# A brief introduction to experimental evolution

Feb, 2019;
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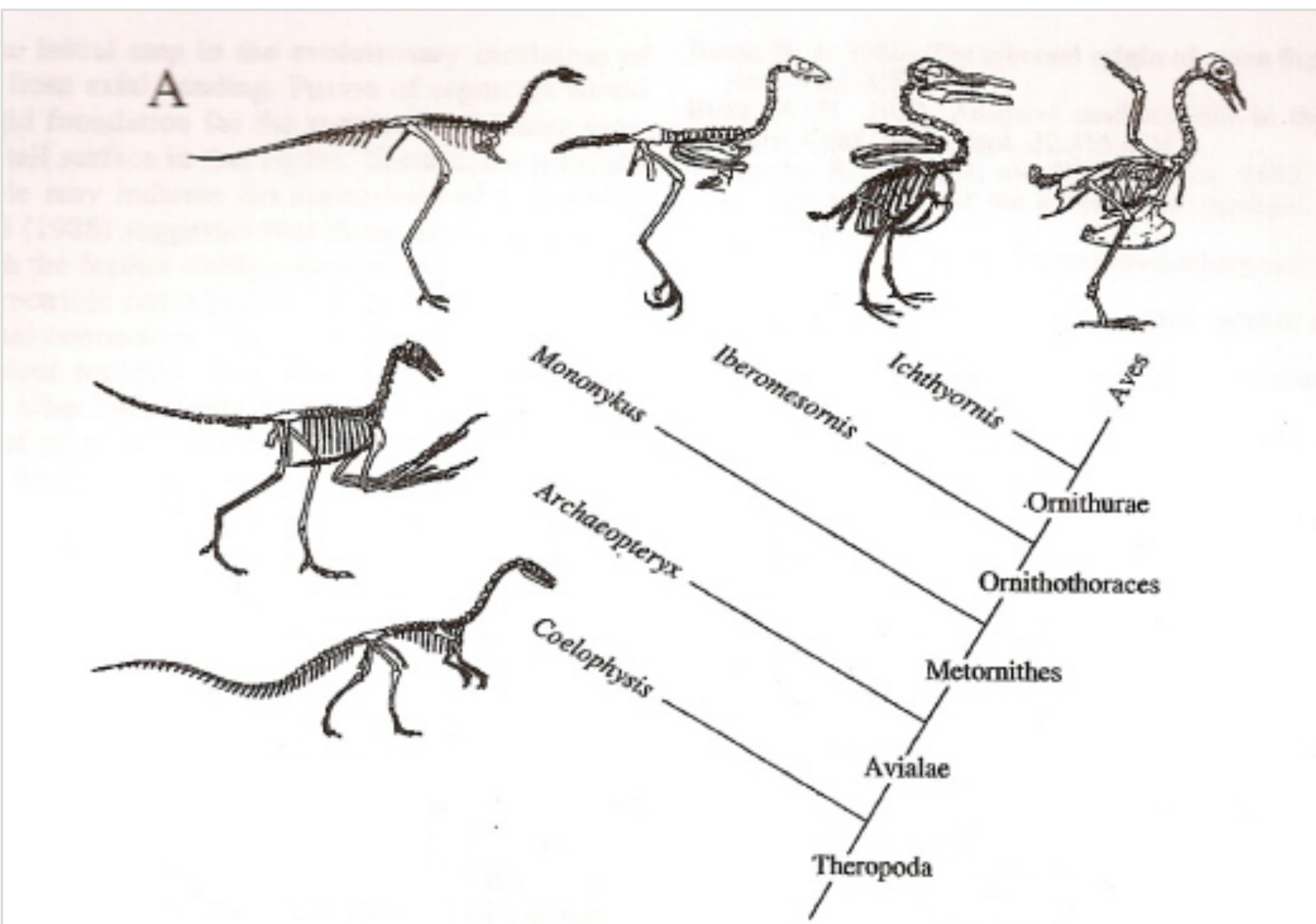
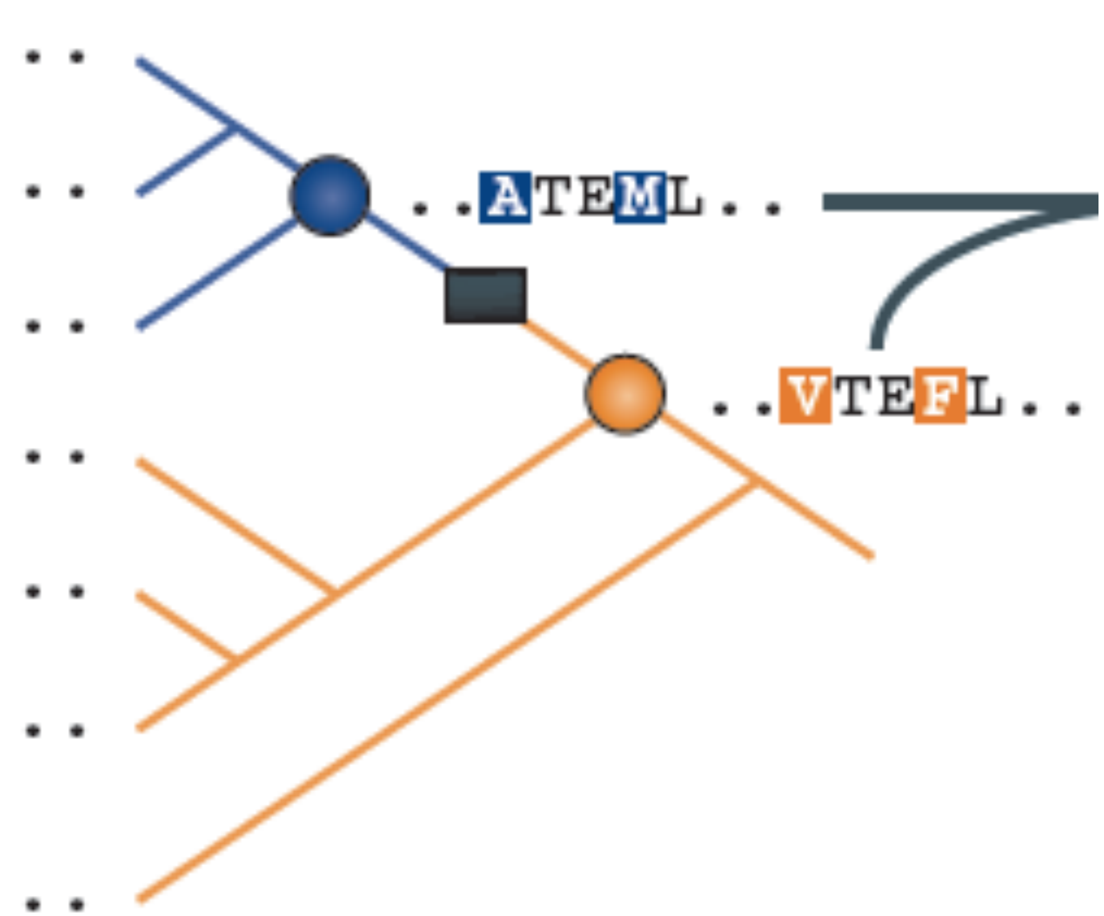
# Evolutionary change?

# Studying evolutionary change

## 1. Fossils



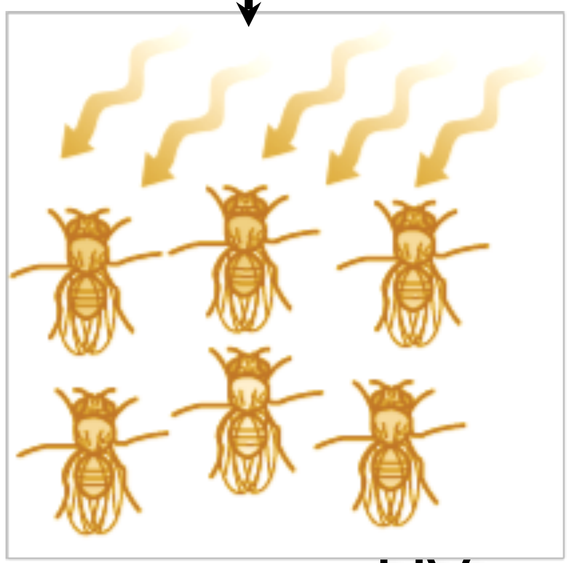

## 2. Comparative studies




history, introduction

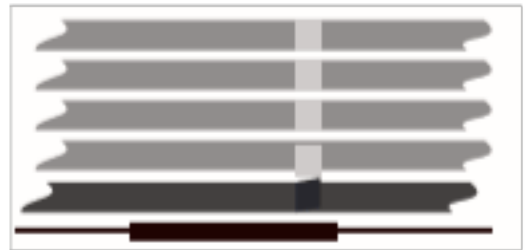
# Studying evolutionary change

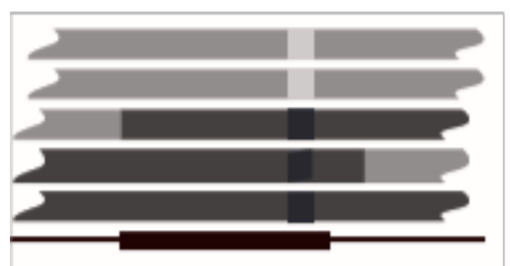
ancestral state

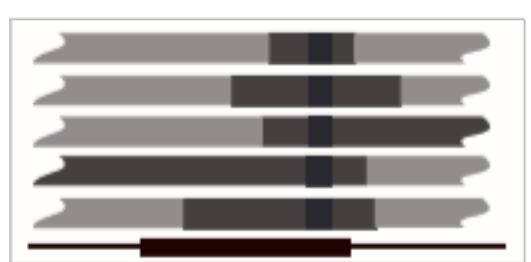


response to UV

evolved state



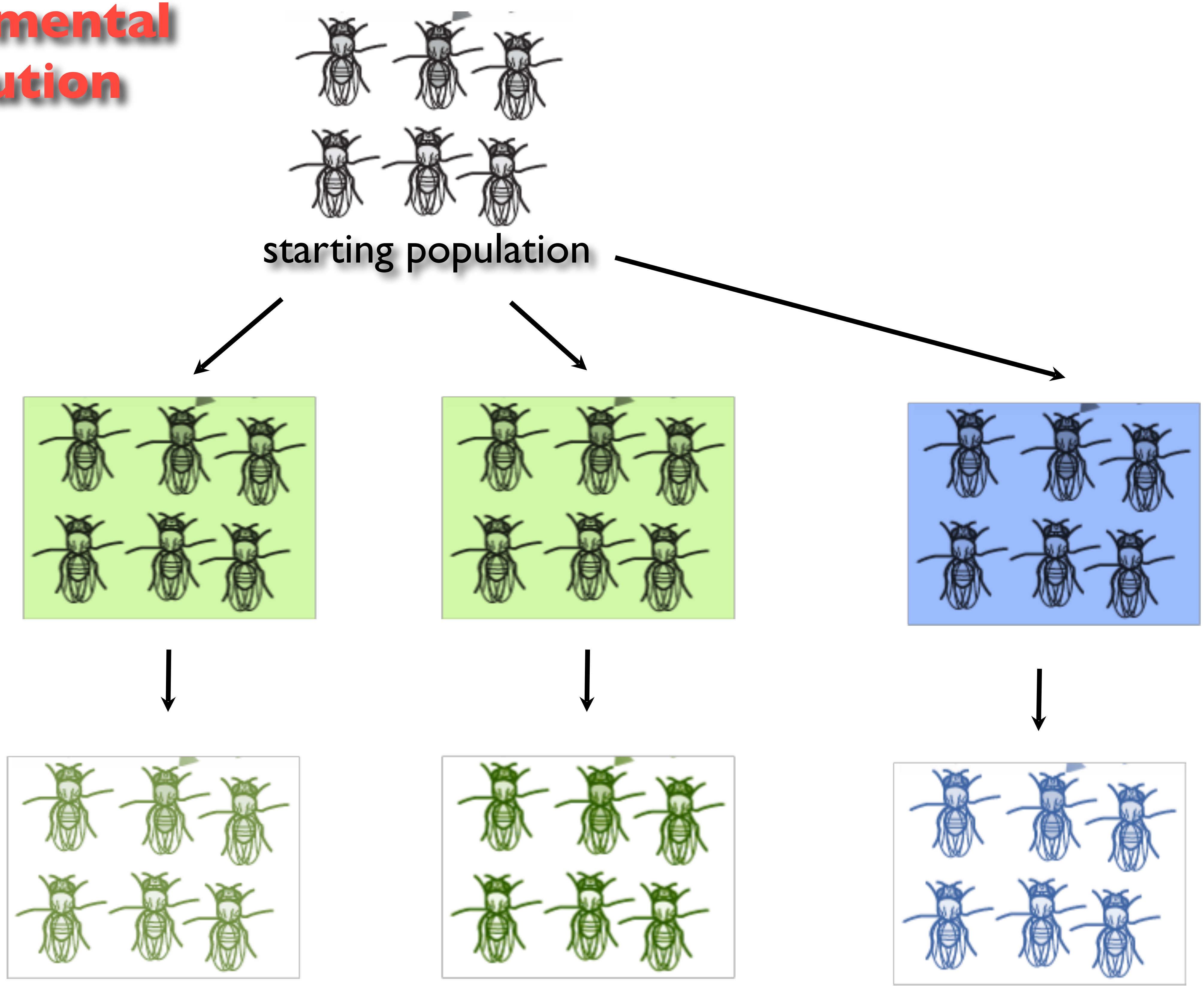




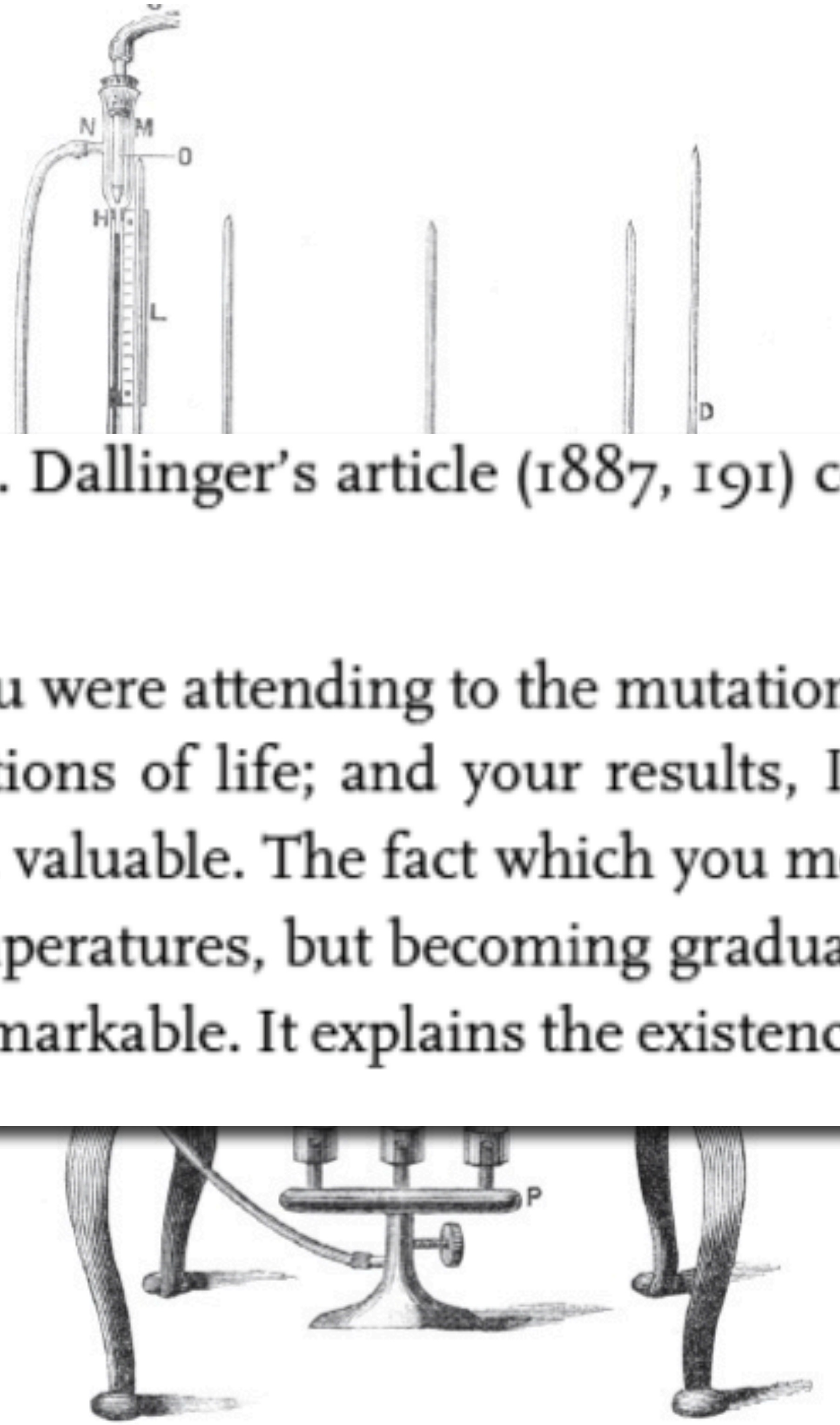

history, introduction

# Studying evolutionary change - Evolution in action

**3. Experimental Evolution**



# First direct test of natural selection (WH Dallinger, 1887)

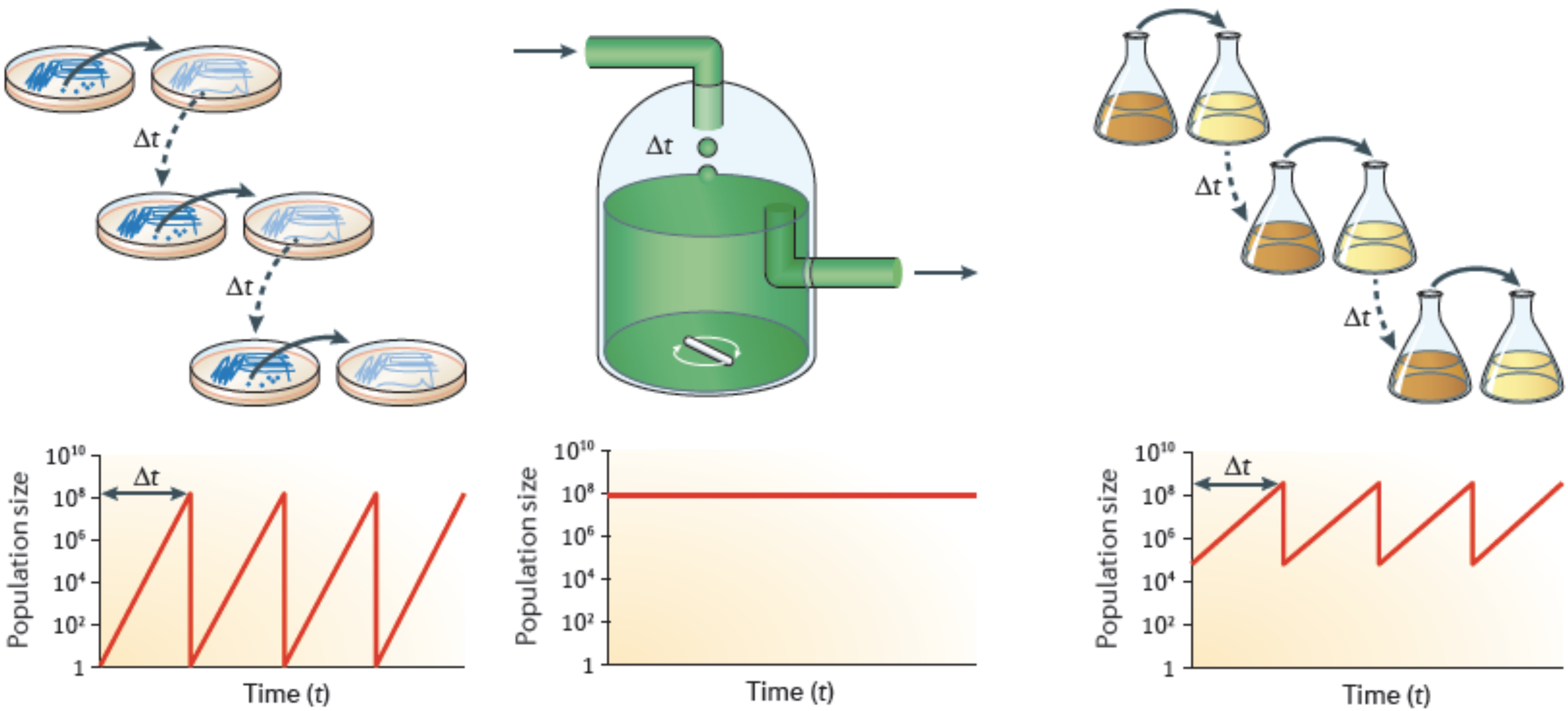


from his selection results. Dallinger's article (1887, 191) contains an insightful evaluation from Darwin:

> I did not know that you were attending to the mutation of the lower organisms under changed conditions of life; and your results, I have no doubt, will be extremely curious and valuable. The fact which you mention about their being adapted to certain temperatures, but becoming gradually accustomed to much higher ones, is very remarkable. It explains the existence of algae in hot springs.

history,
introduction

**Bottlenecks:** **Continuous culture:** **Serial transfers:**




Barrick & Lenski 2003

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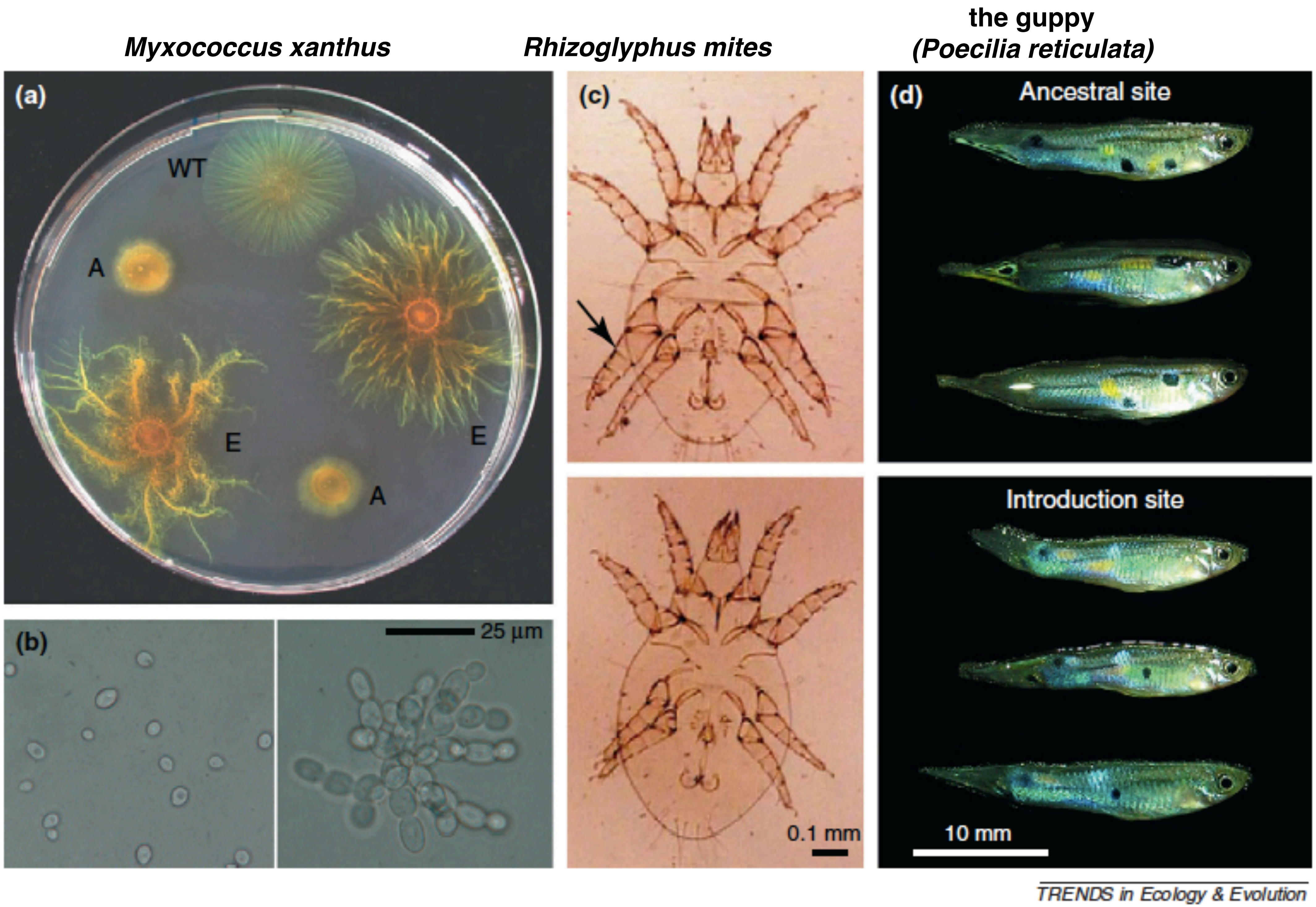
# Model organisms




Kawecki *et al.* 2012

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**How do we quantify adaptation?**
**Fitness, relative fitness.**

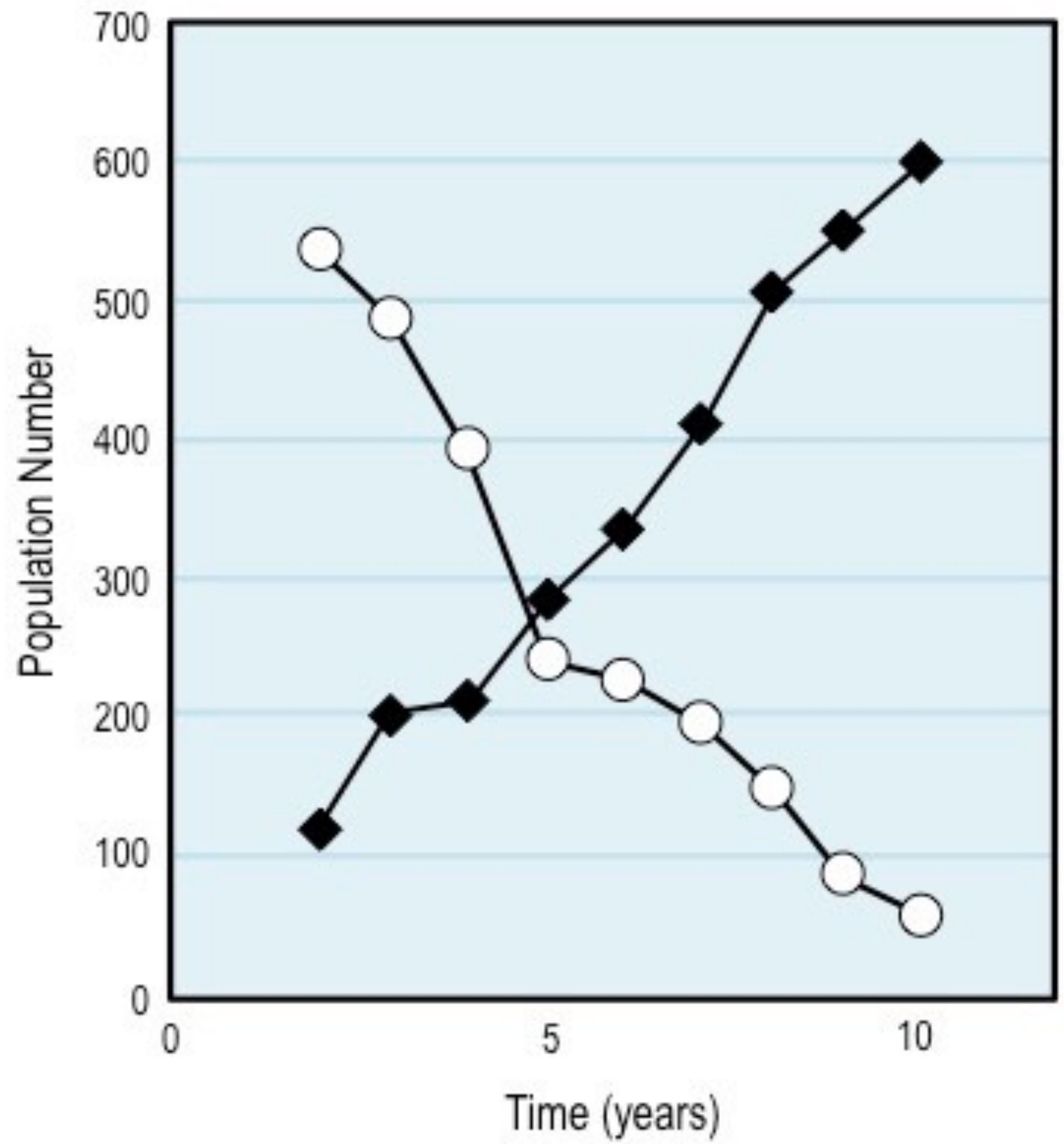
quantifying adaptation

# Adaptive evolution

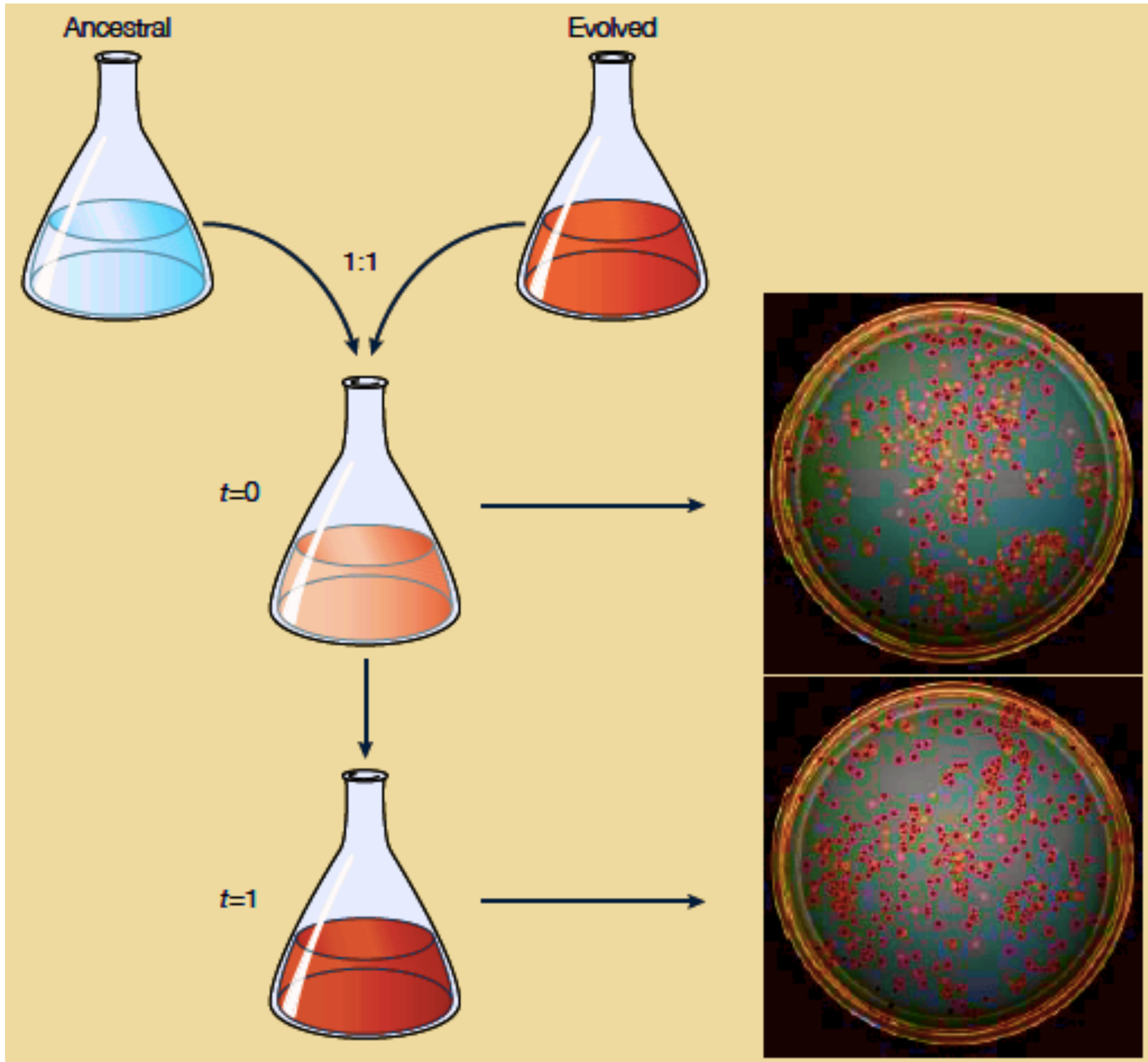
Unpolluted Environment

Polluted Environment

# Adaptive evolution

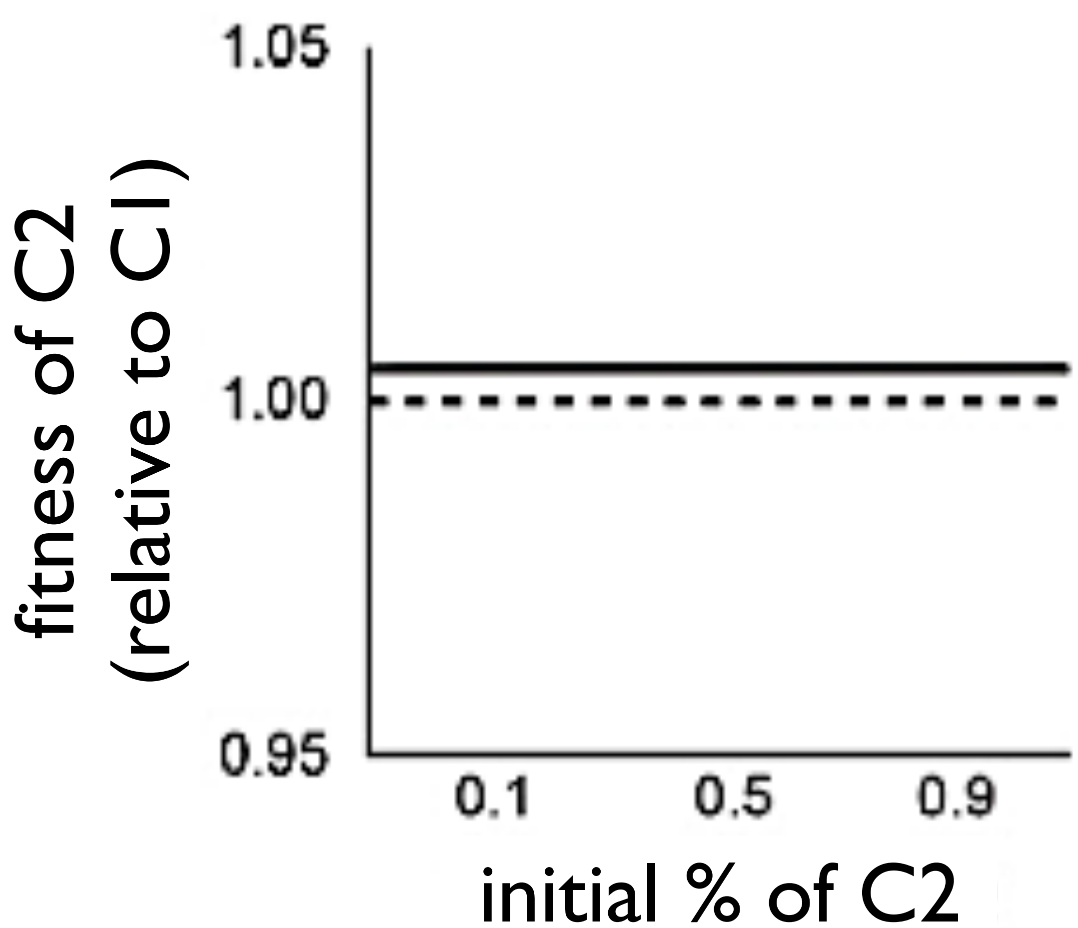

# How do we quantify adaptive change?



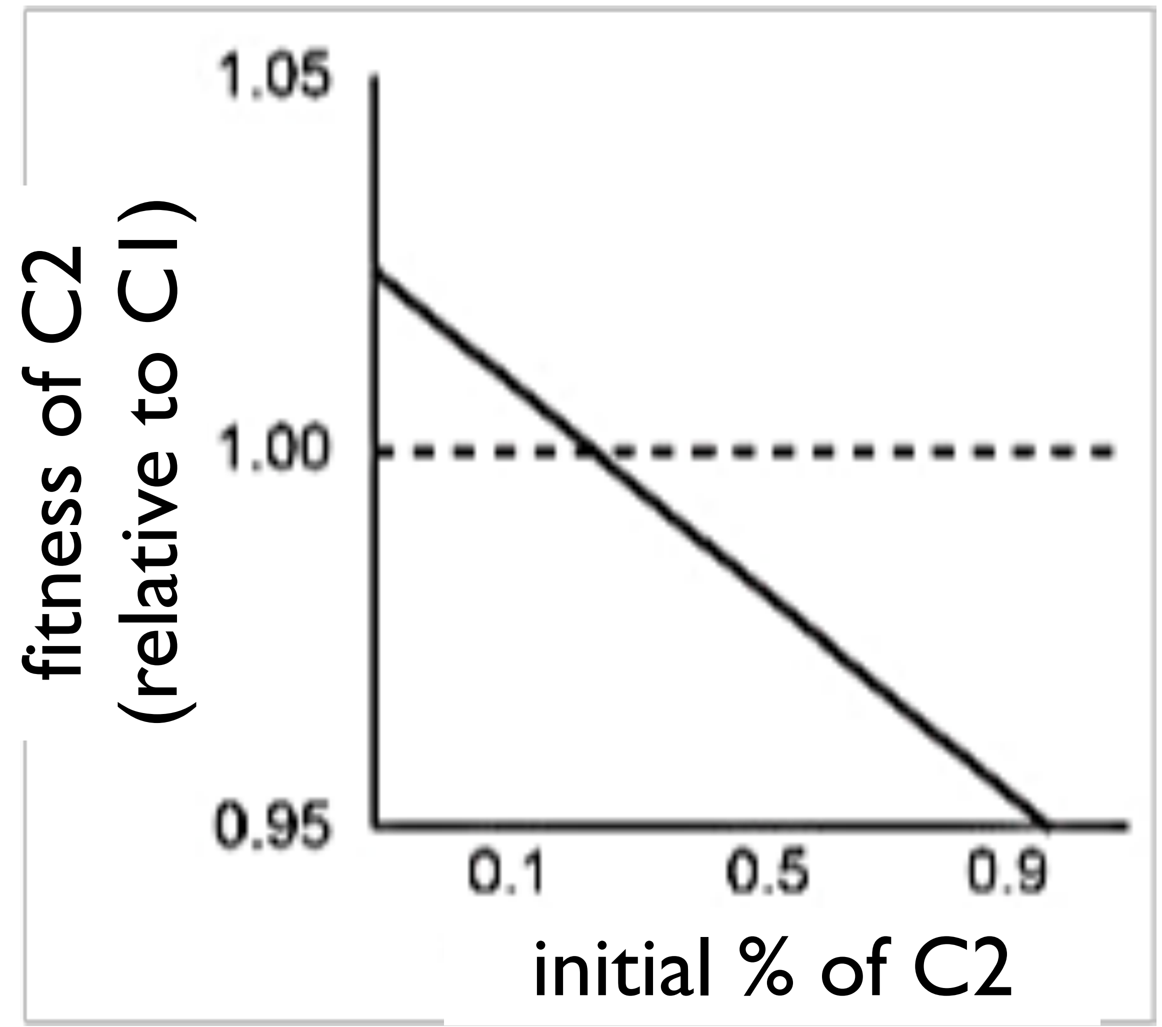

Elena & Lenski 2003

quantifying adaptation

# Relative fitness




Measuring growth rate independently is OK

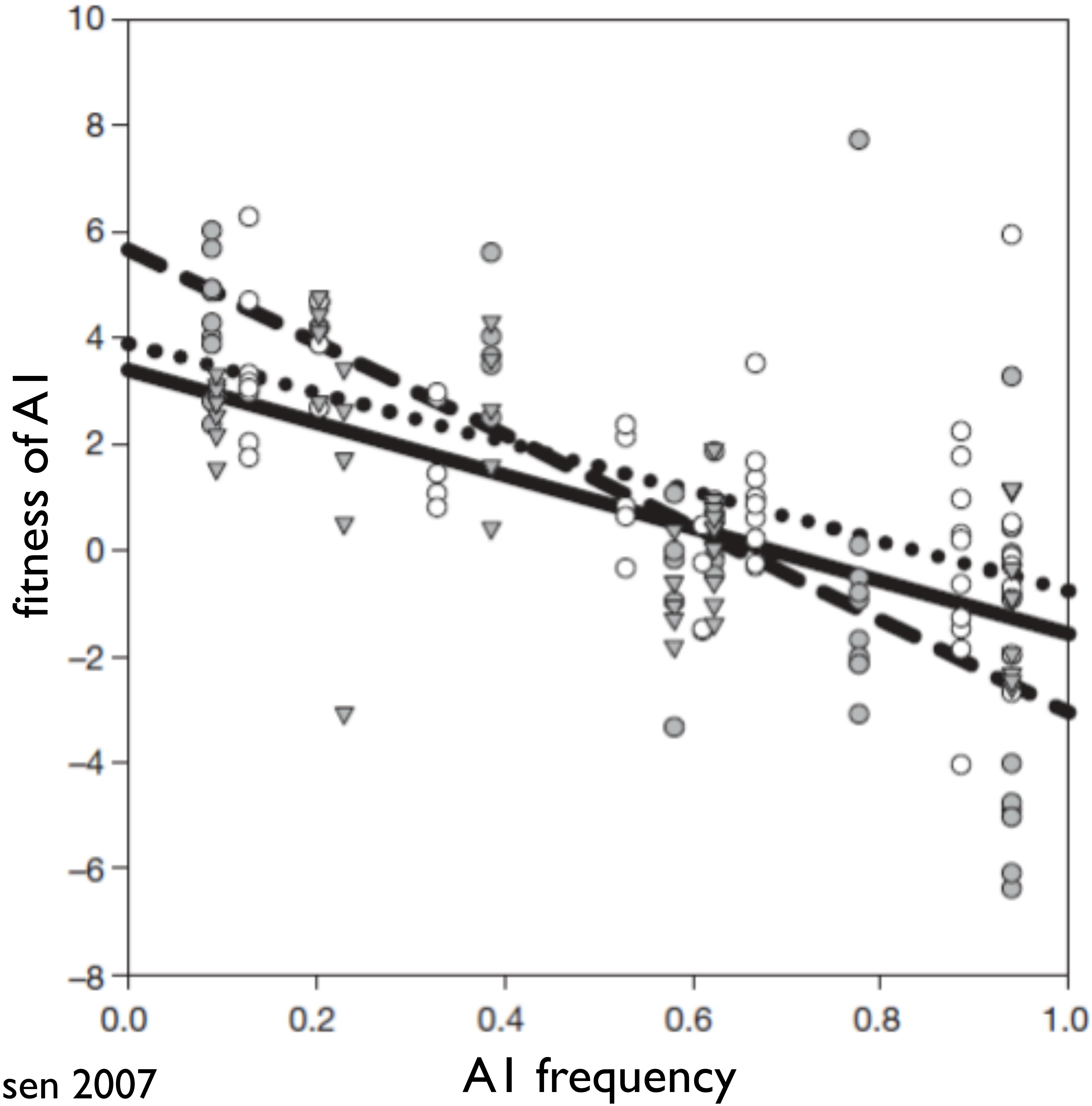



Co-culturing is necessary

Maddamsetti *et al*. 2015

quantifying adaptation

# Nature “cares” about the relative fitness



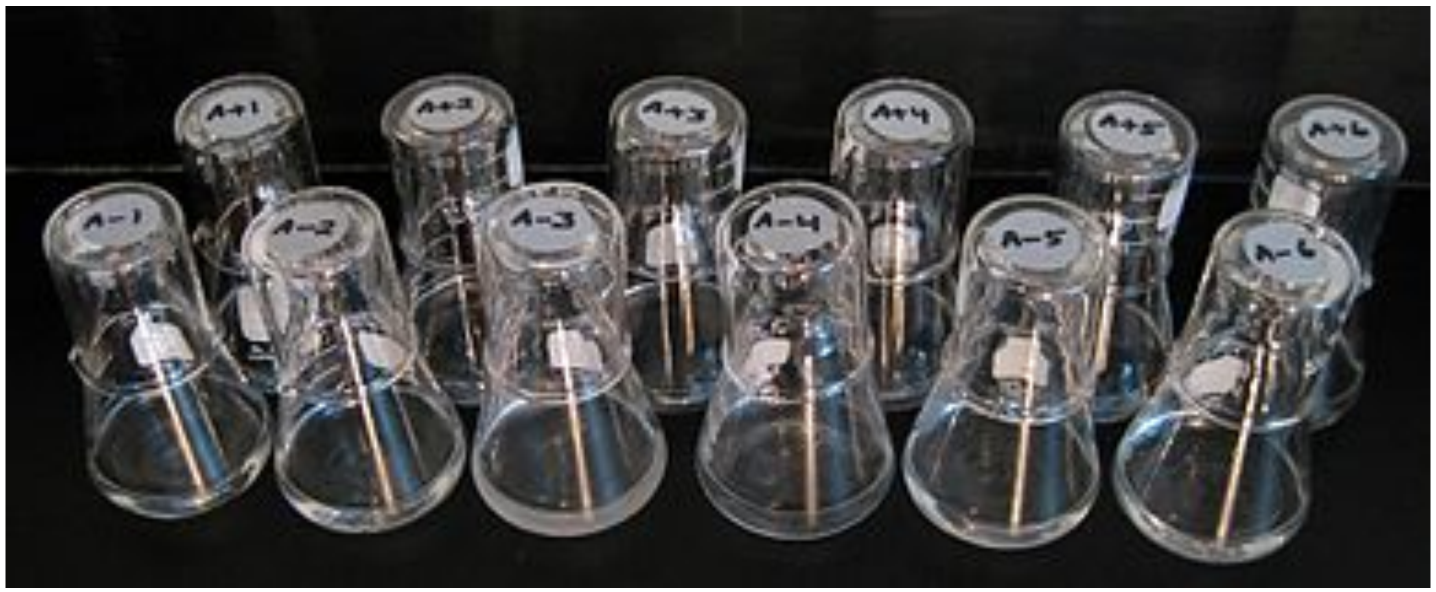

Meyer & Kassen 2007

quantifying adaptation

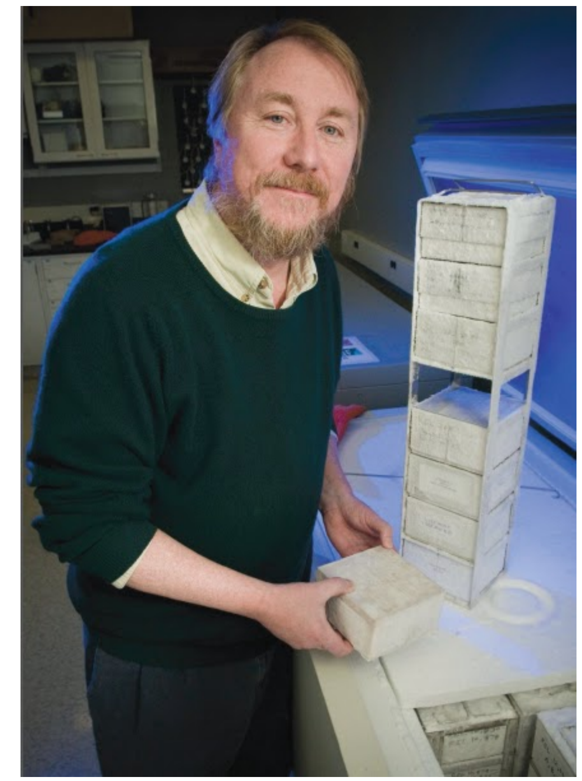
# Dynamics of evolutionary adaptation in response to selection

# Lenski's long term experimental evolution study

Richard Lenski




Liquid culture

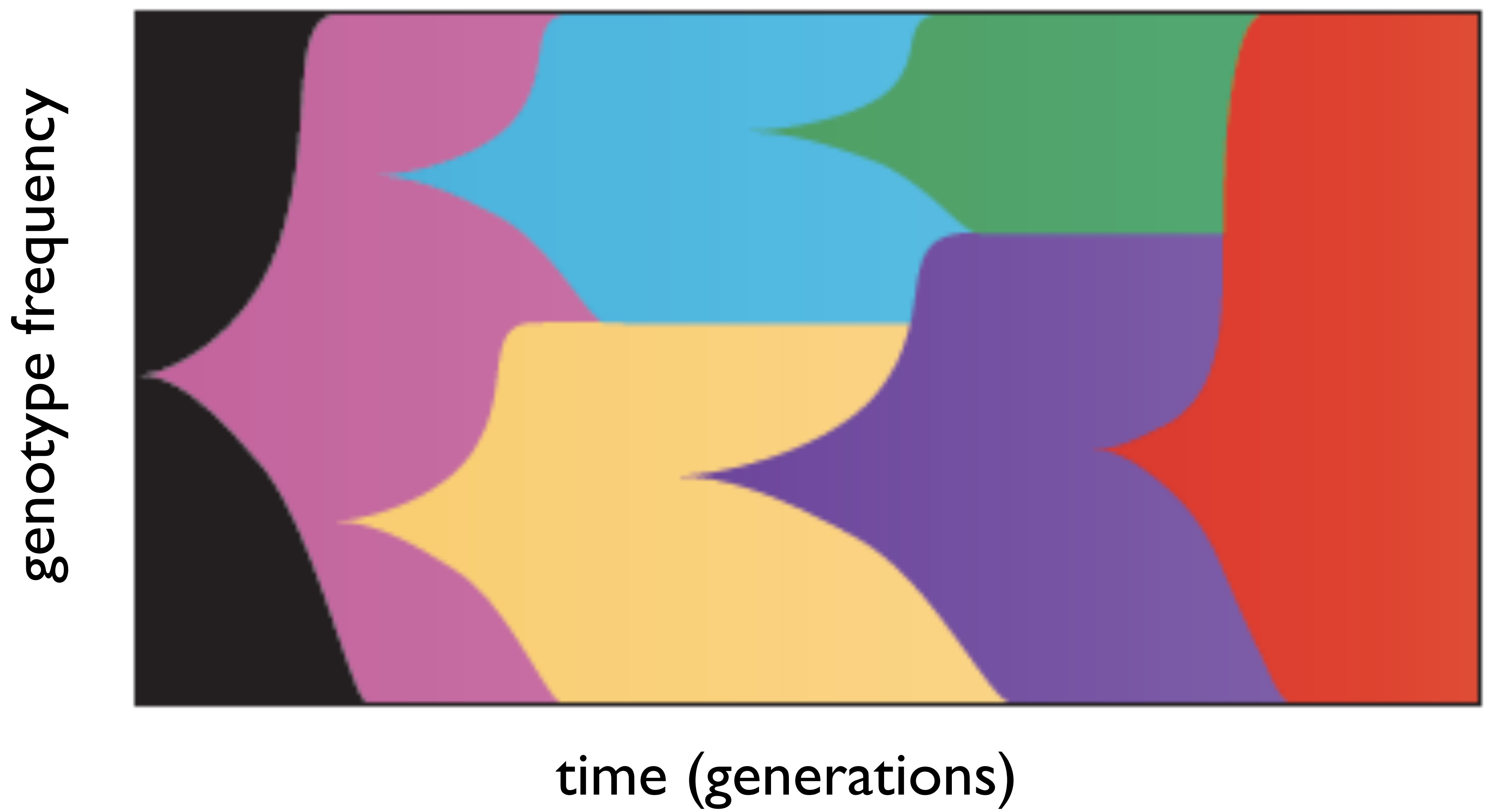


1) Is adaptation a slow process?
2) Multiple local optimums?
3) How repeatable?

adaptation

# Adaptation in clonal & asexual organisms

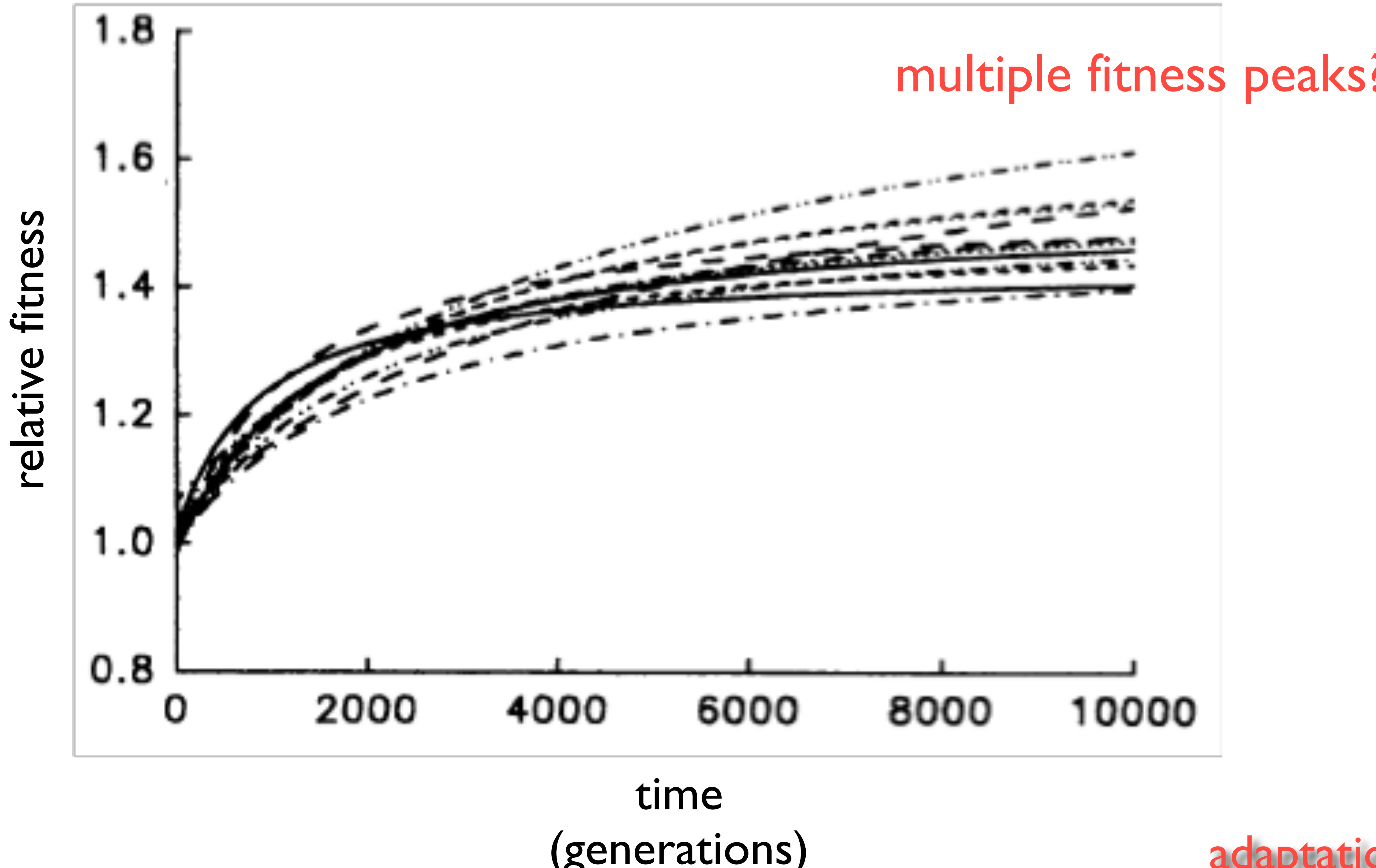
- Isogenic ancestor




Barrick and Lenski 2013

adaptation
Muller Plot

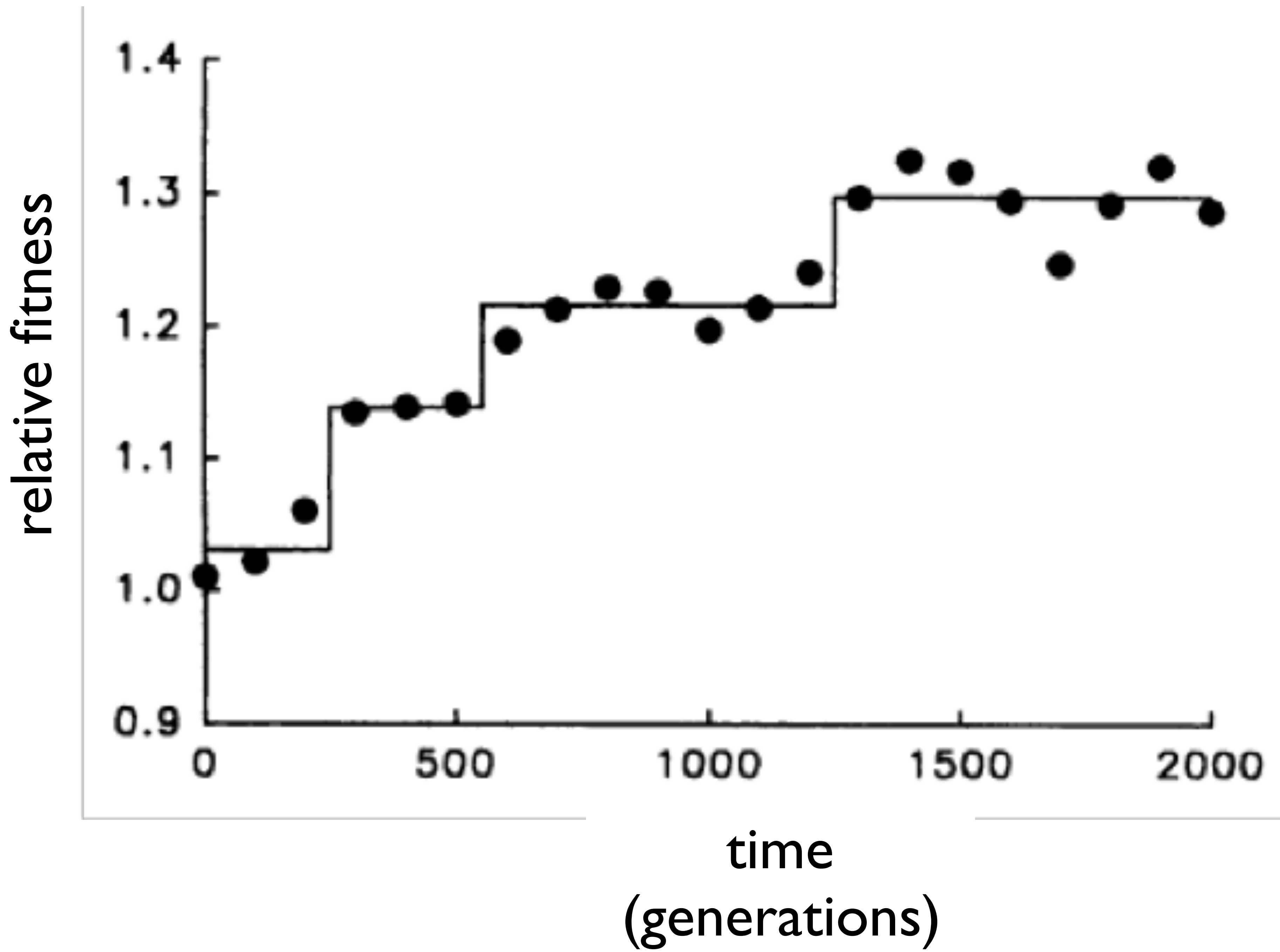
# 10000 generations of adaptive evolution




Lenski & Travisano 1994

adaptation
(*E.coli*)

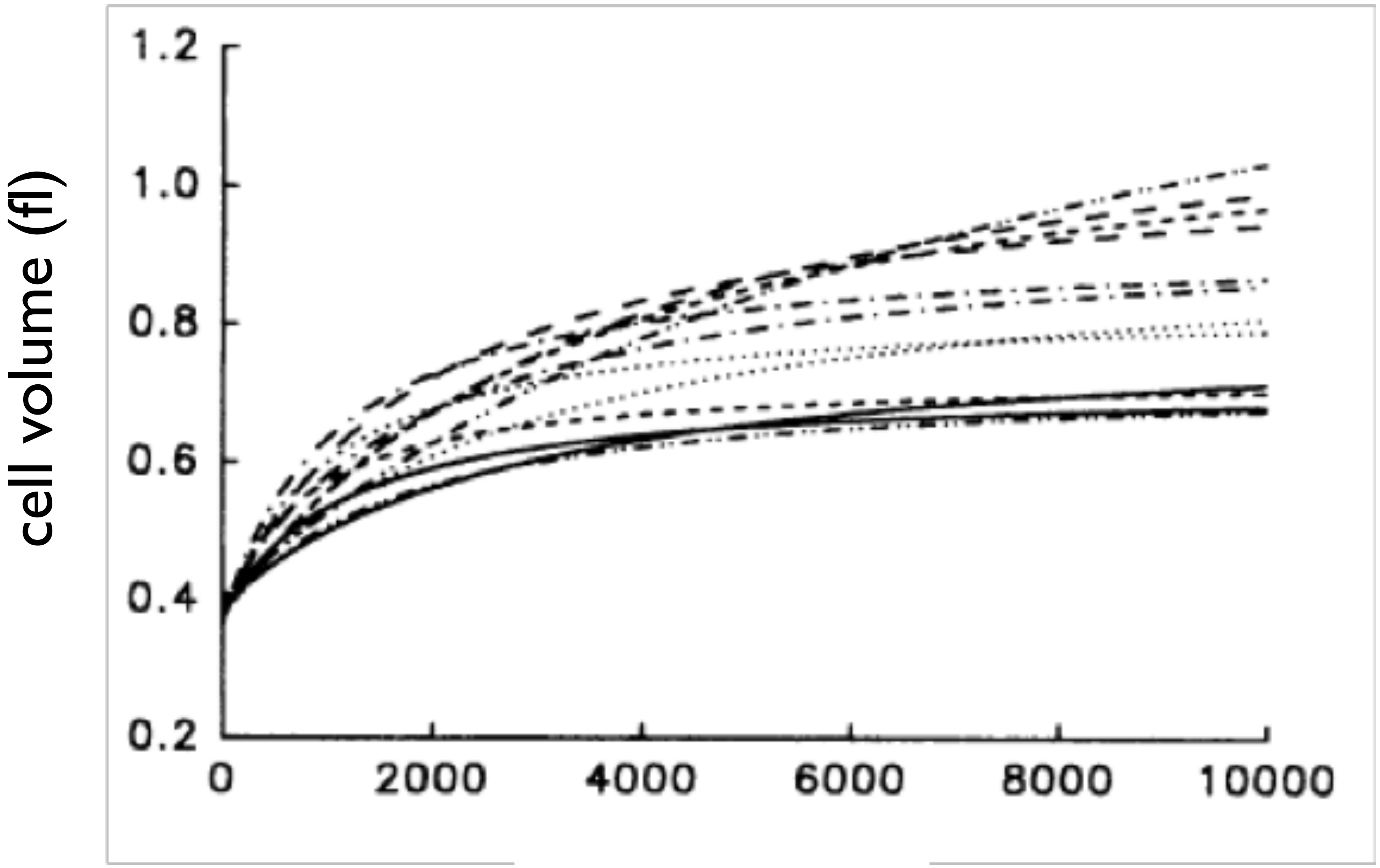
# Dynamics of change in relative fitness




Lenski & Travisano 1994

adaptation
(*E.coli*)

# Phenotypic change?

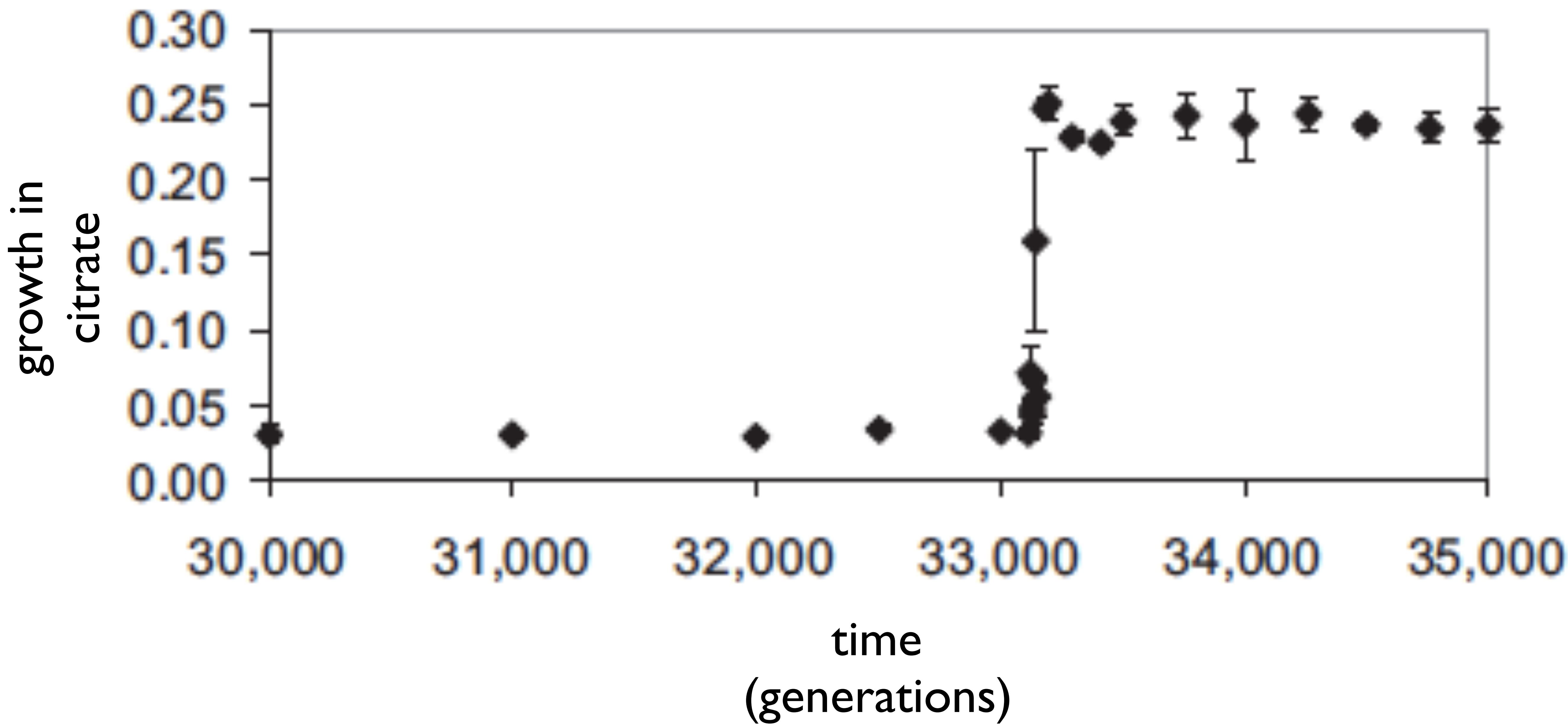



time
(generations)

adaptation, phenotypic change
(*E.coli*)

Lenski & Travisano 1994

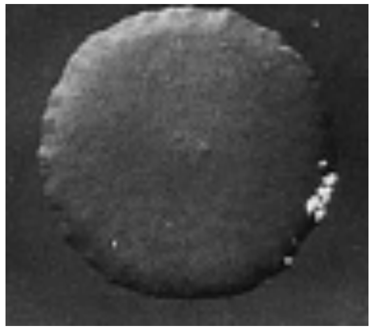
# Evolution of a novel trait: citrate consumers




Blount *et al.* 2006

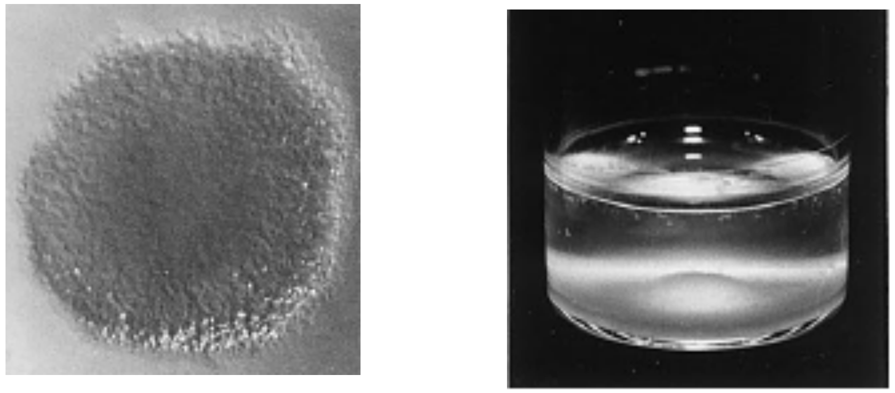
adaptation (*E.coli*)

# Evolution of novel morphs

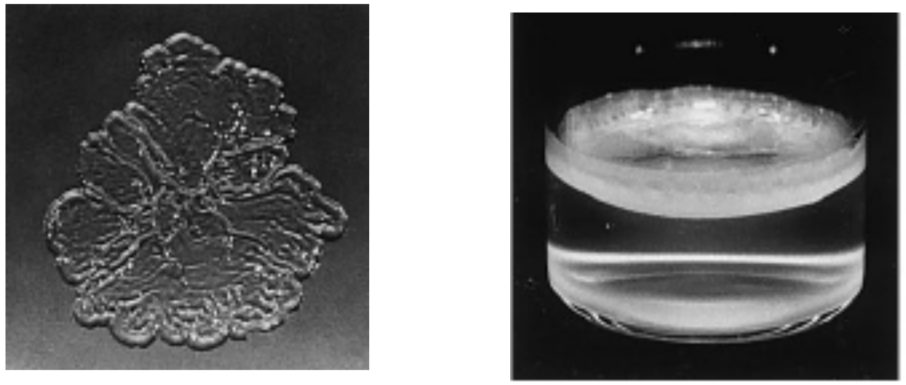


*Pseudomonas*
(smooth)

3 x 24 h



fuzzy



wrinkly

smooth

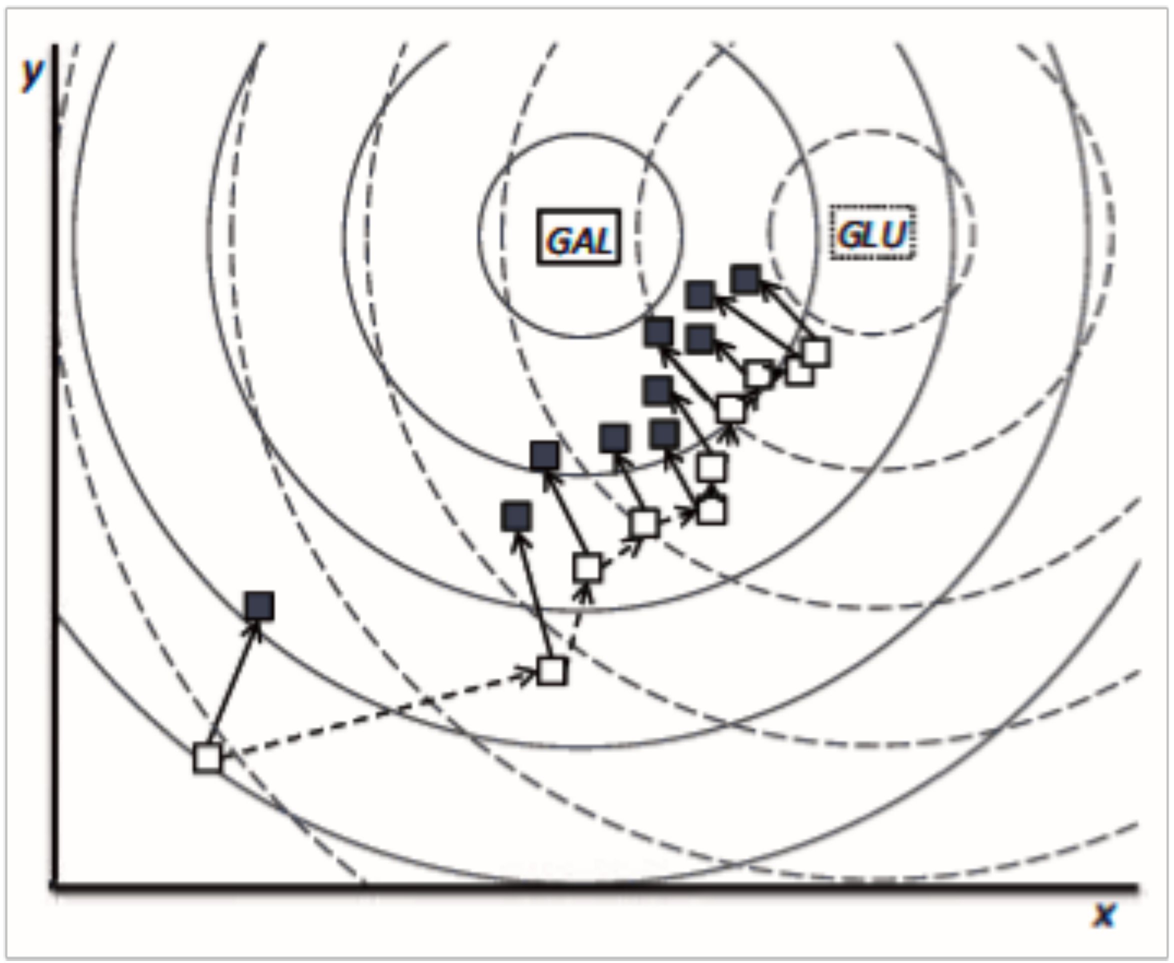
adaptation
(*Pseudomonas*)

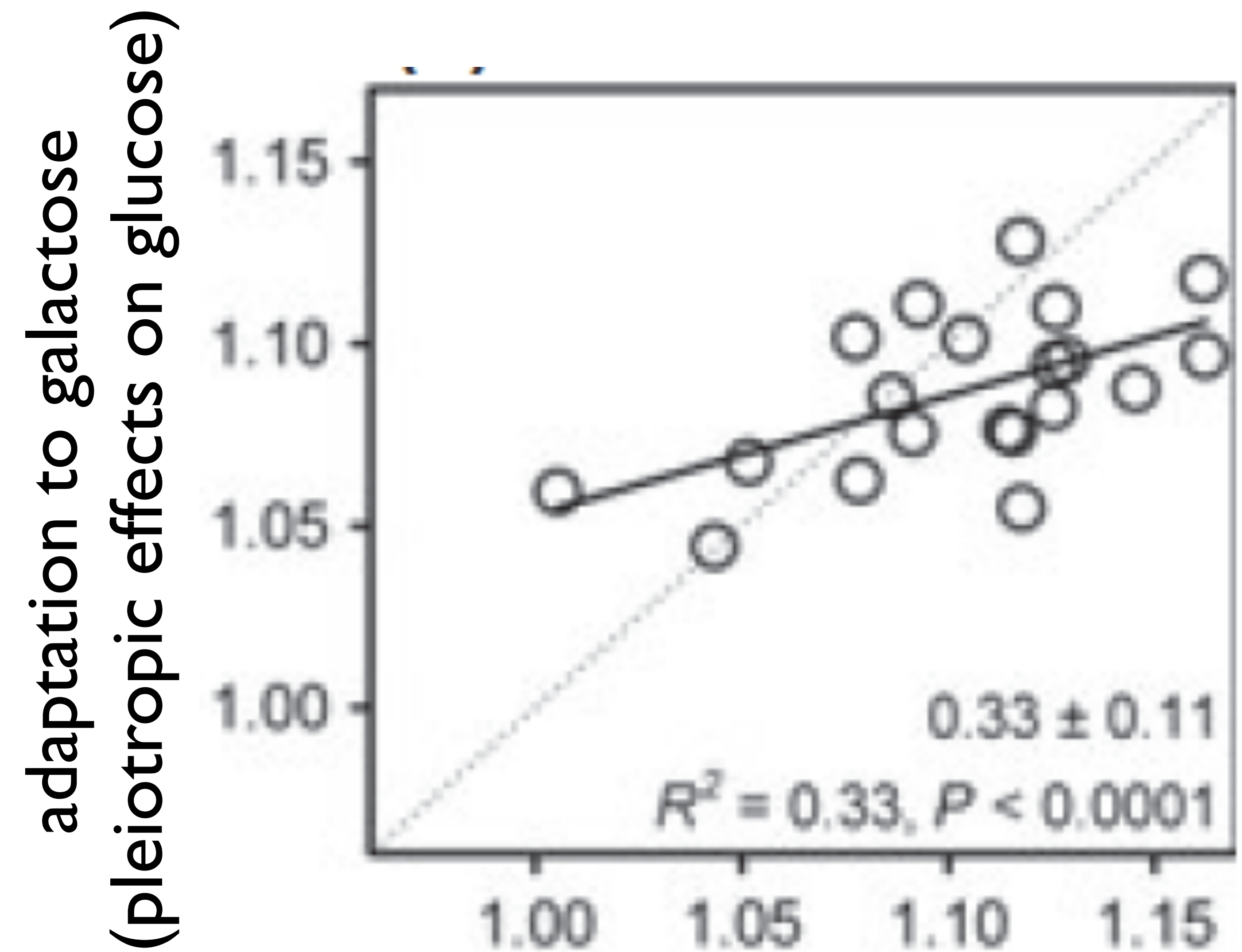
Rainey & Travisano 1998

# Cost of adaptation, sex

adaptation,
trade-off

# Pleiotropic effects of beneficial mutations



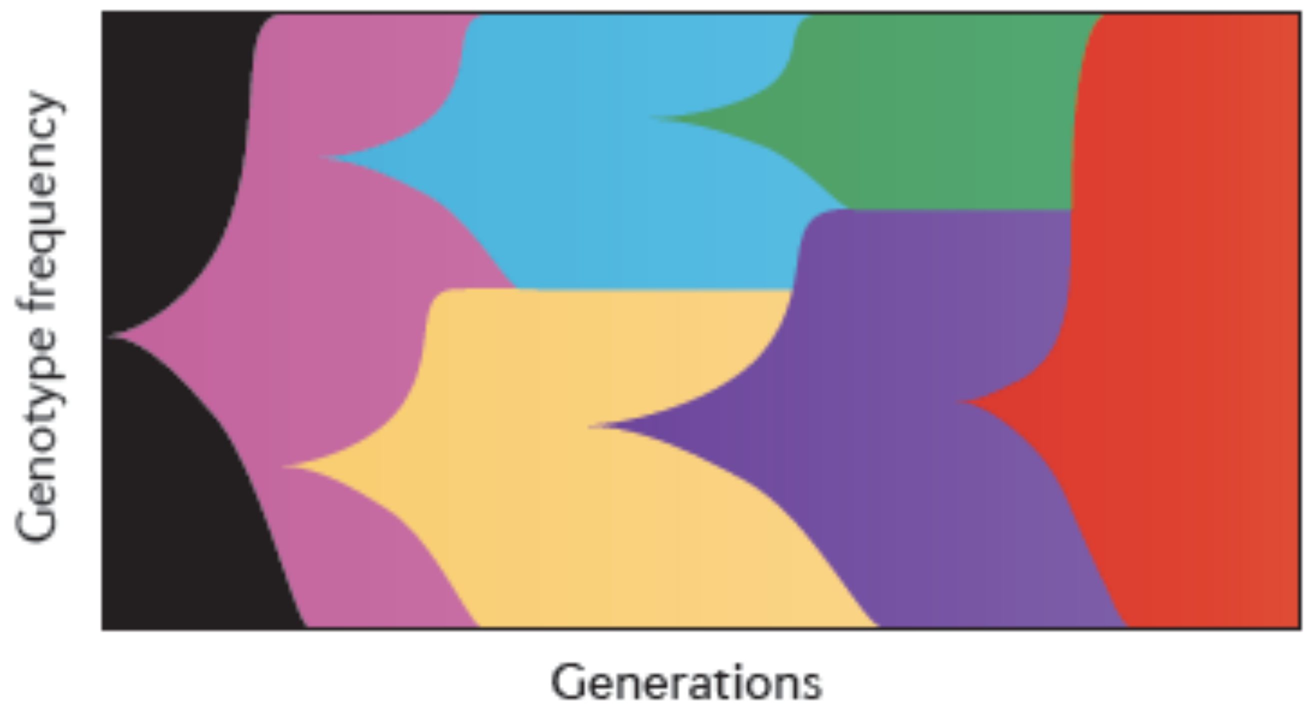

no selection on galactose

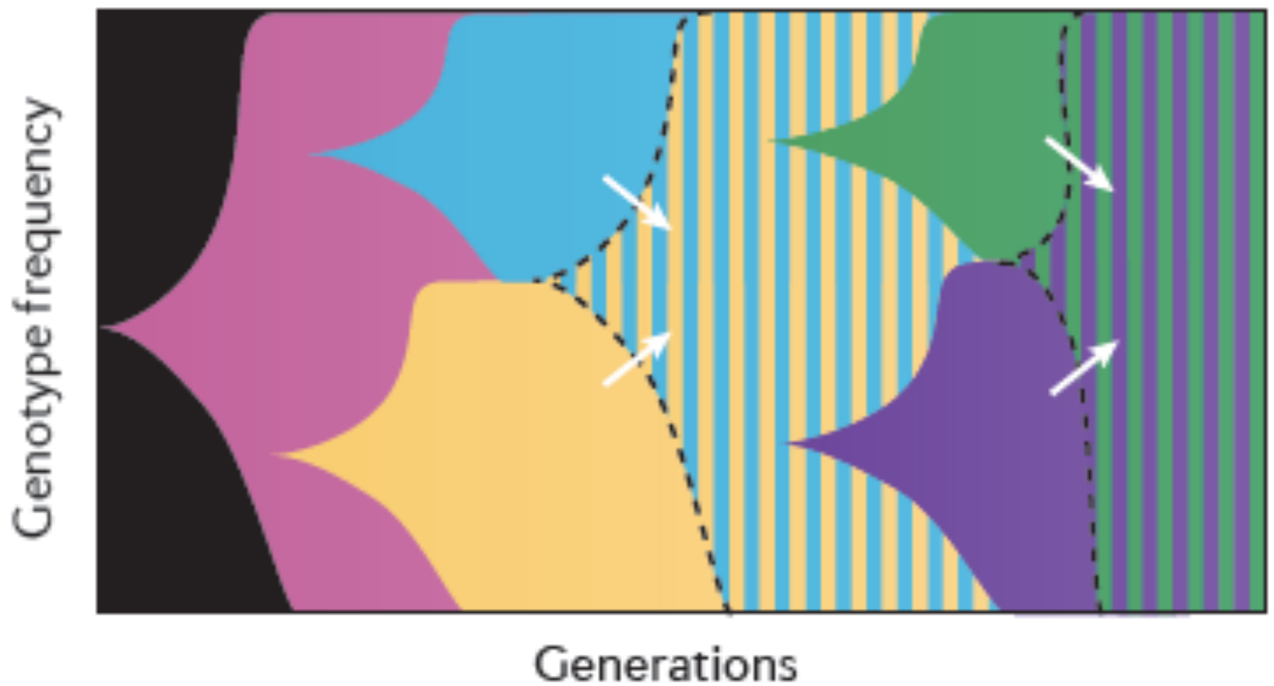
adaptation, trade-off
(yeast)

Jasmin & Zeyl 2013

# Sex/recombination & rate of adaptation

Sex/recombination?

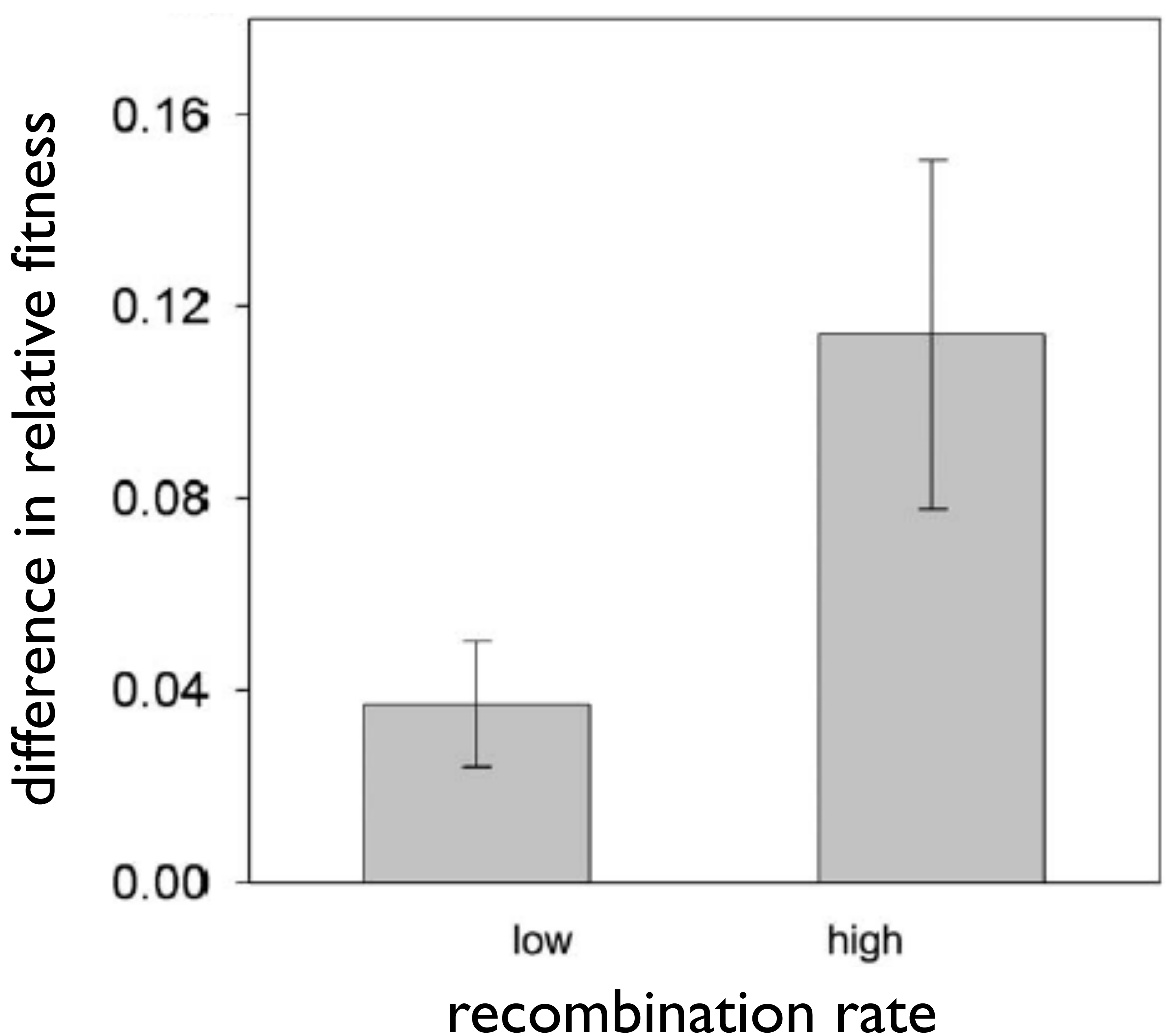



Barrick & Lenski 2013

rate of adaptation
Muller Plot

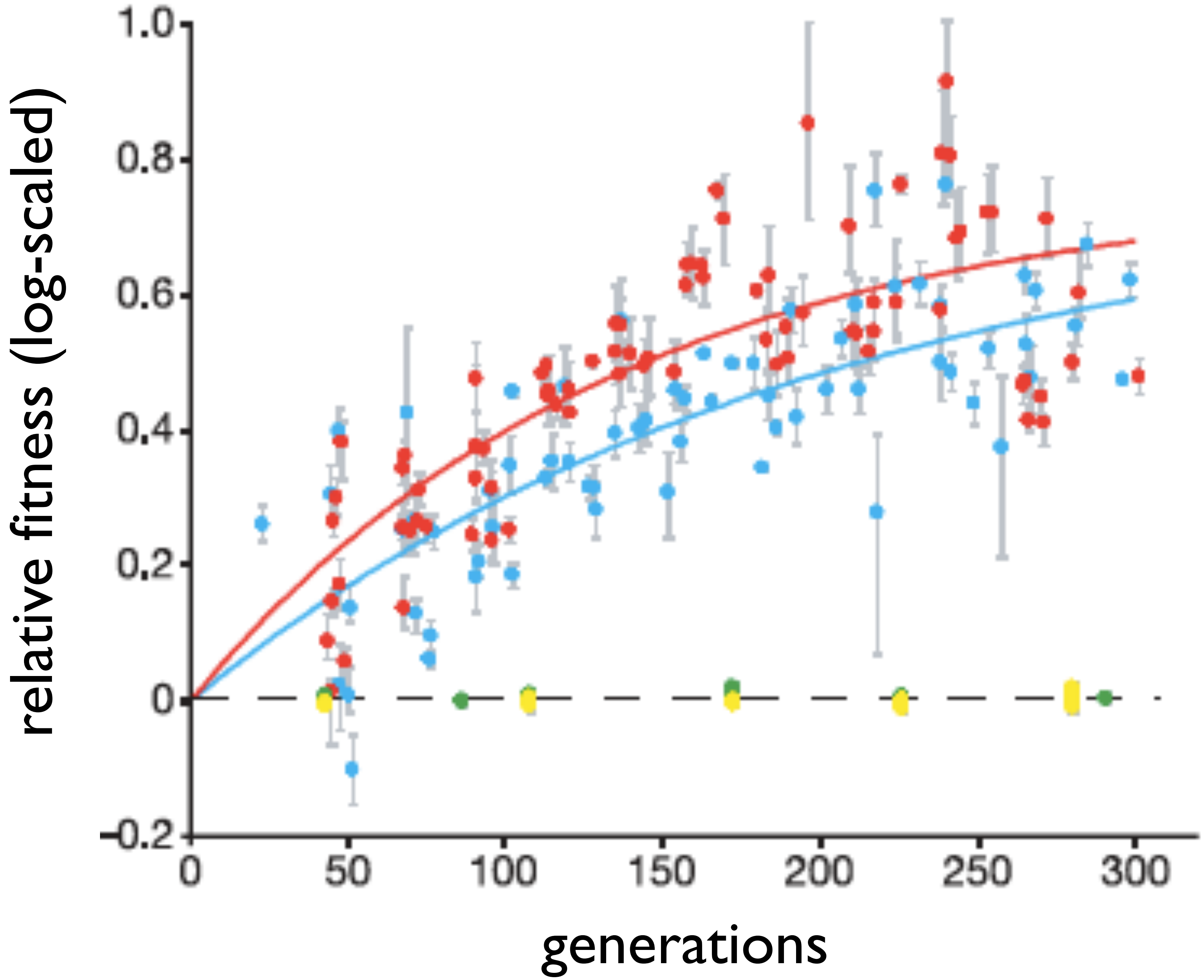
# Sex/recombination & rate of adaptation




rate of adaptation, bacteria

Cooper 2007

# Sex/recombination & rate of adaptation




sexual

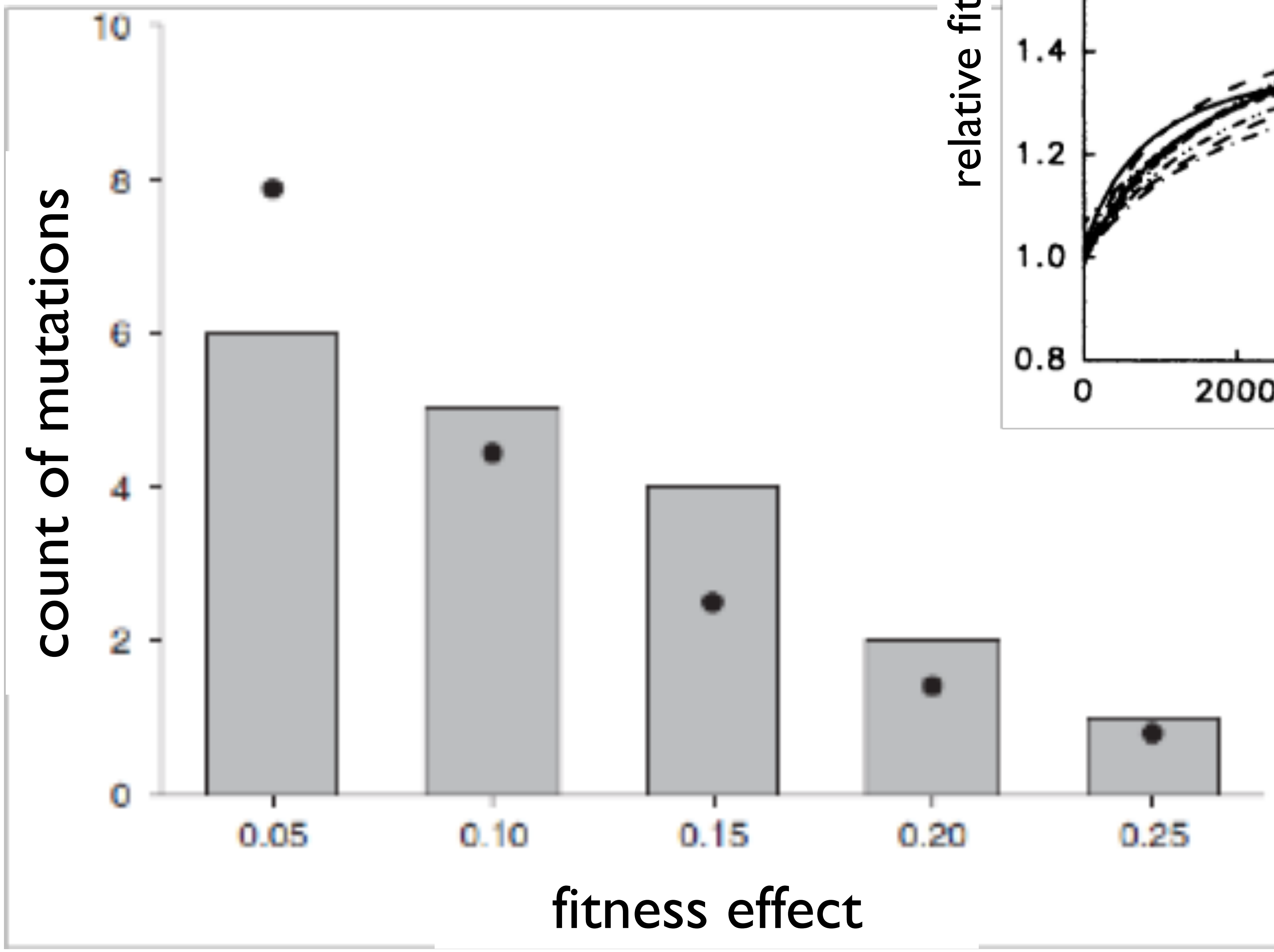
asexual

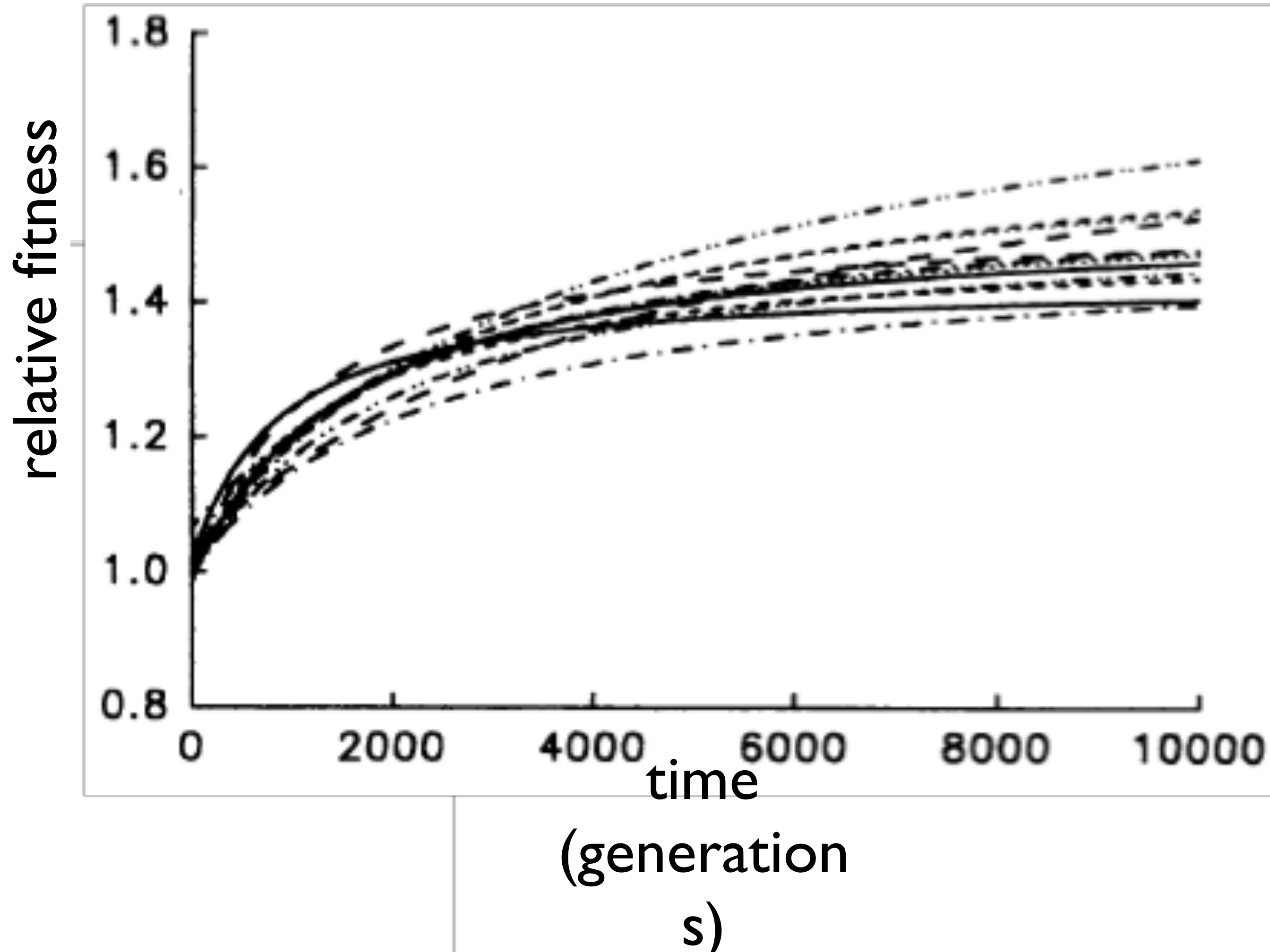
rate of adaptation
yeast

Goddard *et al.* 2005

# Genetic/genomic bases of adaptation

# Fitness effects of beneficial mutations




Kassen & Bataillon 2006

# Alleles & their fitness effects

**Table 2 | Tests of fitness effect in competition between isogenic constructs**

| Gene or region | Fitness effect (%) | Significance |
|---|---|---|
| *topA* | 13.3 | *** |
| *pykF** | 11.1 | *** |
| *spoT* | 9.4 | *** |
| *nadR*† | 8.1 | *** |
| *glmU* promoter | 4.9 | *** |
| *fis* | 2.9 | *** |
| *rbs* operon† | 2.1 | *** |
| *malT* | 0.4 | ** |
| *ompF*‡ | −9.7 | ** |

Barrick *et al.* 2009

# “Tape of life”: Parallel mutations

**Table 1 | Frequency of parallel mutations in 11 other independently evolved lines**

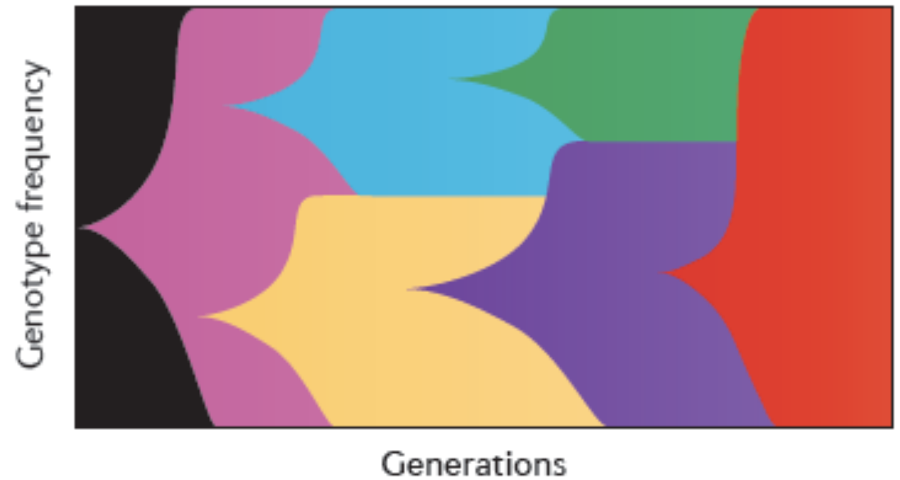
| Gene or region | Function | Parallel mutations (%) |
|---|---|---|
| *nadR* | Transcriptional regulator | 100 |
| *pykF* | Pyruvate kinase | 100 |
| *rbs* operon | Ribose catabolism | 100 |
| *malT* | Transcriptional regulator | 64 |
| *spoT* | Stringent response regulator | 64 |
| *mrdA* | Cell-wall biosynthesis | 45 |
| *infB* | Translation initiation factor 2 | 45* |
| *fis* | Nucleoid-associated protein | 27 |
| *topA* | DNA topoisomerase I | 27 |
| *pcnB* | Poly(A) polymerase | 27 |
| *ompF* | Outer-membrane porin | 18* |
| *rpsD* | 30S ribosomal protein | 18* |
| *rpsM* | 30S ribosomal protein | 0 |
| *glmU* promoter | Cell-wall biosynthesis | 0 |

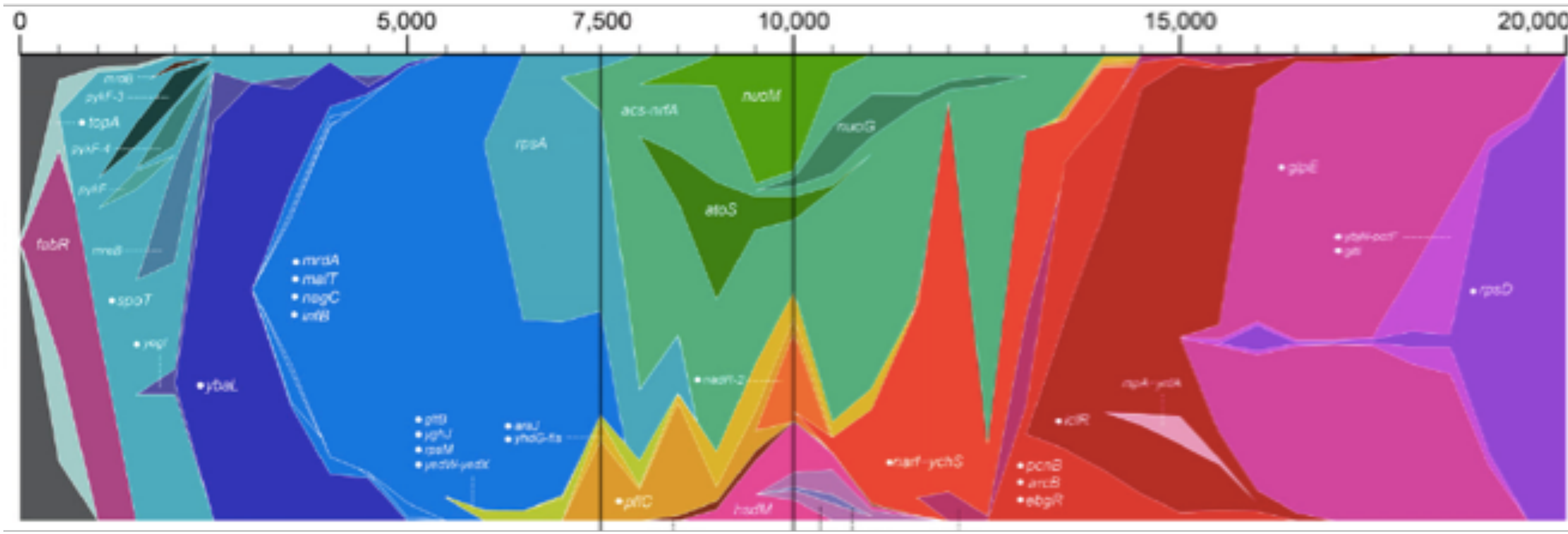
* In addition to populations with substitutions, one or more others were polymorphic.

Barrick *et al.* 2009

tape of life

# Muller plots from NGS data



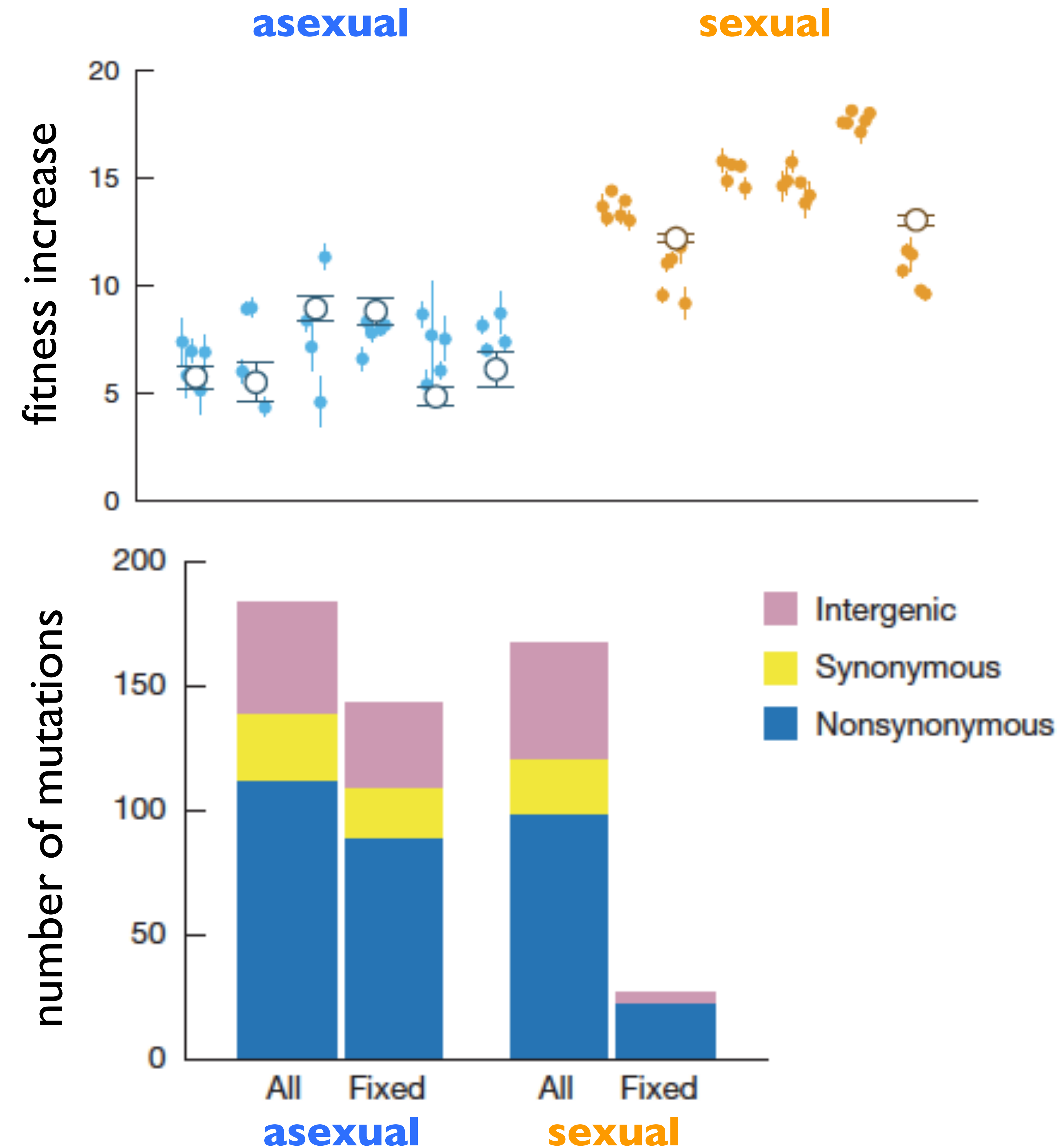

frequency

time (generations)

Maddamsetti *et al.* 2015

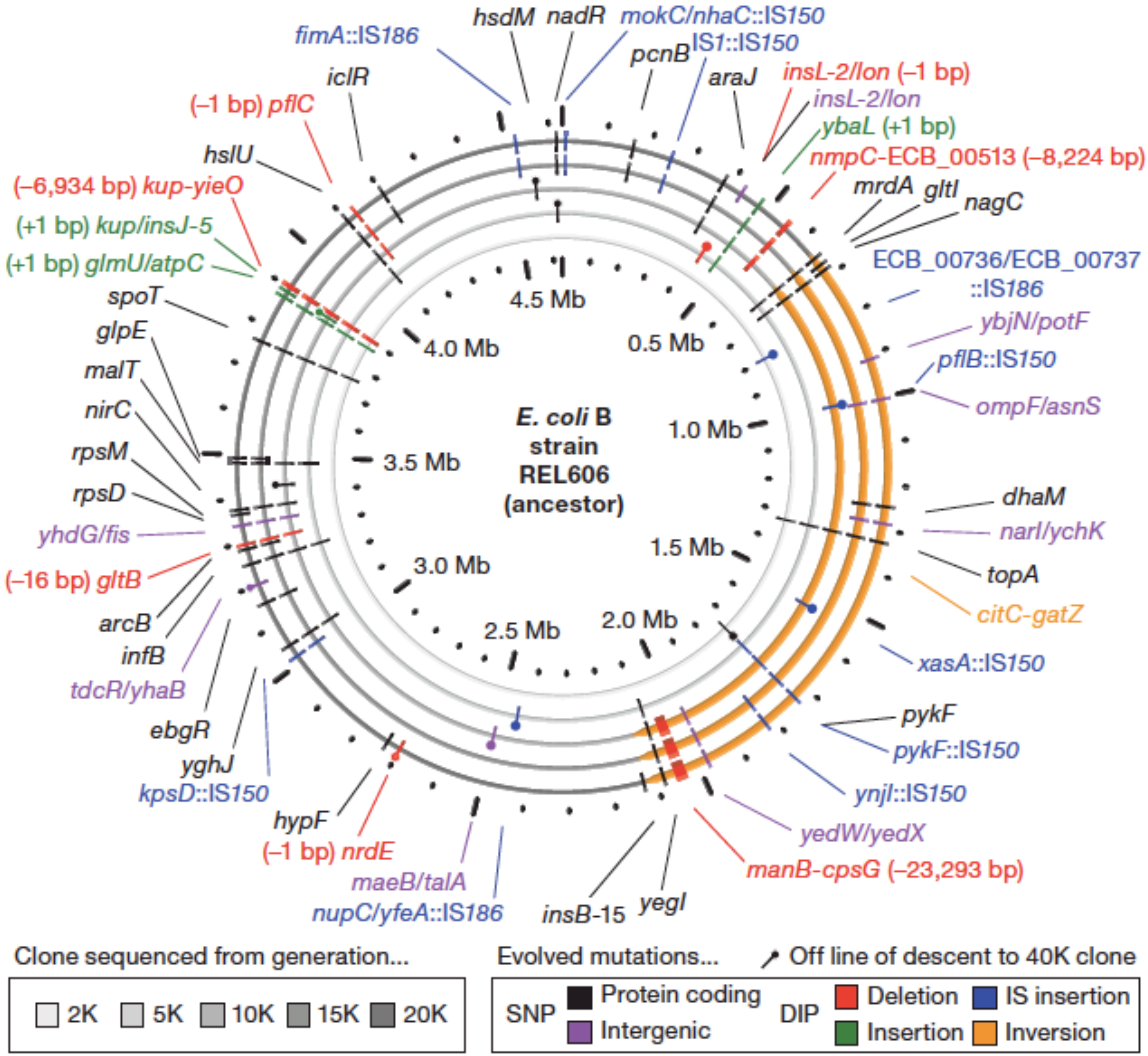
genetics of adaptation

# Genetics of adaptation: sex




genetics of adaptation

McDonald *et al.* 2016



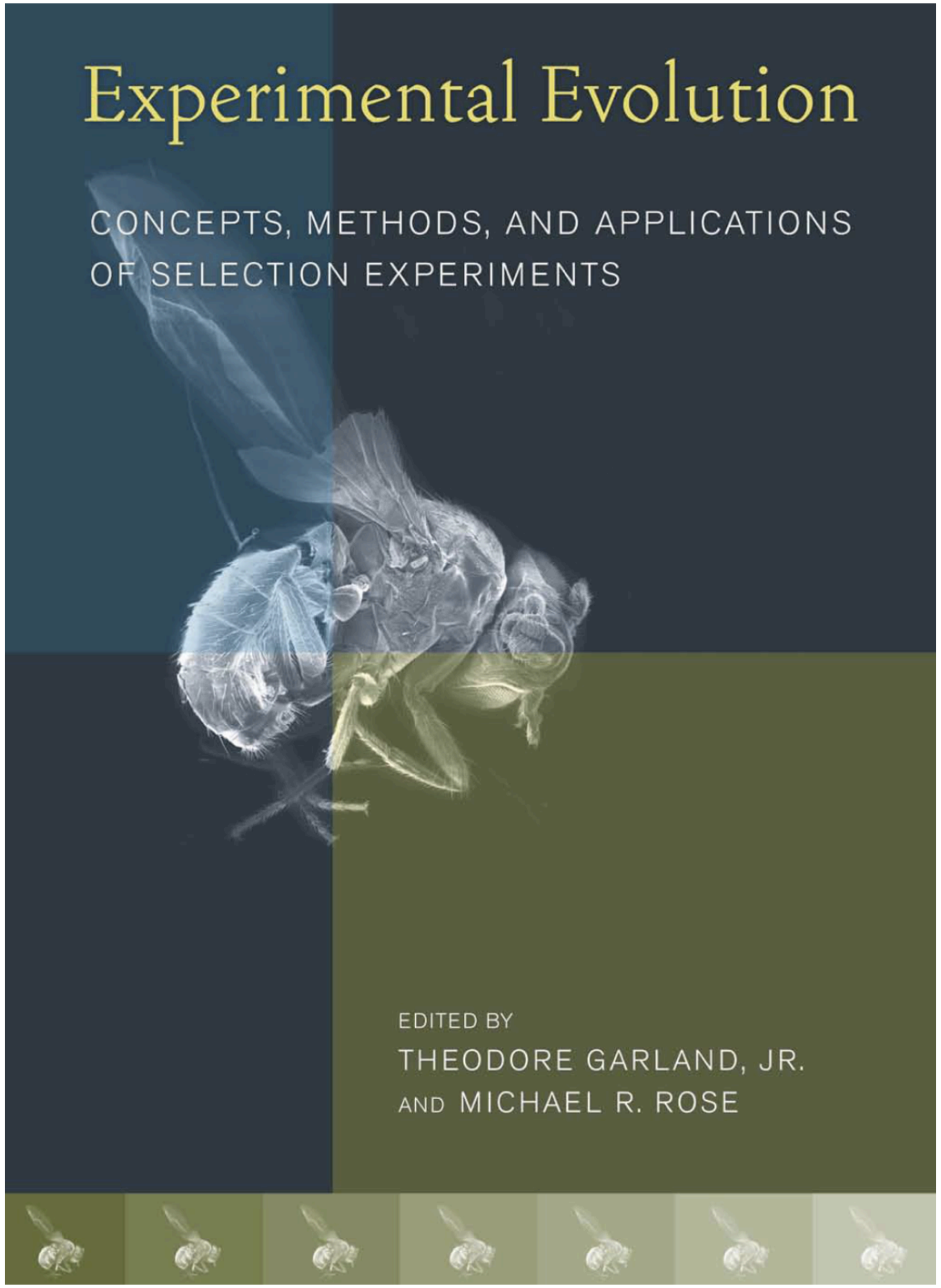

Barrick *et al.* 2009

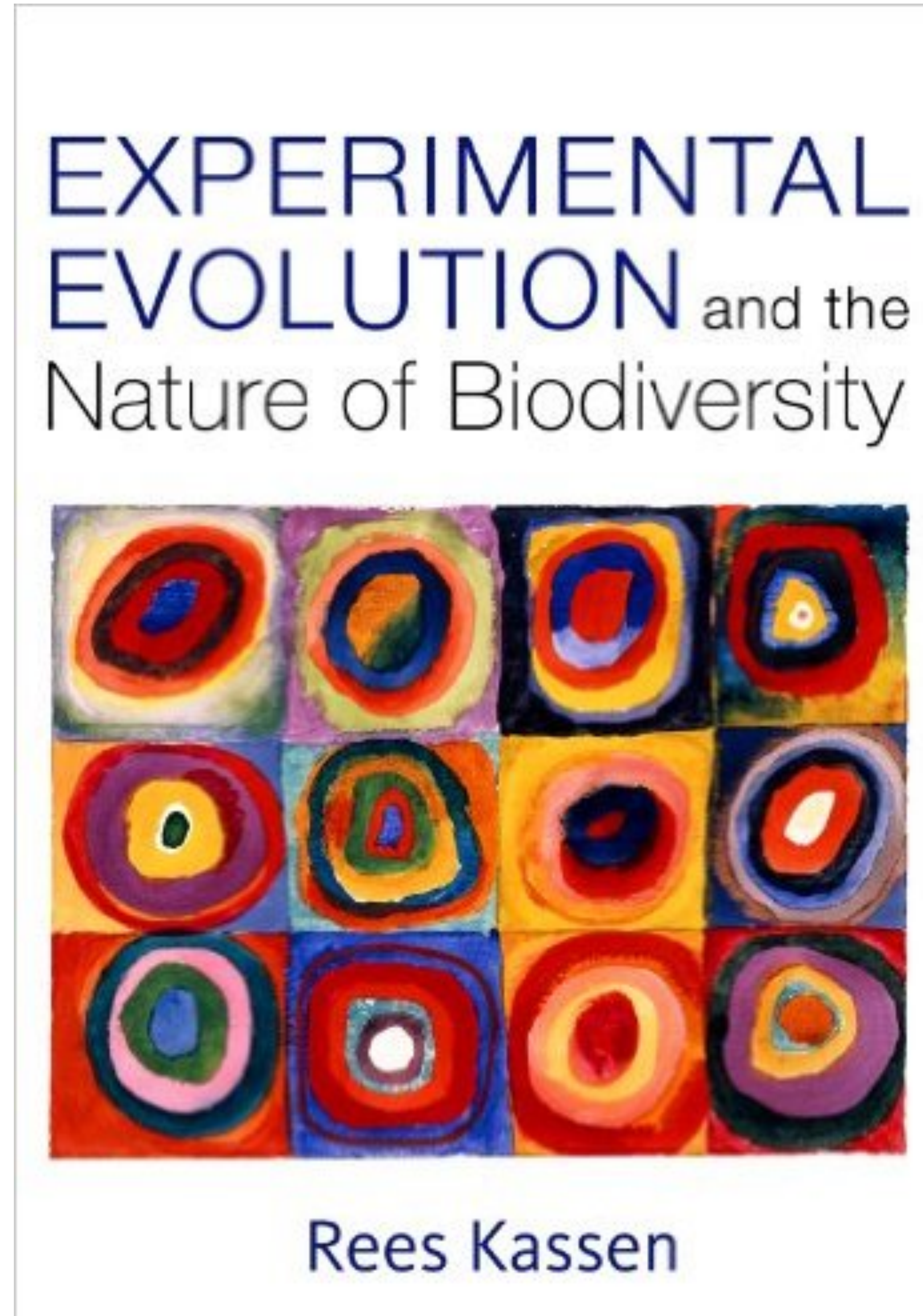
genetics of adaptation

# Limitations of experimental evolution

too simplified,
growth parameters are not widely applicable,
nutrient levels are arbitrarily selected,
ignores ecological complexity

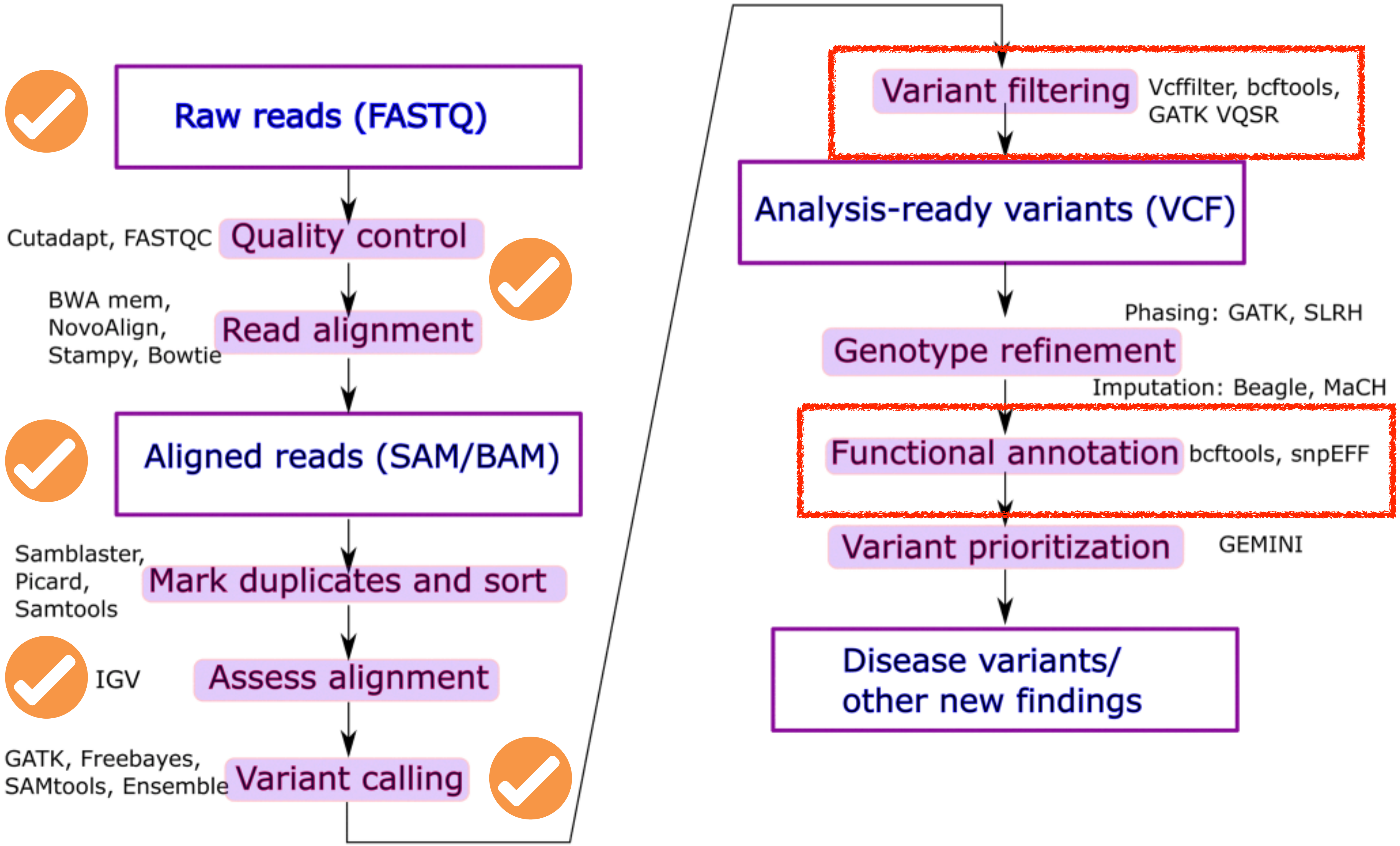
# Further reading



# UYGULAMA

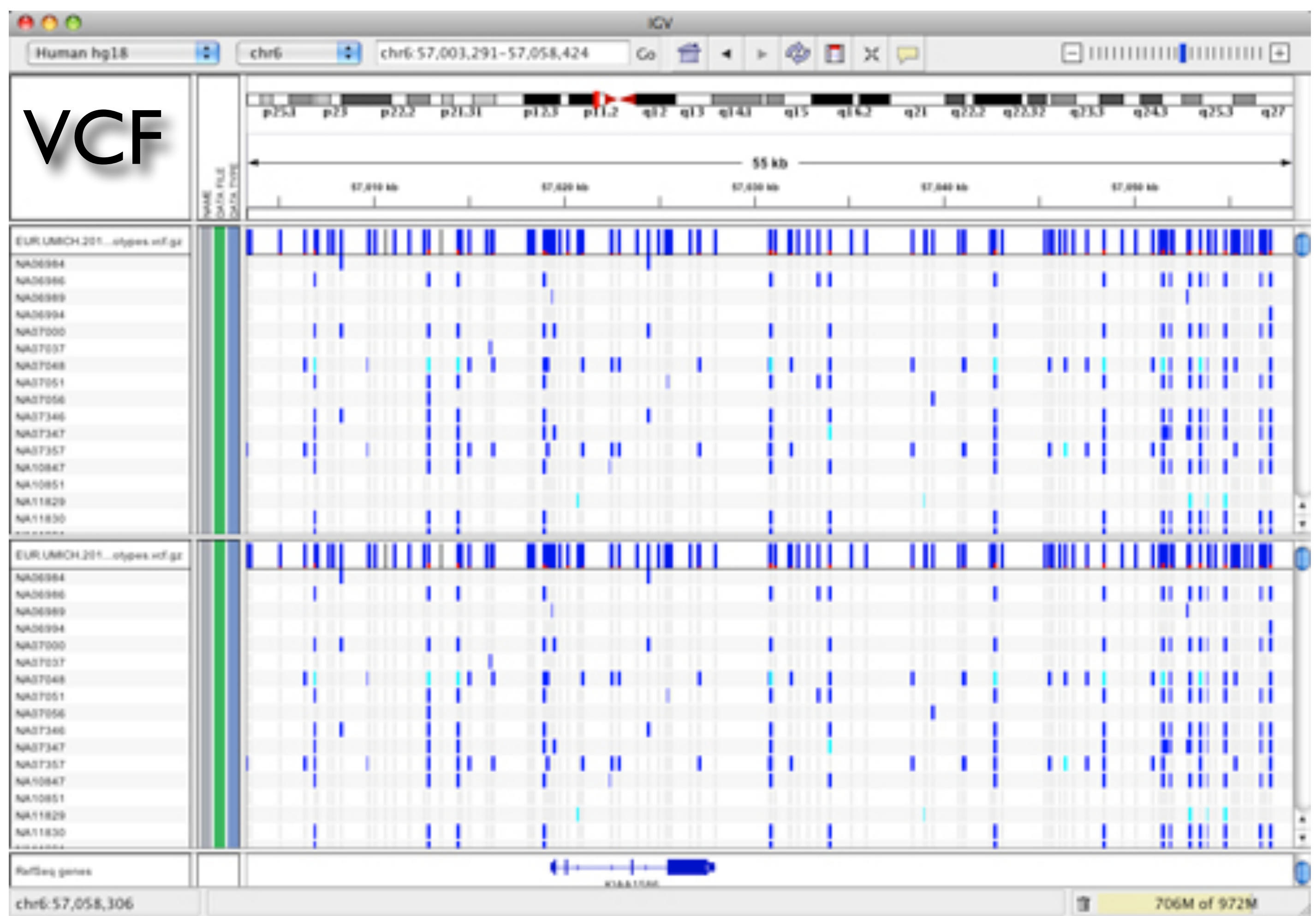
# Uygulama


Raw reads (FASTQ)
Cutadapt, FASTQC
Quality control
BWA mem,
NovoAlign,
Stampy, Bowtie
Read alignment
Aligned reads (SAM/BAM)
Samblaster,
Picard,
Samtools
Mark duplicates and sort
IGV
Assess alignment
GATK, Freebayes,
SAMtools, Ensemble
Variant calling
Variant filtering
Vcffilter, bcftools,
GATK VQSR
Analysis-ready variants (VCF)
Phasing: GATK, SLRH
Genotype refinement
Imputation: Beagle, MaCH
Functional annotation
bcftools, snpEFF
Variant prioritization
GEMINI
Disease variants/
other new findings

Find variants (VCF files) in ancestor

Compare Using bcftools isec

Find variants (VCF files) in evolved



# Tesekkurler

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