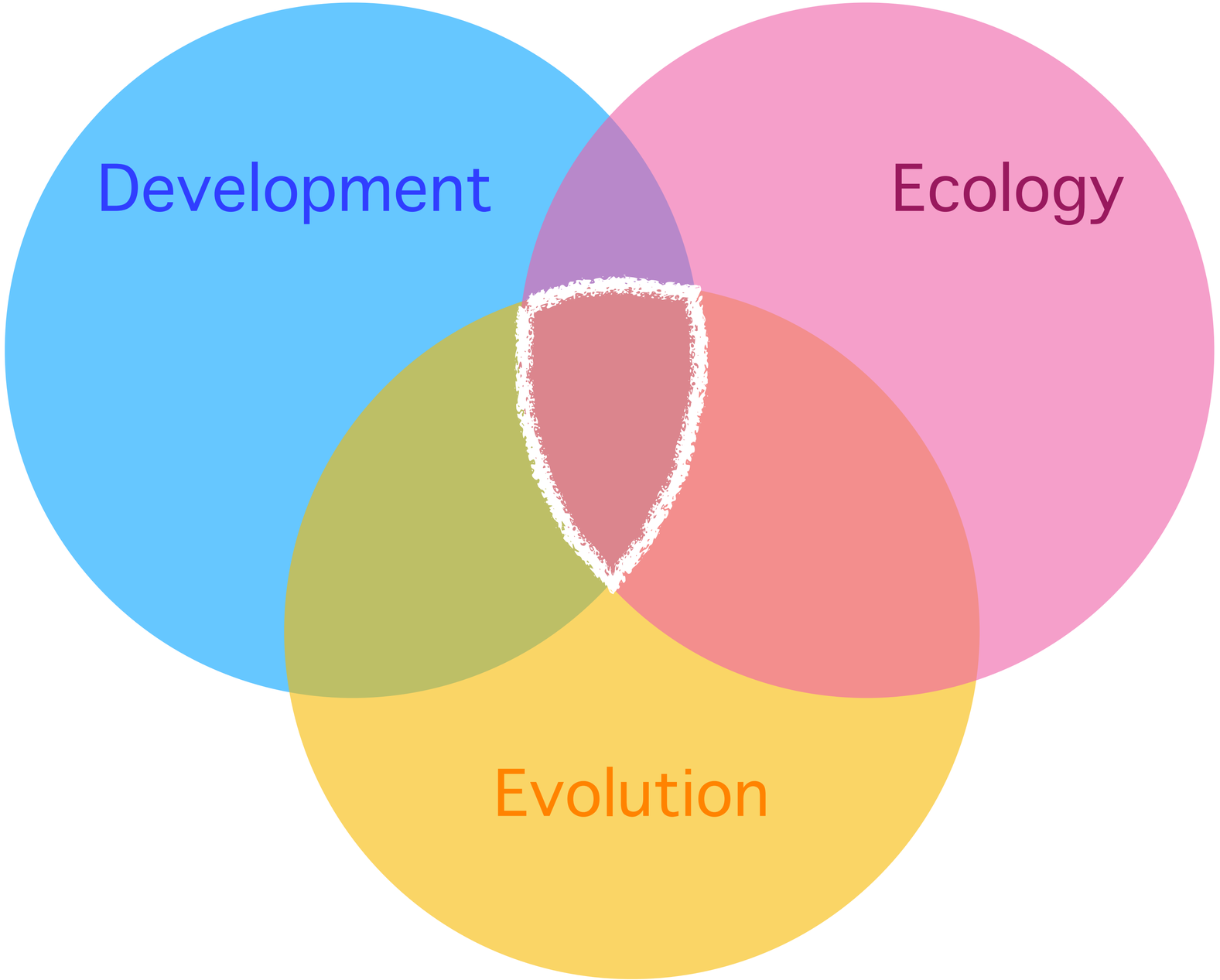
Aplicaciones y Discusiones en Desarrollo Animal II

Christoph Liedtke
Ivan Gomez-Mestre
Estación Biológica de Doñana


Development
Ecology
Evolution

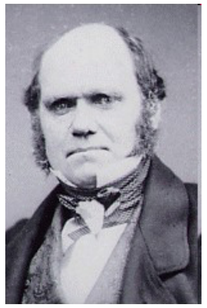
OUTLINE

- Why Eco-Evo-Devo? - The environment is crucial
- Adaptation and Phenotypic plasticity
- Environmentally-induced transcriptomics
- Genetic accommodation

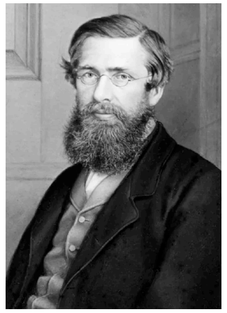
What is evolution?

“Evolution consists of changes in the heritable traits of a population of organisms as successive generations replace one another.”

National Academy of Sciences, USA, 2015



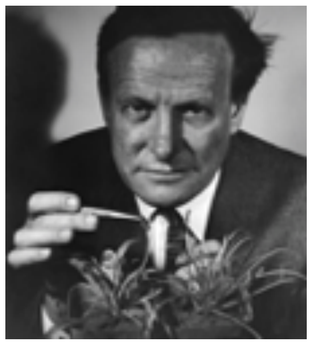
Darwin



Wallace

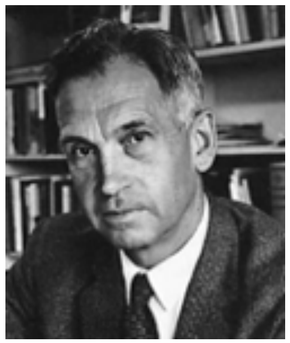
Mendel

Huxley

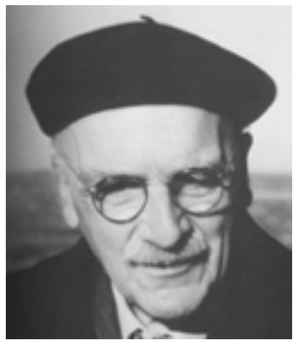


Stebbins

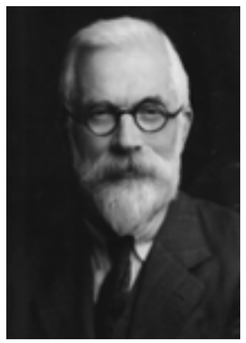
Simpson



Mayr



Haldane



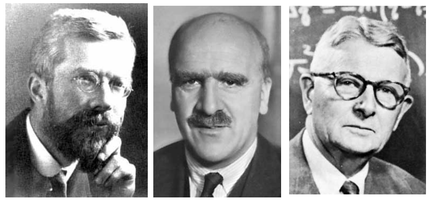
Fisher

Wright

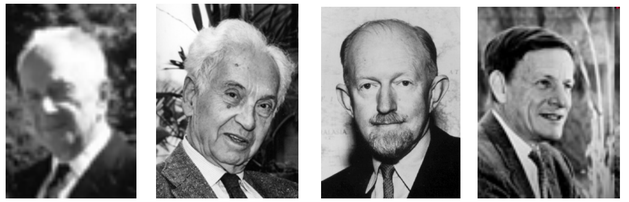
Dobzhansky

The Modern Synthesis

1936-1947



The Modern Synthesis



- Populations harbour genetic variation that emerges randomly through mutation and recombination.

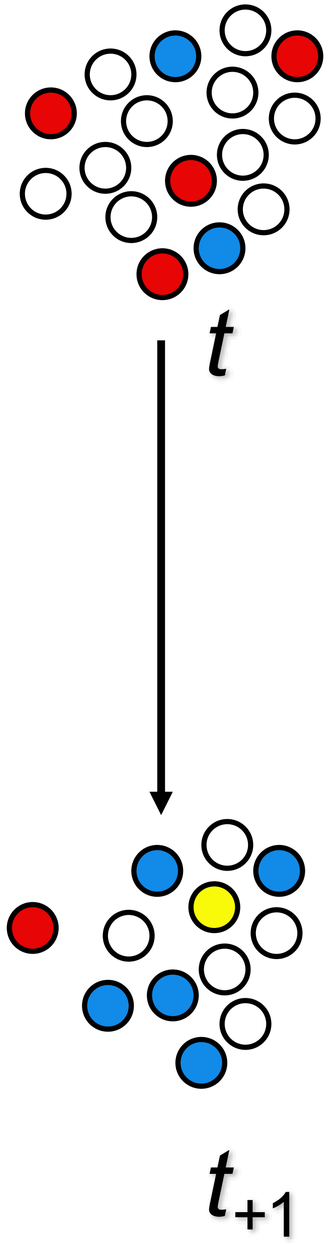
- Populations evolve through changes in allele frequencies due to drift, gene flow, and especially, natural selection.

- The majority of genetic variants have a small phenotypic effect, so that the resulting phenotypic changes are gradual.

- Diversification occurs through speciation, which is mostly the result of reproductive isolation between allopatric populations.

- These processes, operating over long enough timescales, give rise to cumulative changes of such magnitude that the resulting species are grouped at higher taxonomic levels.

Descent with heritable modification



- *Drift*
- *Selection*
- *Migration*
- *Mutation*

Mutation
Gene flow
Drift
Selection

+ 3.8 billion years = MACROEVOLUTION

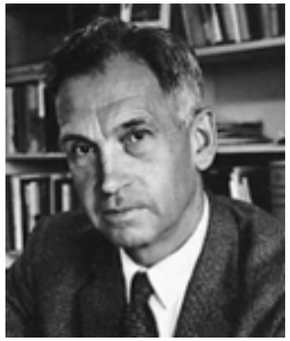
‘*The basic evolutionary mechanisms—mutation, migration, genetic drift, and natural selection—can produce major evolutionary change if given enough time*’

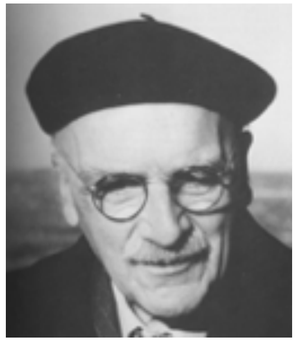
The Modern Synthesis (1936-1947)

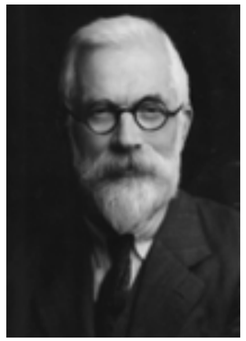

Huxley


Stebbins


Simpson


Mayr


Haldane


Fisher


Wright


Dobzhansky



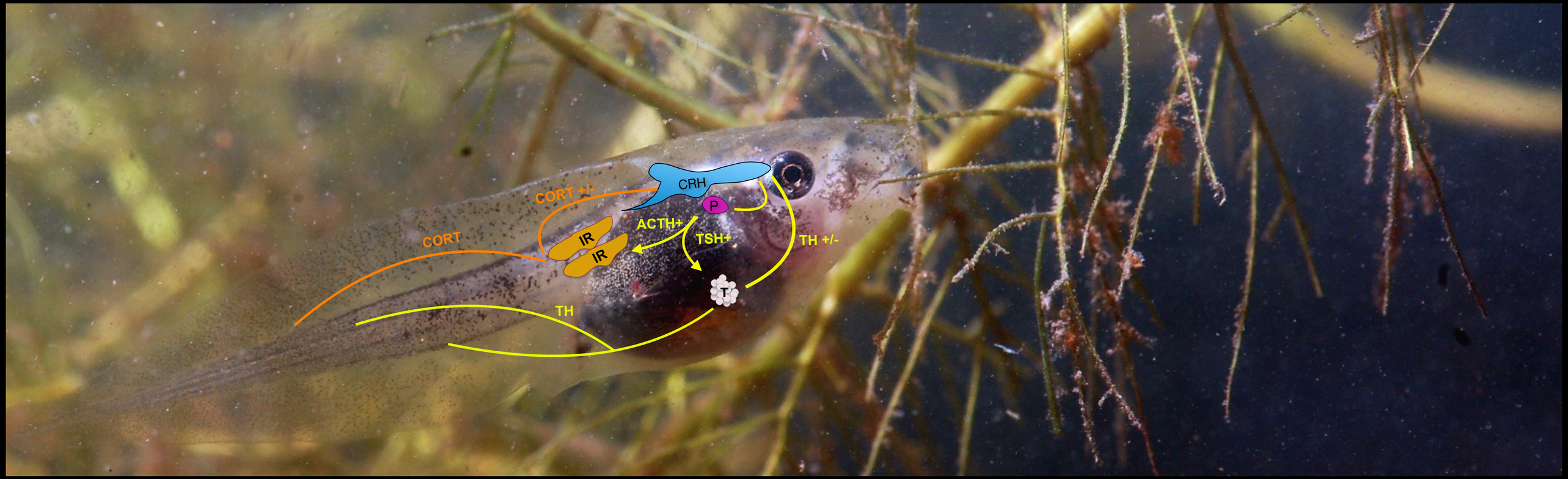




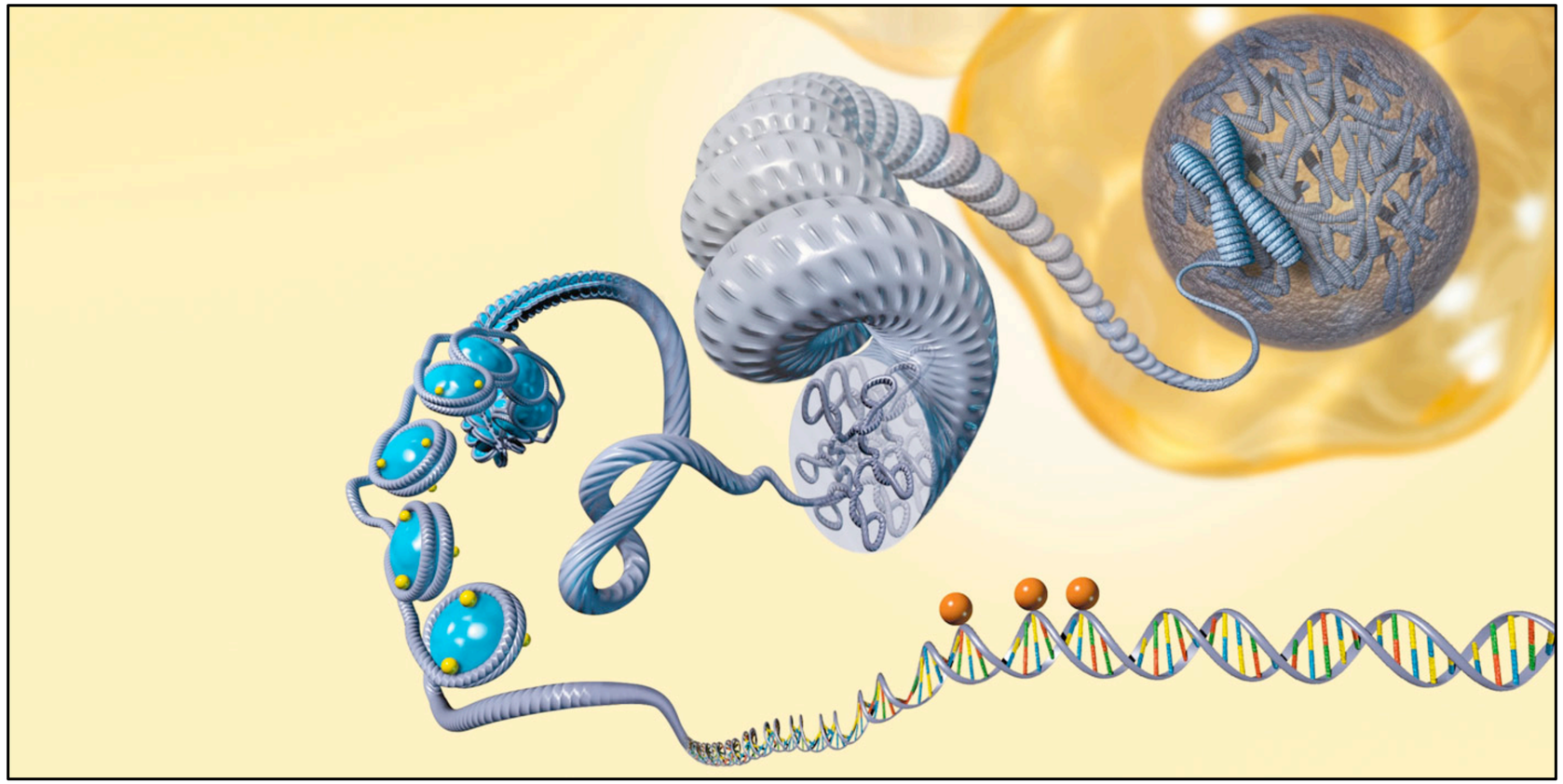


Organisms use environmental cues to assess environmental suitability

…then react adjusting their behaviour, morphology or physiology accordingly



Environmental stimuli epigenetic regulation of gene expression

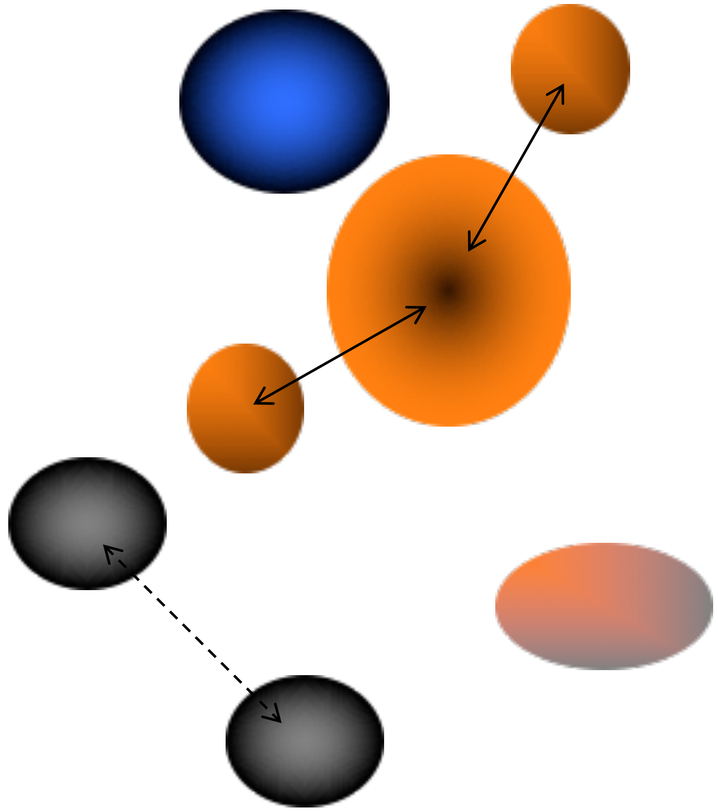


Phenotypes result from interaction between
ENVIRONMENT and GENOME

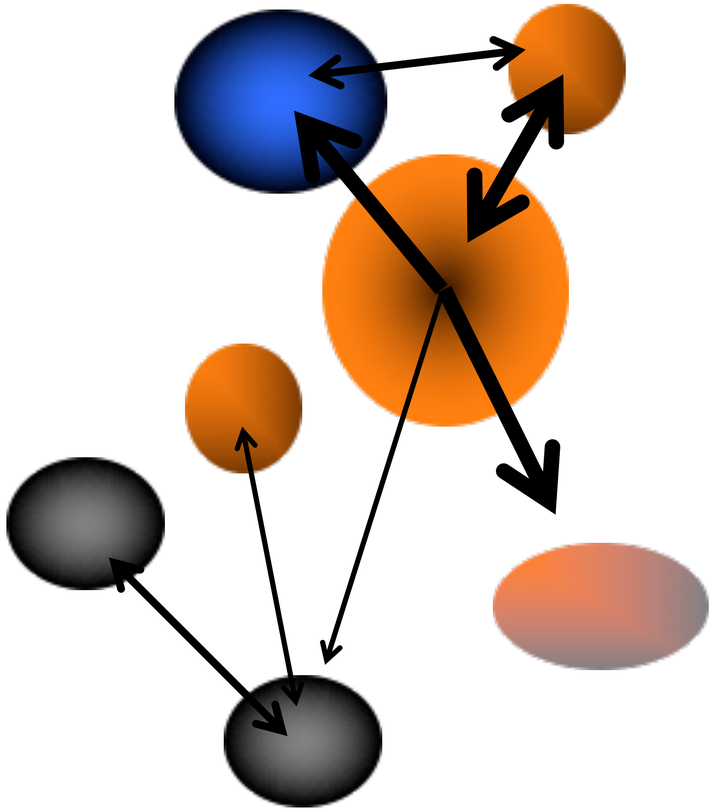
VOL. 160, NO. 2 THE AMERICAN NATURALIST AUGUST 2002

Metapopulation Structure Favors Plasticity over Local Adaptation

Sonia E. Sultan[1,*] and Hamish G. Spencer[2,†]

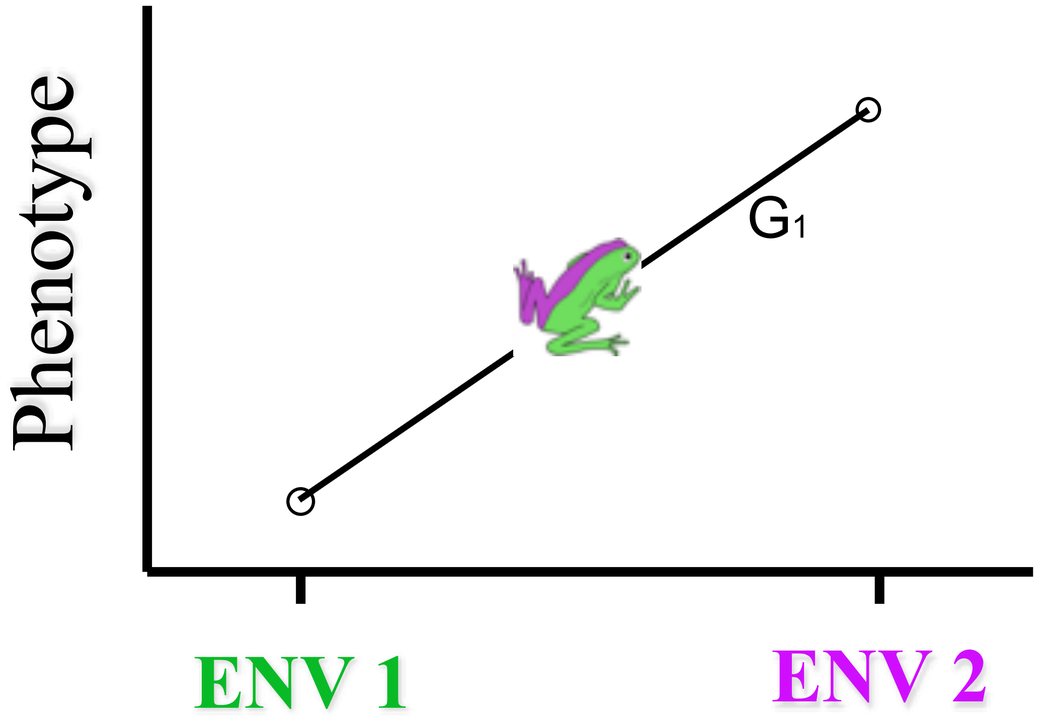


Local adaptation of fixed phenotypes

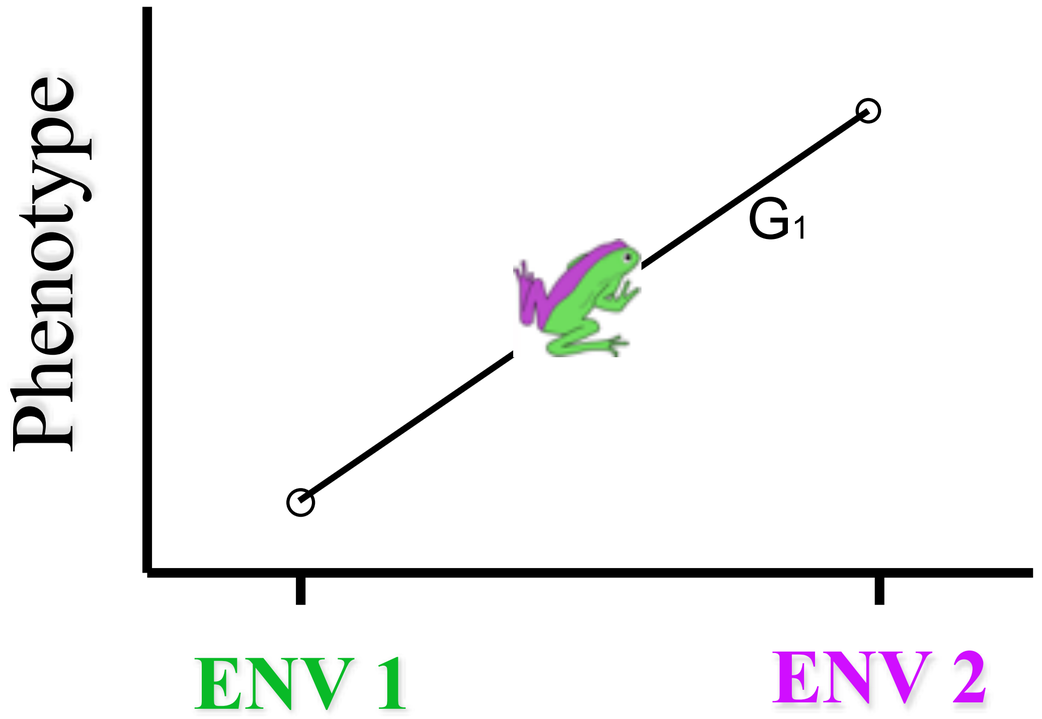


Adaptive phenotypic plasticity

Phenotypic plasticity



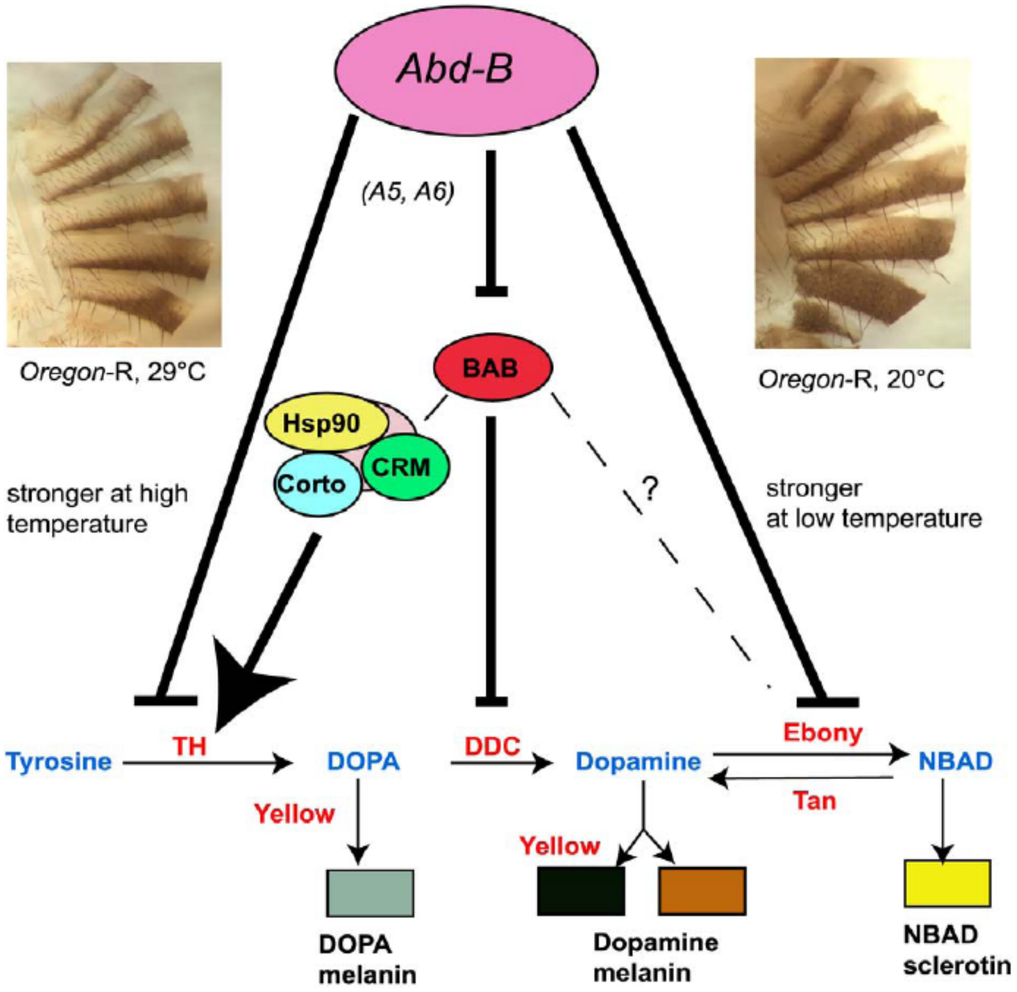
Adaptive phenotypic plasticity



If/When:

- Environmental heterogeneity
- Fitness trade off
- Reliable cues
- Heritable basis
- Fitness benefits outweigh costs

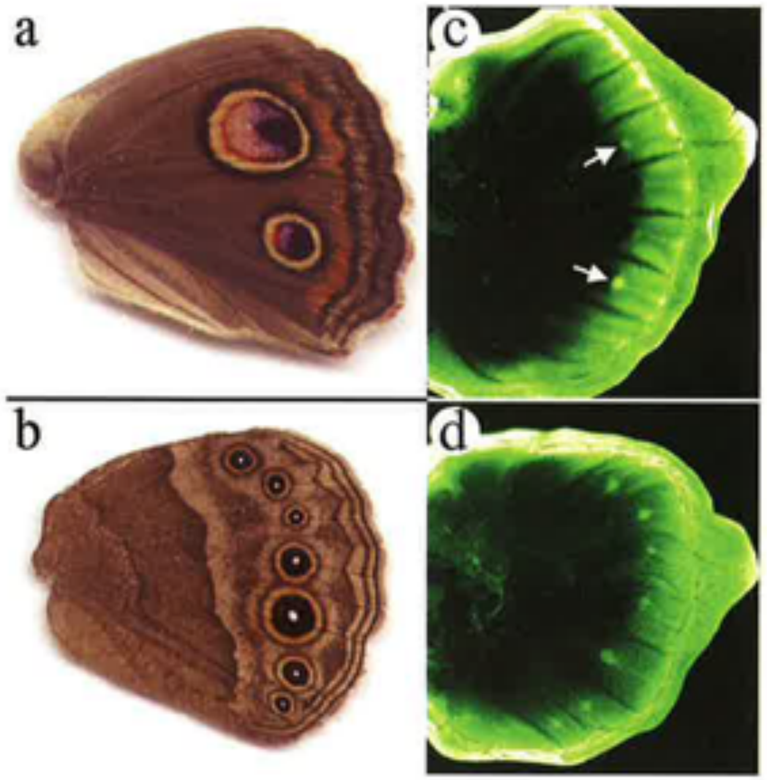
Environmental input is essential in development



Gibert et al. 2007, *PLoS Gen*

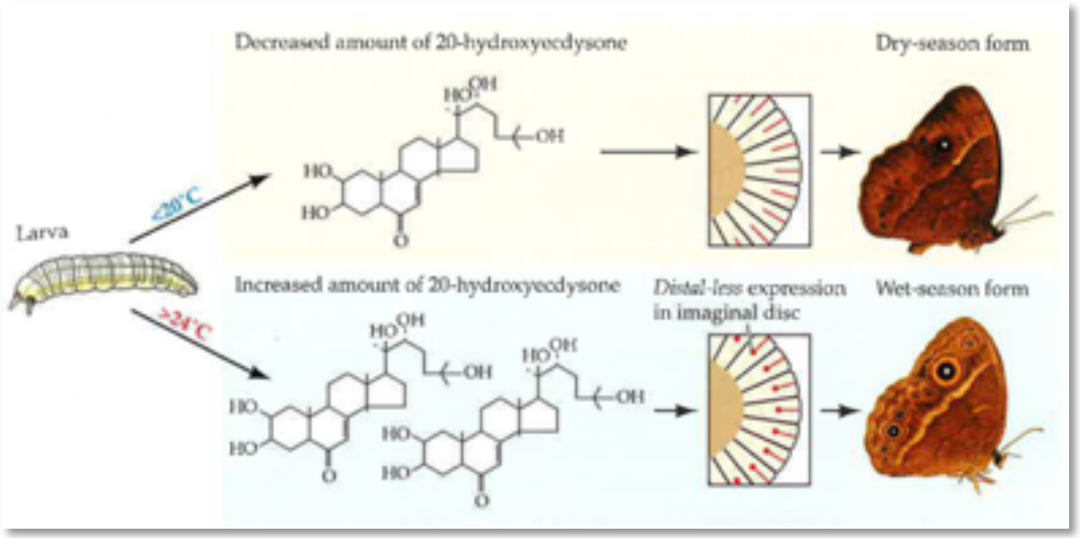
Environmental input is essential in development

Dll expression marks the formation of eyespots



Brakefield et al 1996 *Nature*

…but *Dll* expression is dependent upon temperature and results in seasonal morphs



Brakefield & Reitsma 1991

Environmental input is essential in development

Summer morph

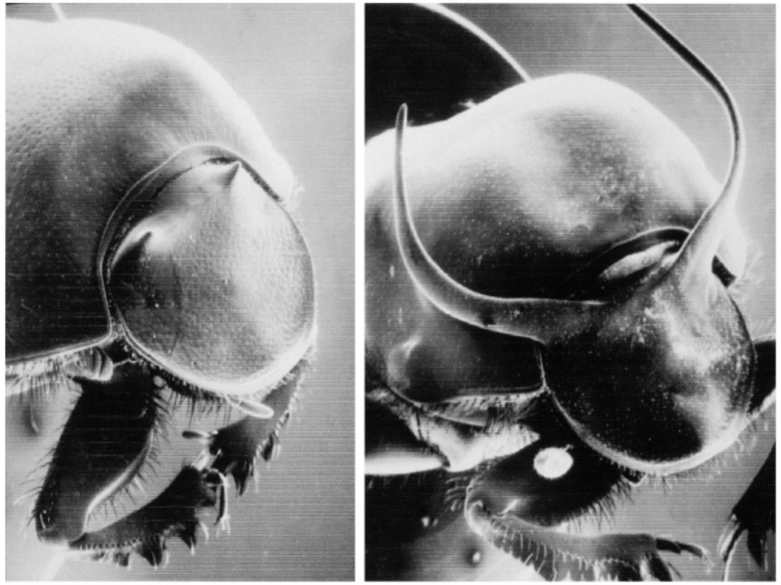
Spring morph

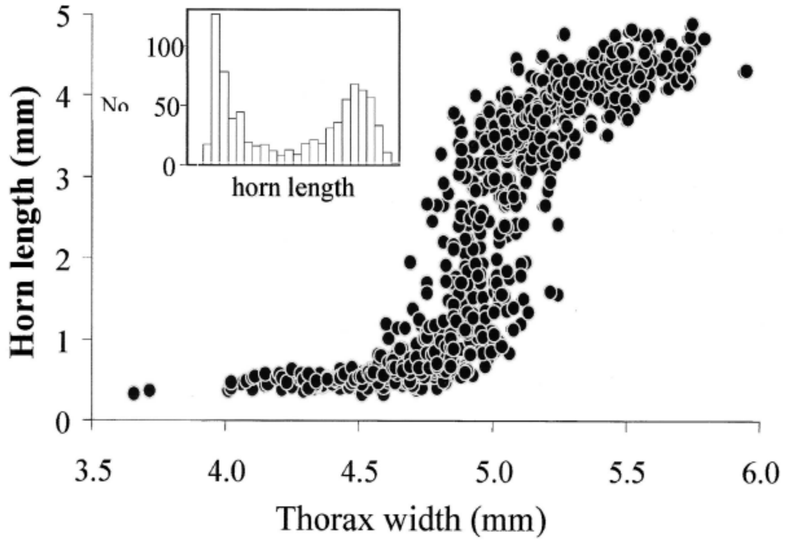
Araschnia levana, Windig & Lammar 1999 Evol Ecol

Environmental input is essential in development

Nemoria arizonaria, Greene 1989 Nature

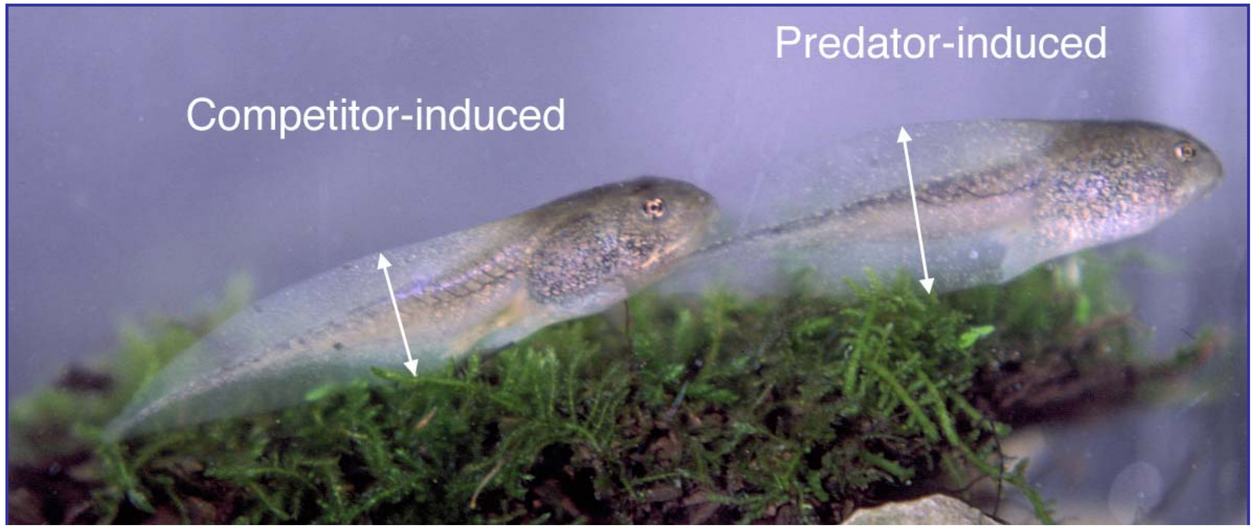
Environmental input is essential in development





Moczek Lab

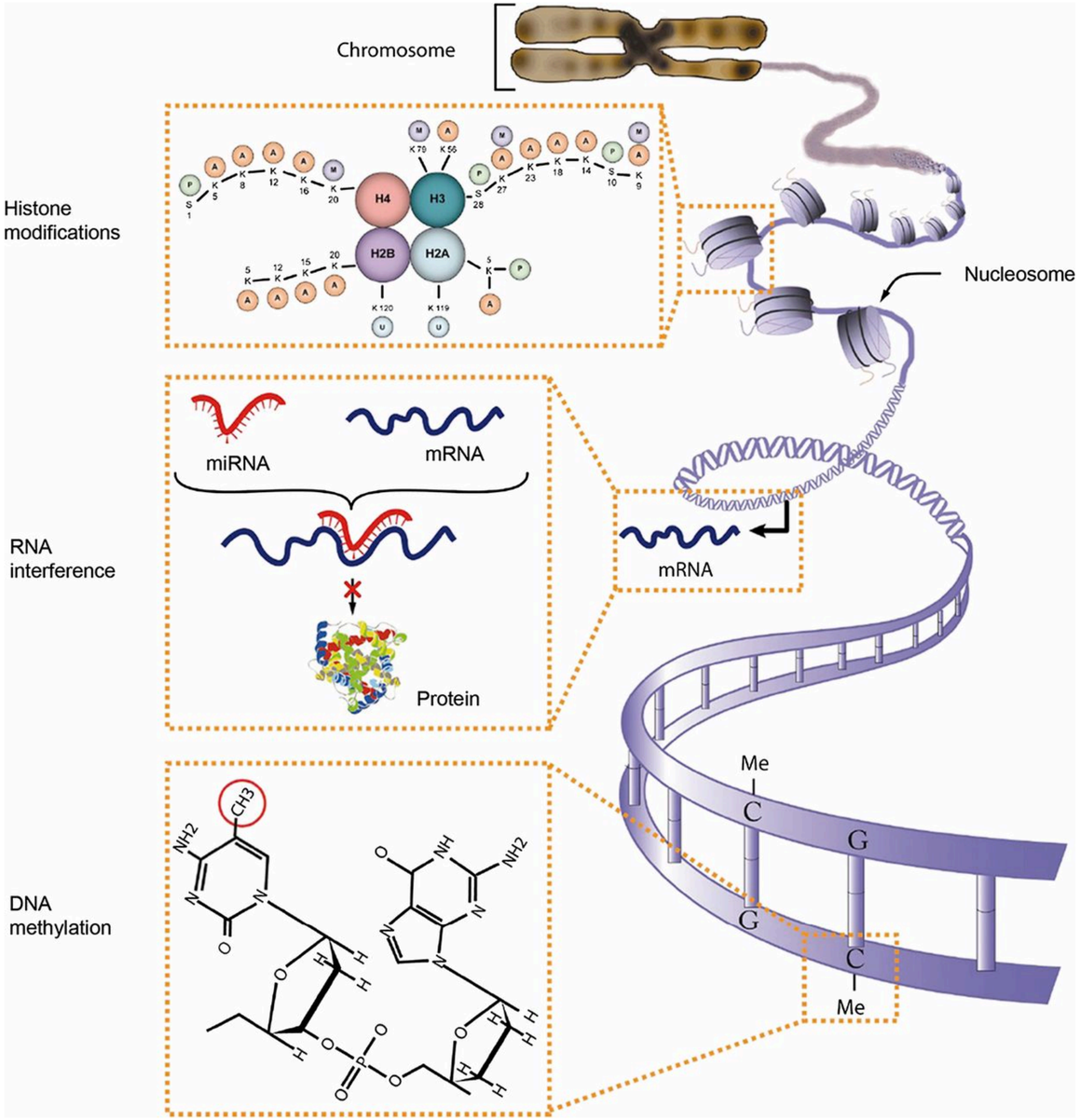
Environmental input is essential in development



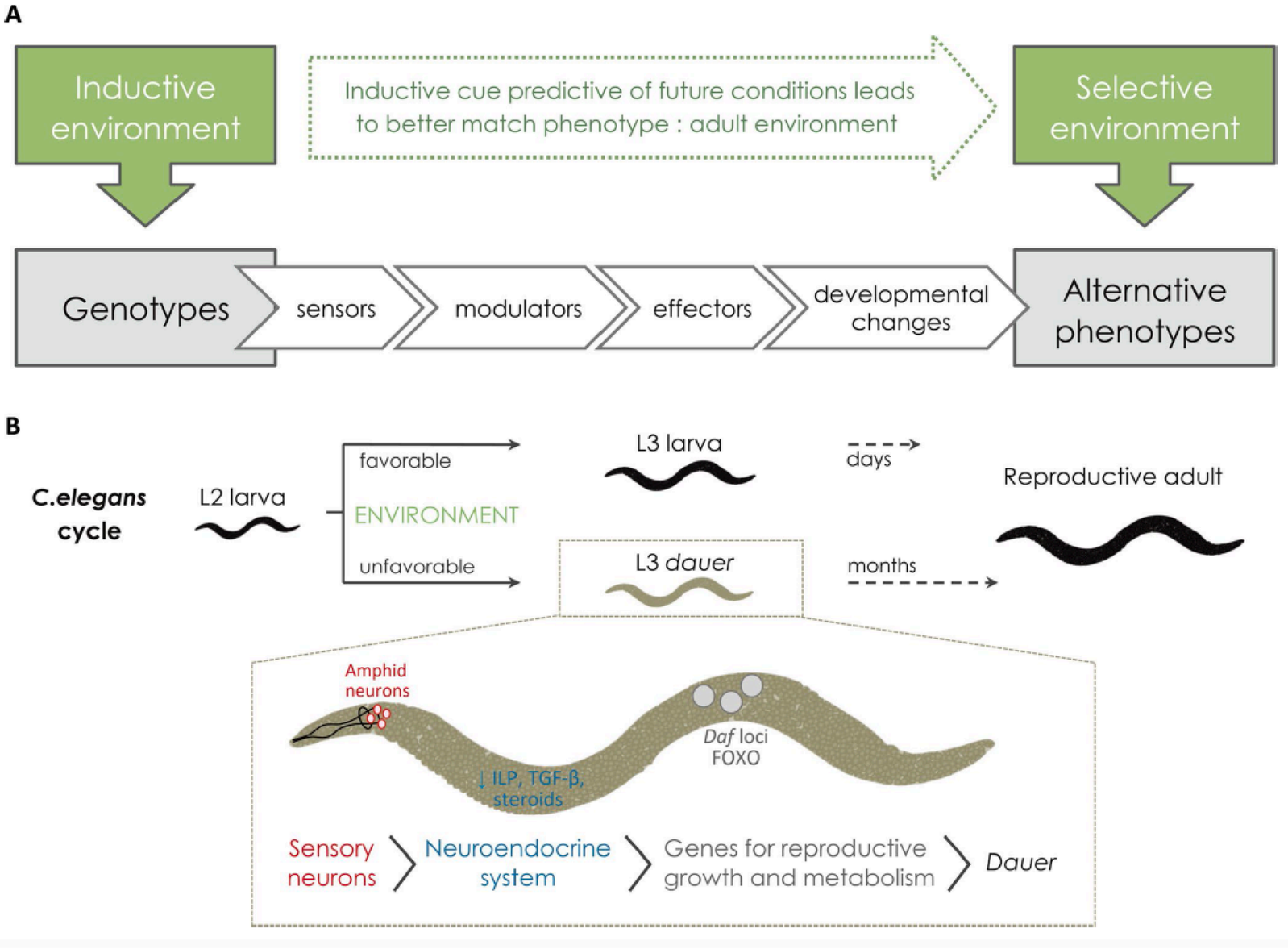
Relyea Lab

Eco-Evo-Devo
EBD

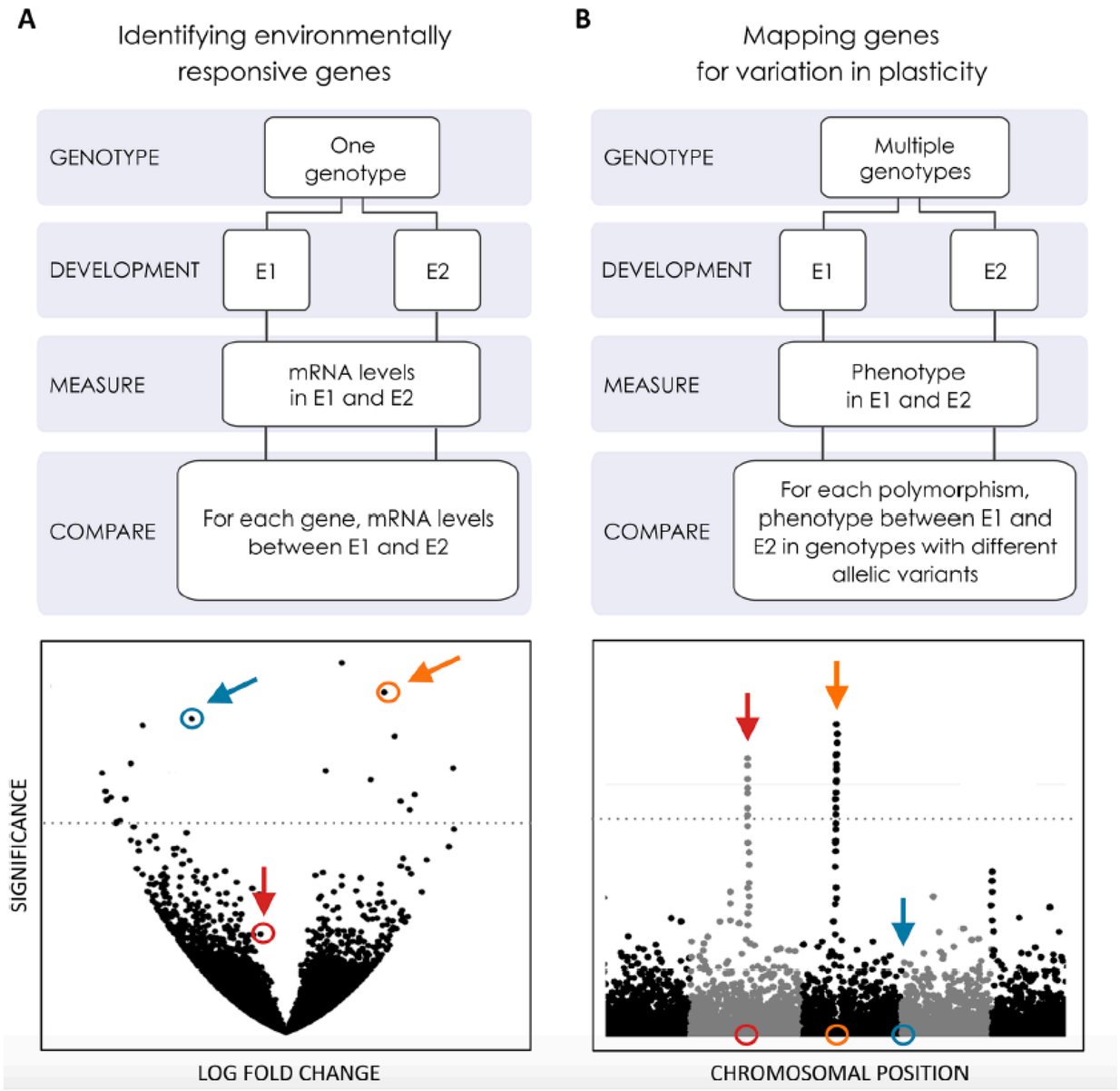
Epigenetic changes translate environmental input into changes in gene expression



Environment > Genotype > Phenotype



Molecular quest for plasticity: transcriptomics and mapping studies



Predator- and prey-driven gene expression in salamander brains

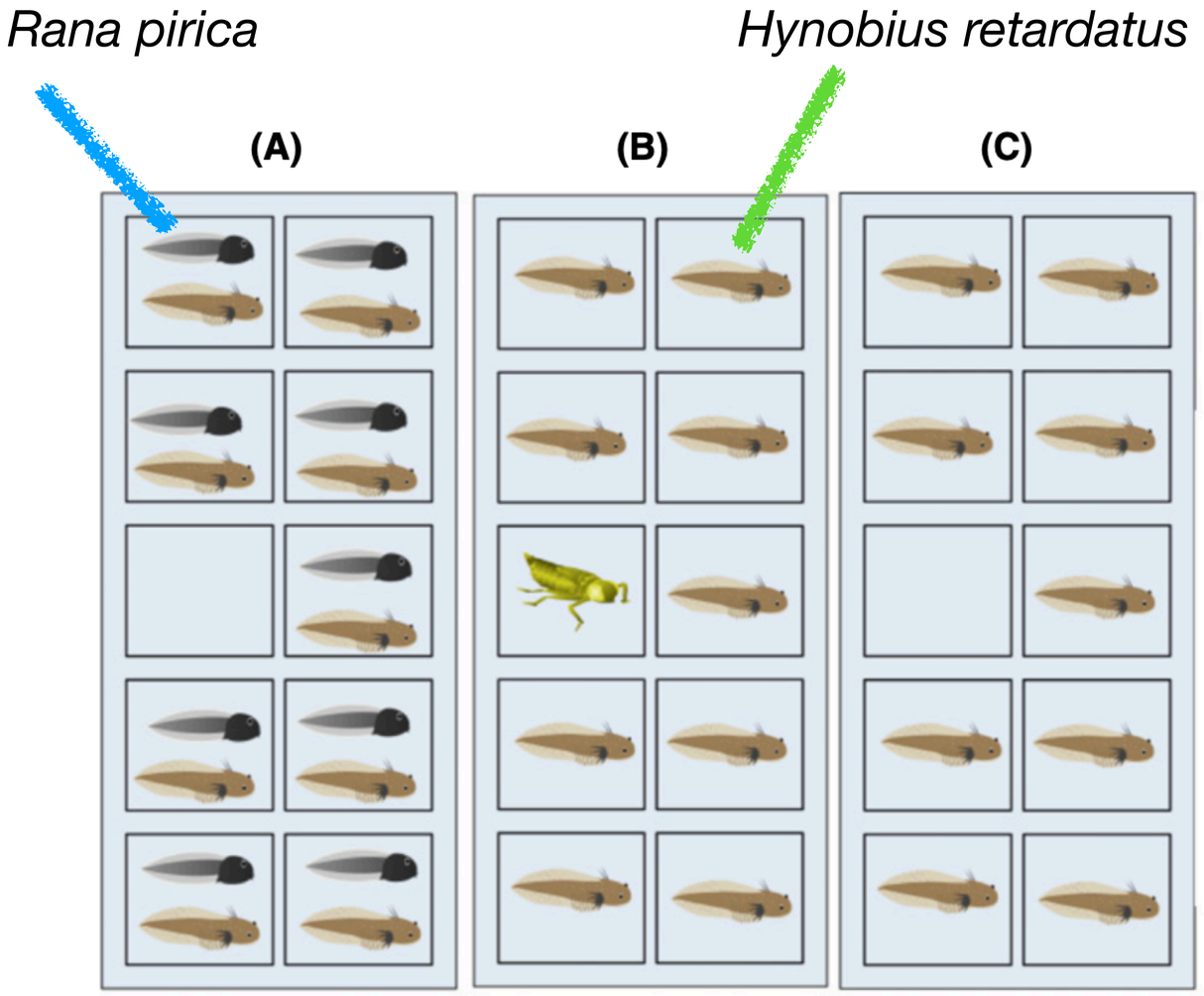
MOLECULAR ECOLOGY

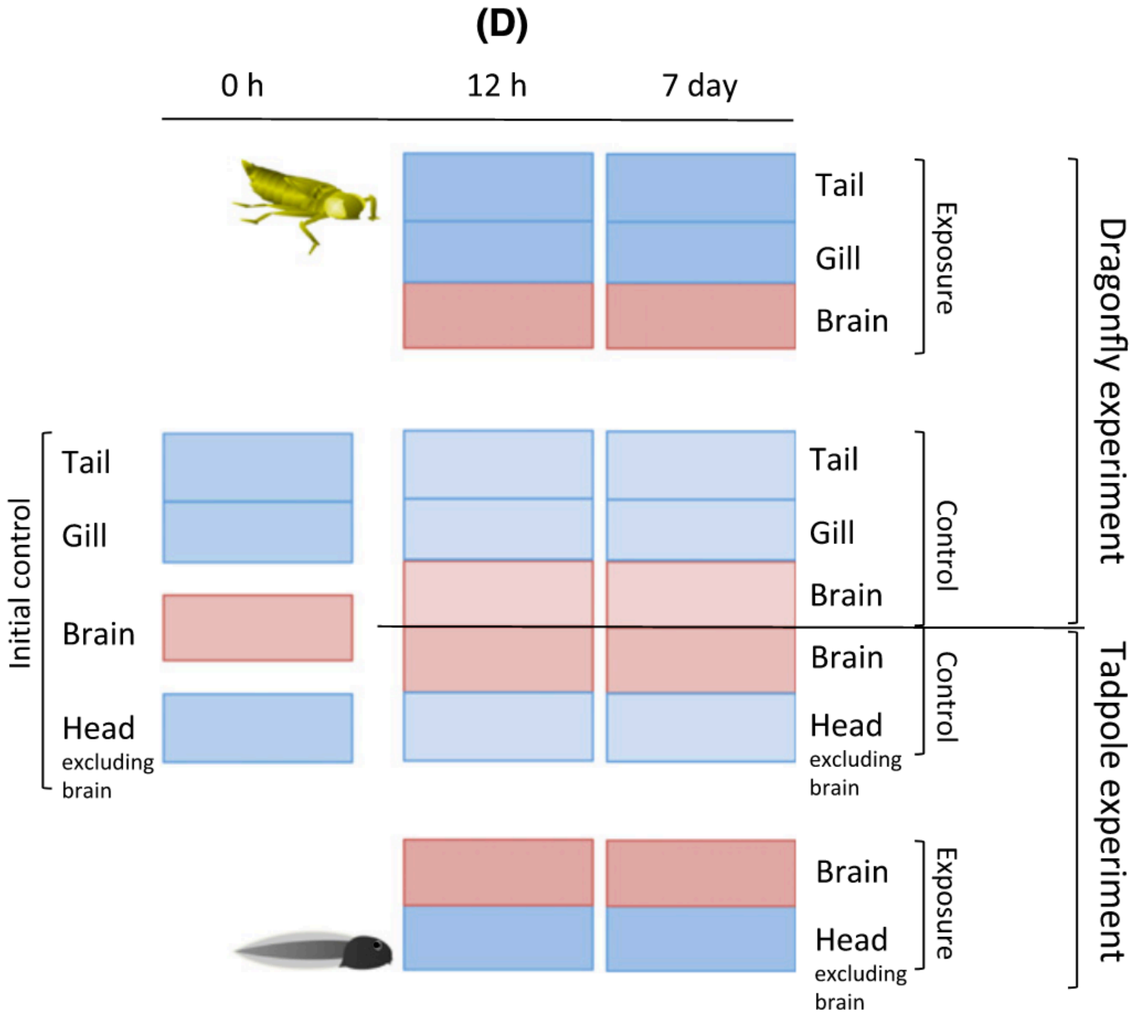
Molecular Ecology (2015) **24**, 3064–3076 doi: 10.1111/mec.13228

Transcriptome analysis of predator- and prey-induced phenotypic plasticity in the Hokkaido salamander (*Hynobius retardatus*)

MASATOSHI MATSUNAMI,*† JUN KITANO,‡ OSAMU KISHIDA,§ HIROFUMI MICHIMAE,¶ TORU MIURA† and KINYA NISHIMURA*

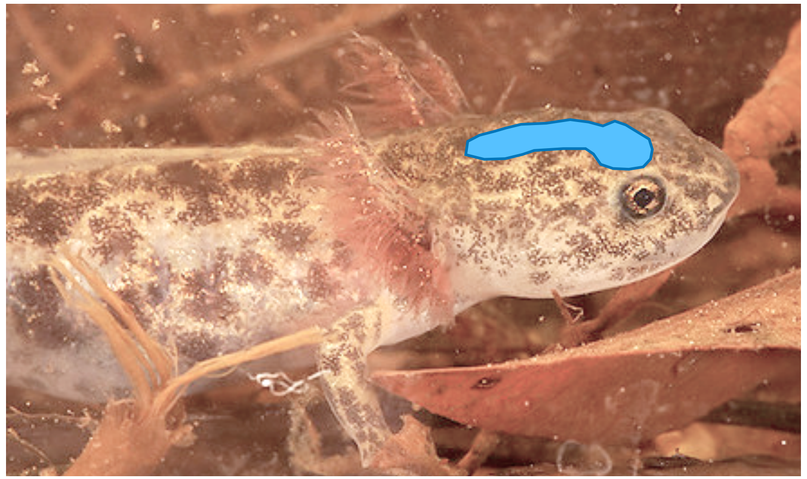
Predator- and prey-driven gene expression in salamander brains

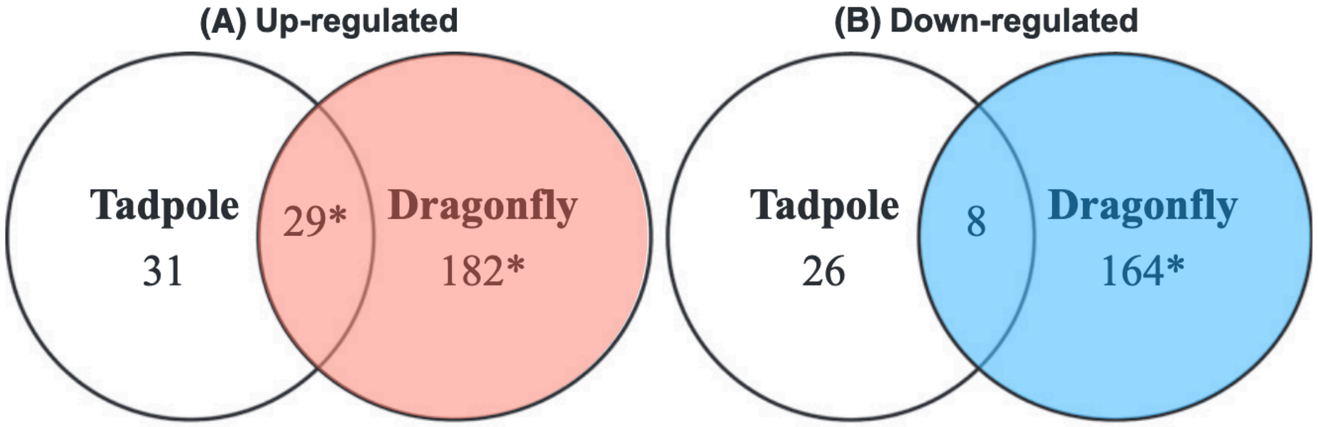


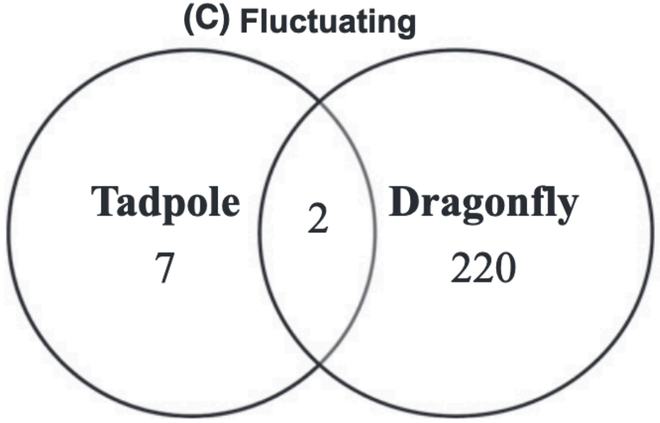


Matsunami et al. 2015 Mol Ecol

Predator- and prey-driven gene expression in salamander brains







"If more genes are involved in the expression of one alternative phenotype than in the expression of the other [..], the former plasticity may require more complicated developmental changes"

Catabolism
Oxidative stress

Neural development
Locomotion

Matsunami et al. 2015 Mol Ecol

Transcriptomics of salinity adaptation in a treefrog

ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

Molecular mechanisms of local adaptation for salt-tolerance in a treefrog

Molly A. Albecker | Adam M. M. Stuckert | Christopher N. Balakrishnan | Michael W. McCoy

"These animals and their spawn are immediately killed (with the exception as far as known, of one Indian species) by sea-water."

—Charles Darwin (1872)

Transcriptomics of salinity adaptation in a treefrog

ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

Molecular mechanisms of local adaptation for salt-tolerance in a treefrog

Molly A. Albecker | Adam M. M. Stuckert | Christopher N. Balakrishnan | Michael W. McCoy

Herpetological Monographs, 29, 2015, 1–27

OCCURRENCE OF AMPHIBIANS IN SALINE HABITATS: A REVIEW AND EVOLUTIONARY PERSPECTIVE

GARETH R. HOPKINS[1] AND EDMUND D. BRODIE, JR

Department of Biology and the Ecology Center, Utah State University, Logan, UT 84322, USA

Transcriptomics of salinity adaptation in a treefrog

ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

Molecular mechanisms of local adaptation for salt-tolerance in a treefrog

Molly A. Albecker | Adam M. M. Stuckert | Christopher N. Balakrishnan | Michael W. McCoy

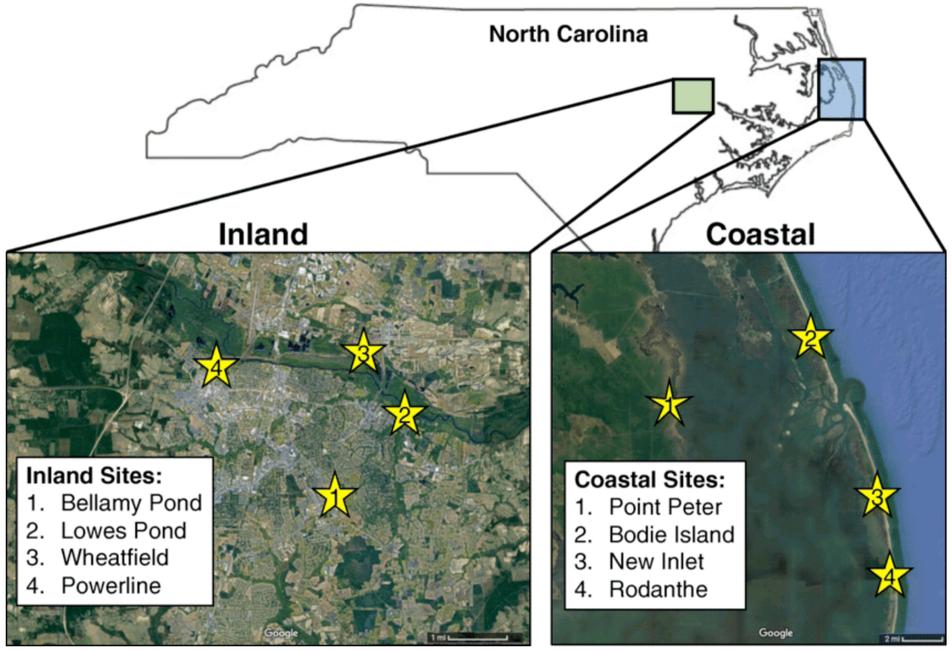
Transcriptomics of salinity adaptation in a treefrog

ORIGINAL ARTICLE

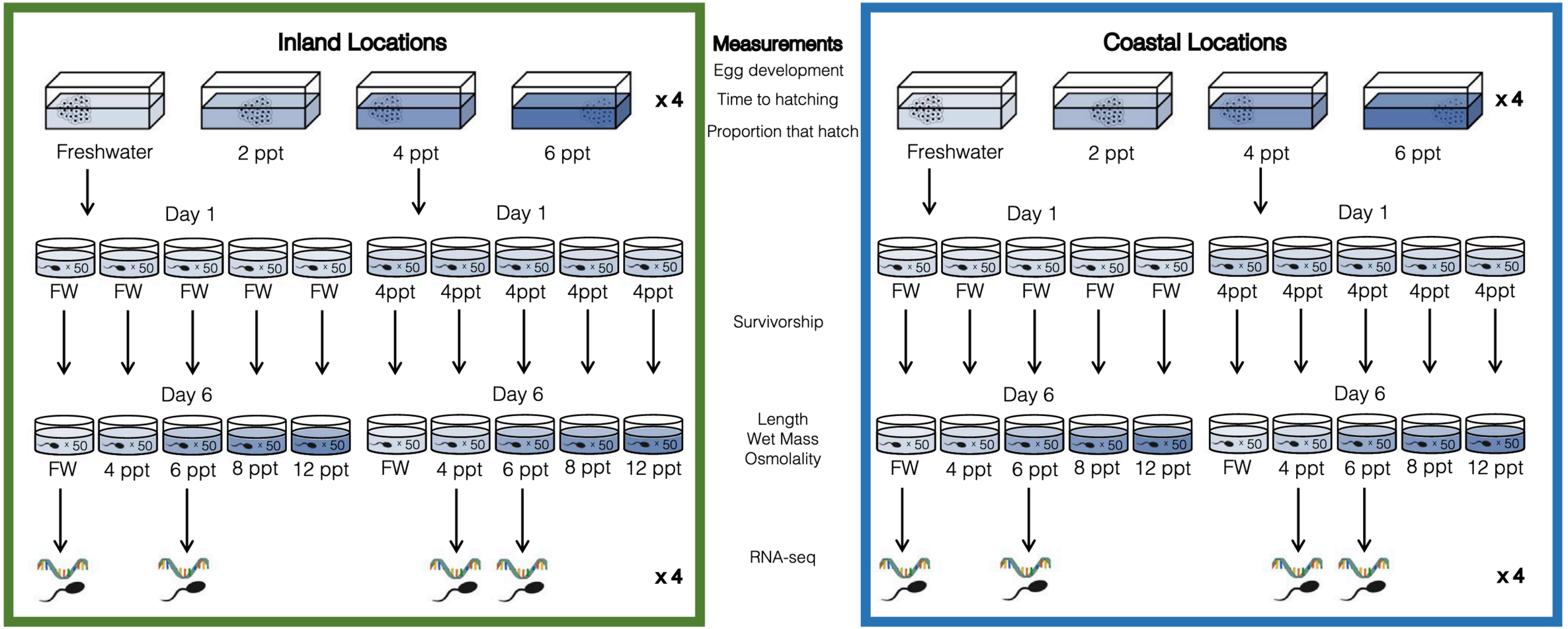
MOLECULAR ECOLOGY WILEY

Molecular mechanisms of local adaptation for salt-tolerance in a treefrog

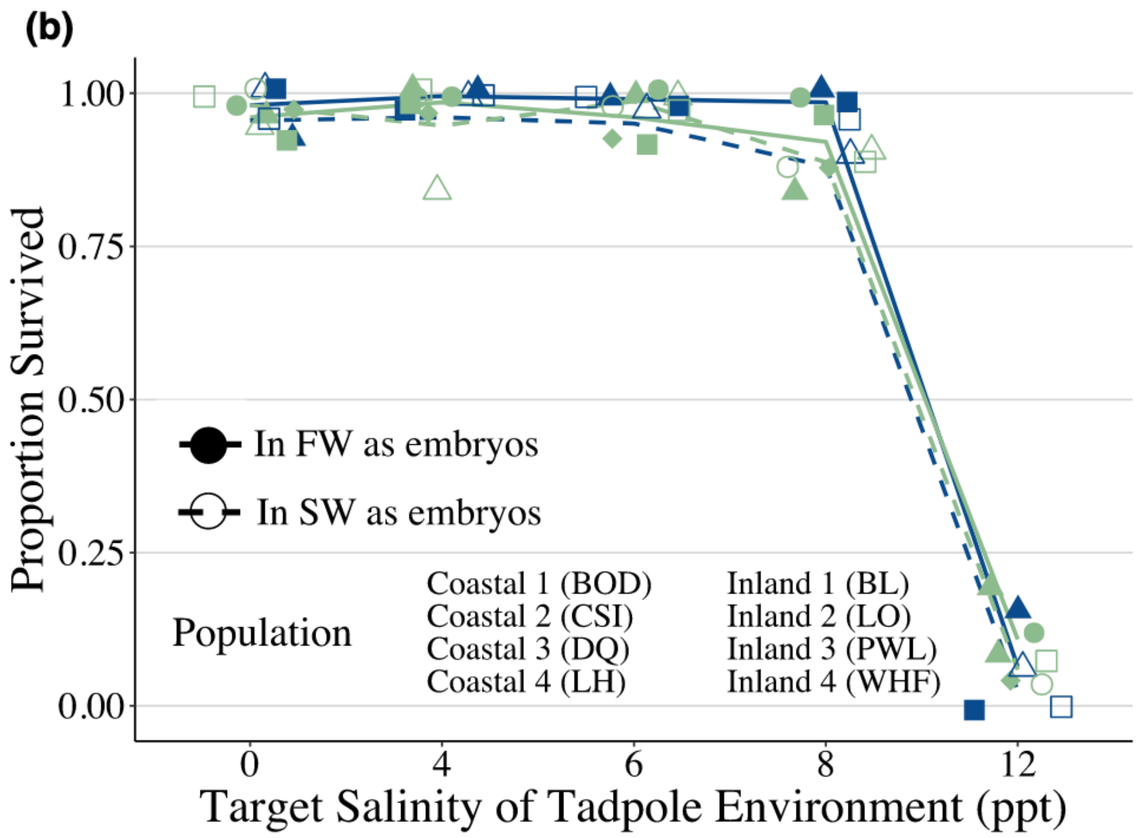
Molly A. Albecker | Adam M. M. Stuckert | Christopher N. Balakrishnan | Michael W. McCoy

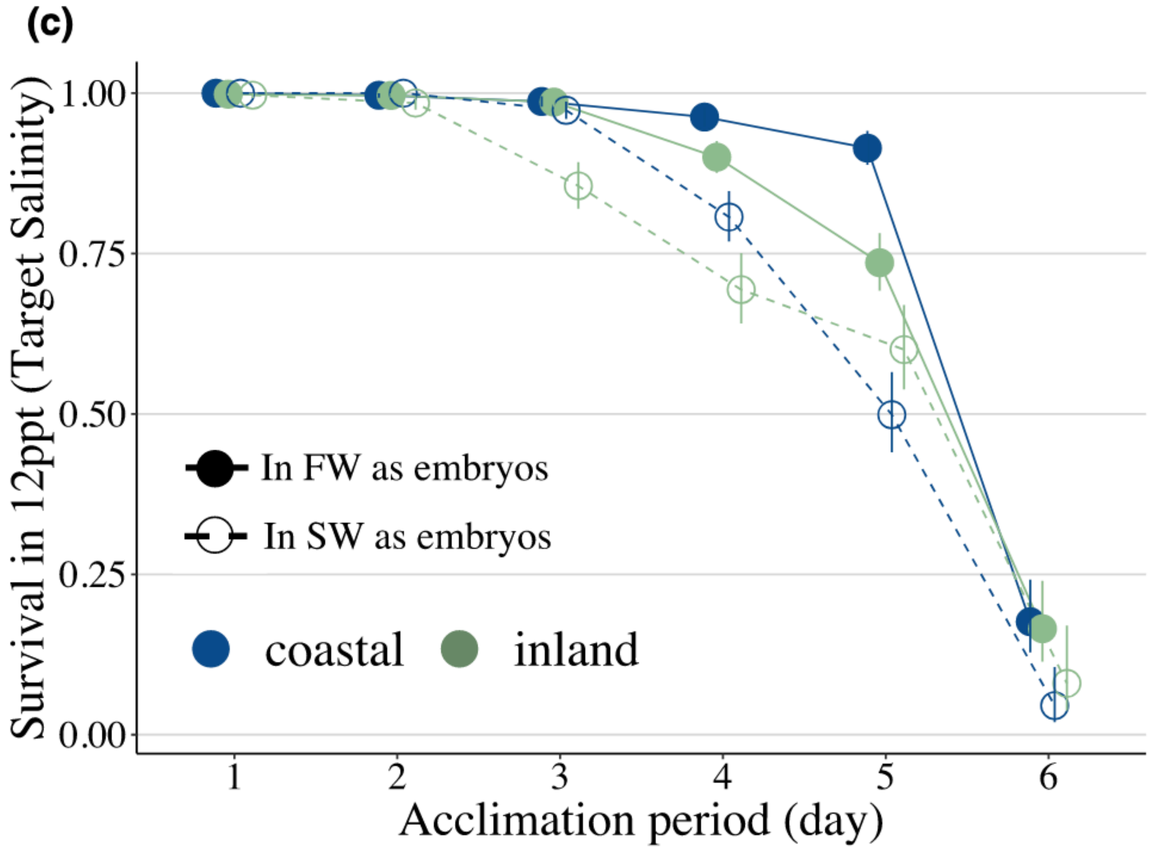


Transcriptomics of salinity adaptation in a treefrog

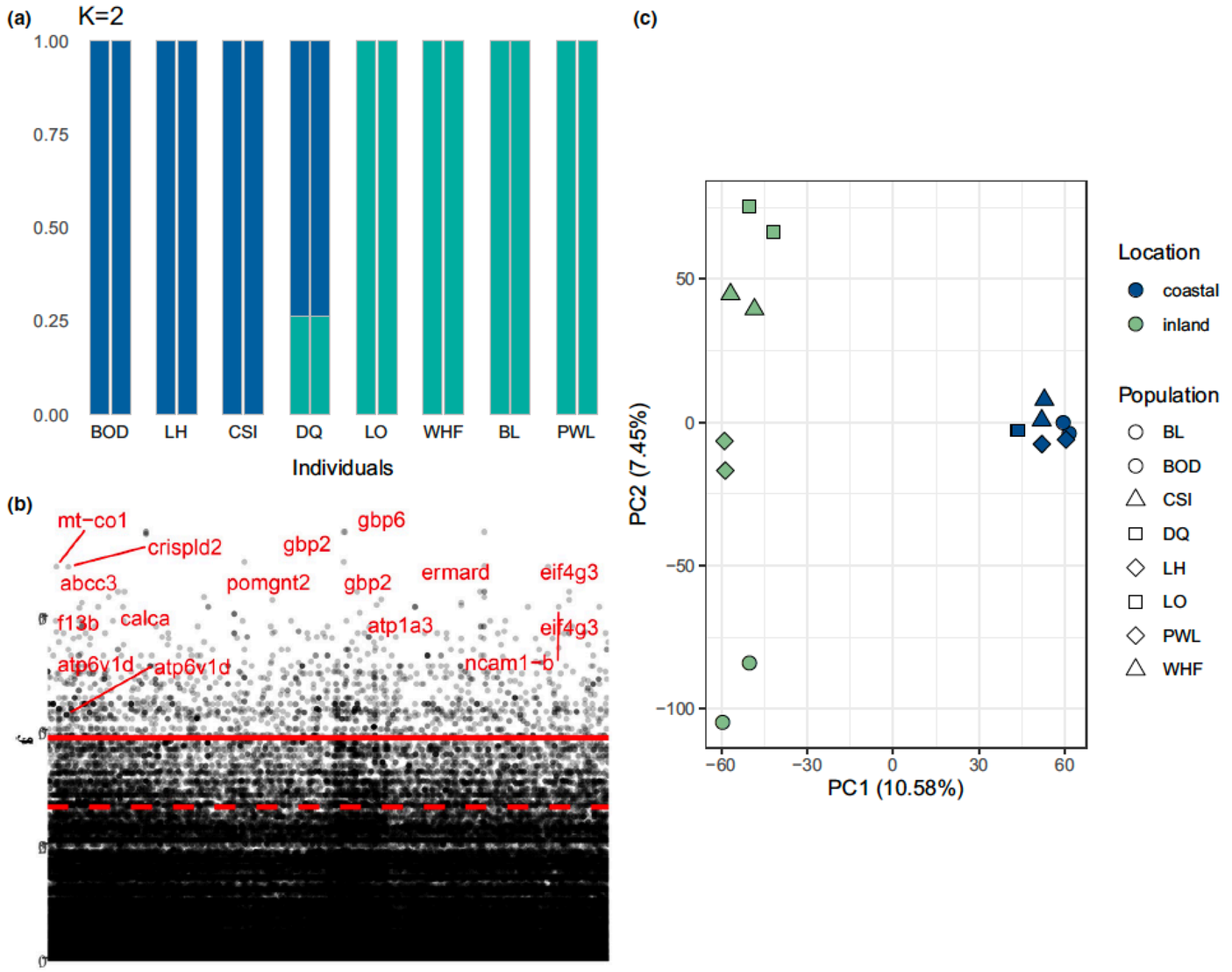


Transcriptomics of salinity adaptation in a treefrog

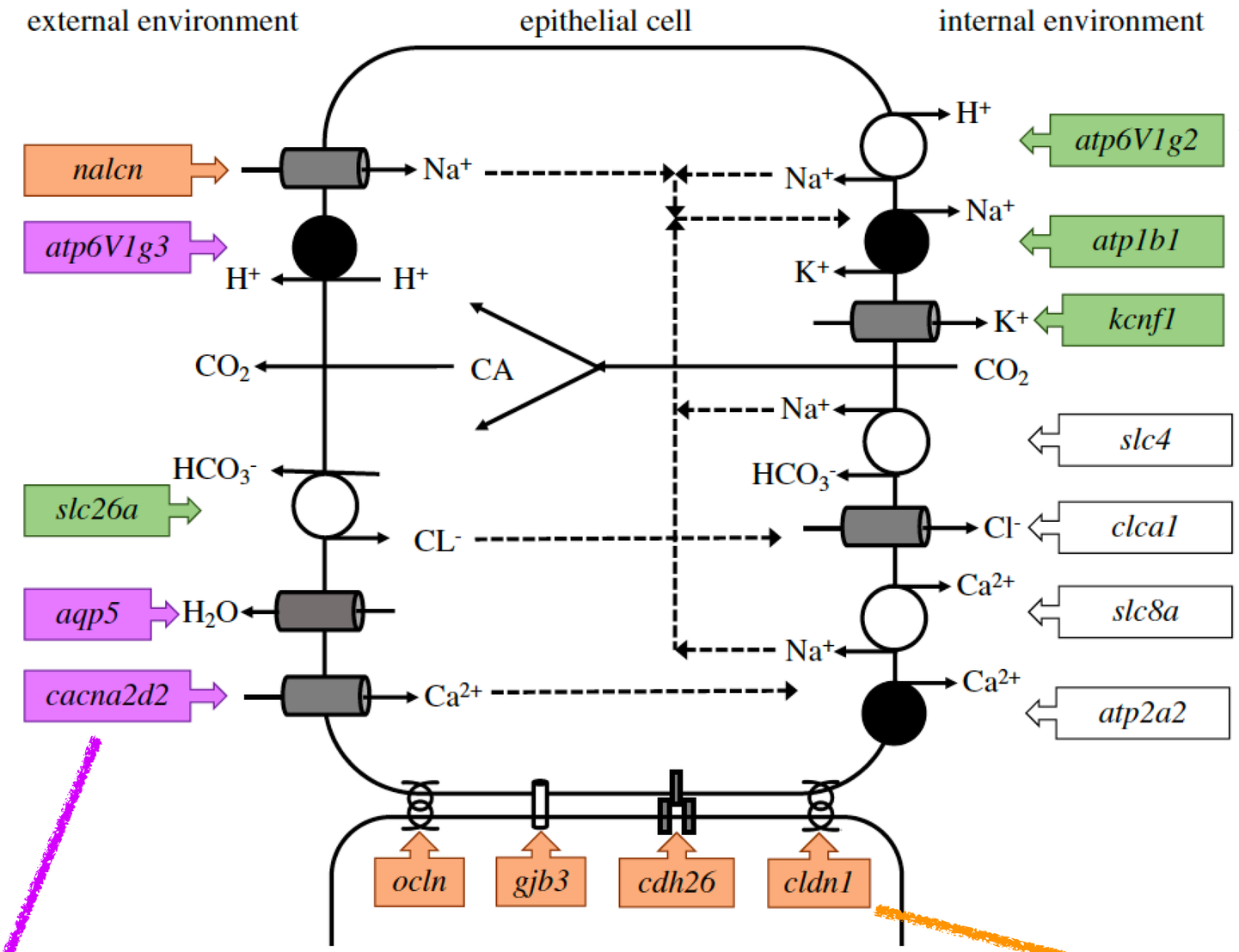




Transcriptomics of salinity adaptation in a treefrog



Transcriptomics of salinity adaptation in a treefrog



Upregulated in coastal populations

Also gpd1:
Glycerol as osmolyte

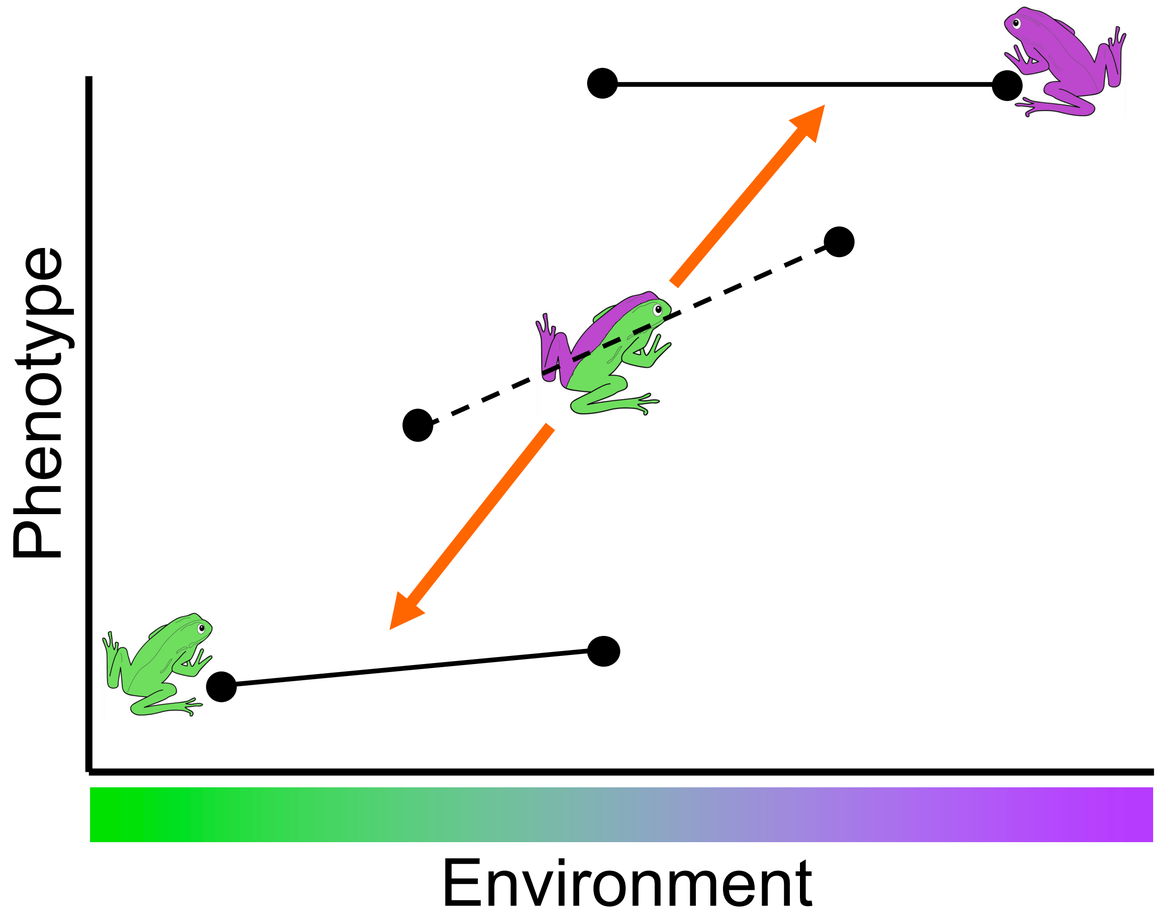
Regulated by salinity exposure

Downregulated in coastal populations in FW

Ok, organisms alter their gene expression in response to environmental changes…

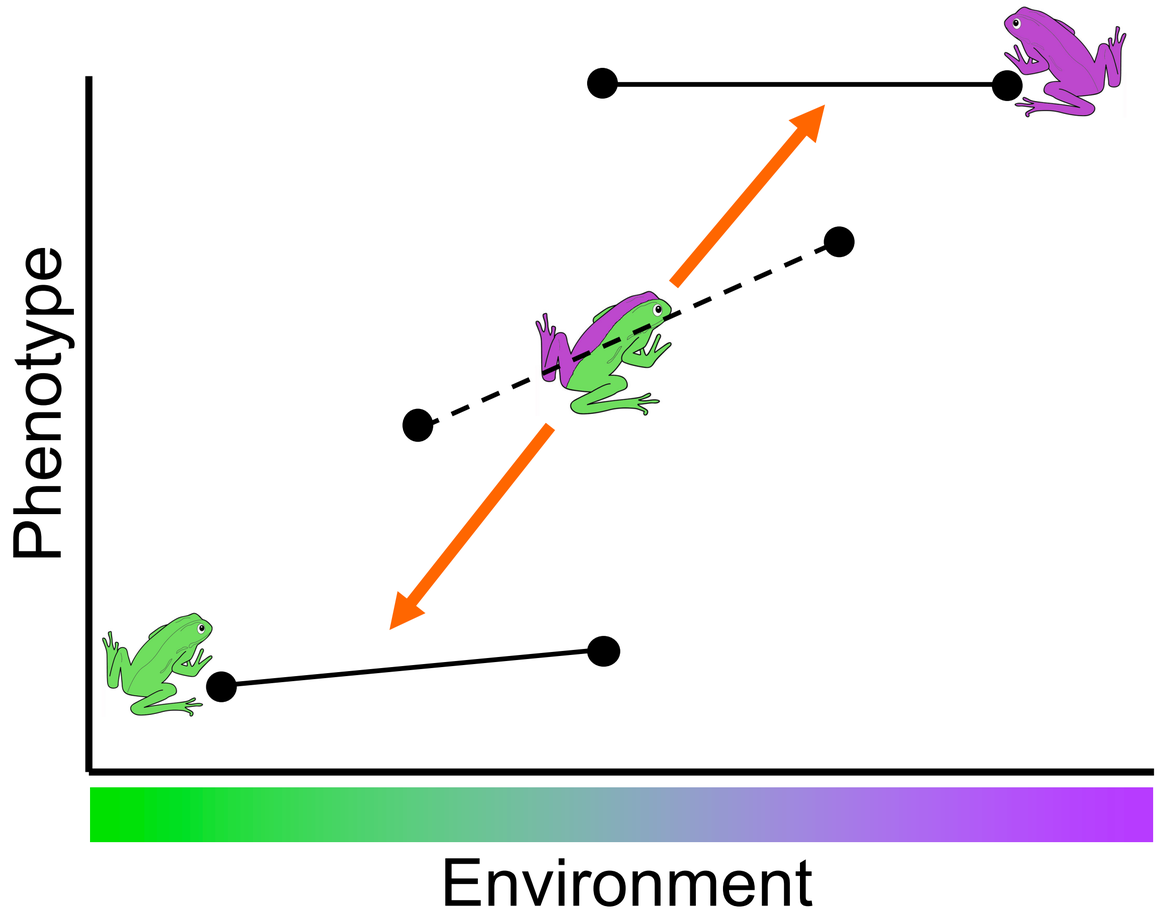
so what?

Ancestral plasticity can diverge under selection into constitutive differences



Ancestral plasticity can diverge under selection into constitutive differences:

Genetic accommodation



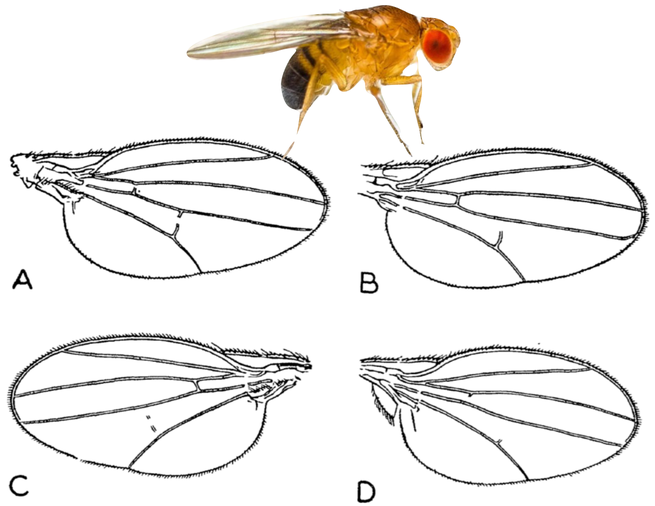
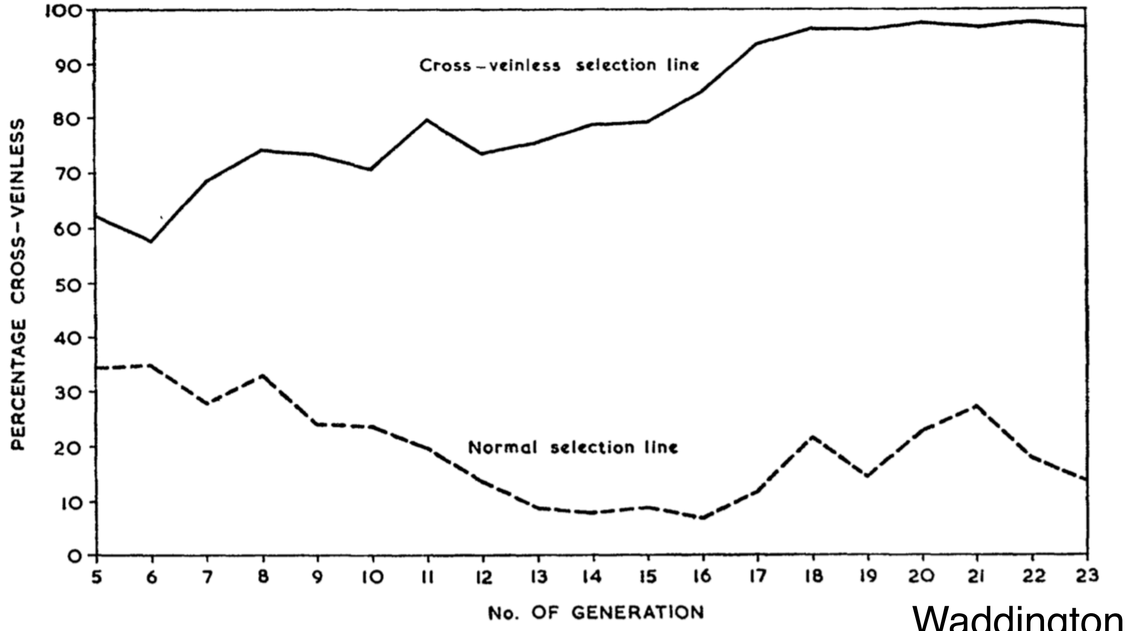
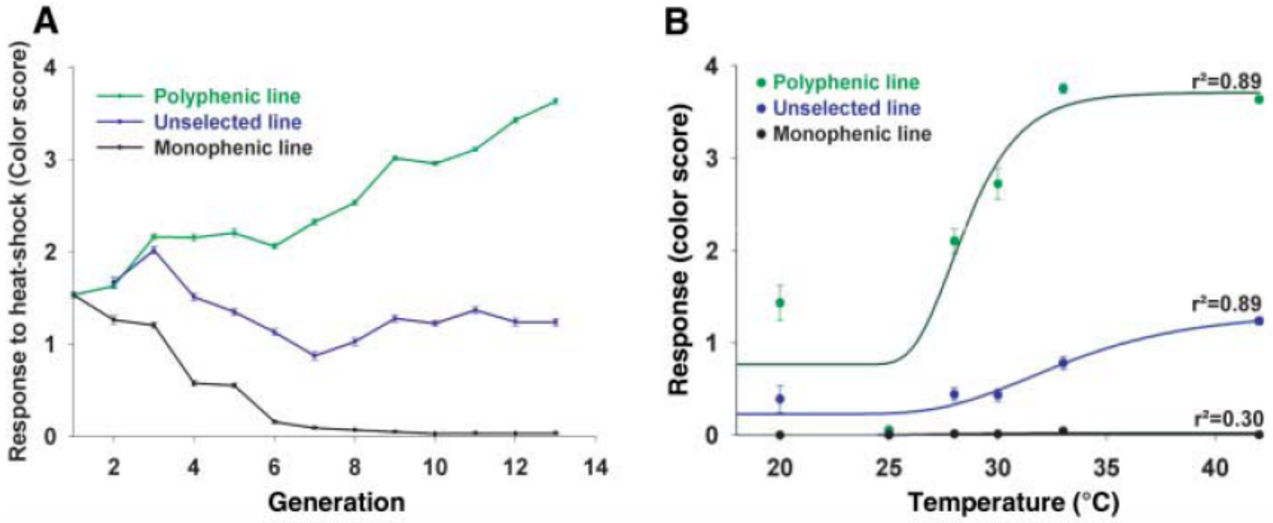


FIG. 1. Four crossveinless wings: *a* grade 4, *b* grade 3, *c* grade 2, *d* grade 1.

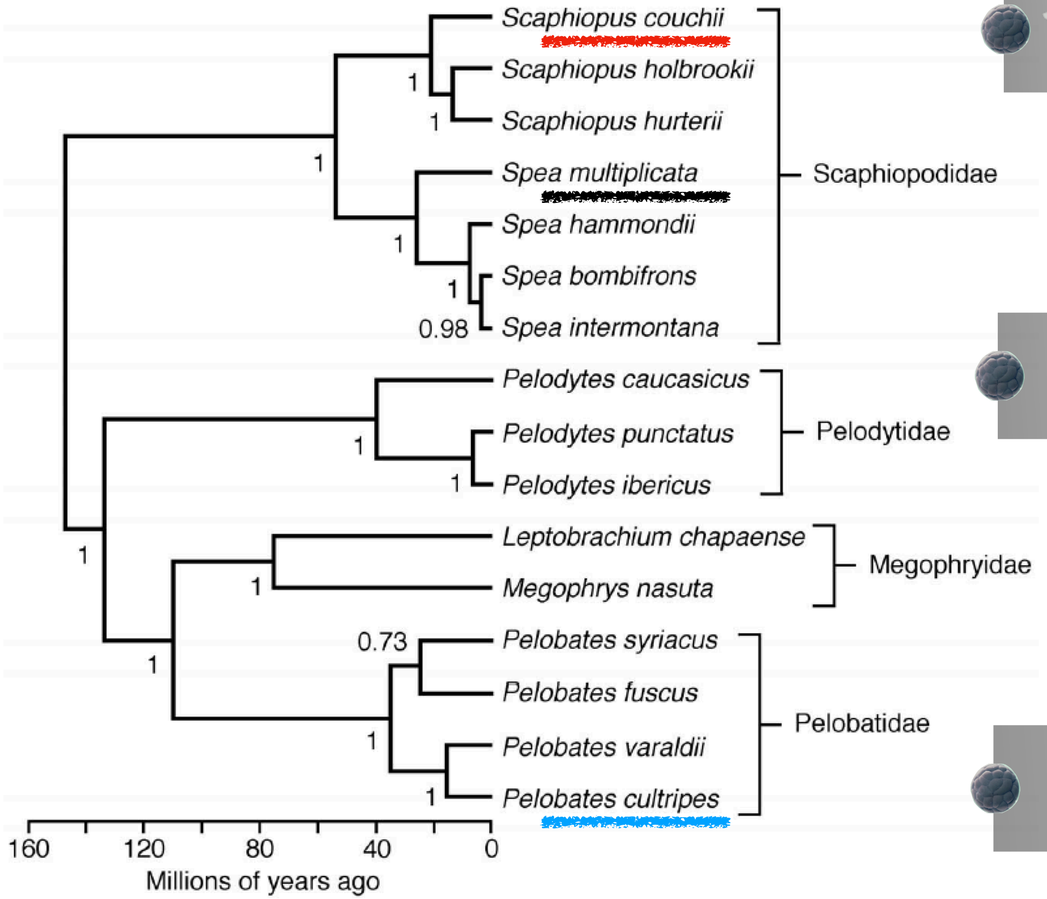


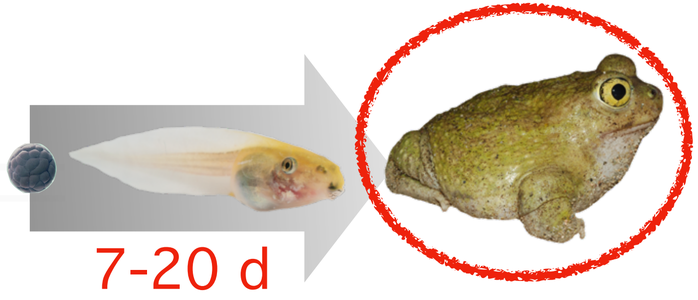
Waddington 1953 Evolution

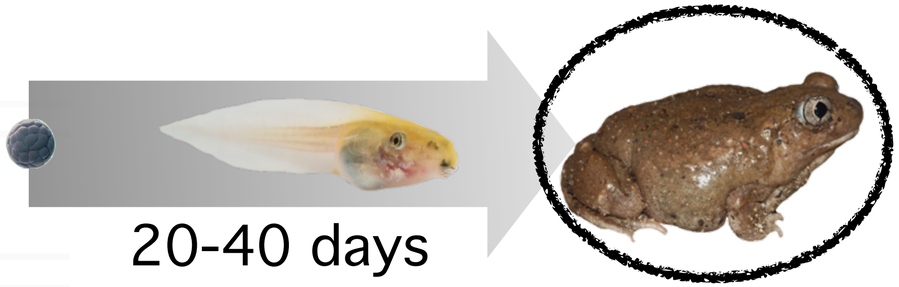


Suzuki & Nijhout 2006 Science

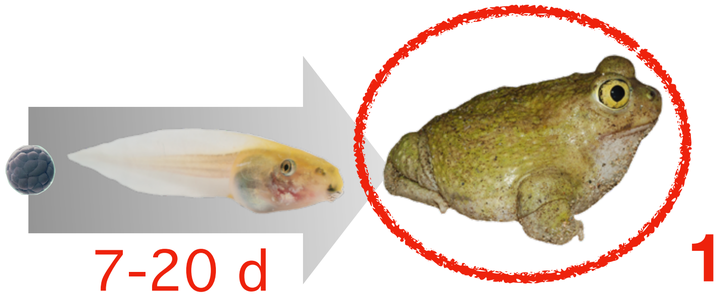
Evolutionary divergence in developmental rate - Spadefoot toads







Larval period is positively associated with genome size



7-20 d

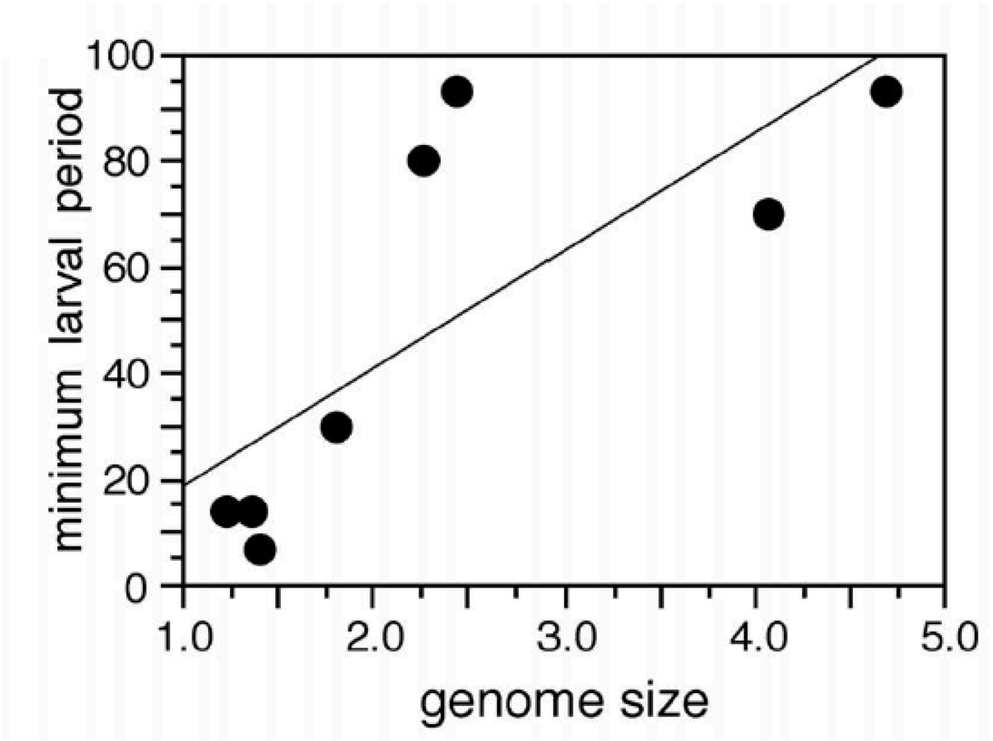
1.5 Gb

20-40 days

1.8 Gb

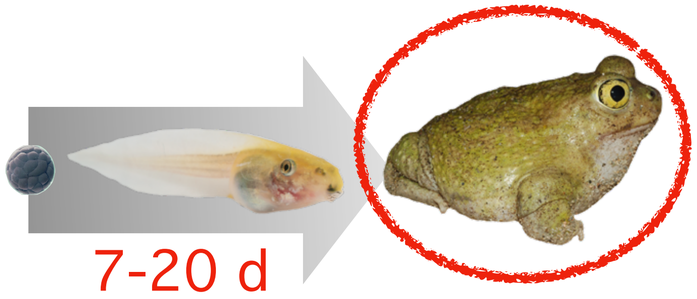
90-180 days

4.2 Gb

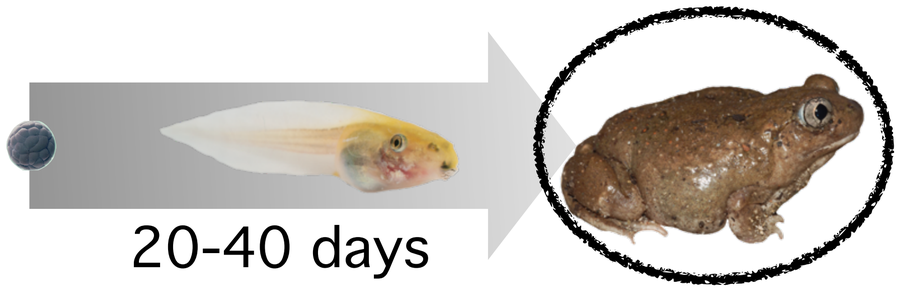


Zeng et al. PLoS One 2016

Species have evolved different degrees of developmental plasticity

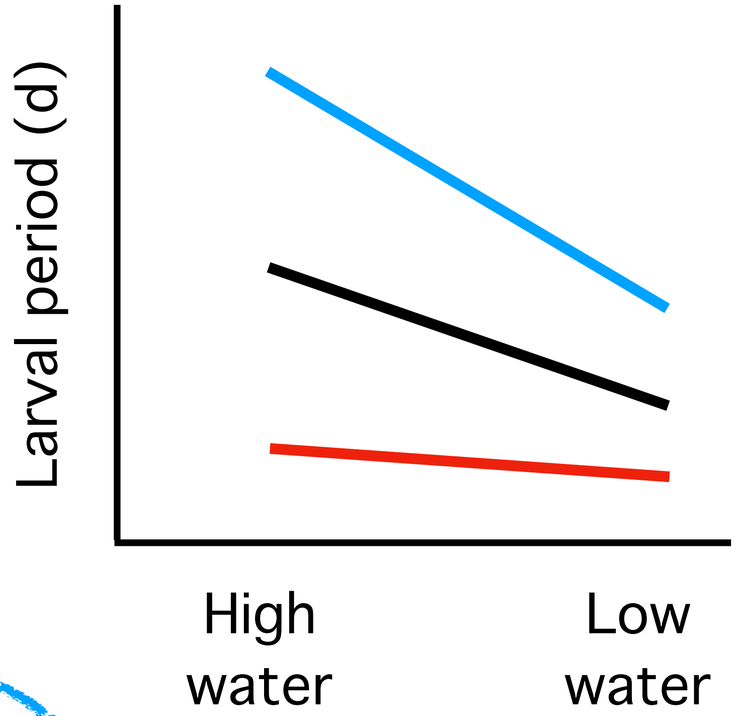


7-20 d



20-40 days

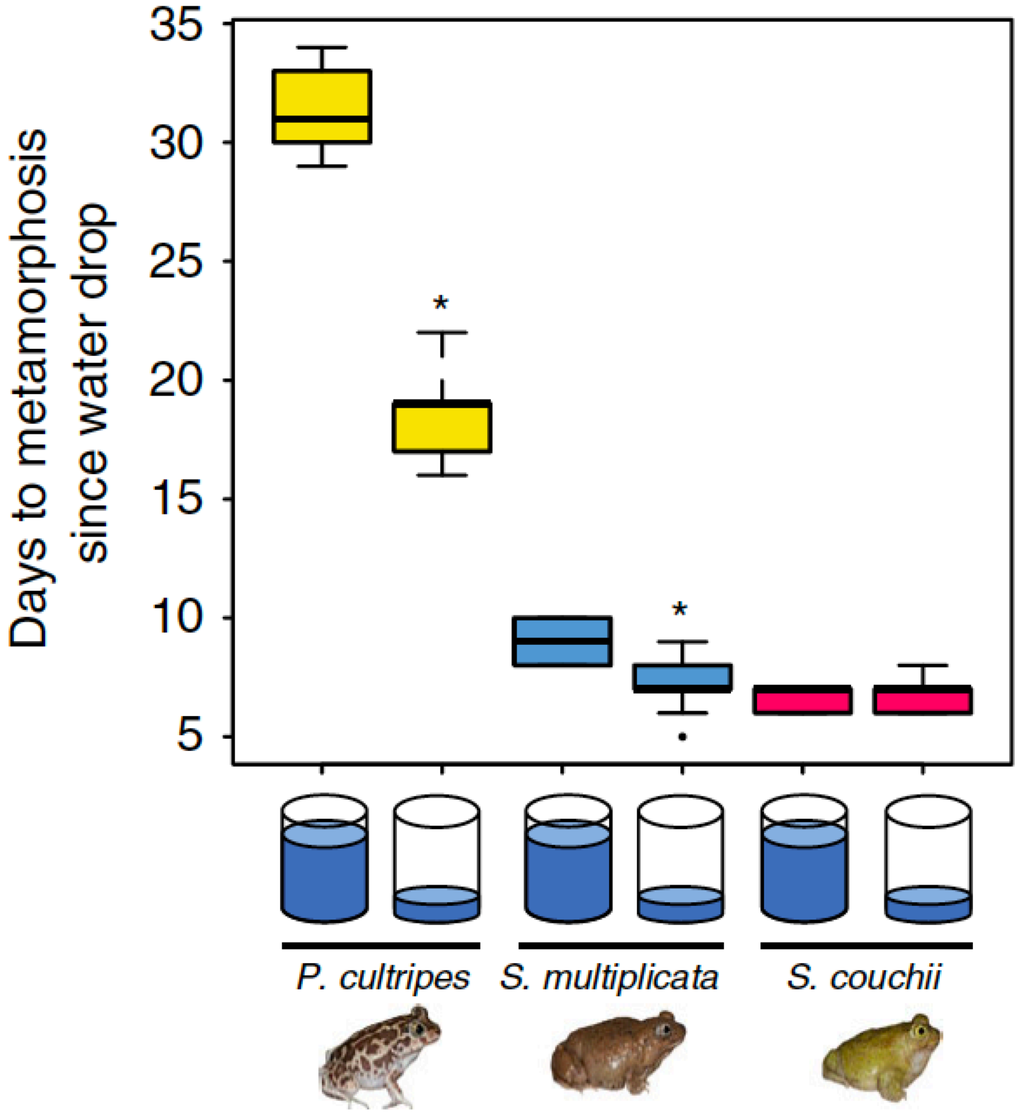
90-180 days

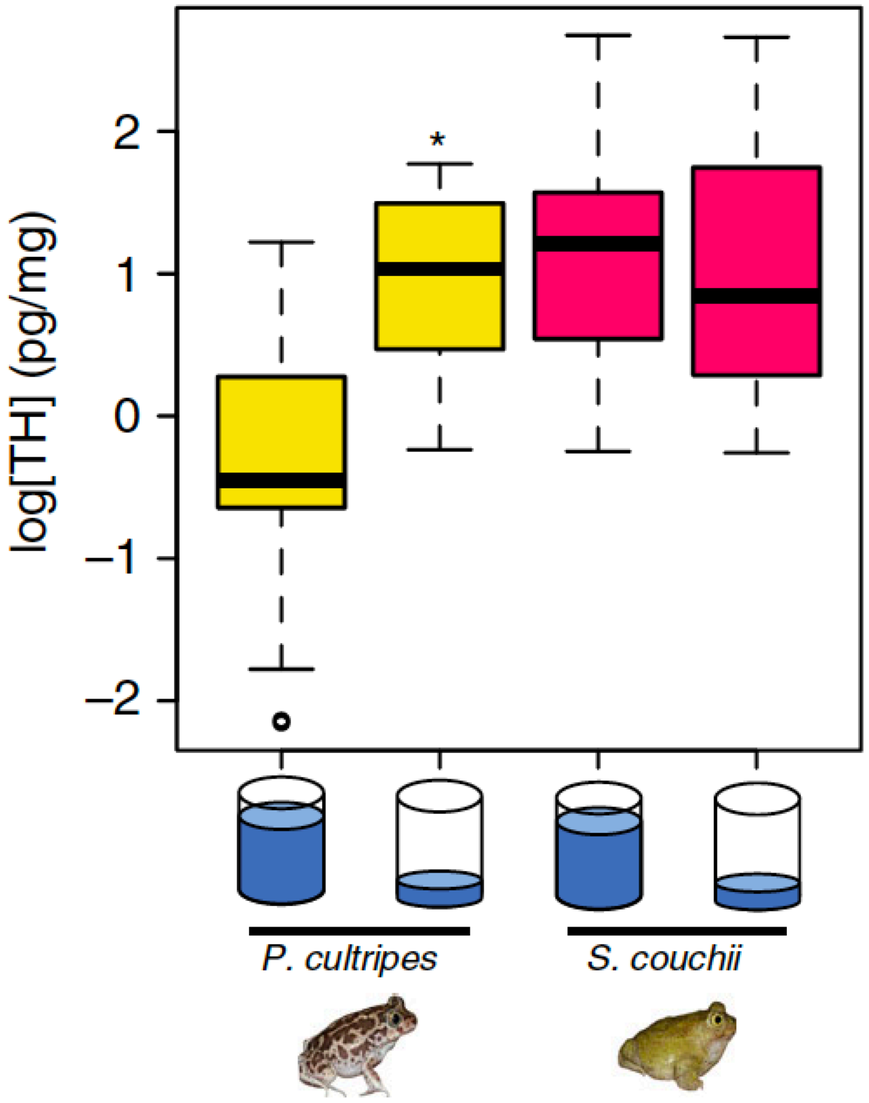


Gomez-Mestre & Buchholz PNAS 2006

Kulkarni et al. J Evol Biol 2011

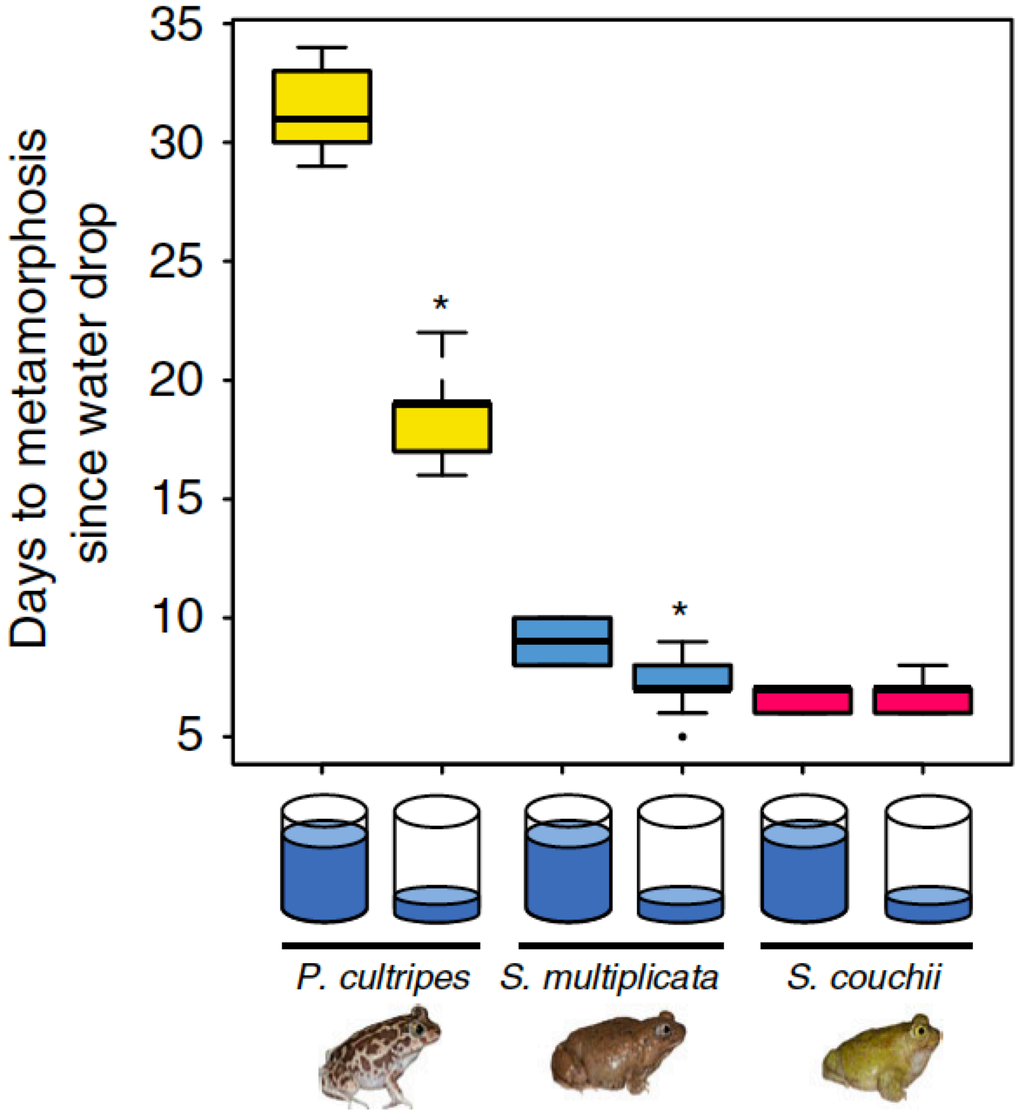
Within-species plasticity mirrors among-species differences

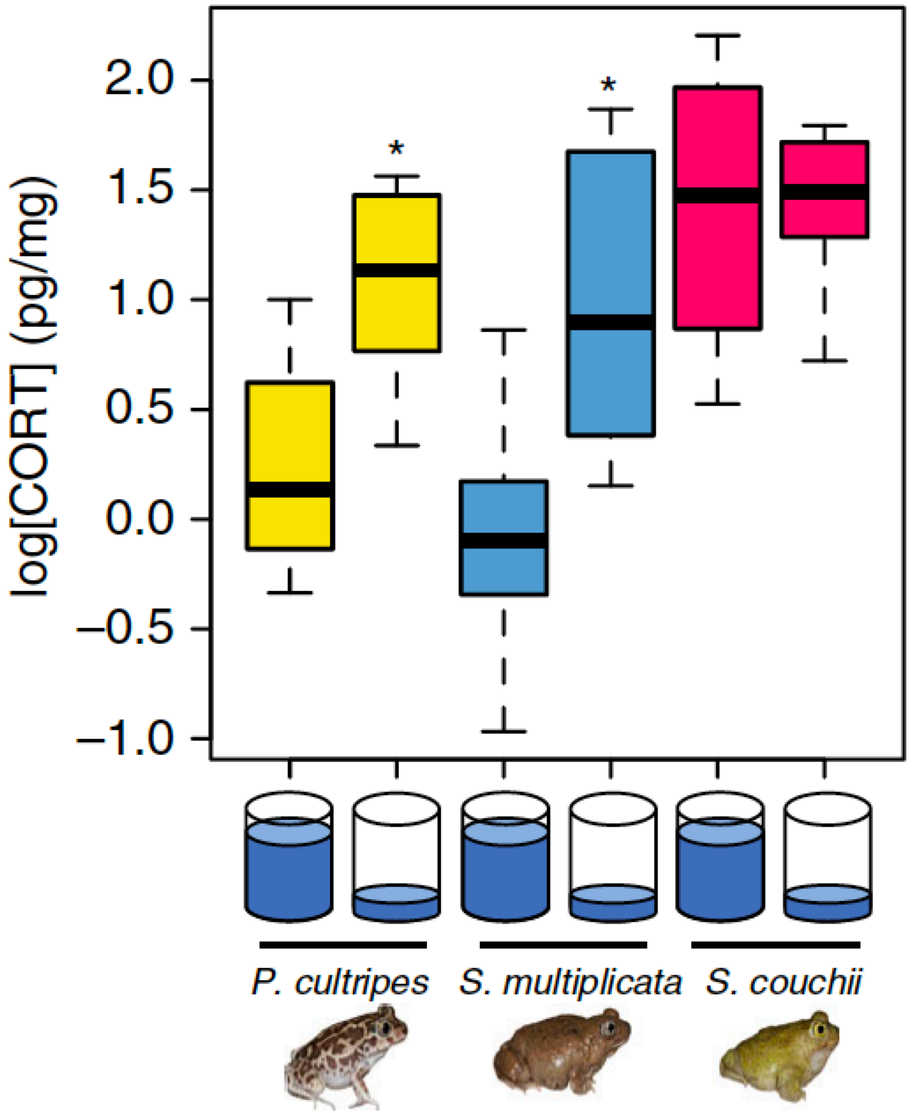




Kulkarni et al. Nature Comms 2017

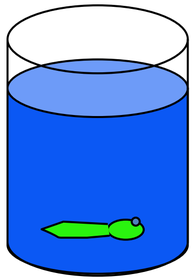
Within-species plasticity mirrors among-species differences

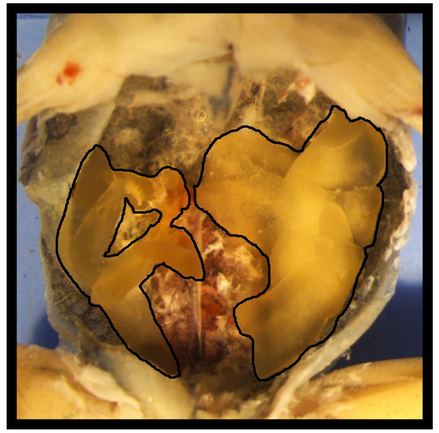


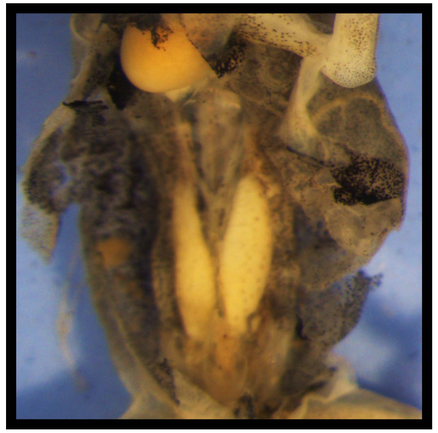


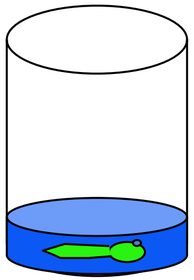
Kulkarni et al. Nature Comms 2017

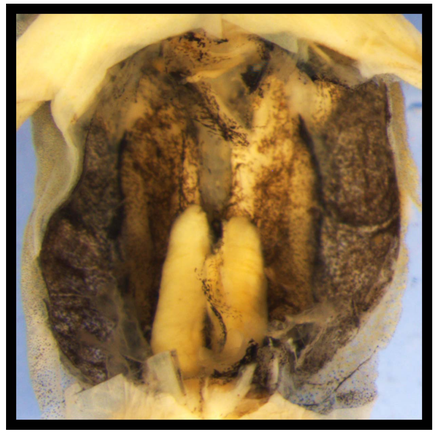
Within-species plasticity mirrors among-species differences



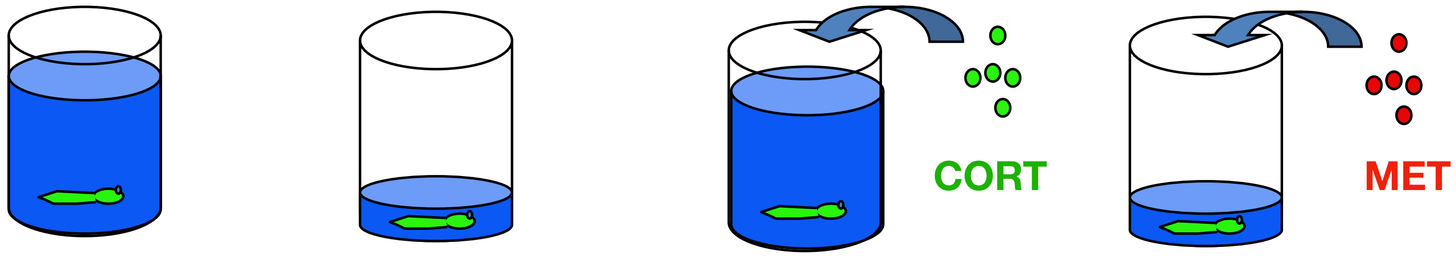


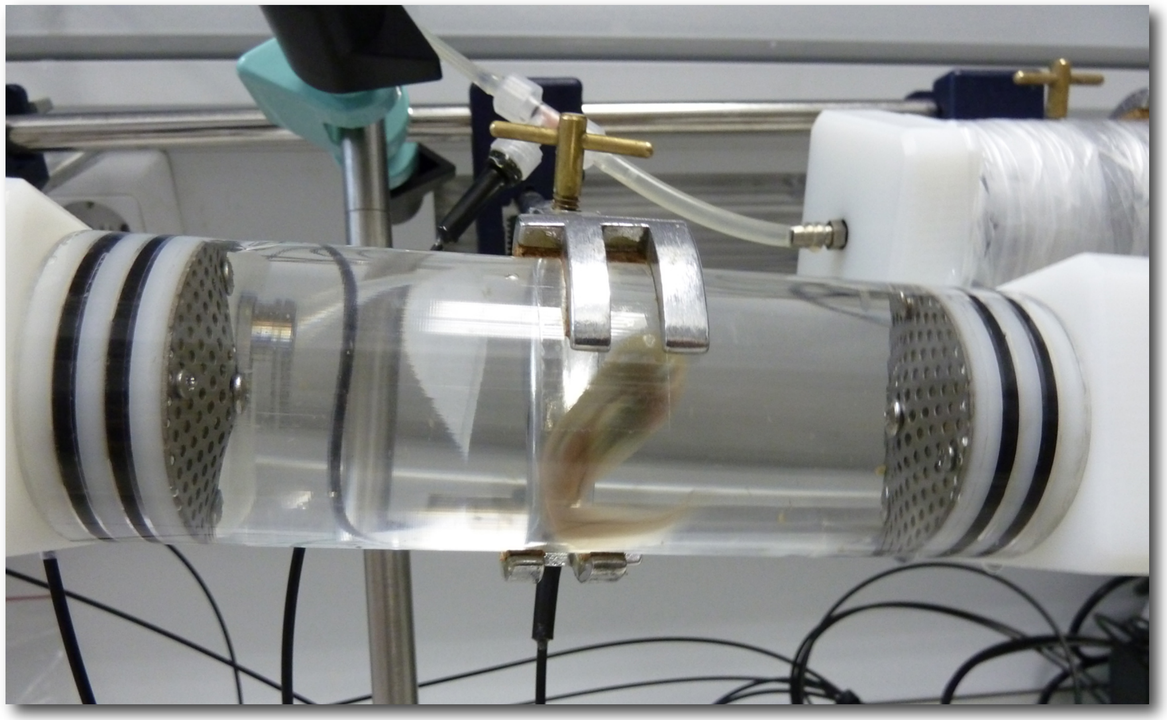




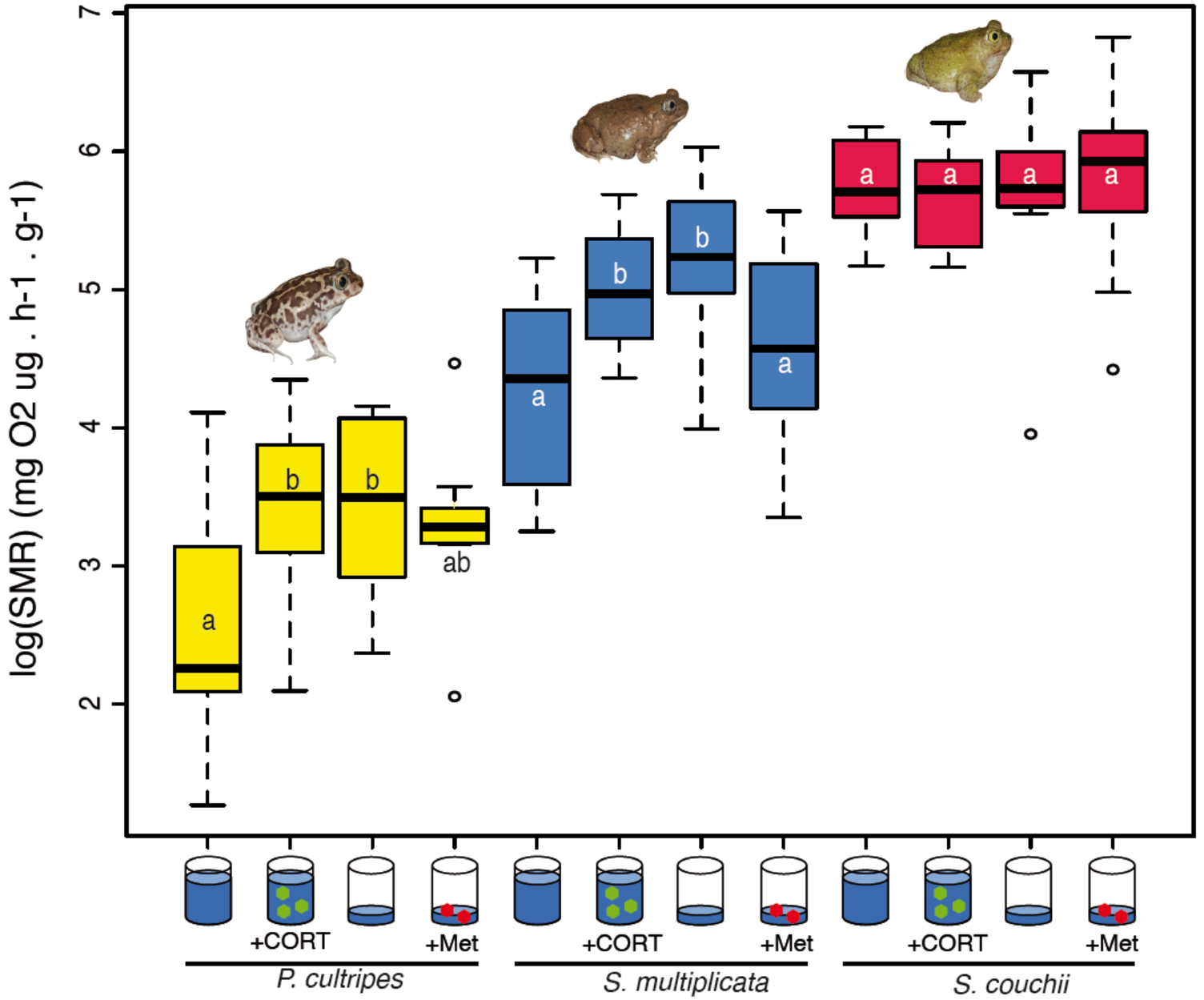


How does metabolic rate vary within and among species?



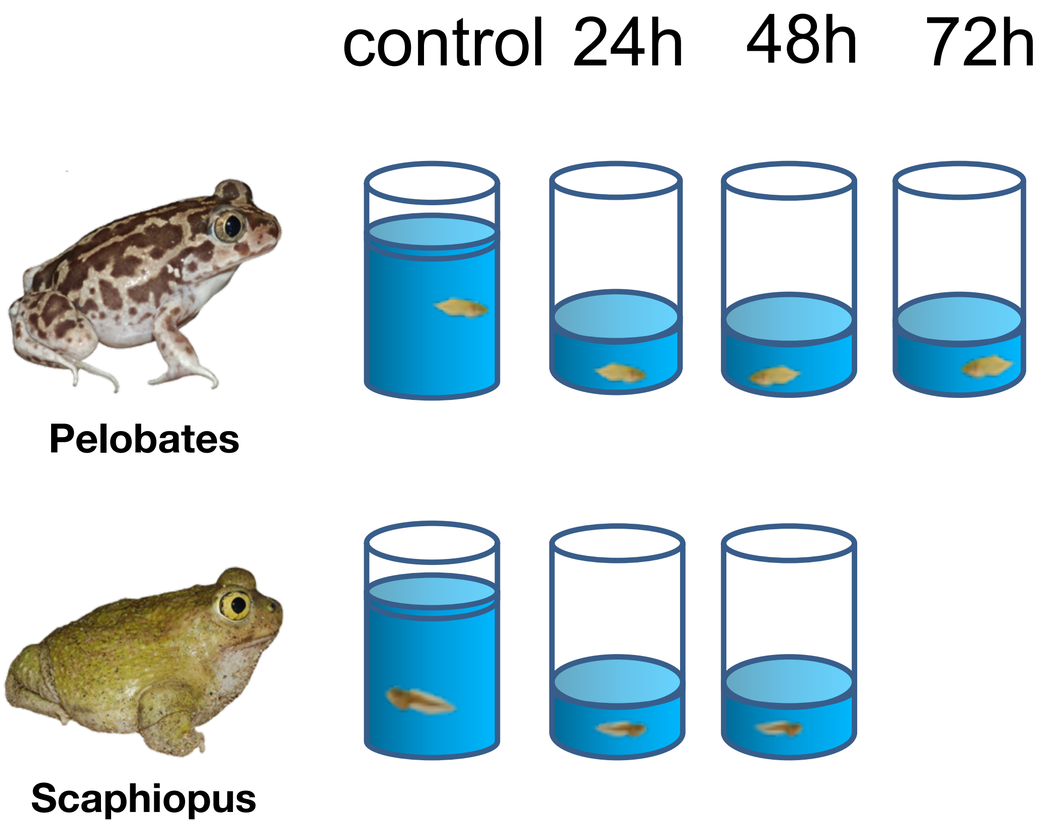


How does metabolic rate vary within and among species?



Kulkarni et al. Nature Comms 2017

How does gene expression vary in response to water level?



ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

Cross-species transcriptomics uncovers genes underlying genetic accommodation of developmental plasticity in spadefoot toads

Hans Christoph Liedtke[1] | Ewan Harney[2] | Ivan Gomez-Mestre[1]

Liedtke et al. 2019 G3
Liedtke et al. 2022 DNA Research

ARTICLES
https://doi.org/10.1038/s41559-020-1202-x
nature ecology & evolution
Check for updates

Nutrition-responsive gene expression and the developmental evolution of insect polyphenism

Sofia Casasa[1]✉, Eduardo E. Zattara[1,2]✉ and Armin P. Moczek[1]

nature COMMUNICATIONS

ARTICLE

Received 18 Oct 2016 | Accepted 9 Mar 2017 | Published 15 May 2017

DOI: 10.1038/ncomms15213 OPEN

Transcriptomic and macroevolutionary evidence for phenotypic uncoupling between frog life history phases

Katharina C. Wollenberg Valero[1,†], Joan Garcia-Porta[2], Ariel Rodríguez[3,†], Mónica Arias[4,5,*], Abhijeet Shah[4,6,*], Roger Daniel Randrianiaina[3,7,*], Jason L. Brown[8], Frank Glaw[9], Felix Amat[10], Sven Künzel[11], Dirk Metzler[4], Raphael D. Isokpehi[1] & Miguel Vences[3]

ORIGINAL ARTICLE

MOLECULAR ECOLOGY

Cross-species transcriptomics uncovers genes underlying genetic accommodation of developmental plasticity in spadefoot toads

Hans Christoph Liedtke[1] | Ewan Harney[2] | Ivan Gomez-Mestre[1]

Zhu *et al. BMC Genomics* (2018) 19:422
https://doi.org/10.1186/s12864-018-4790-y

BMC Genomics

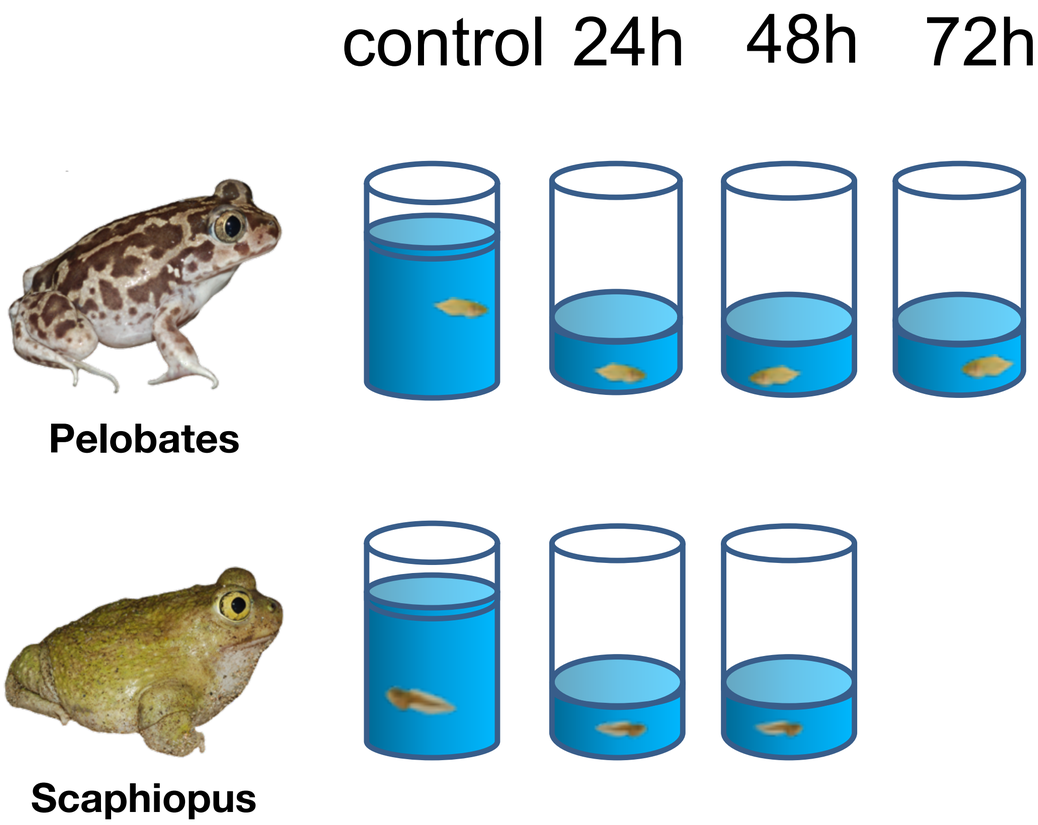
RESEARCH ARTICLE Open Access

CrossMark

Transcriptomics reveals the molecular processes of light-induced rapid darkening of the non-obligate cave dweller *Oreolalax rhodostigmatus* (Megophryidae, Anura) and their genetic basis of pigmentation strategy

Wei Zhu[1], Lusha Liu[1], Xungang Wang[1,2], Xinyu Gao[1], Jianping Jiang[1*] and Bin Wang[1*]

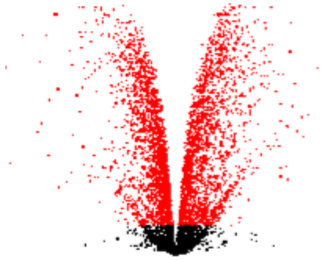
How does gene expression vary in response to water level?



- Standardized conditions
- Control + 2 or 3 treatments
- 3 biological replicates

- Total RNA extraction from whole body
- Illumina (HiSeq2000) ~30 mil. reads per sample

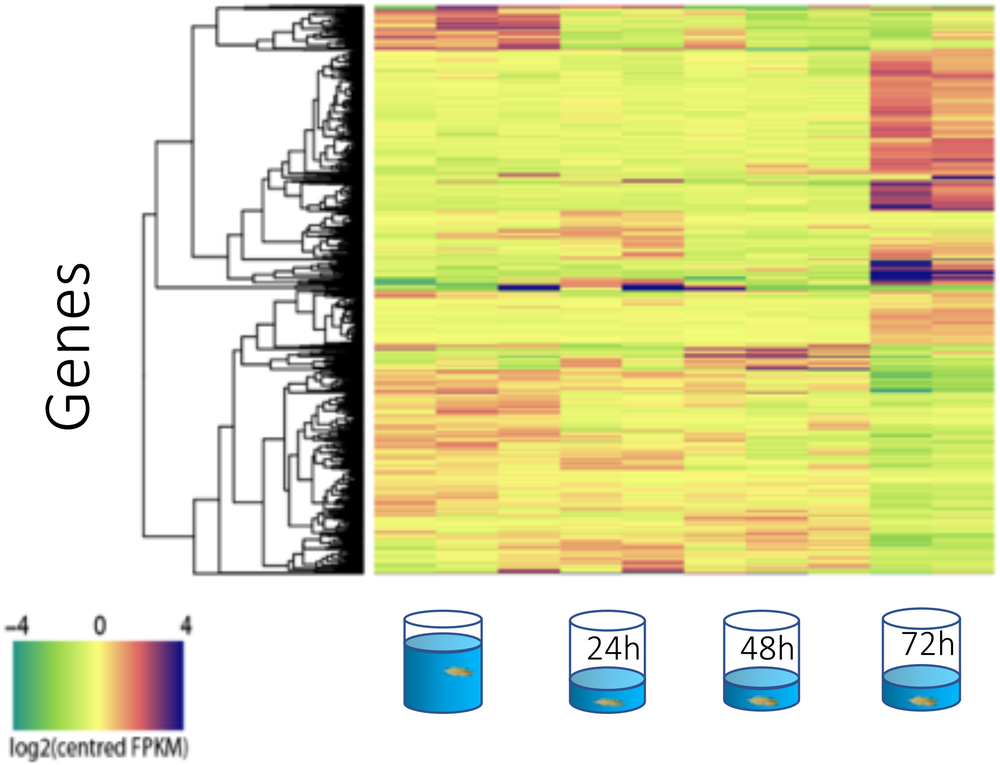
- *De novo* transcriptome assembly and annotation using Trinity + Trinotate
- Differential expression analysis using Kallisto and EdgeR + GOseq

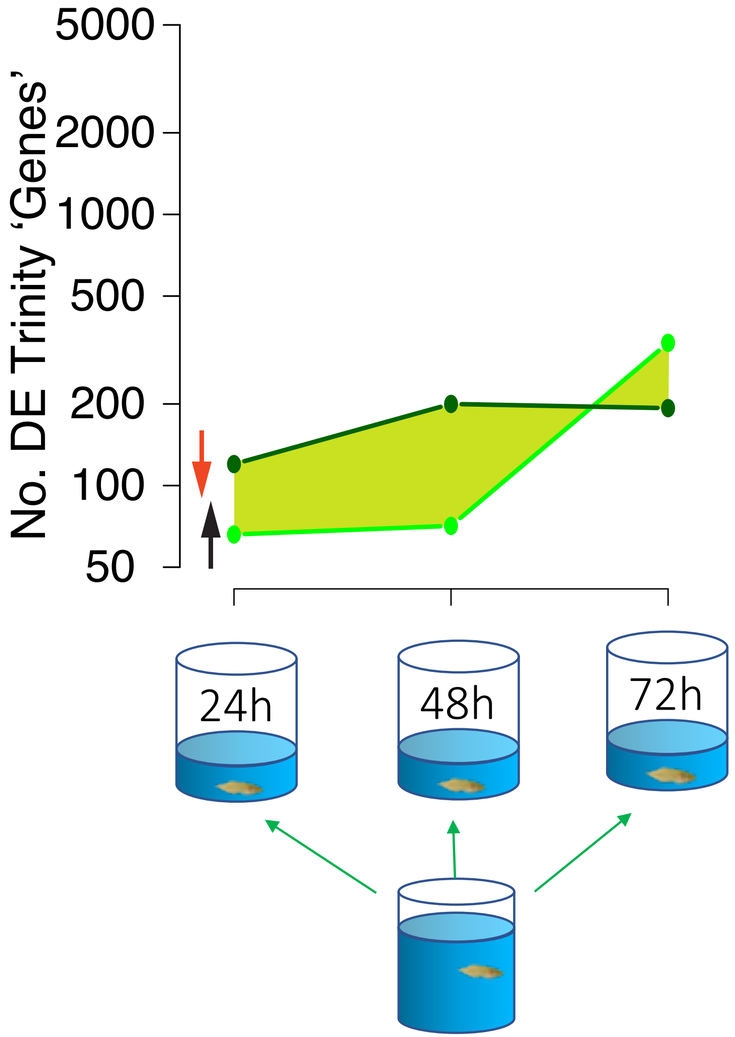


Liedtke et al. 2019 G3
Liedtke et al. 2022 DNA Research

Pelobates - time lag and extensive down regulation

1236 DE Trinity ‘Genes’
(0.29% of transcriptome)

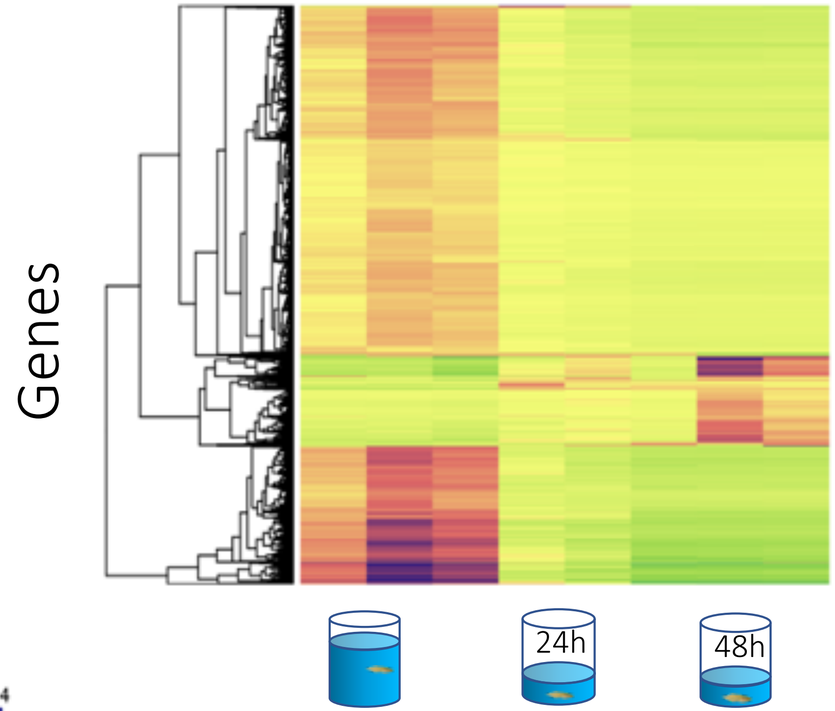




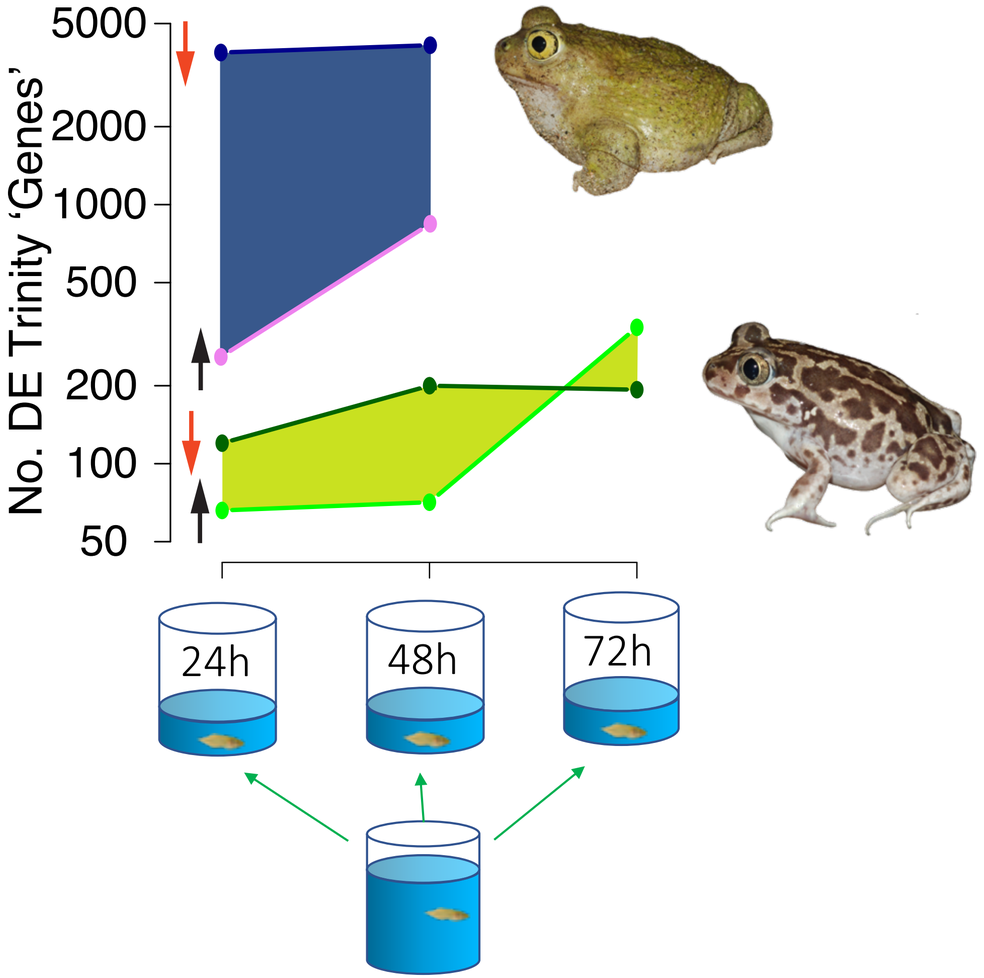
Liedtke, Harney, Gomez-Mestre 2021 Mol Ecol

Scaphiopus - faster response, greater response

5015 DE Trinity ‘Genes’
(1.32% of transcriptome)

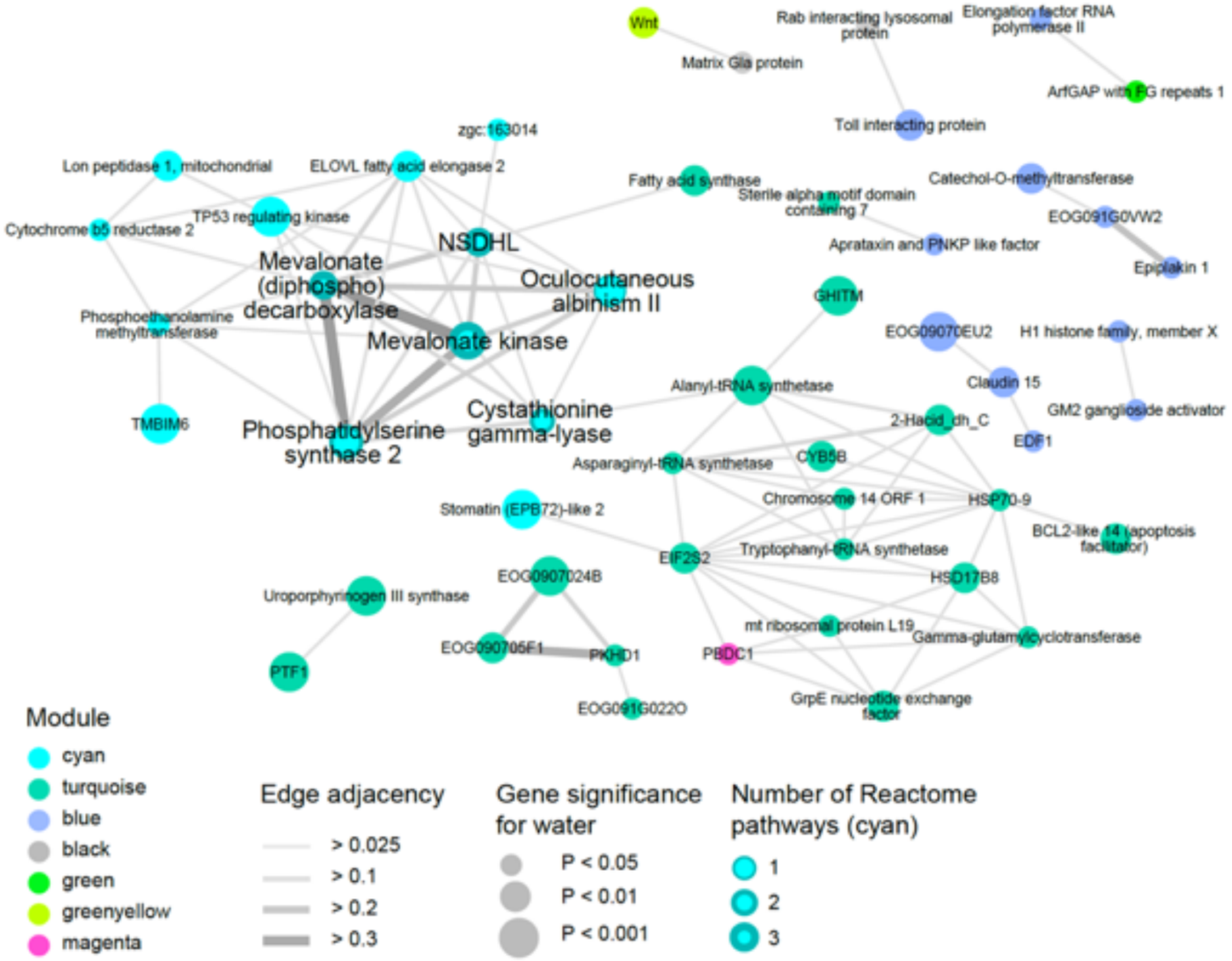


LogFC>2, p<0.05

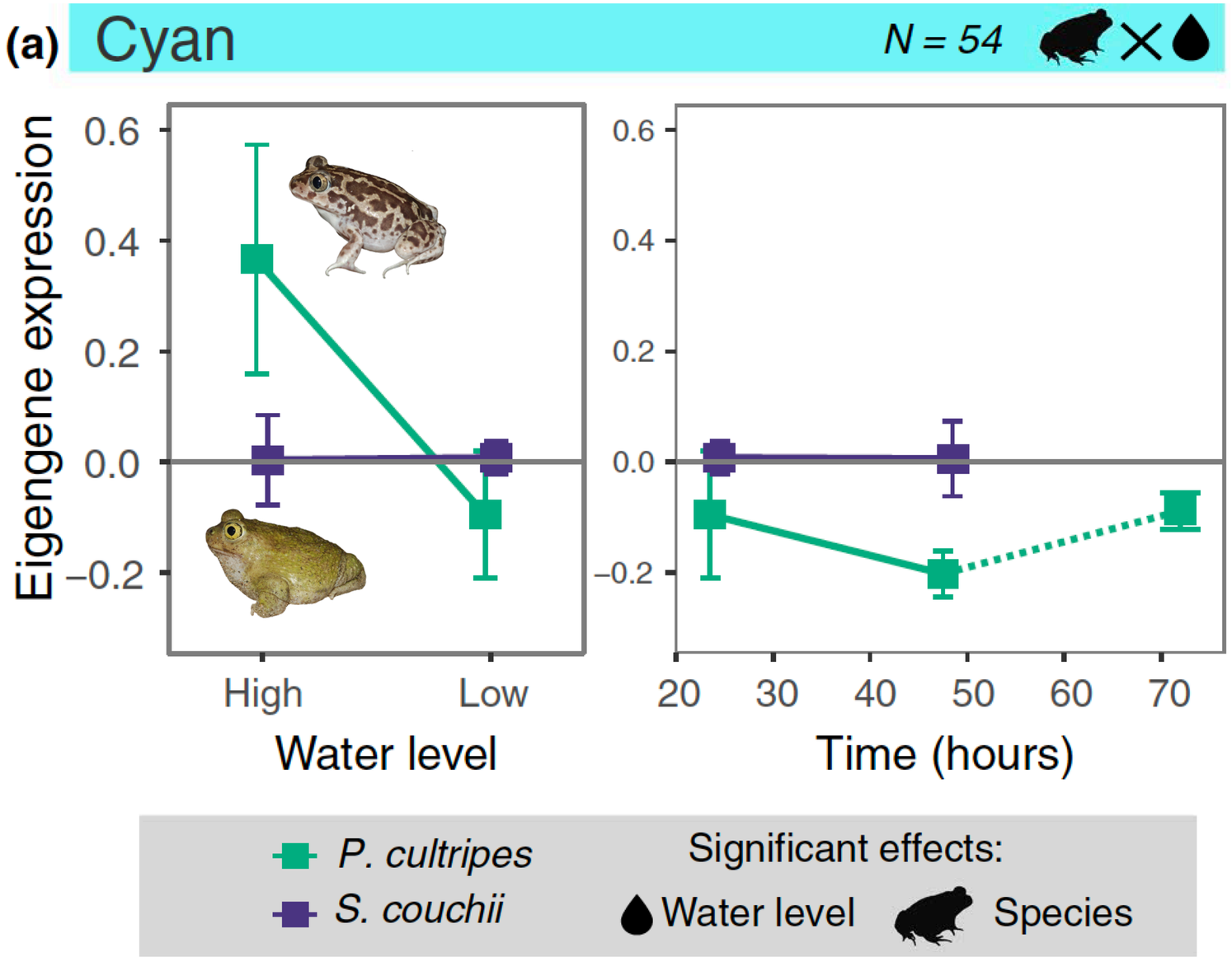


Liedtke, Harney, Gomez-Mestre 2021 Mol Ecol

WGNCA - gene cluster associated with species x environment



WGNCA - gene cluster associated with species x environment



Cholesterol and steroid biosynthesis and metabolism

Liedtke, Harney, Gomez-Mestre 2021 Mol Ecol