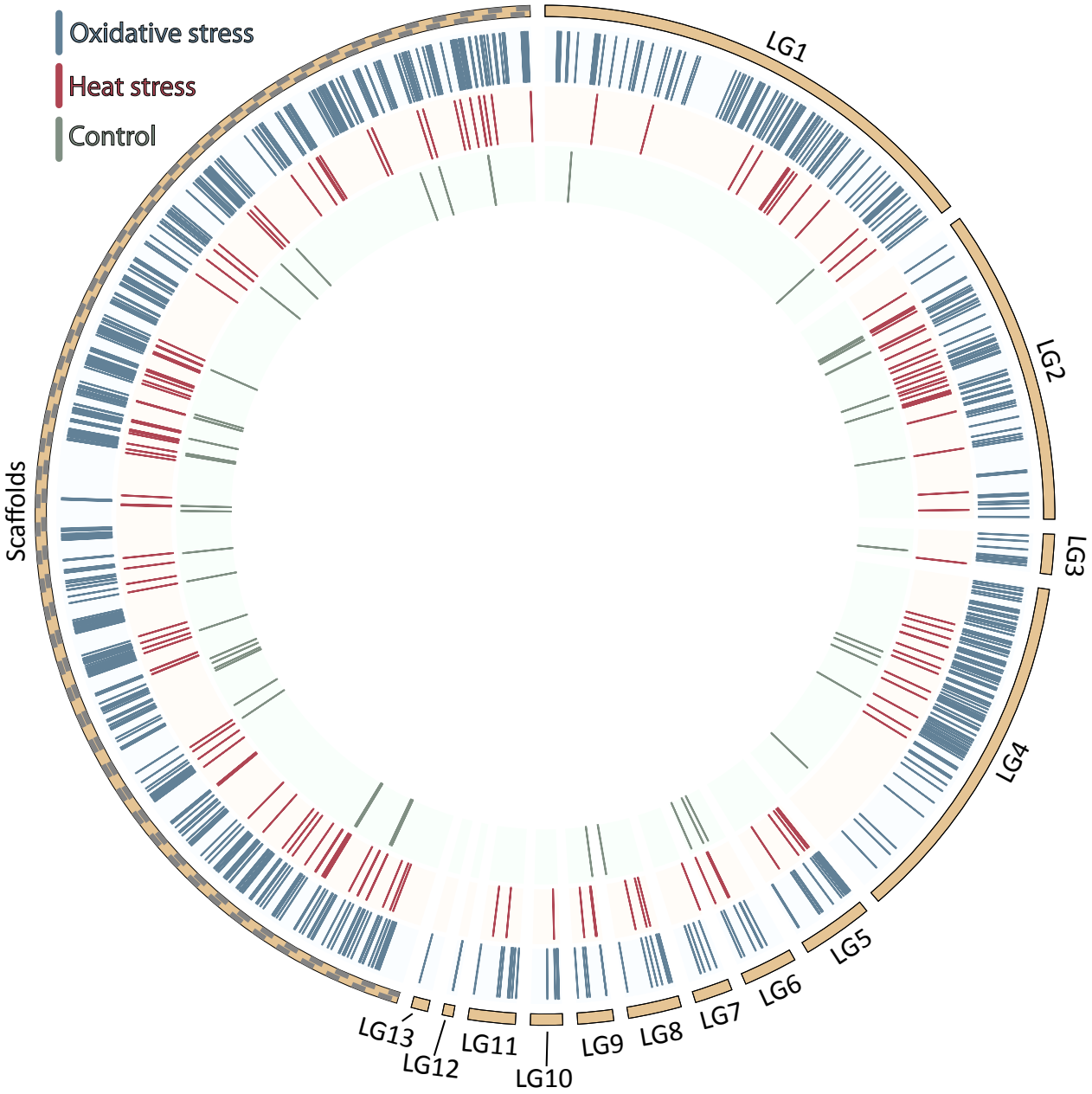
Themes

- Sufficiency of quantitative genetics theory
- Experimental evolution as a closed inferential system



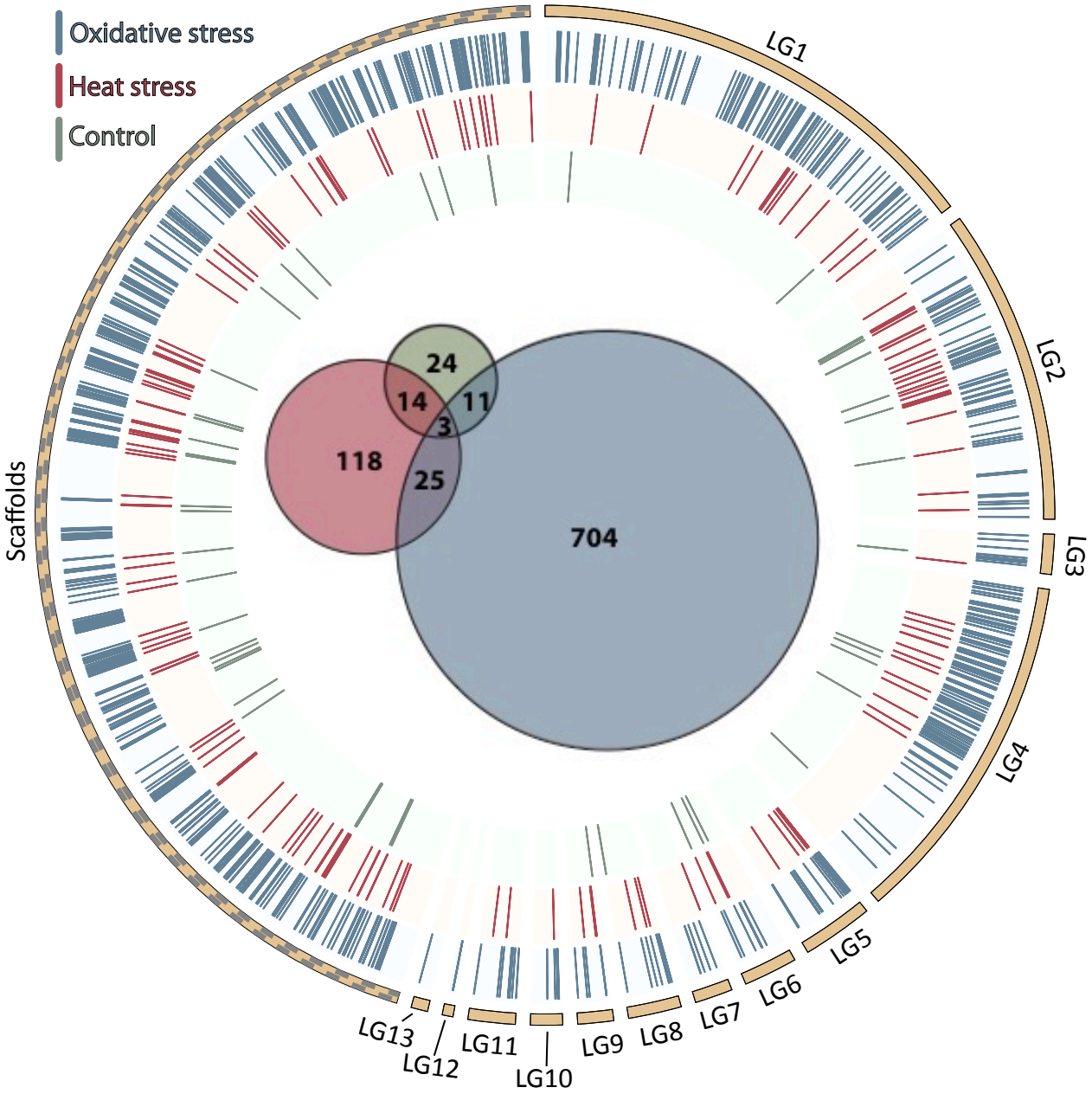
Variation in pleiotropy across complex genetic networks

Constitutive changes in gene expression



Kristin Sikkink
Christine O'Connor

Constitutive changes in gene expression



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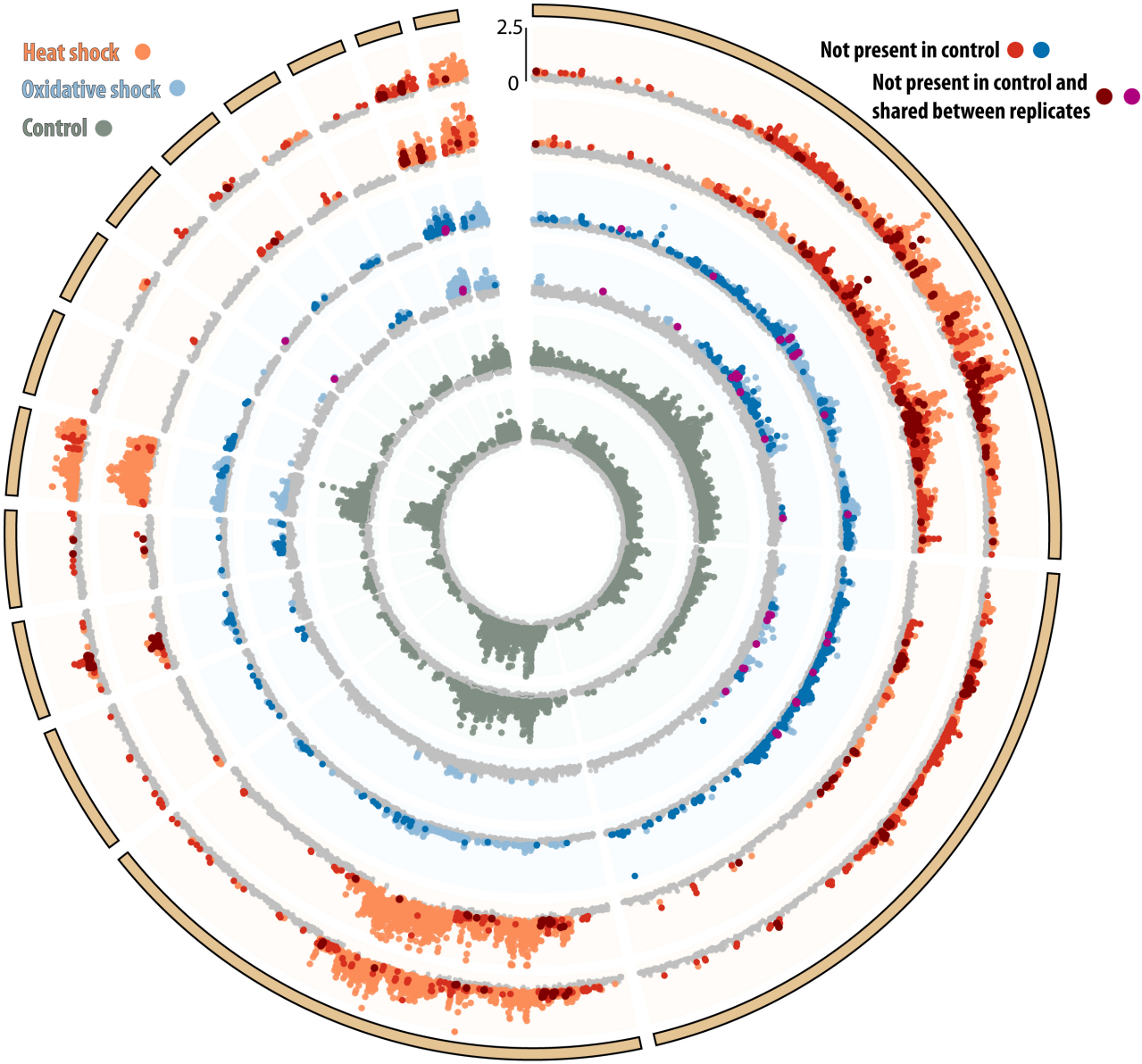
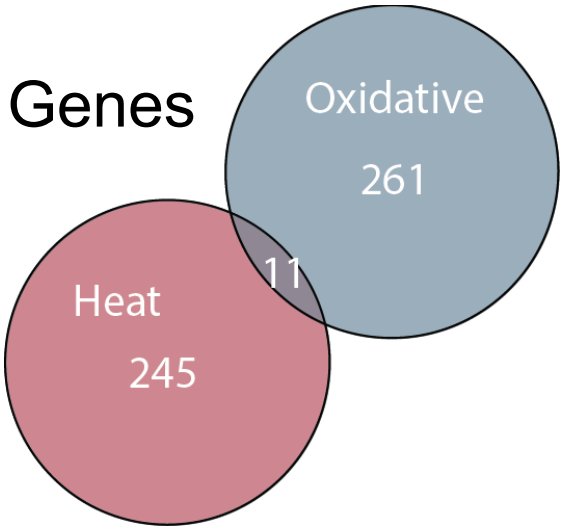
Genomic basis of evolutionary change

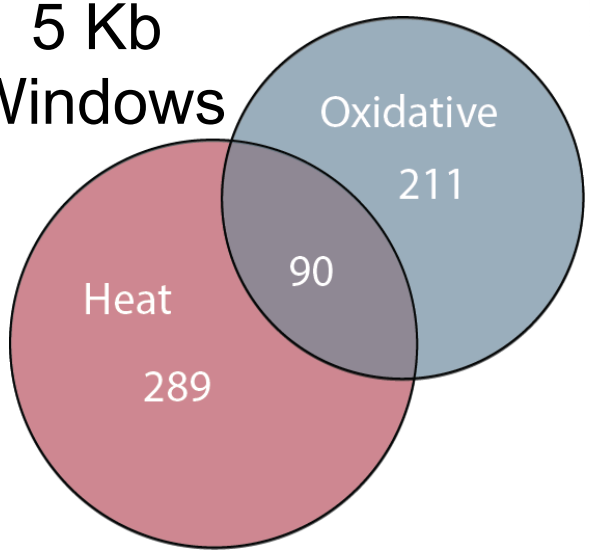


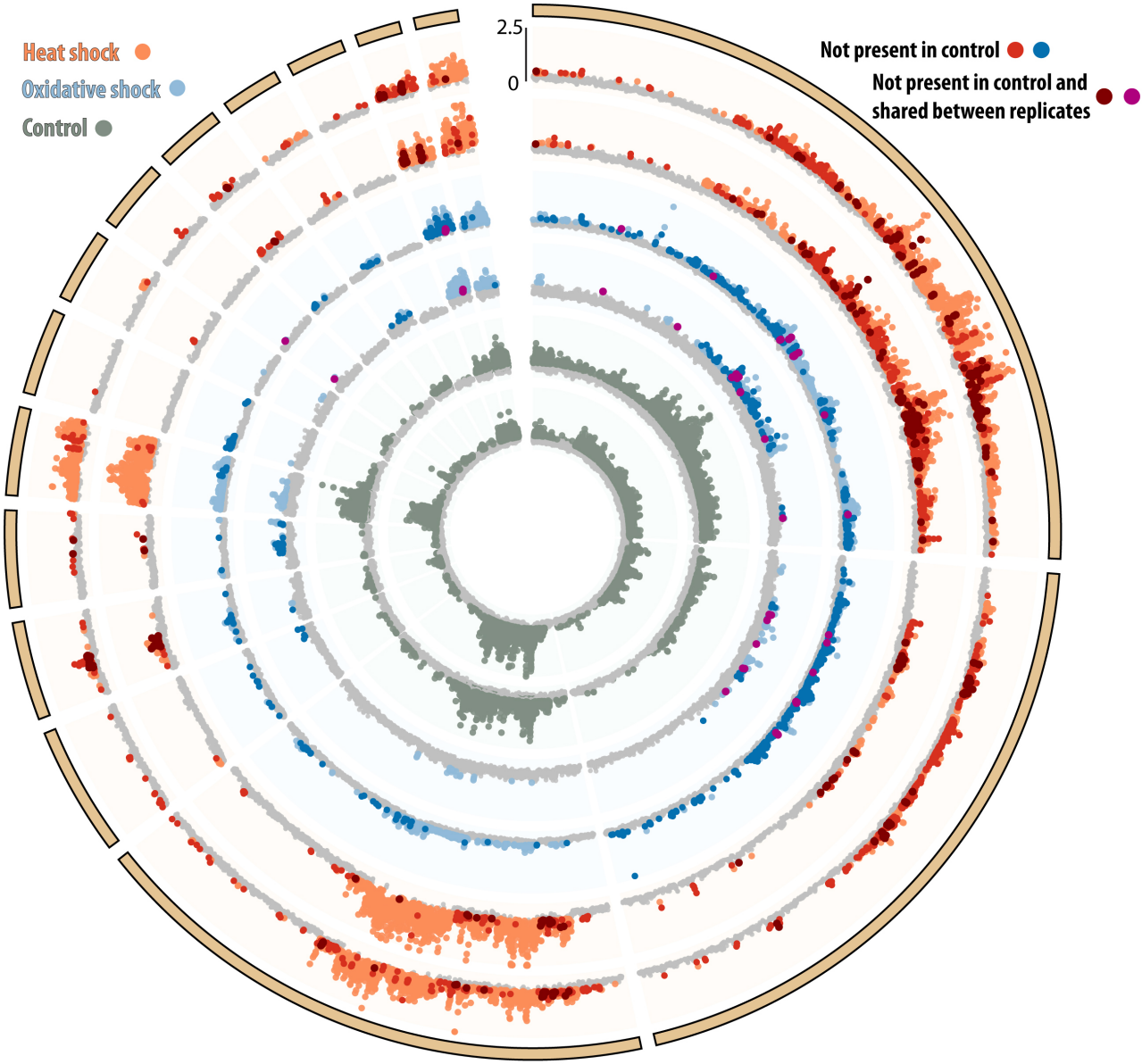
Genomic basis of evolutionary change

Genes

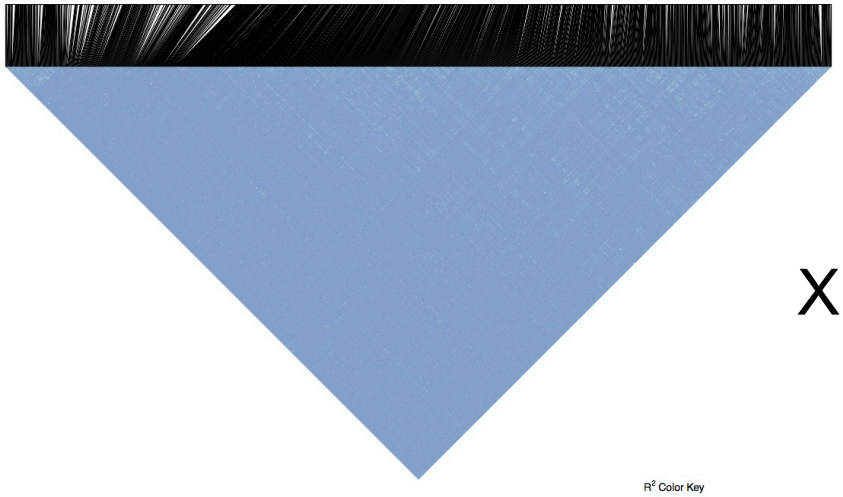


5 Kb Windows

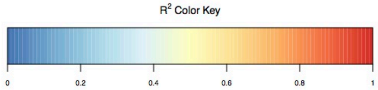


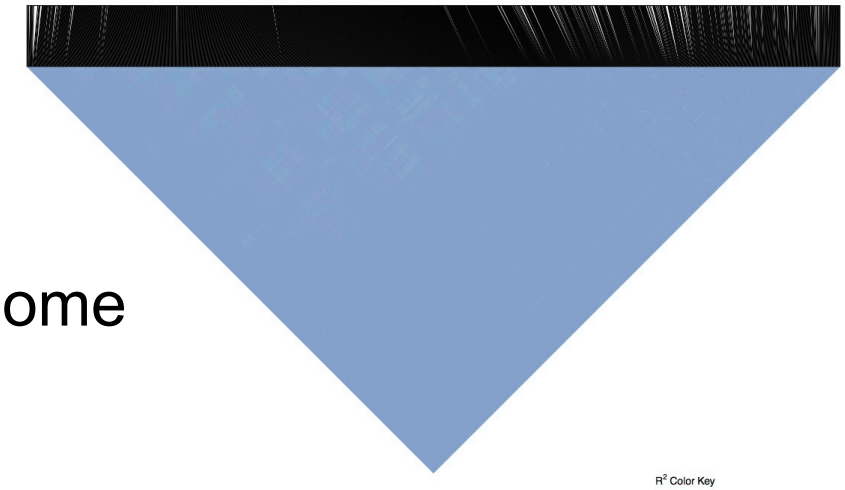


Selective sweeps?

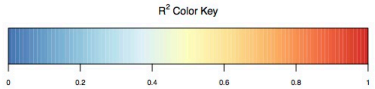


X Chromosome





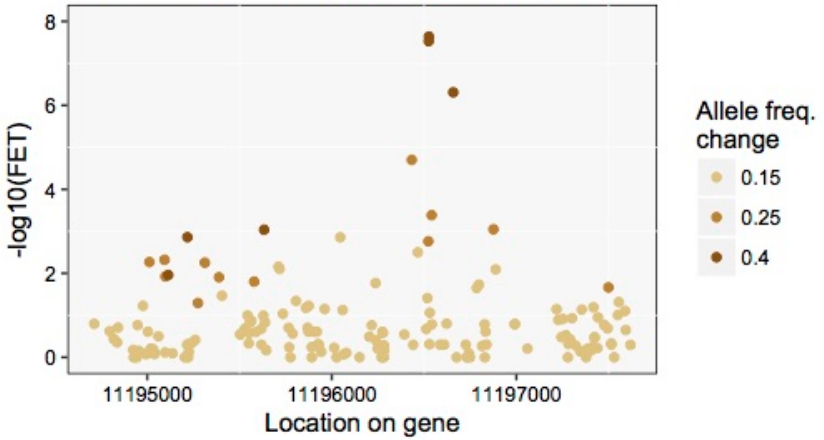
3rd Chromosome

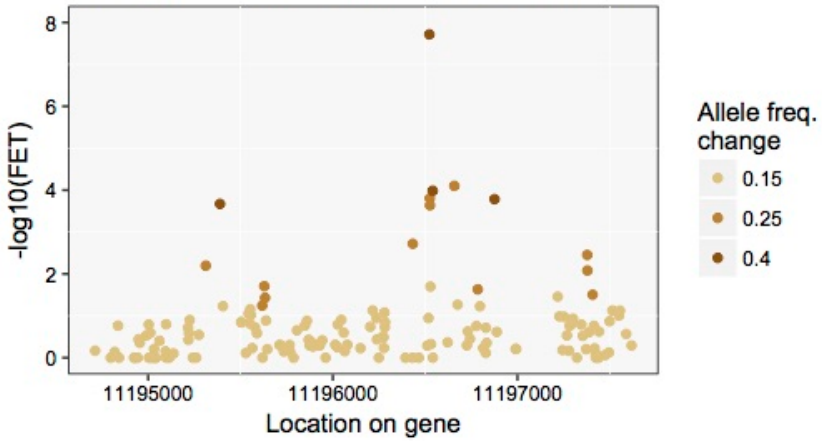


Localized mapping

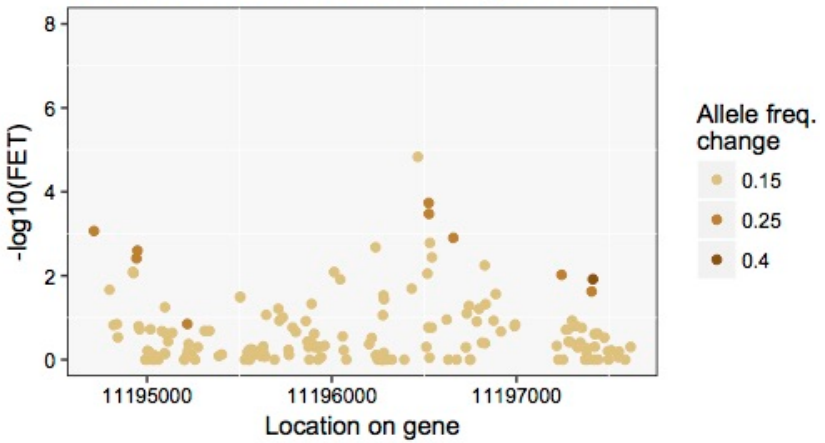
Putative epidermal growth factor

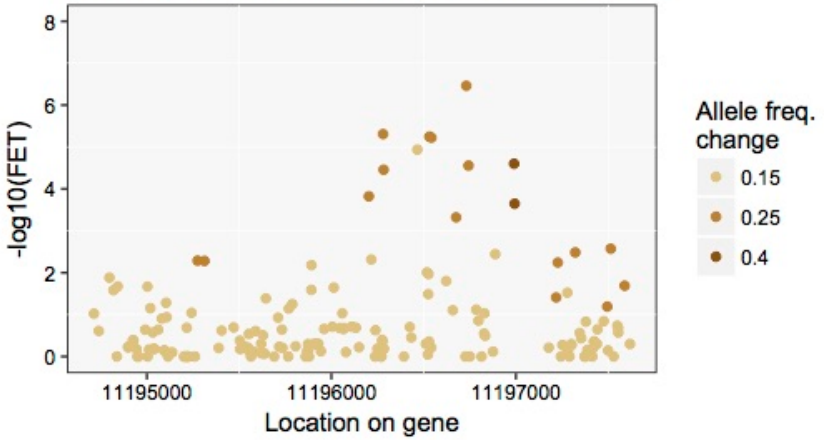
Heat shock resistance





Oxidative shock resistance





Pleiotropic sieve

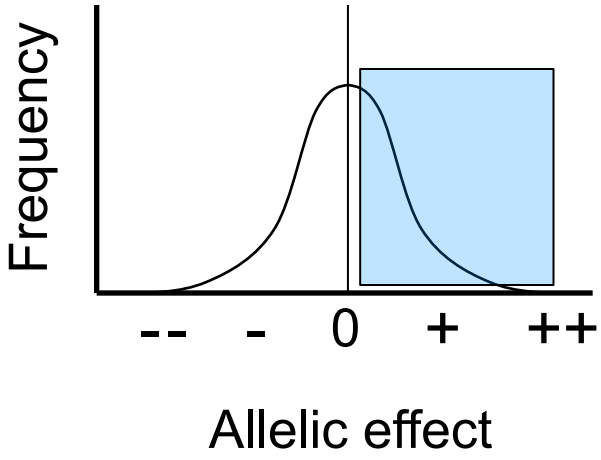
Number of phenotypic records in WormBase:	434,920
Number of unique gene-phenotype associations:	66,968
Number of unique phenotypic classes associated with genes:	1,918

Gene	Description	Phenotypes
pop-1	Wnt pathway TCF/LEF family TF important for cell migration and cell fate	122
daf-2	Insulin receptor important for dauer decision, stress-response, longevity, others	111
gld-1	RNA-binding protein important for multiple aspects of germline development	79
daf-16	FOXO transcription factor downstream of *daf-2*, implicated in similar processes	77
mpk-1	MAP kinase, involved in vulval cell fate specification, cell migration, immunity, others	75

Themes

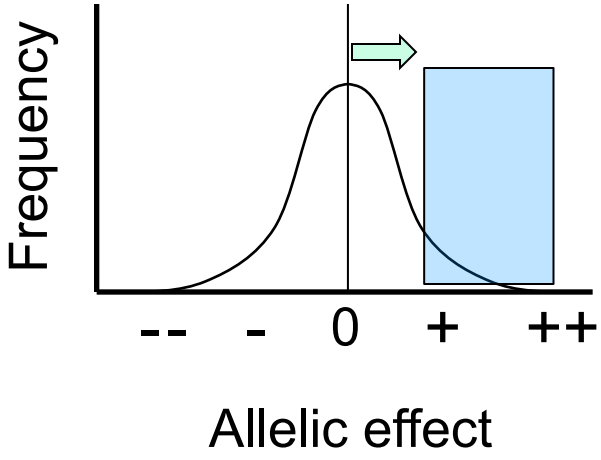
- Sufficiency of quantitative genetics theory
- Experimental evolution as a closed inferential system
- Complex genetic basis of natural variation

Migration as an affect-size filter



No migration

Selection: effect > $4N_e s$

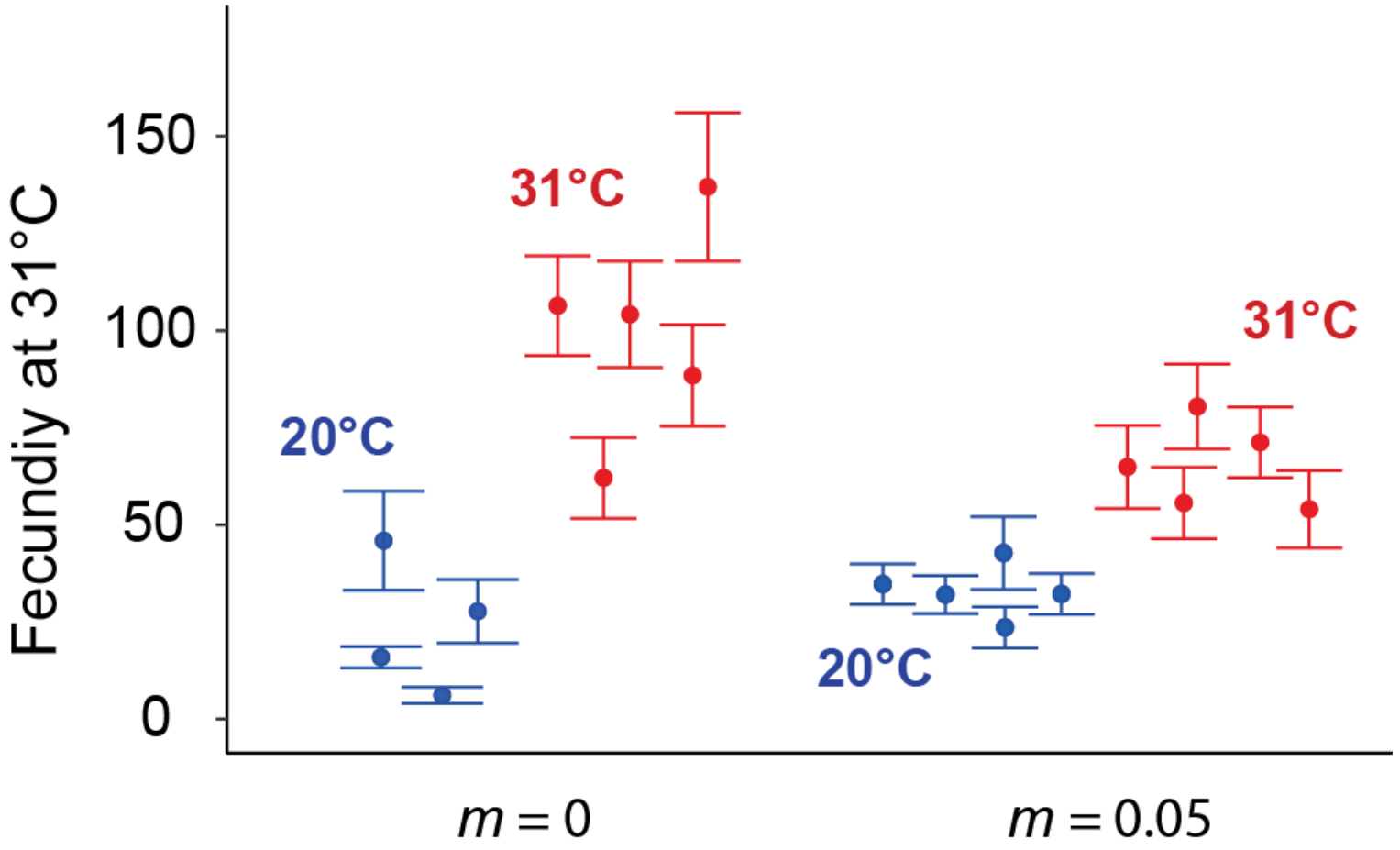


With migration from non-selected pop

Selection: effect > $4N_e s >> 4N_e m$

Divergence under migration-selection balance

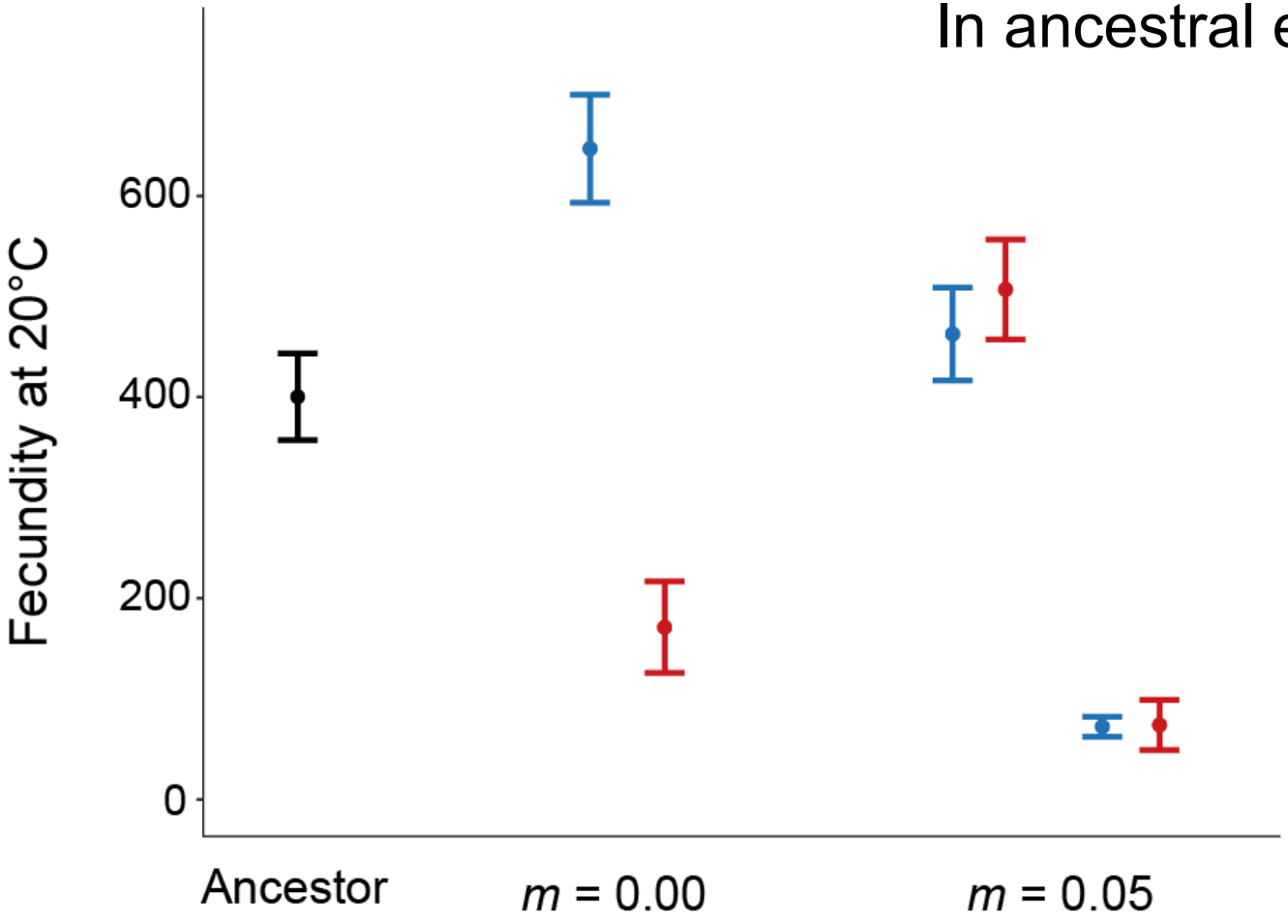
In novel environment



30 generations of chronic exposure

Cost of migration

In ancestral environment



Summary

- Rapid evolution of increased stress response
- Evidence for independent genetic basis, but depends on environment
- Many genes responsible
- Molecular pleiotropies match quantitative genetic expectations, not mutational ones
- No clear network signal (yet)
- Complex adaptations are complex
- Disparate components of genetics are moving toward reconciliation but have a ways to go

Acknowledgments

Strain Development

Tim Ahearne
Rose Reynolds
Chad Smith

Stress selection experiment

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Rose Reynolds
Heather Archer

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Genomic analysis

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John Willis
Thom Nelson

Microfluidics

Stephen Banse
Ben Blue
Joseph North