

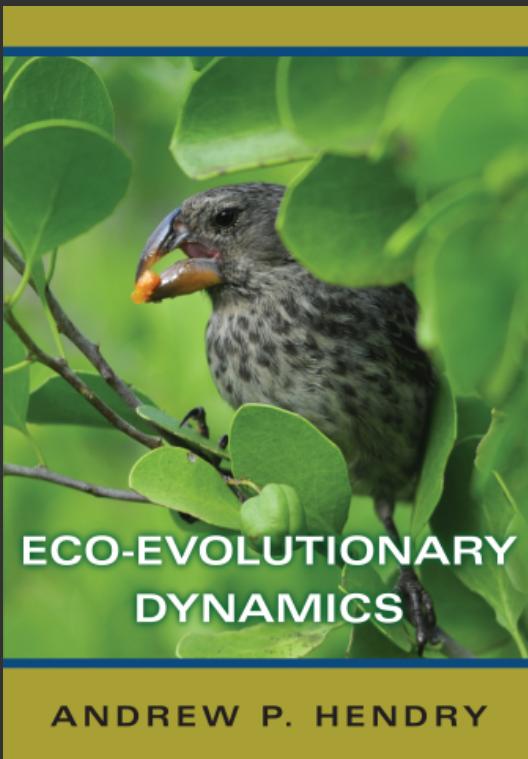
Adaptive Phenotypic Plasticity and Epigenetics

Kevin Wong

BIO 594 | Feb. 28 2019

Outline

Phenotypic Plasticity



- Q1: What is phenotypic plasticity?**
- Q2: Is plasticity adaptive?**
- Q3: What are the cost-benefits of plasticity?**
- Q4: Does plasticity promote or constrain genetic evolution?**
- Q5: How can we quantify phenotypic plasticity?**

Outline

Epigenetics

Annual Review of Marine Science

Marine Environmental Epigenetics

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Q1: What is epigenetics?

Q2: Epigenetic effect vs inheritance

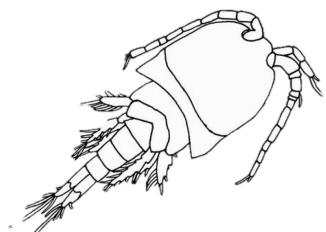
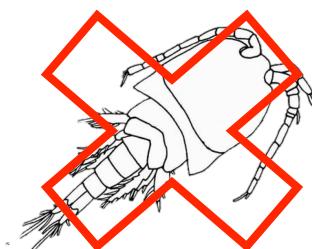
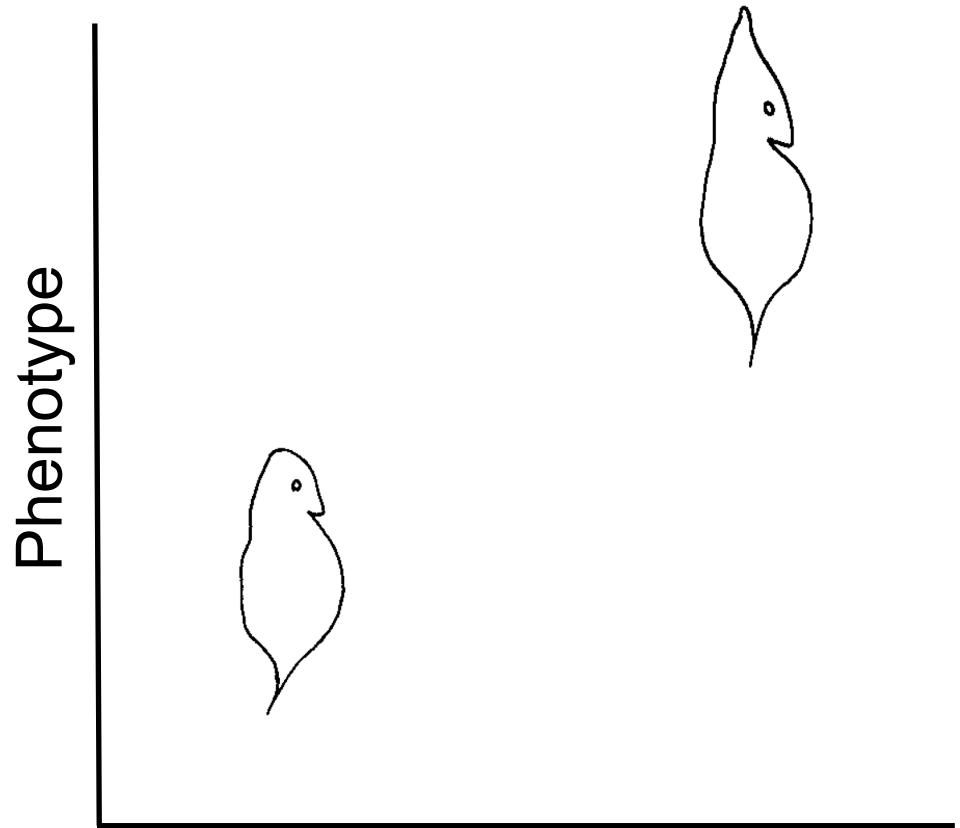
Q3: What are epigenetic mechanisms?

Q4: How can we quantify epigenetics?

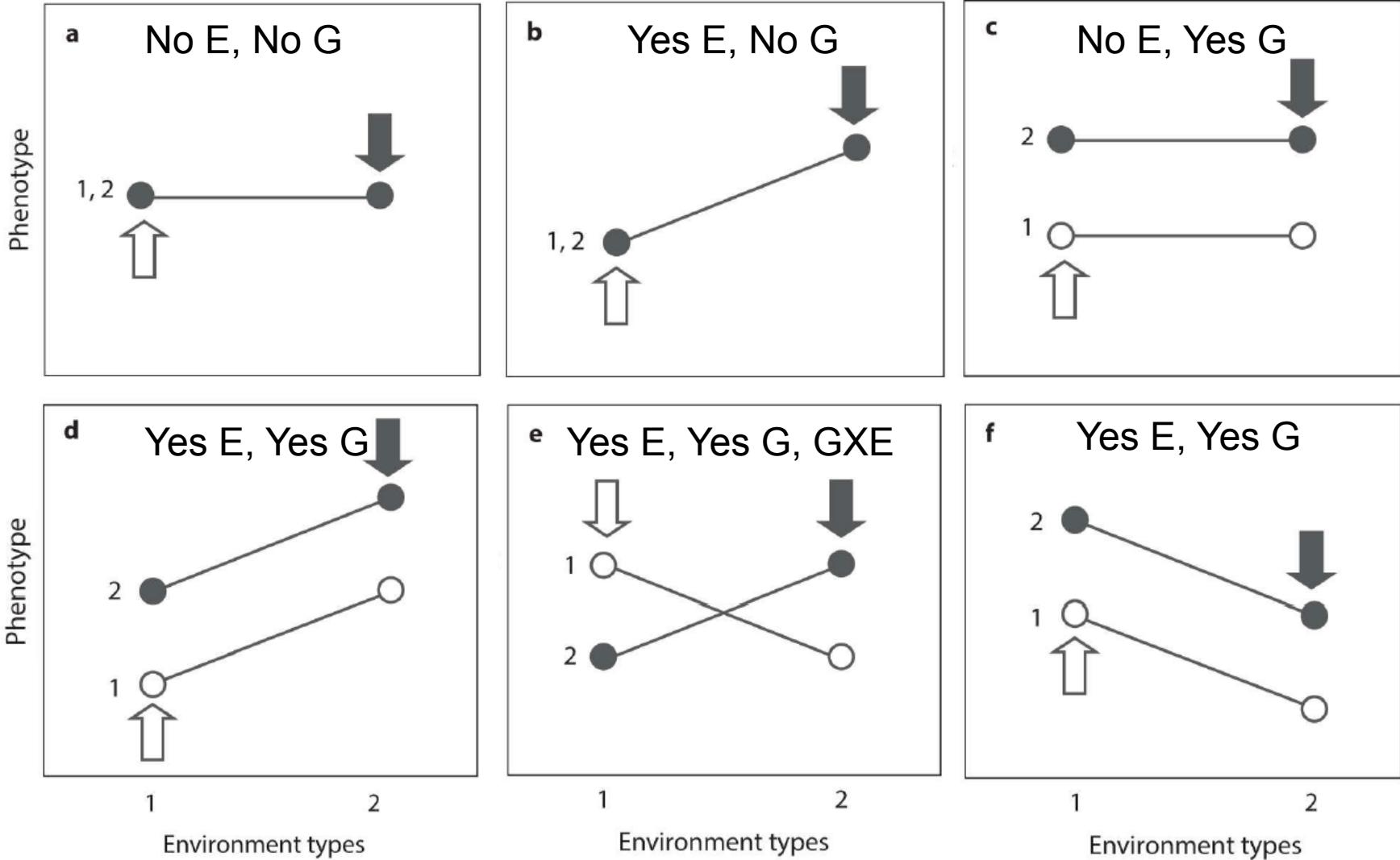
Q5: What is the epigenetic role in environmental acclimatization?

Q1: What is phenotypic plasticity?

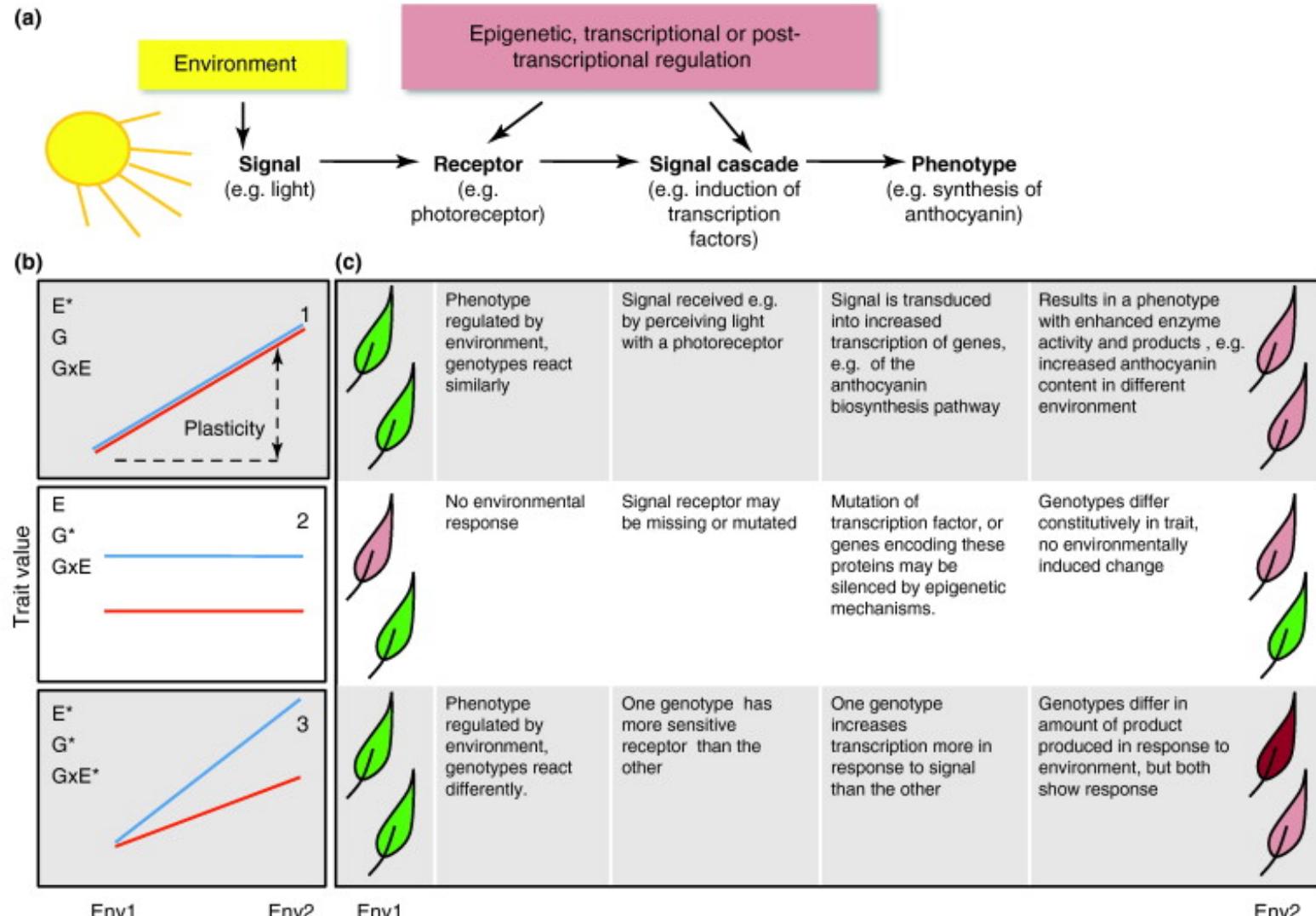
“The ability of one genotype to express different phenotypes in different environments”



Environment (E), Genotype (G), or both (GXE)?



Plasticity and Reaction Norms



Q1: What is phenotypic plasticity?

Within-generation (WGP)

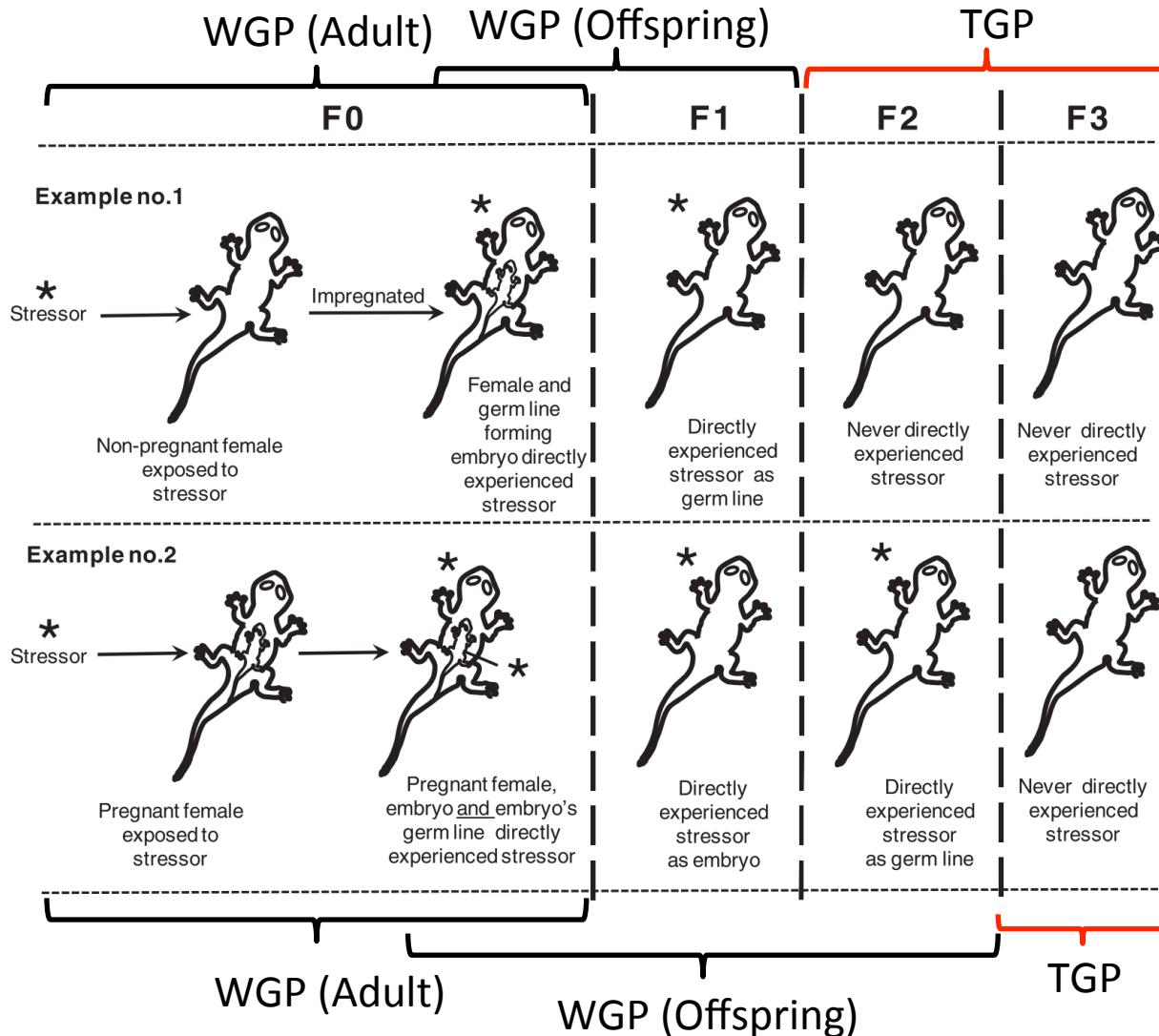
- A change in phenotype within the same individual under altered environmental conditions

Trans-generational (TGP)

- Differences in offspring phenotype that occur due to the interaction between the current generation and previous generation's environmental conditions

But what defines different generations?

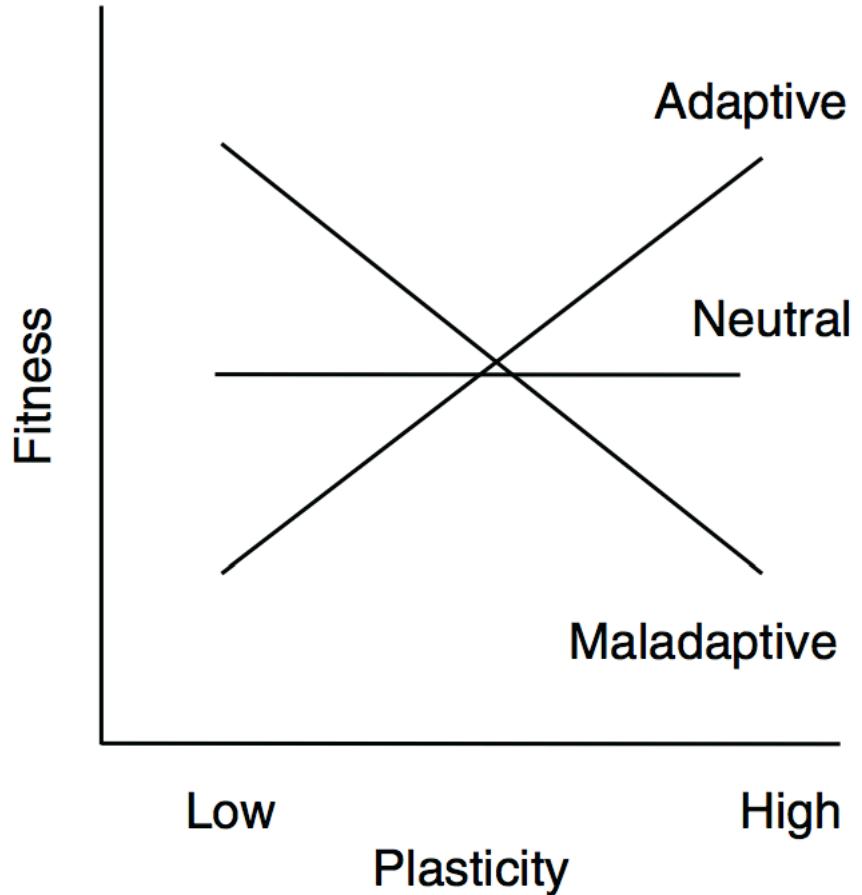
Types of plasticity: WGP and TGP



Q2: Is plasticity adaptive?

“Plasticity is sometimes adaptive, sometimes maladaptive, and sometimes neutral”

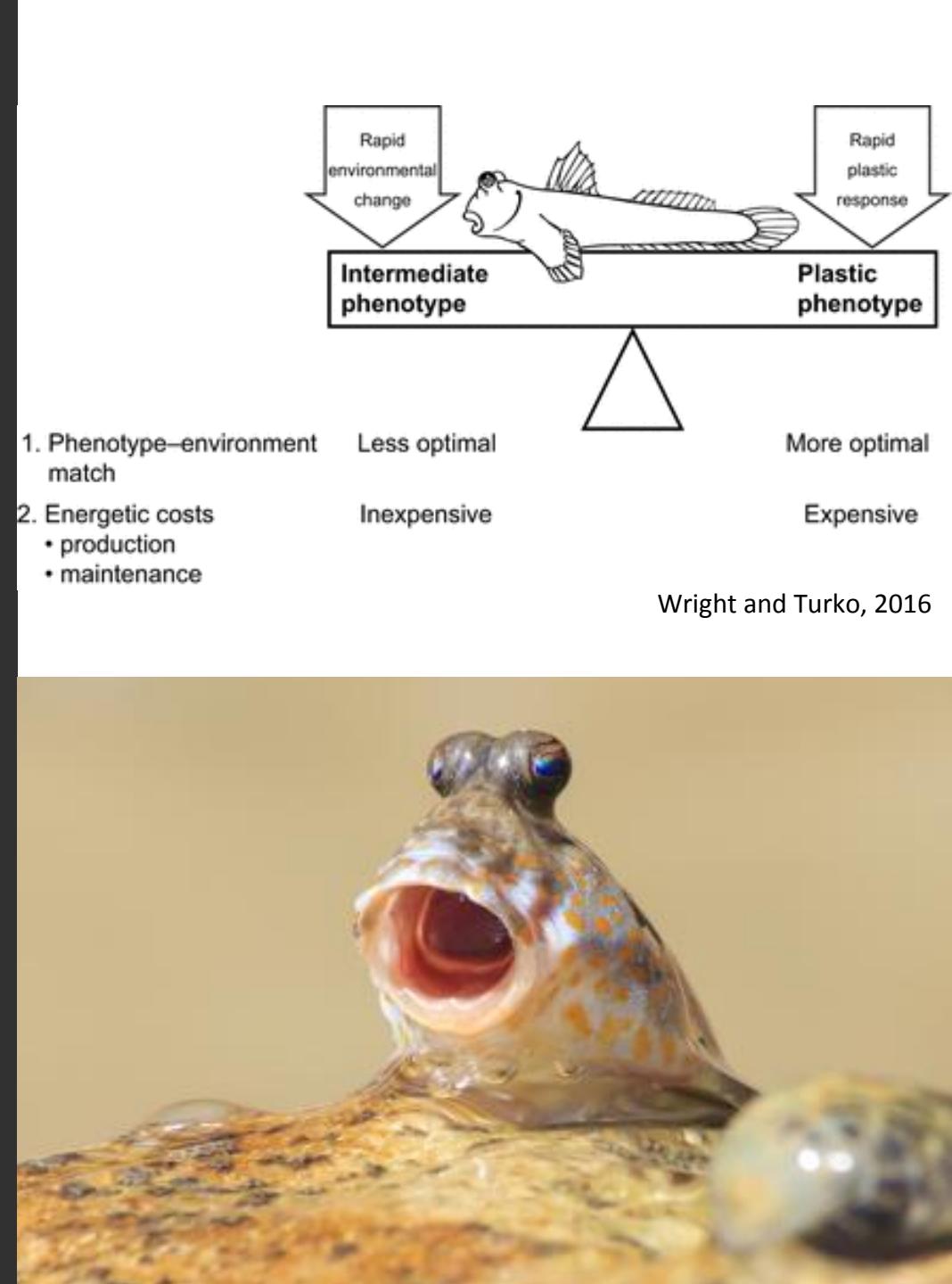
– Andrew Hendry



Q3: What are the cost-benefits of plasticity?

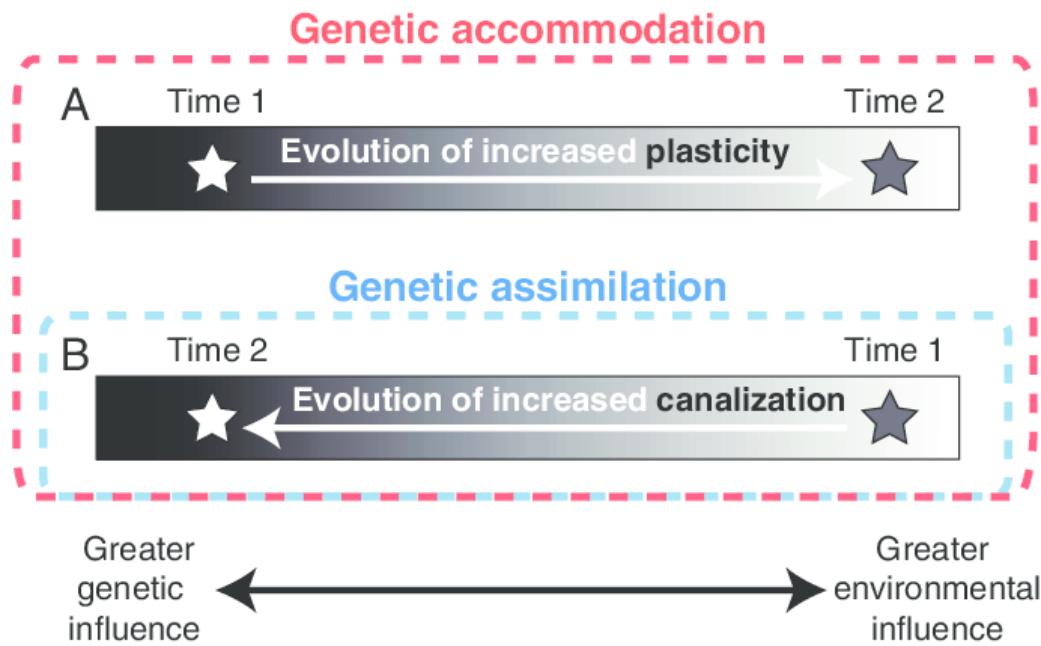
Energetic costs:

- Building new structures (and reversing)
- Maintenance costs for detecting environmental change
- Lag time effects – when is it worth it?



Q5: Does plasticity promote or constrain evolution?

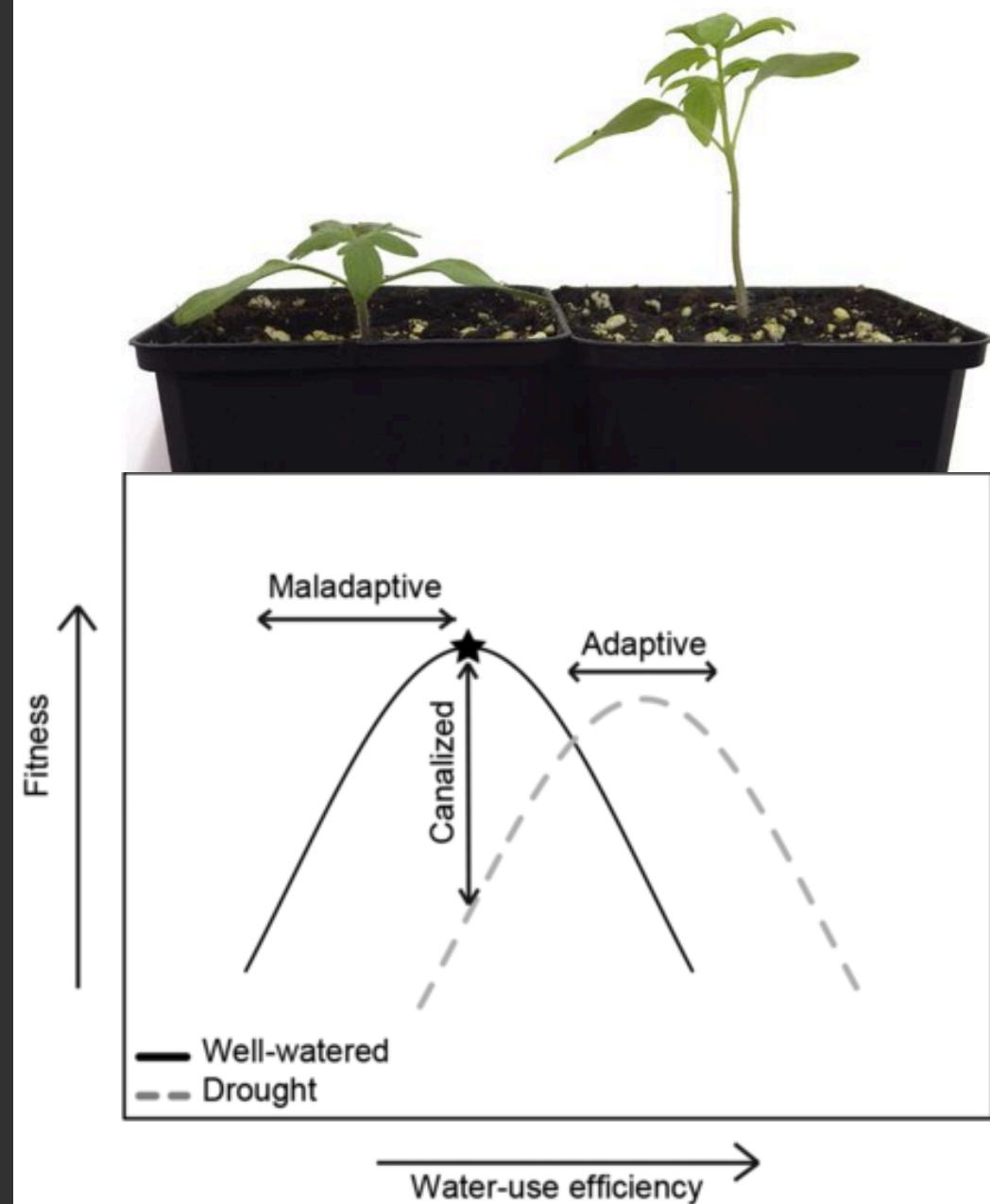
Genetic canalization
Genetic assimilation



Q4: Does plasticity promote or constrain evolution?

Genetic canalization

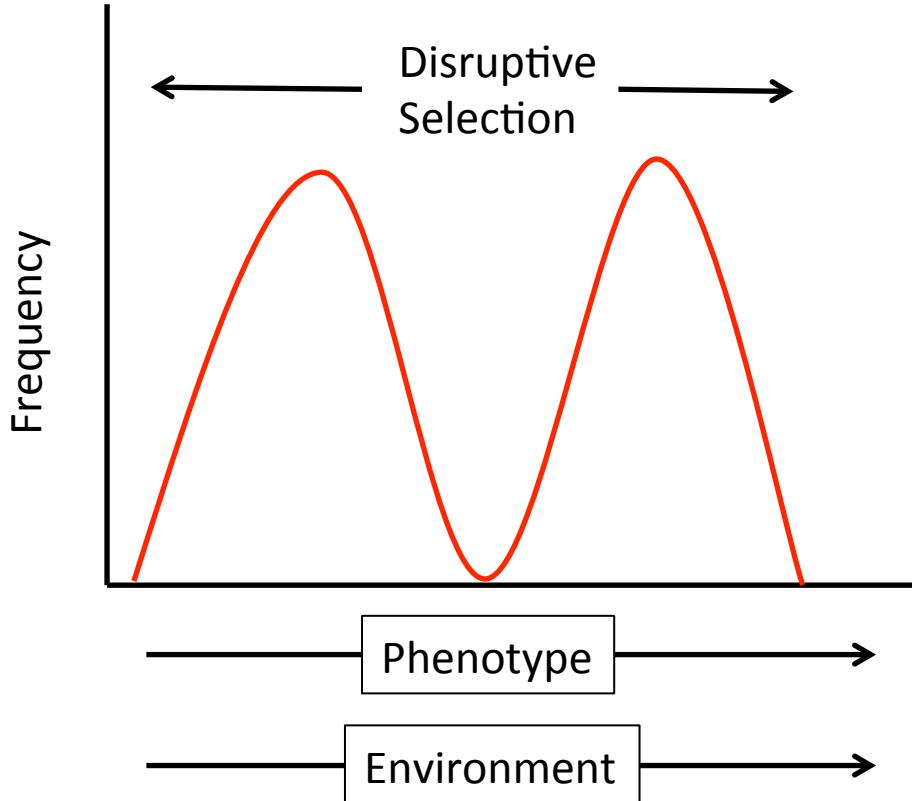
- Phenotypic robustness to environmental change



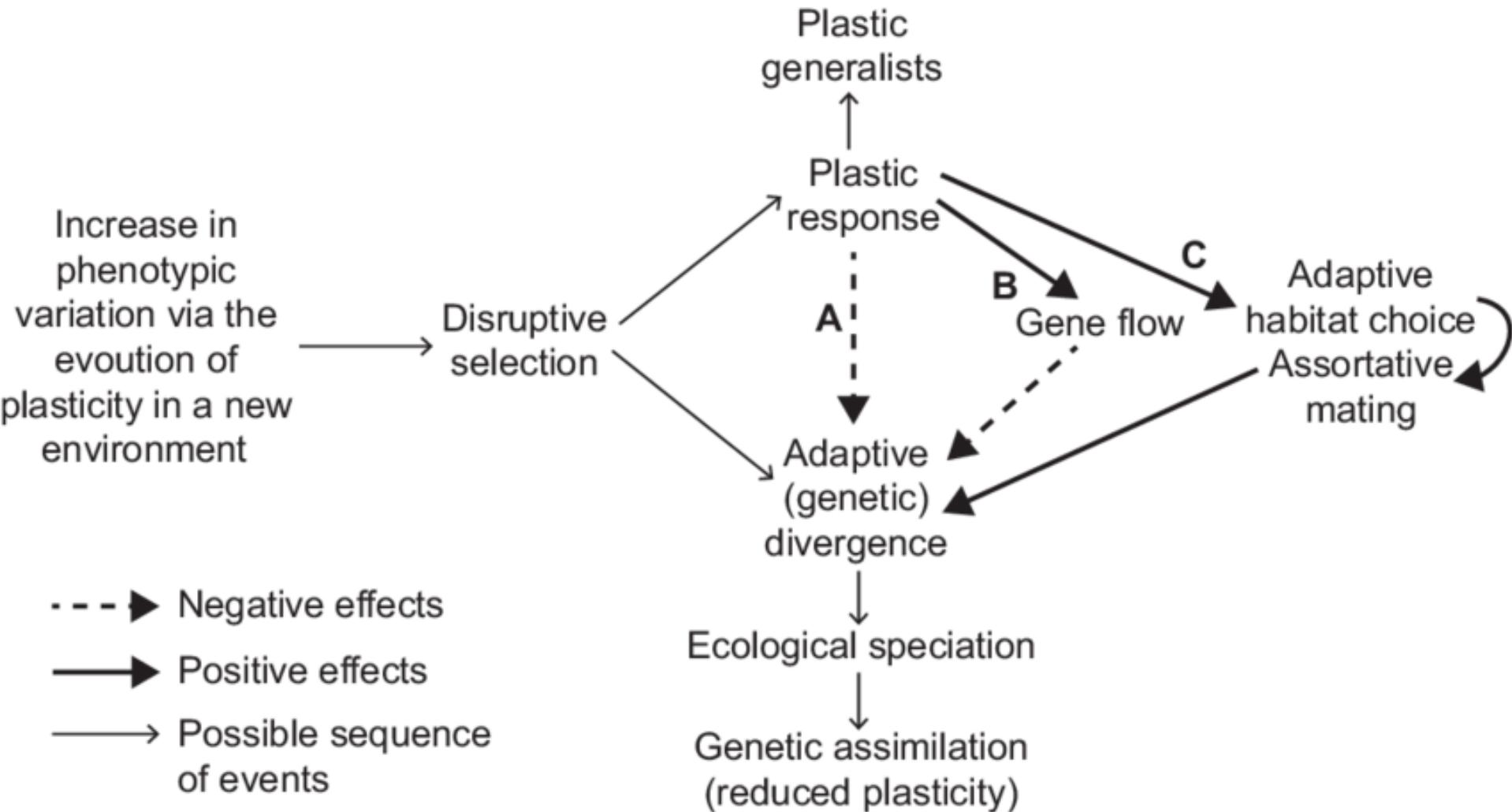
Q4: Does plasticity promote or constrain evolution?

Genetic assimilation

- When a change on phenotype in response to an environmental change is selected for
- Does this increase or decrease long term plasticity?

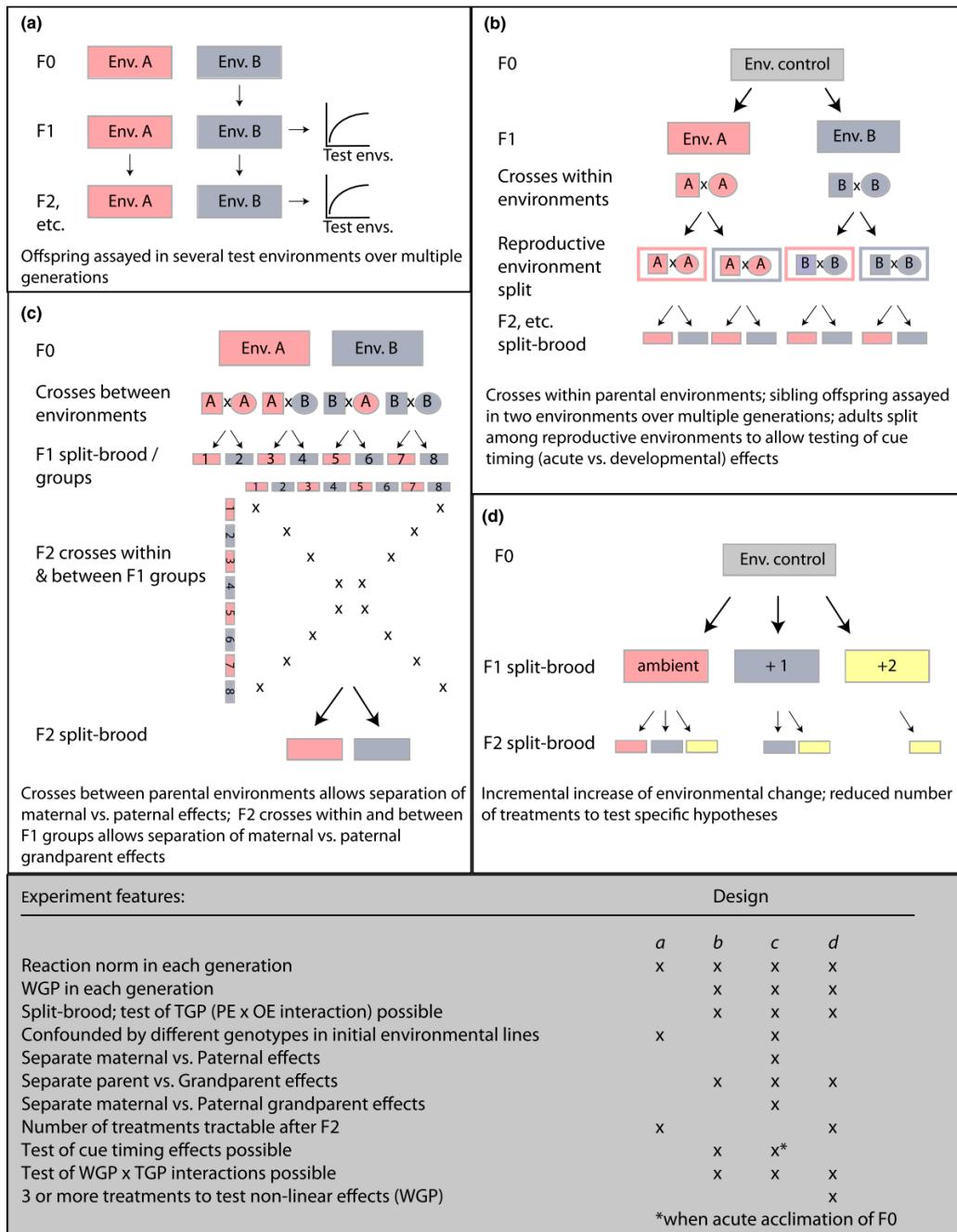


Does this increase or decrease long term plasticity?



Q5: How can we quantify phenotypic plasticity?

- Experimental Design matching the hypothesis
- Known plastic traits and how to measure them
- Are they heritable?

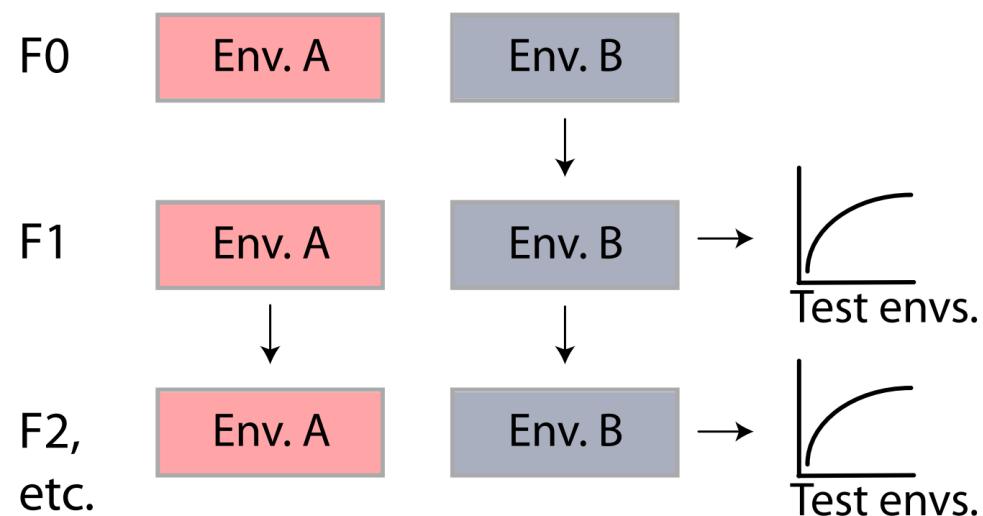


Q5: How can we quantify phenotypic plasticity?

Experimental Design (a):

- Population Level
- Rxn norm for each generation
- Confounded by different genotypes in each environmental line

(a)



Q5: How can we quantify phenotypic plasticity?

Experimental Design (b):

- Rxn norm for each generation
- WGP in each generation
- Split -brood, testing TGP (PE X OE)
- Separate parent/grandparent effects
- Can test for cue timing effects
- Can test WGP X TGP interactions

(b)

F0

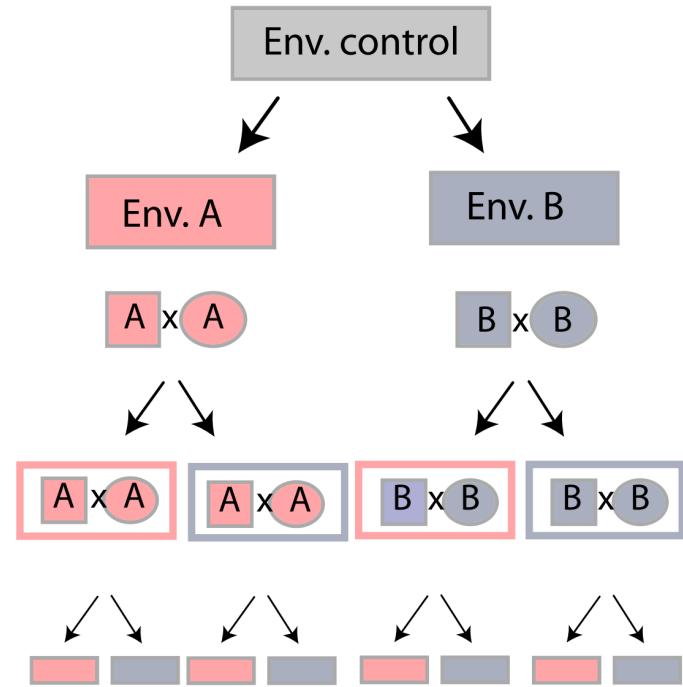
Env. control

F1

Crosses within environments

Reproductive environment split

F2, etc.
split-brood



Q5: How can we quantify phenotypic plasticity?

Experimental Design (c):

- Rxn norm for each generation
- WGP in each generation
- Split -brood, testing TGP (PE X OE)
- Confounded by different genotypes in each environmental line
- Separate maternal/paternal effects
- Separate parent/grandparent effects
- Can test WGP X TGP interactions

(c)

F0

Env. A

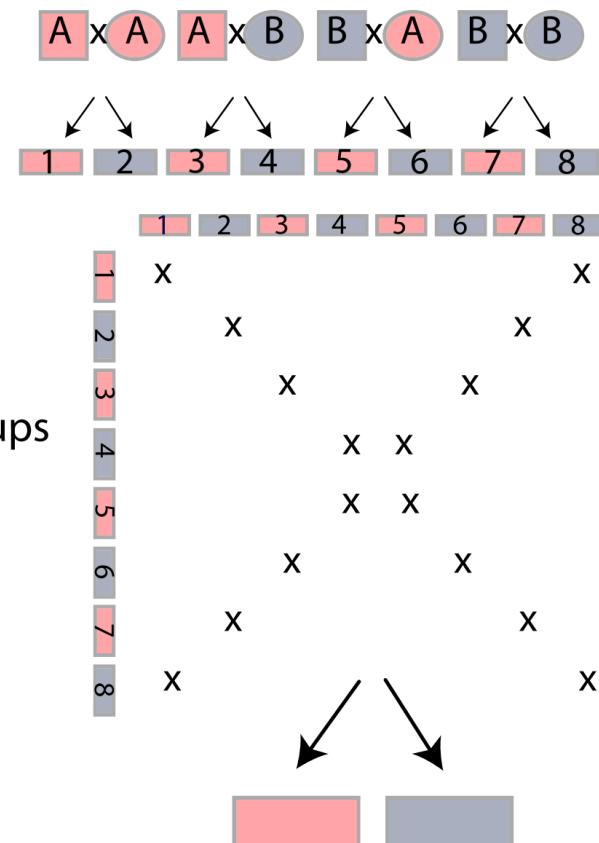
Env. B

Crosses between environments

F1 split-brood / groups

F2 crosses within & between F1 groups

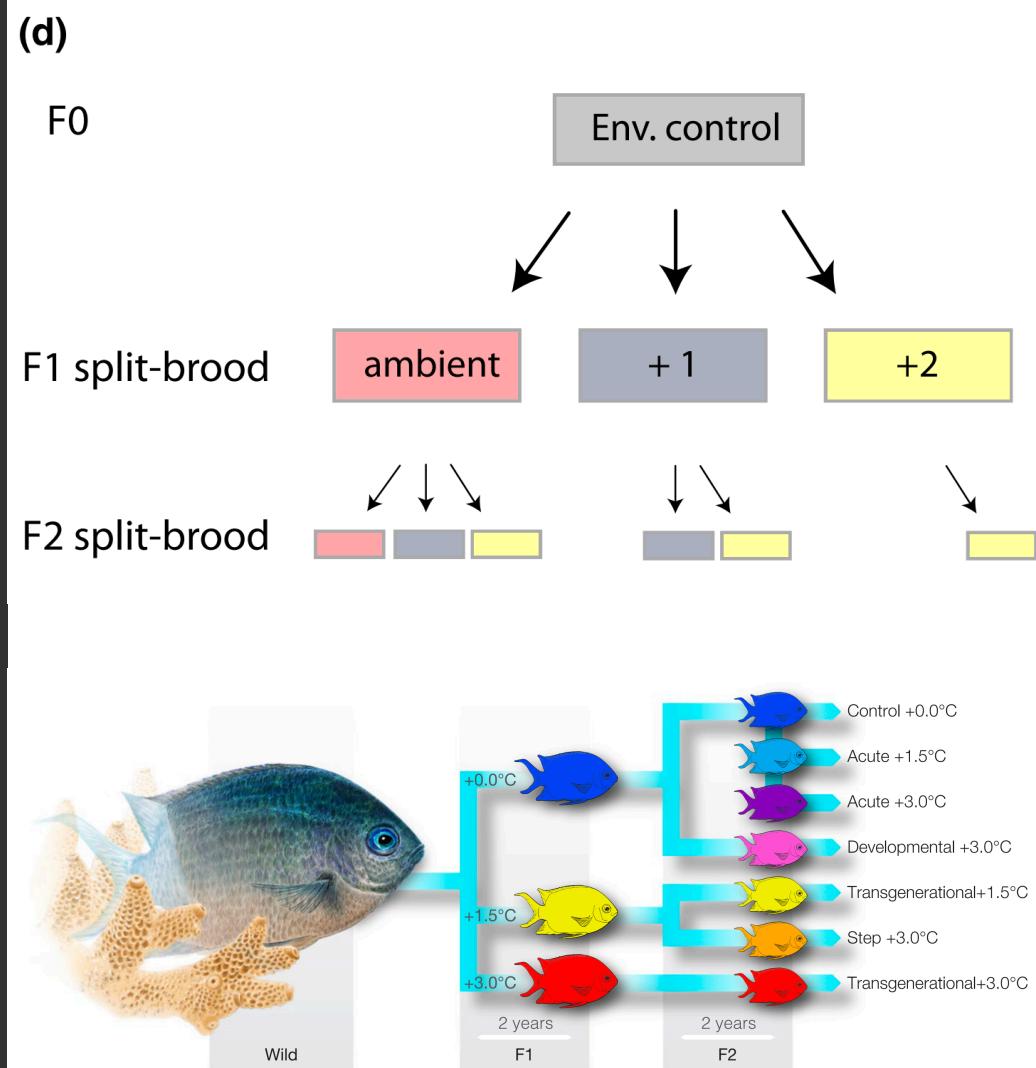
F2 split-brood



Q5: How can we quantify phenotypic plasticity?

Experimental Design (d):

- Rxn norm for each generation
- WGP in each generation
- Split -brood, testing TGP (PE X OE)
- Separate parent/grandparent effects
- Can test WGP X TGP interactions
- Can test for cue timing effects
- 3 or more treatments to test non-linear effects



Outline

Epigenetics

Q1: What is epigenetics?

Q2: Epigenetic effect vs inheritance

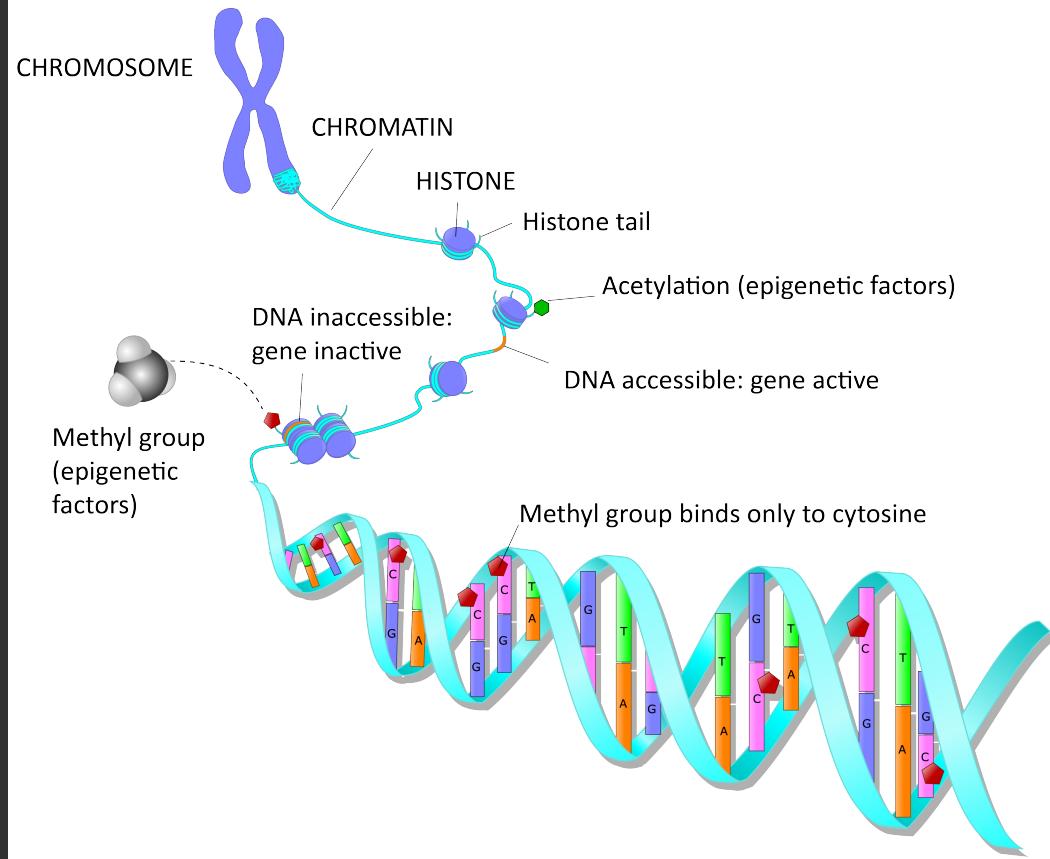
Q3: What are epigenetic mechanisms?

Q4: How can we quantify epigenetics?

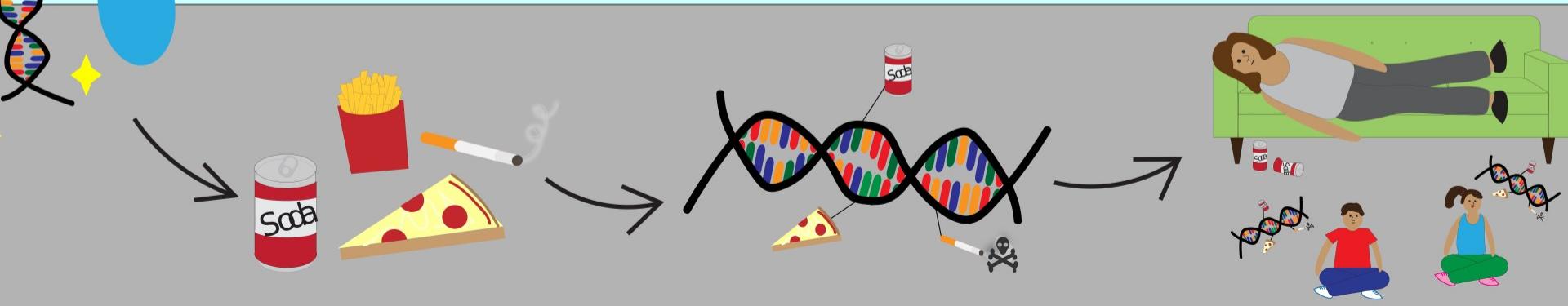
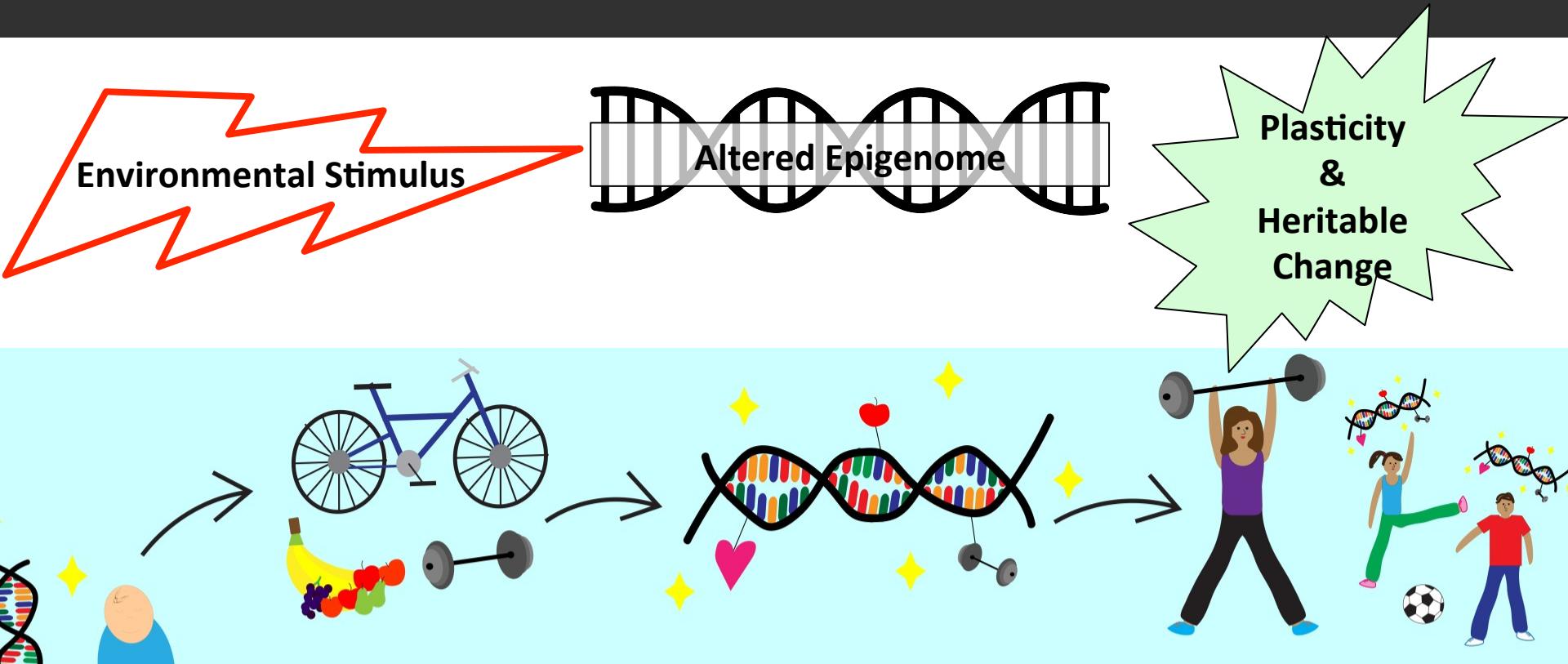
Q5: What is the epigenetic role in environmental acclimatization?

Q1: What is epigenetics?

“Change in **heritable** (mitotic/meiotic) gene function that **cannot** be explained by changes in the DNA sequence”

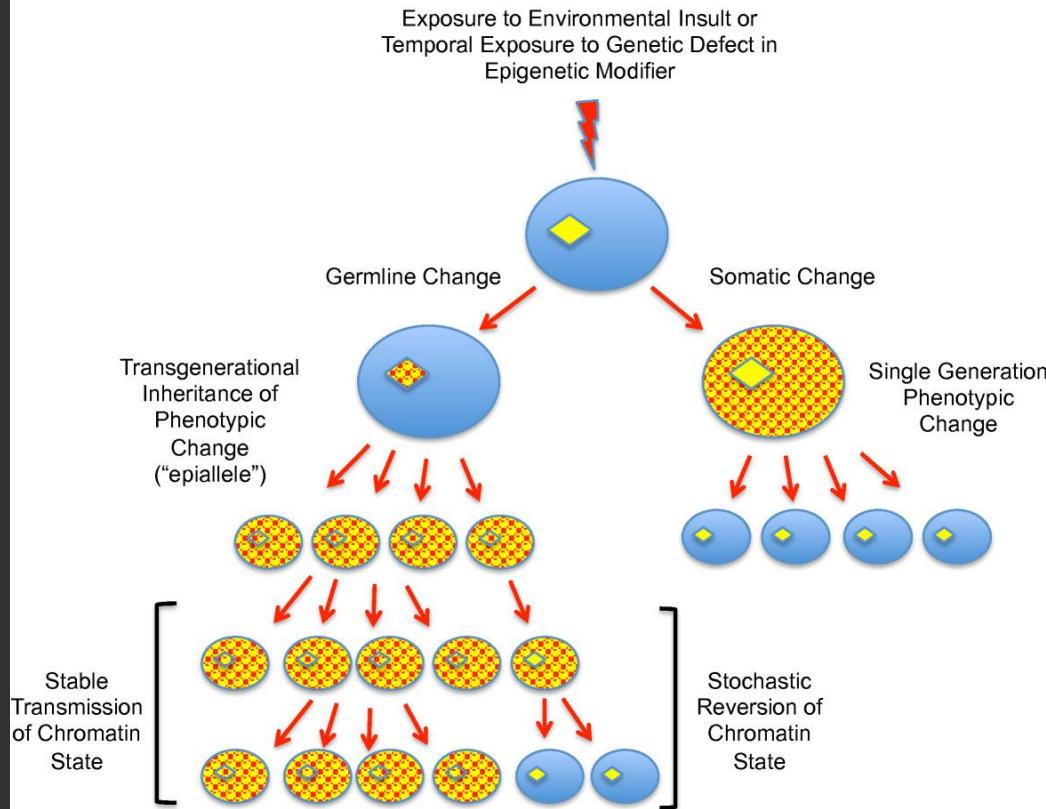


Plasticity and Epigenetics

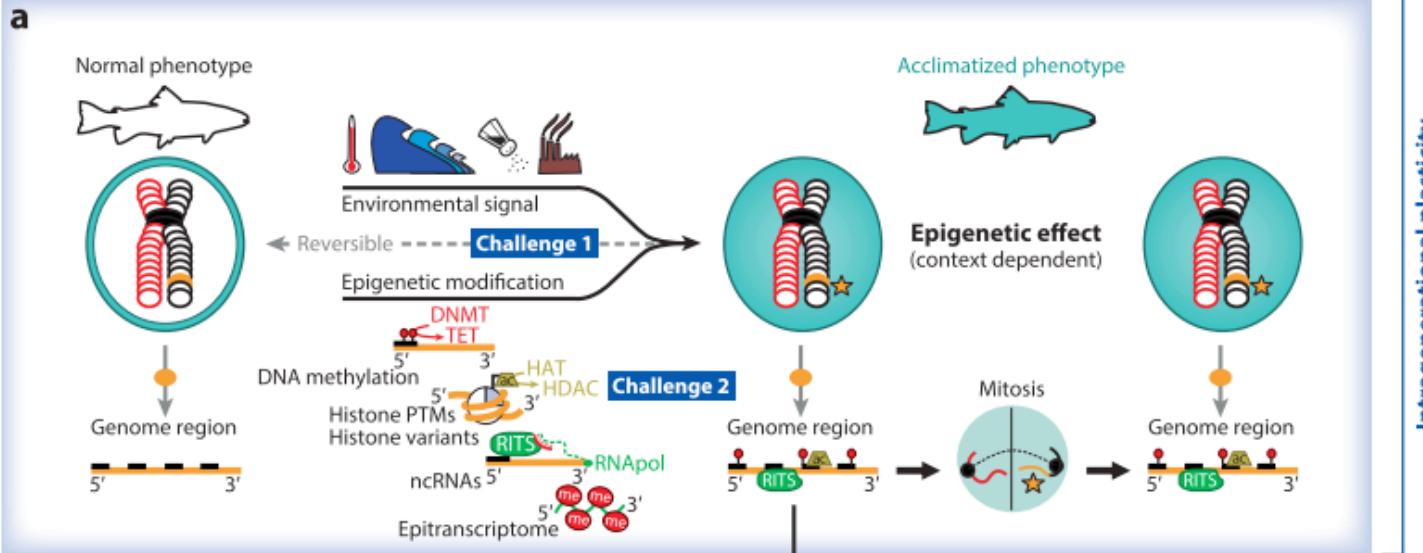


Q2: Epigenetic effect vs inheritance

- Transmission of epigenetic states in the soma and germline
- Epigenetic effects on soma
- Epigenetic inheritance through germline cells

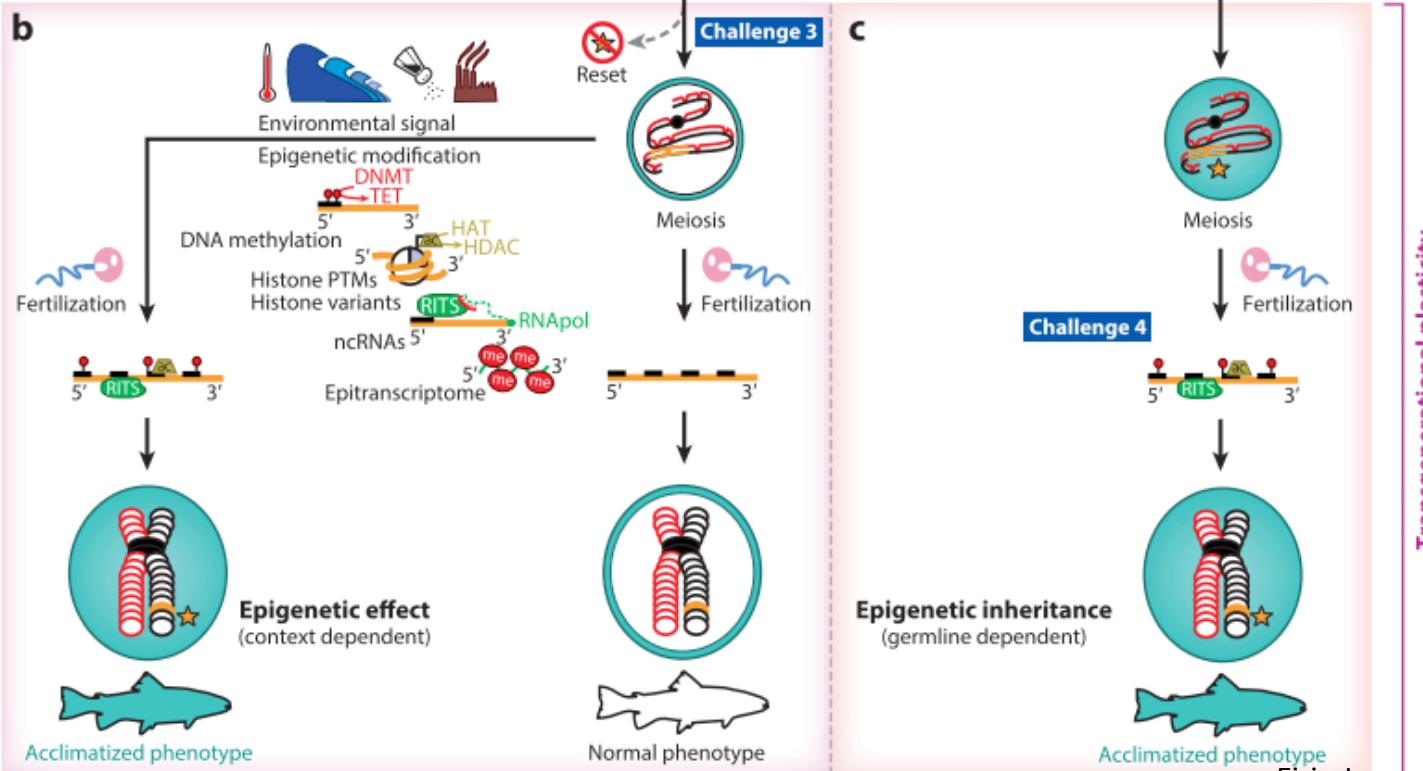


Parental generation



Intragenerational plasticity

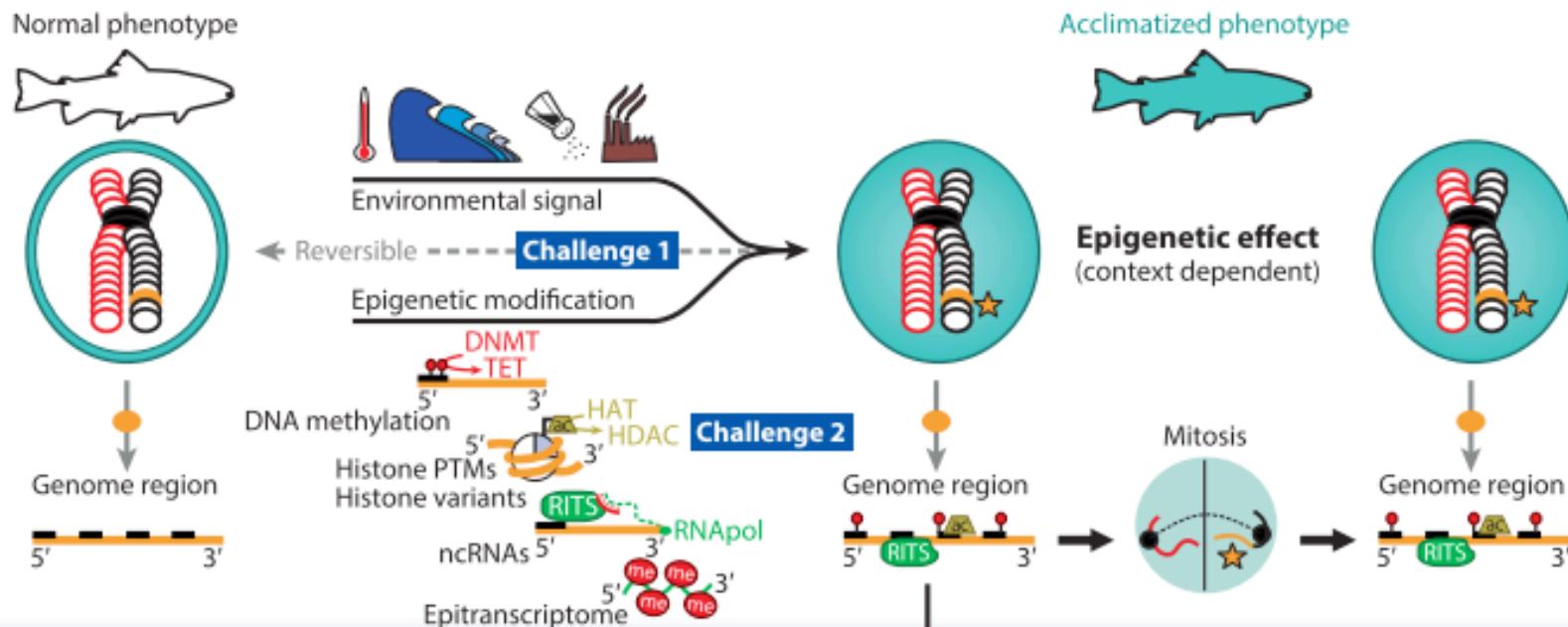
Offspring generation



Transgenerational plasticity

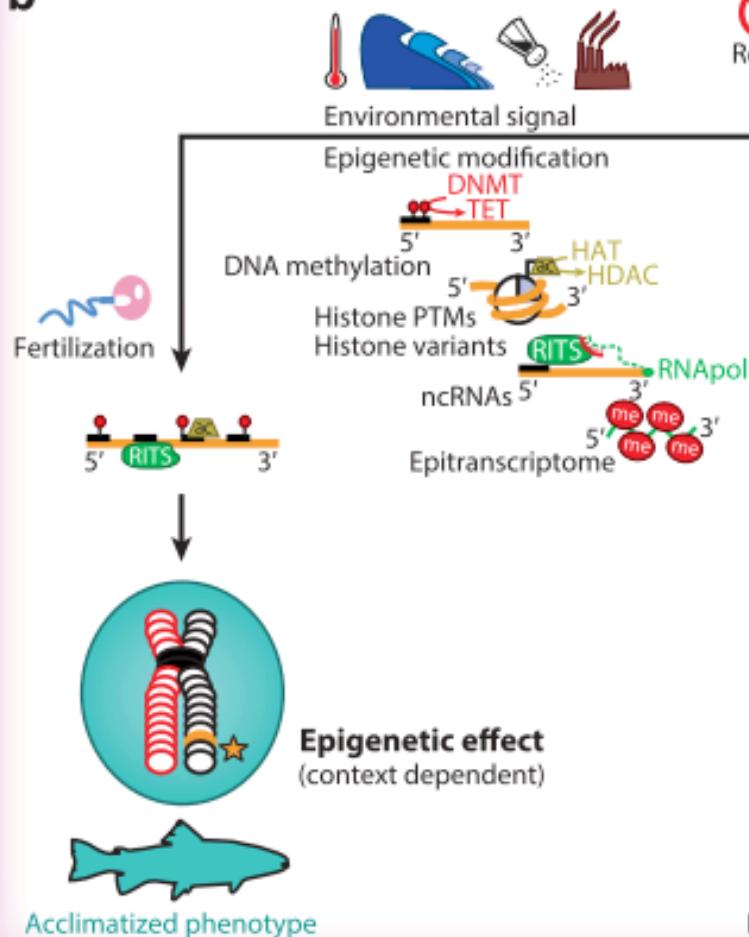
Parental generation

a



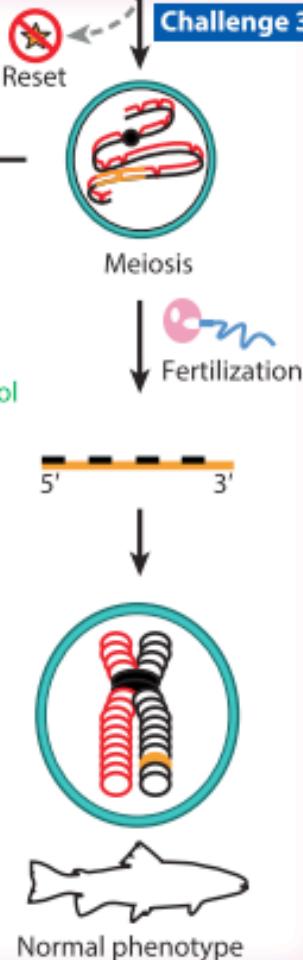
Offspring generation

b

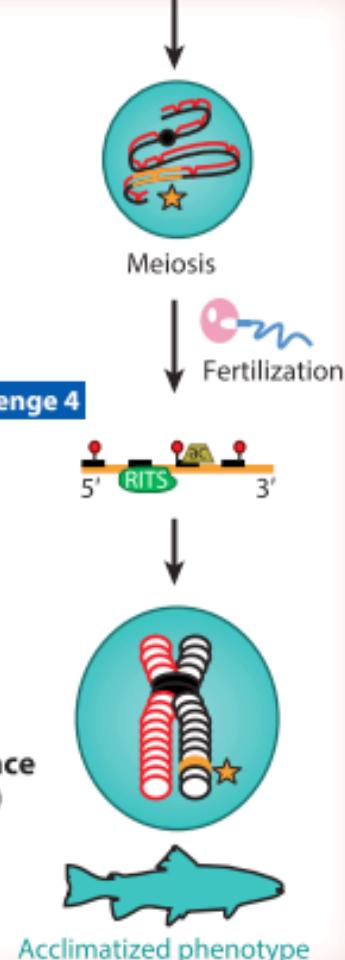


Challenge 3

c

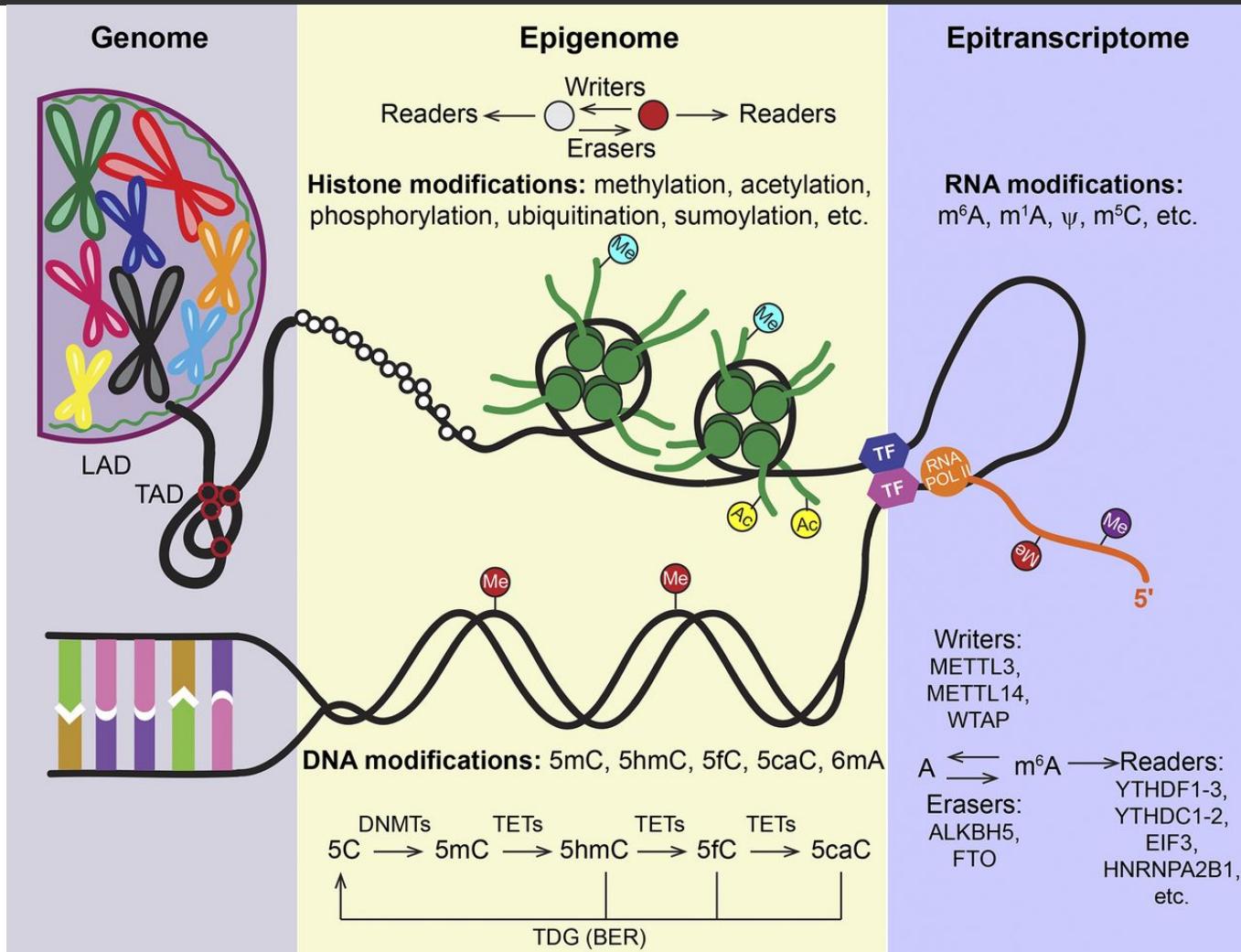


Challenge 4



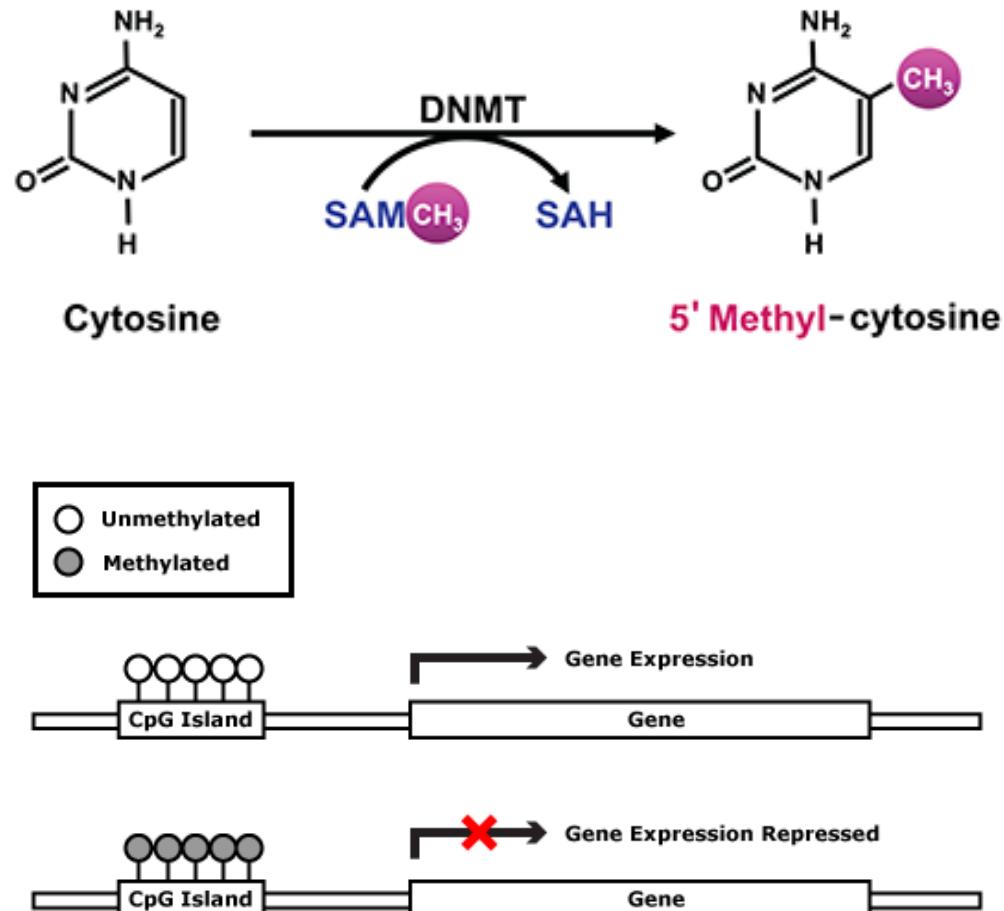
Transgenerational plasticity

Q3: What are epigenetic mechanisms?



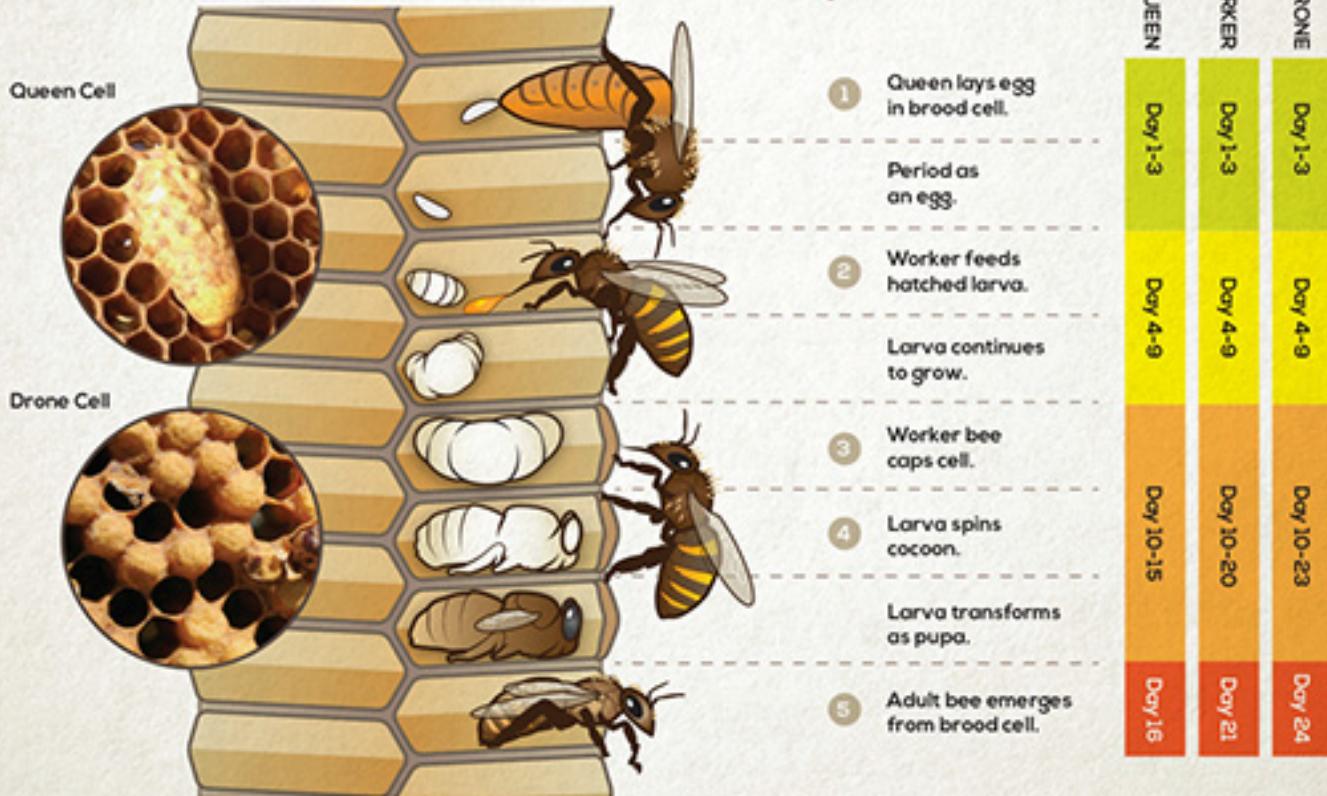
DNA Methylation

- Methyl group added to cytosine molecules by DNMT enzymes
- Can repress transcription in 2 ways:
 - Binding to DNA directly and impede binding of transcriptional proteins (CpG islands)
 - Methylated DNA may be bound by methyl-CpG-binding domain proteins (MBDs)



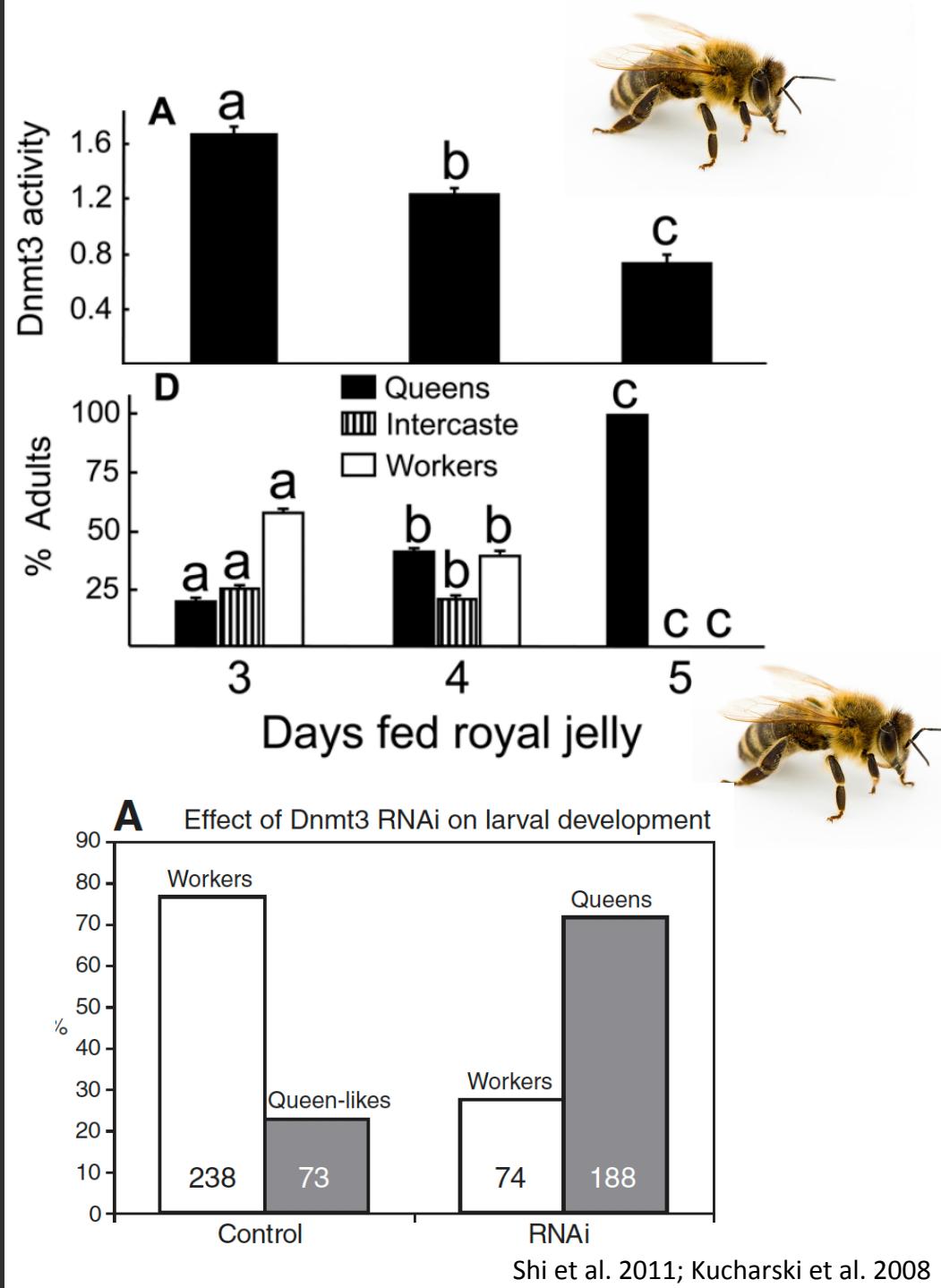
LIFE CYCLE OF THE HONEY BEE

Apis Mellifera

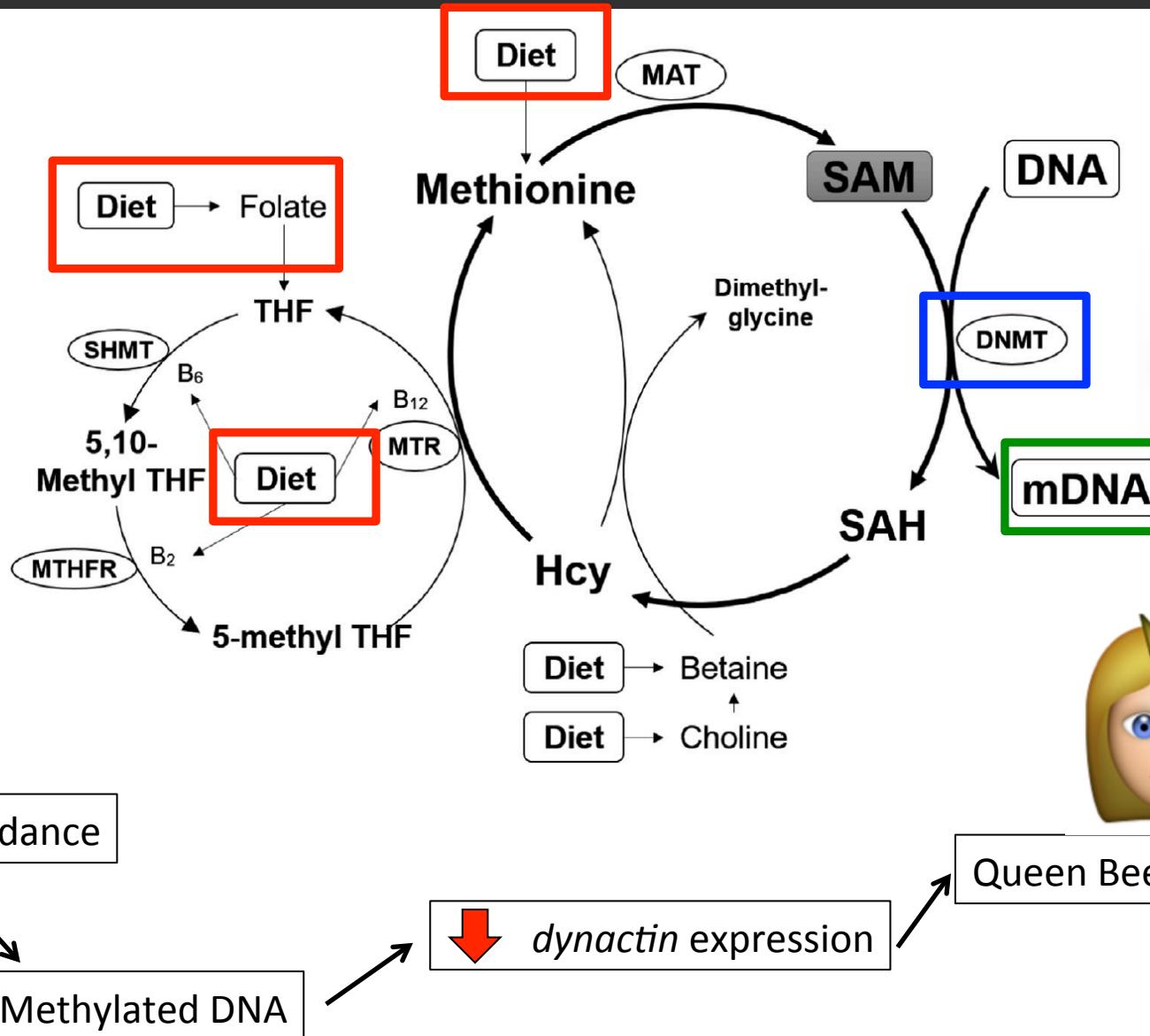


DNA Methylation

- Larvae of *Apis mellifera* (honey bees) can become either queen or workers
- DNA methylation is known to regulate expression patterns of *dyactin p62* gene resulting in altered phenotypes
- When fed royal jelly, repressed DNMT results in queen phenotype



DNA Methylation and Nutrition

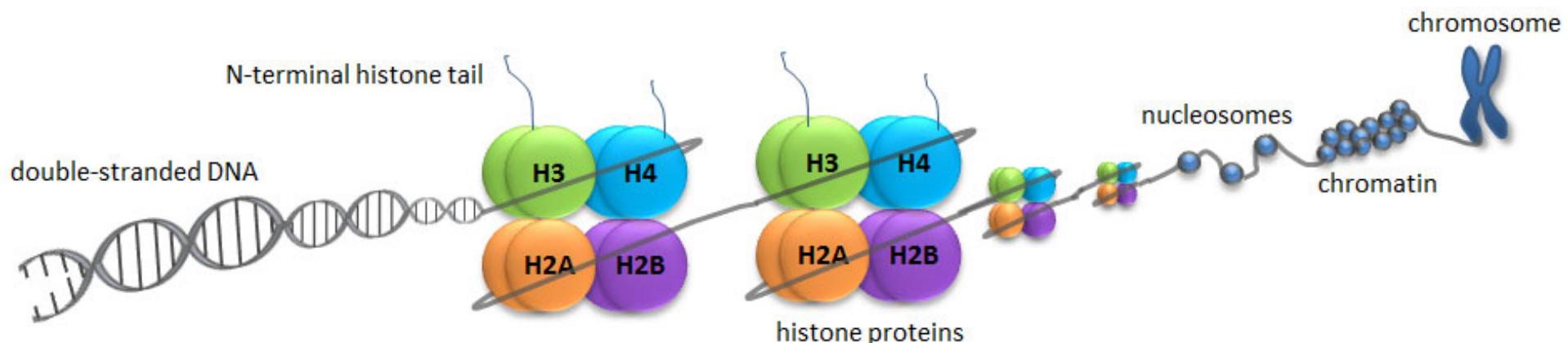


Chromatin Structure

Histone modifications are:

- Methylation
- Phosphorylation
- Acetylation
- Ubiquitylation
- Sumoylation

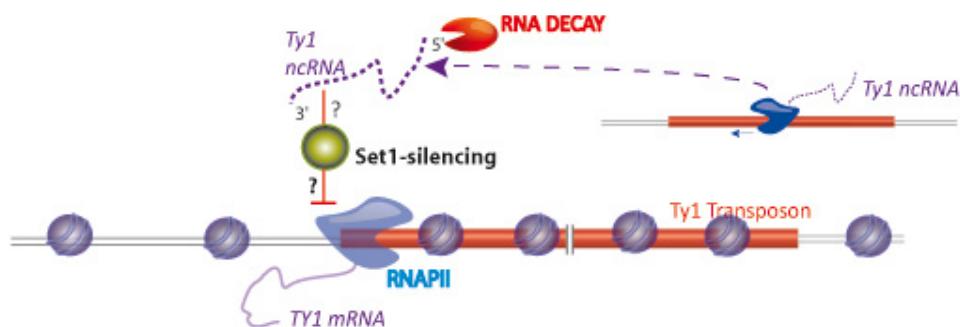
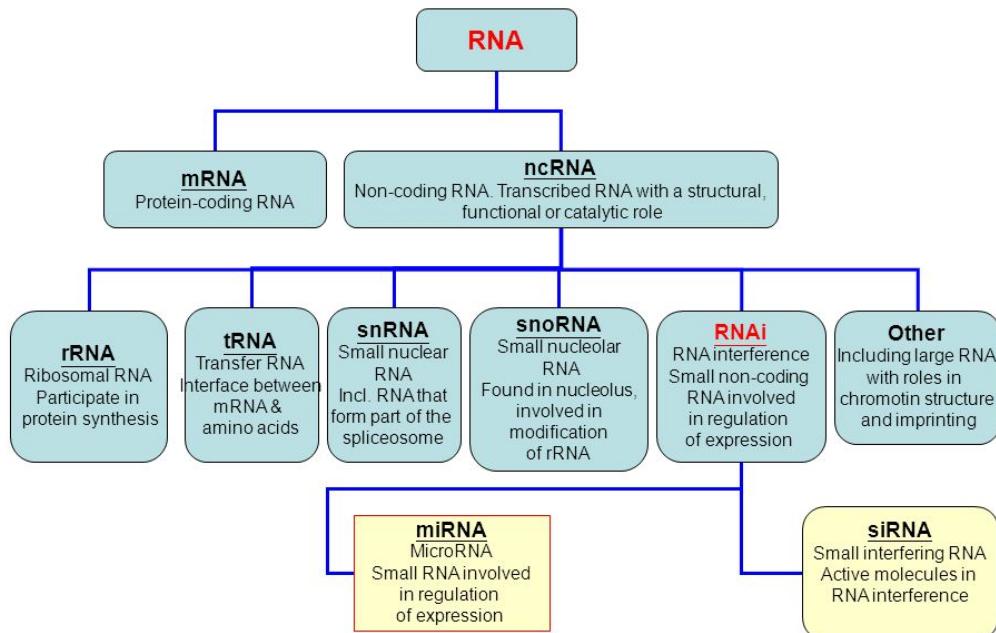
Histone modifications can impact gene expression by altering chromatin structure or recruiting histone modifiers



Non-coding RNA

- Formation of RNA structures that facilitate the recruitment of chromatin modifiers
- Can be horizontally transferred between cells
- Can be methylated like DNA → referred to as “epitranscriptome”

Type of RNA molecules



Q4: How can we quantify epigenetics

- DNA Methylation
 - CpG O/E
 - Global DNA methylation
 - Bisulfite sequencing methods
- Histone Modifications
 - Histone extraction and immuno-detection
 - ChIP sequencing
- Noncoding RNAs
 - sRNA sequencing

Approach	Description ^a	Level of detail	Difficulty ^b	Cost ^c	Advantages	Disadvantages	References ^d
DNA methylation							
CpG O/E	Methylated cytosine has a tendency to undergo deamination to thymine. This can leave a signature of cytosine depletion in the genome that can be quantified by looking at the ratio of observed CpG to expected CpG in silico.	Single-base-pair resolution of historical methylation status	#	\$	Can utilize existing data sets	Cannot examine dynamic or inducible methylation changes	Gardiner-Garden & Frommer 1987
							Dimond & Roberts 2016, Dixon et al. 2010, Gavery & Roberts 2010
HPLC and LC-MS/MS	An HPLC or LC-MS/MS instrument can detect global DNA methylation following digestion of the DNA.	Methylation relative to cytosines in DNA or total DNA	#	\$	Quick and easy	Global signal, low resolution, no ability to assess sequence	Kuo et al. 1980, Song et al. 2005
							Mirbahai et al. 2011, Varriale & Bernardi 2006 (HPLC); none found (LC-MS/MS)
ELISA	Enrichment and quantification of global DNA methylation can be done through the addition of a capture antibody for methylated DNA and a detection antibody, followed by colorimetric or fluorescent detection.	Methylation relative to total DNA	#	\$	Quick and easy	Global signal, low resolution, no ability to assess sequence	NA
							Dabe et al. 2015, García-Fernández et al. 2017, Kuc et al. 2017, Putnam et al. 2016
WGBS	A global picture of DNA methylation with single-base-pair resolution gives the optimal capacity to test hypotheses that go beyond genes or regions to genomic architecture. These data are generated by whole-genome fragmentation, bisulfite conversion, DNA library preparation, and sequencing.	Base pair or whole genome	#####	\$\$\$\$\$	Provides a complete picture of methylation with single-base-pair resolution, facilitates higher-order analyses	Can potentially damage DNA with bisulfite treatment, has a high cost of sequencing for very-low-percentage methylation	NA
							Dabe et al. 2015; Li et al. 2018; Liew et al. 2018a,b; Rondon et al. 2017; Wang et al. 2014

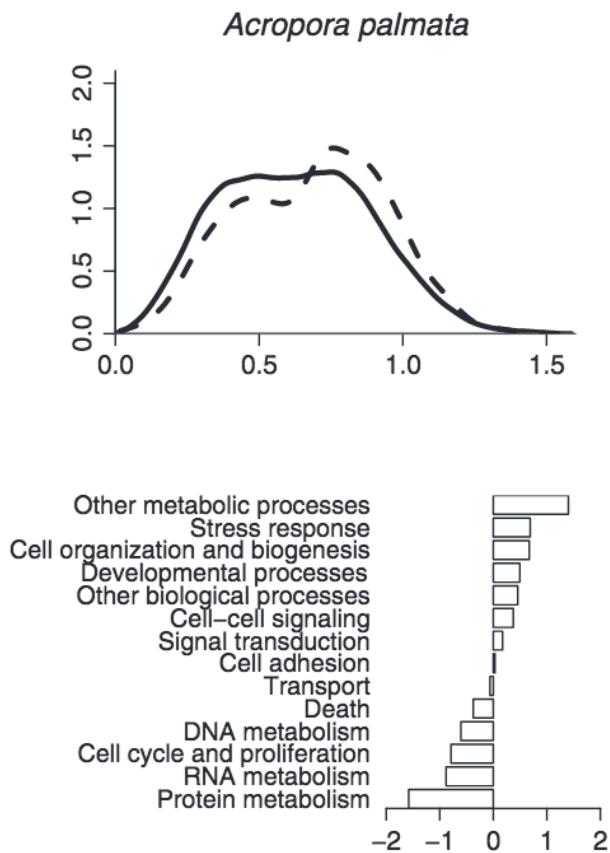
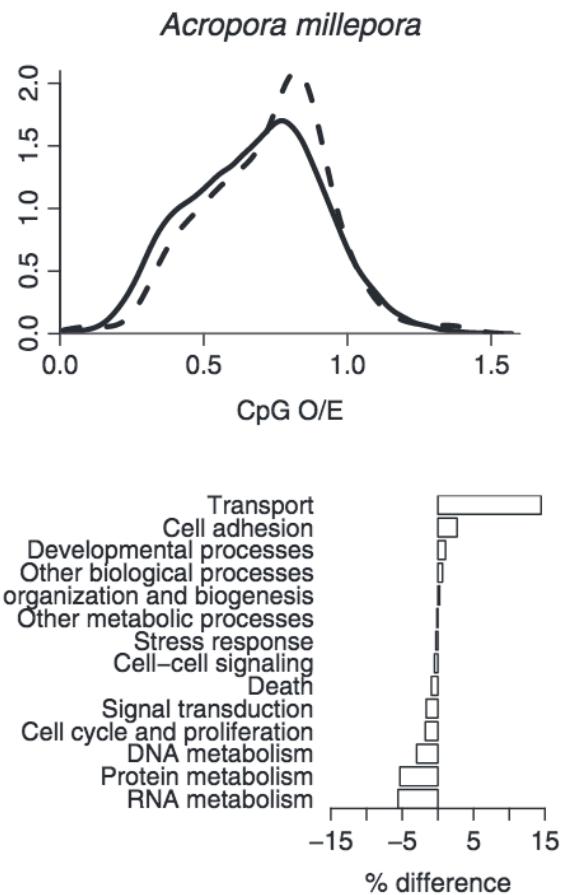
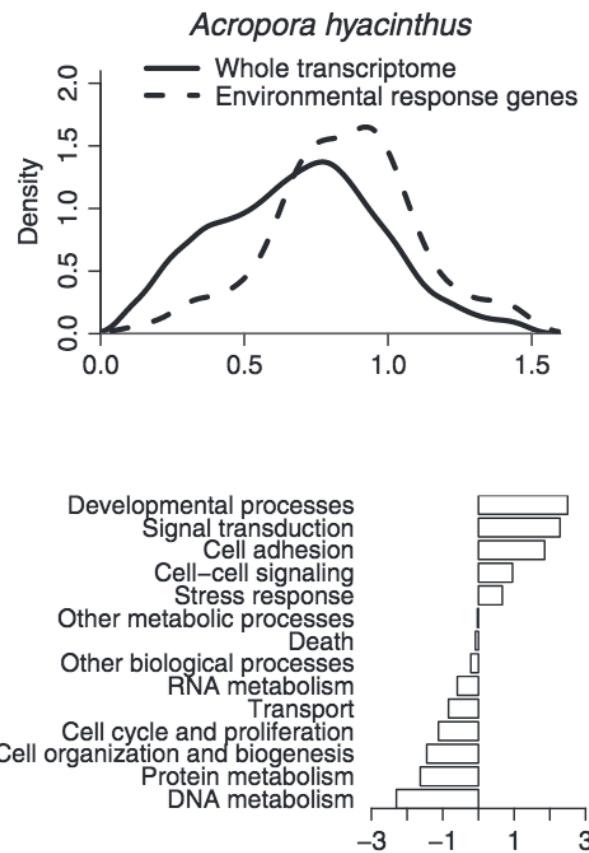
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DNA Methylation: CpG Observed/Expected

- Methylated cytosines convert to thymines over time

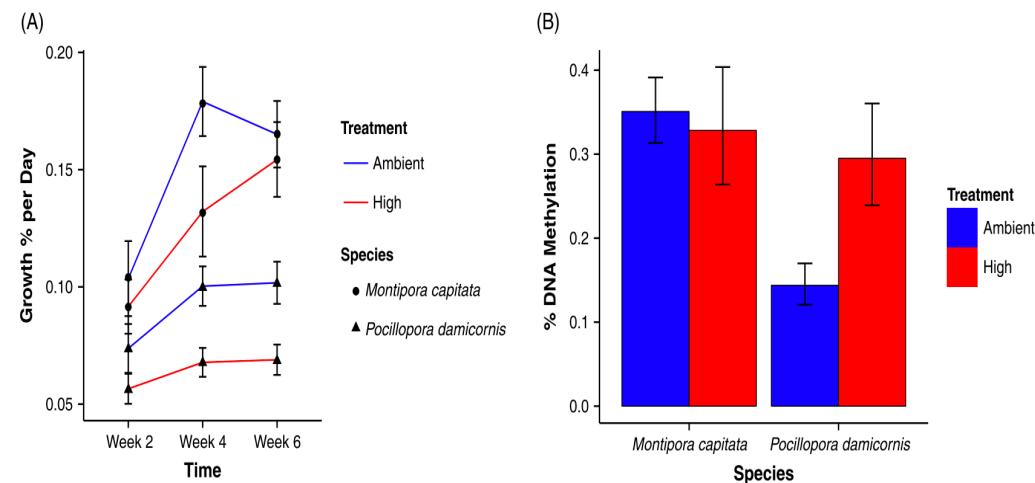
$$\text{CpG O/E} = \frac{\text{number of CpG}}{\text{number of C} \times \text{number of G}} \times \frac{l^2}{l} - 1$$

DNA Methylation: CpG Observed/Expected



DNA Methylation: Global DNA Methylation

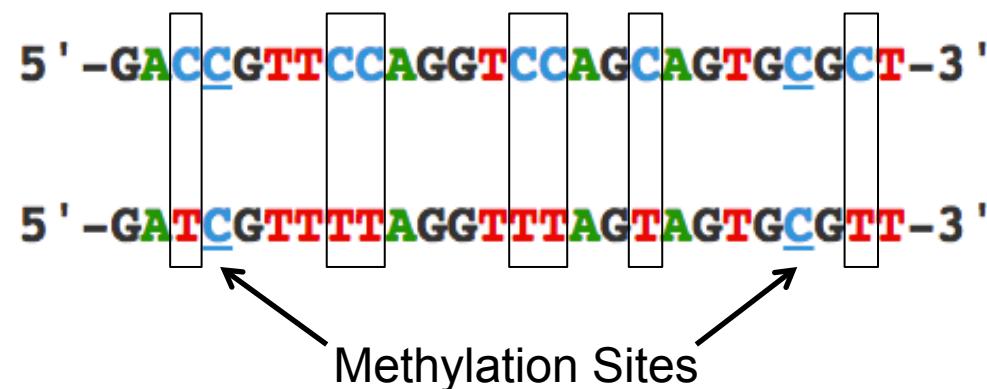
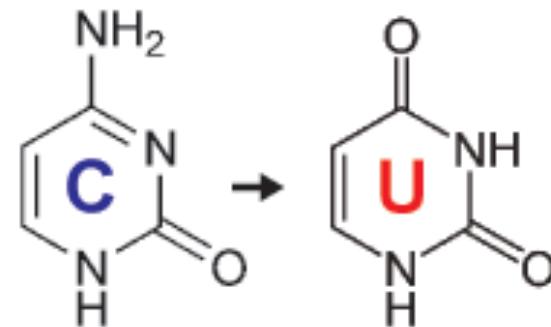
- DNA is bound to strip-wells
- Methylated fraction of DNA is detected using capture and detection anti-bodies
- Quantified colormetrically on a spectrophotometer



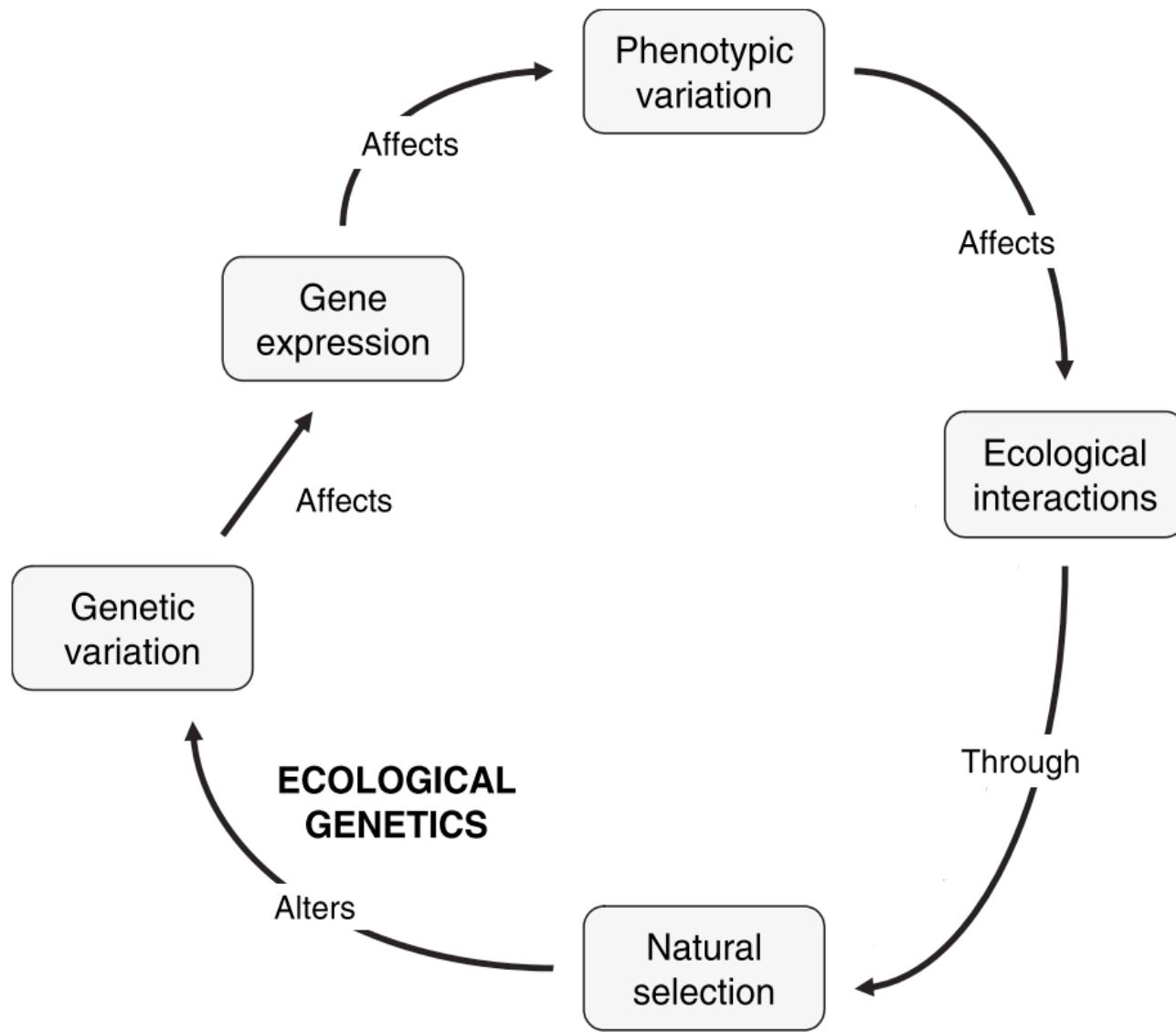
DNA Methylation: Bisulfite Sequencing

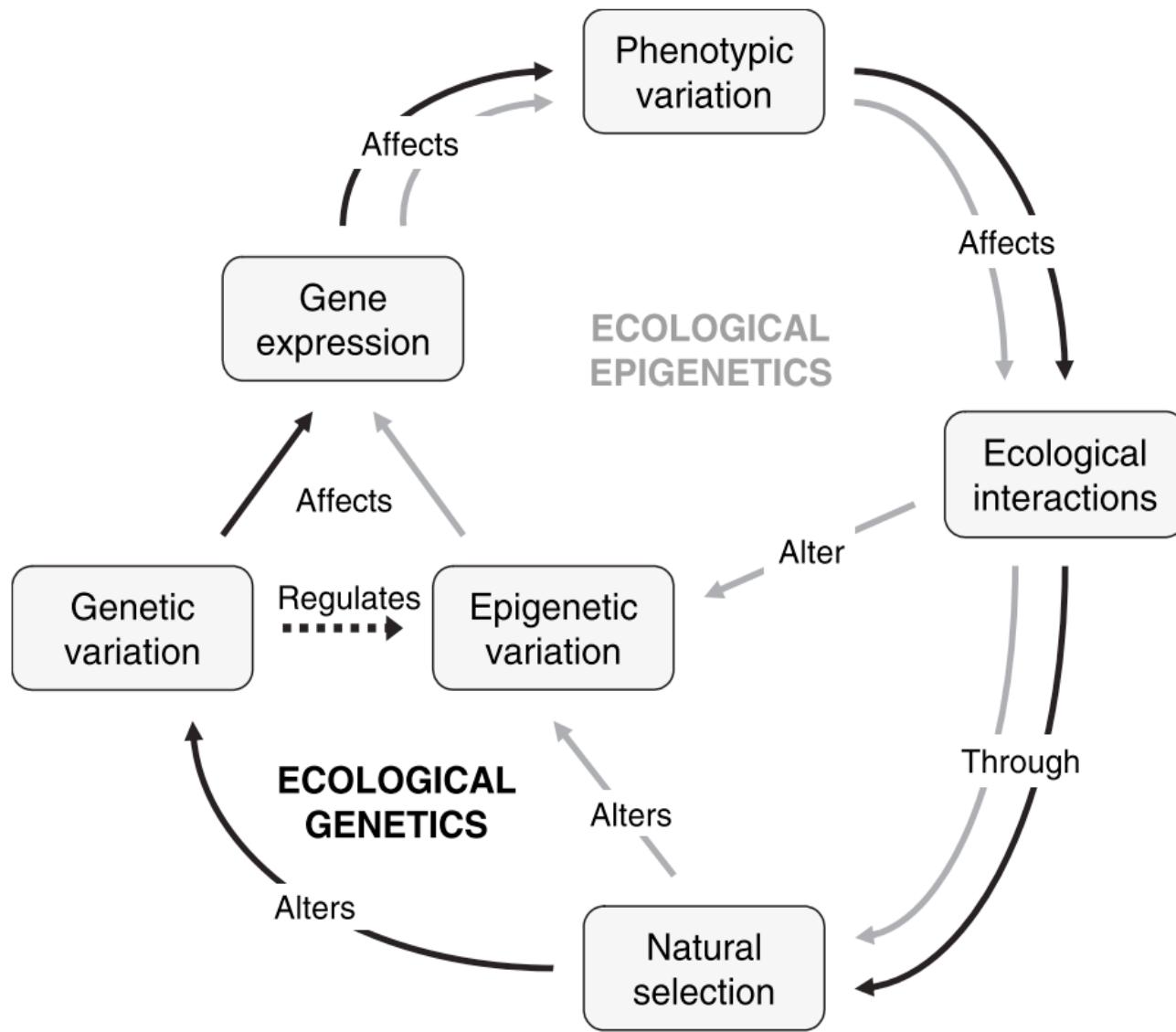
- Gold standard
- Unmethylated cytosines undergo hard bisulfite treatment
- Methylated cytosines are immune to this conversion

Bisulfite Conversion 



Q5: What is the epigenetic role in phenotypic plasticity?





Q5: What is the epigenetic role in environmental acclimatization?

