marbec

MARINE BIODIVERSITY EXPLOITATION & CONSERVATION

Repeated evolution following habitat transitions from marine to freshwater

Dr. Antoine Fraimout

May 9th 2023

MOPGA

IRD Institut de Recherche pour le Développement FRANCE

Ifremer

Université de Montpellier

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INRAE

Main questions

Can populations respond adaptively to habitat changes and can we predict these adaptive changes?

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Is evolution predictable?

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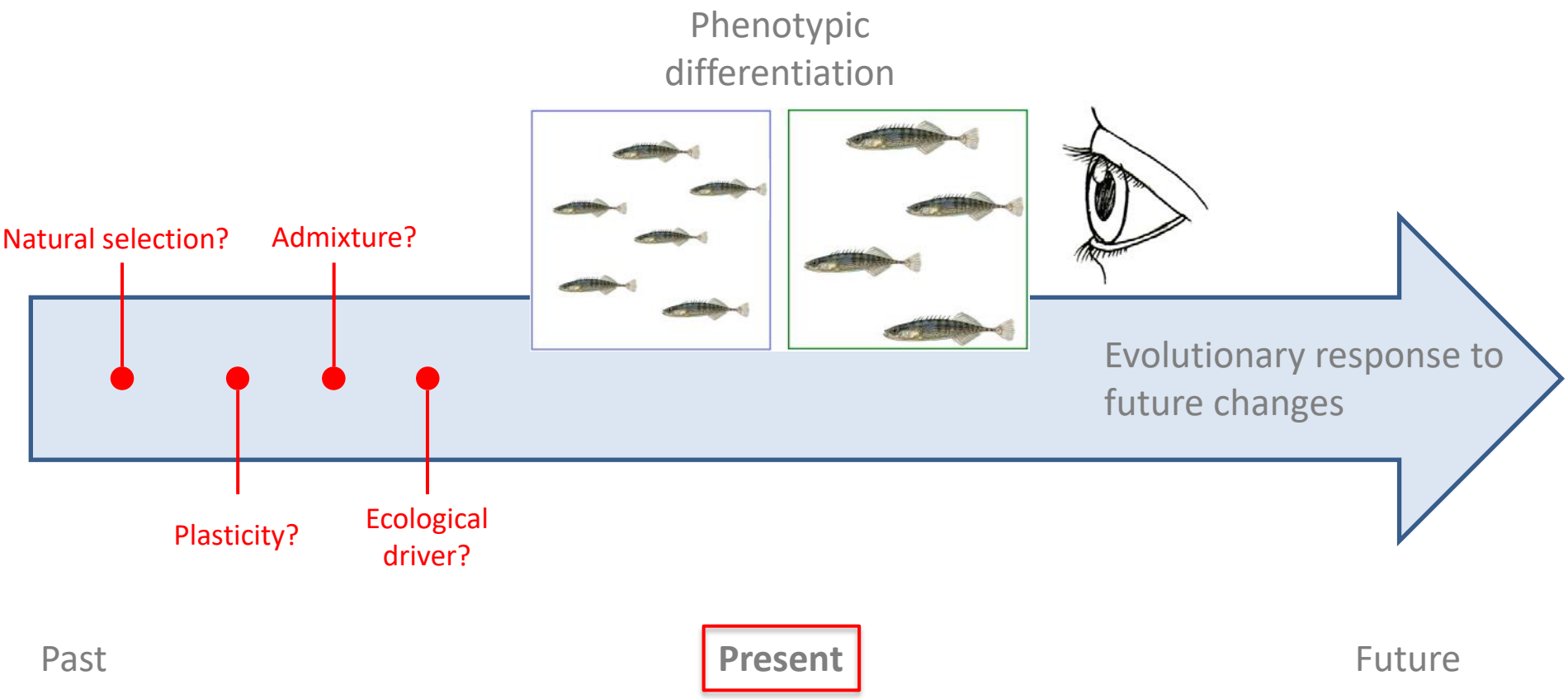
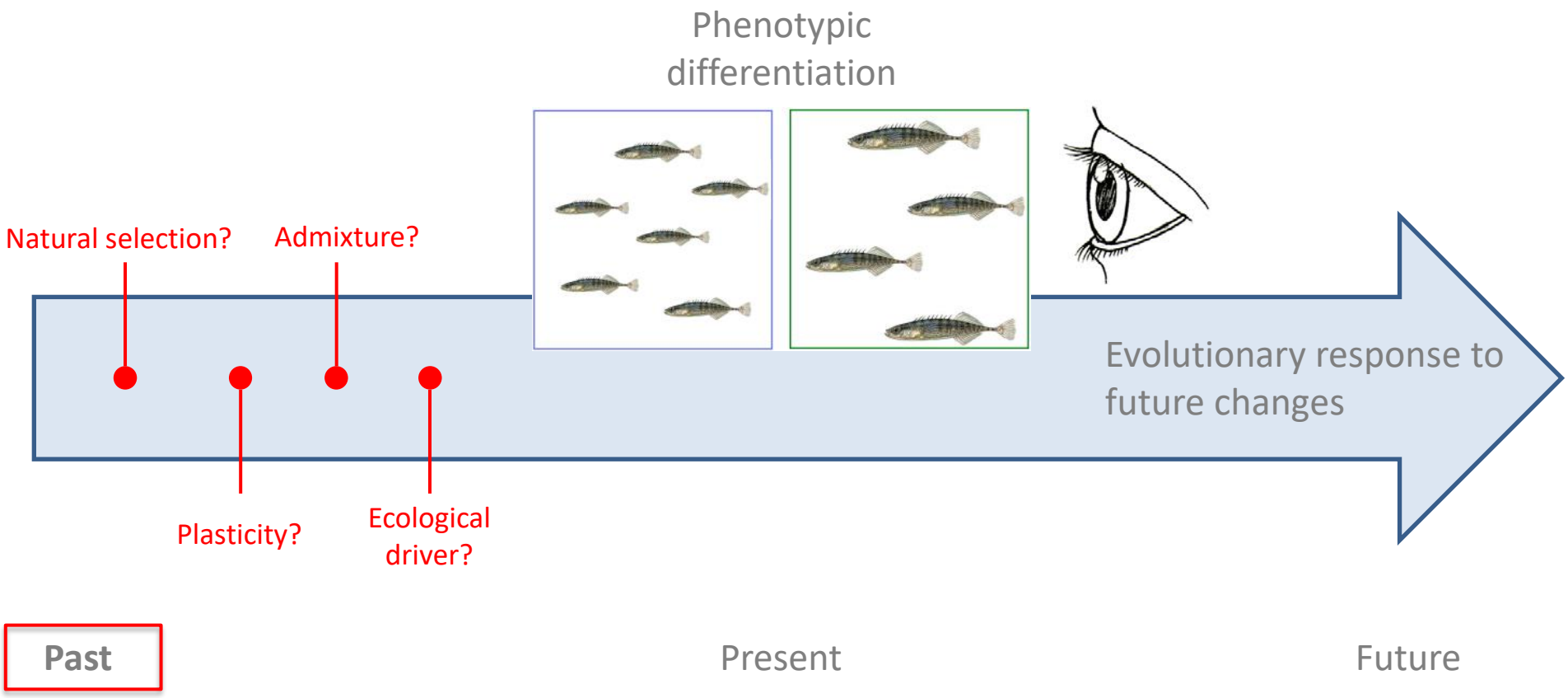
Testimony for evolution by natural selection

Experimental quantitative genetics approach



Experimental quantitative genetics approach



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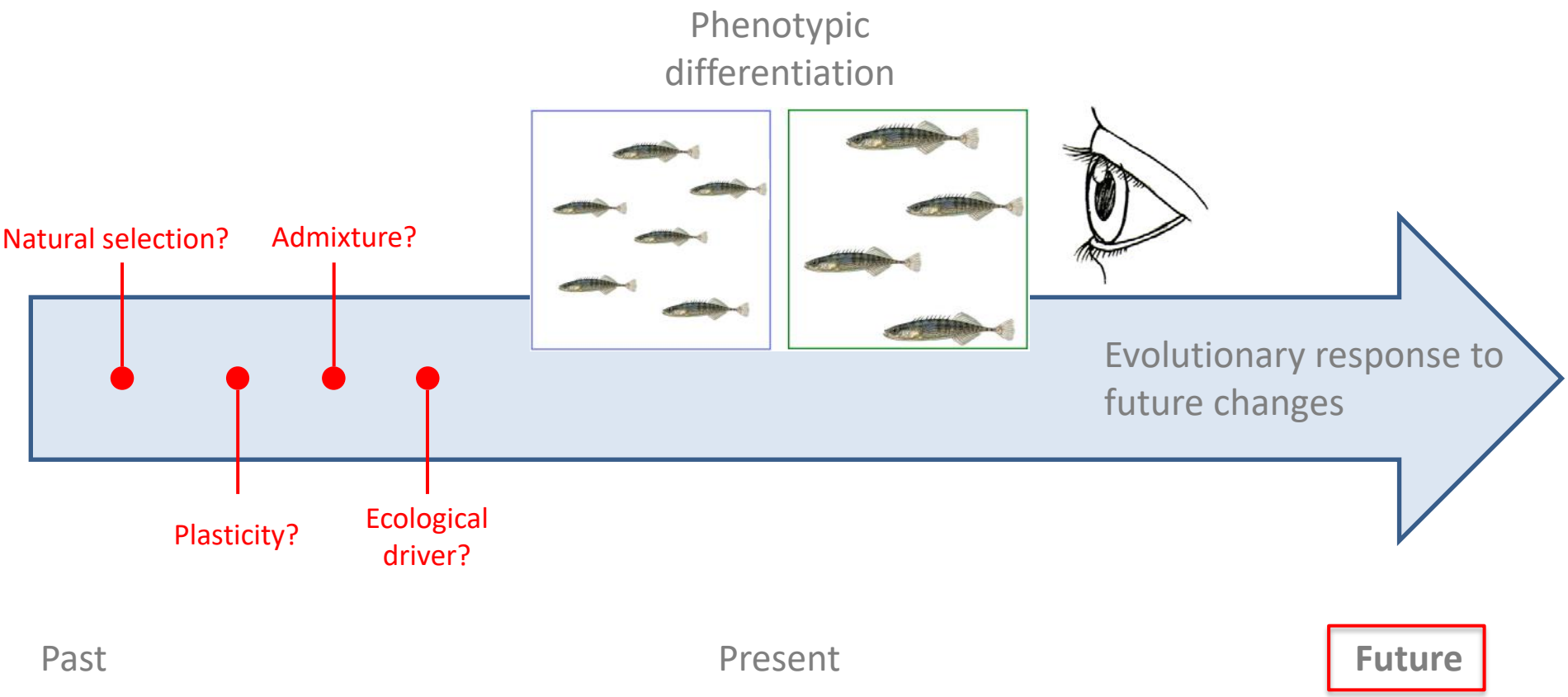
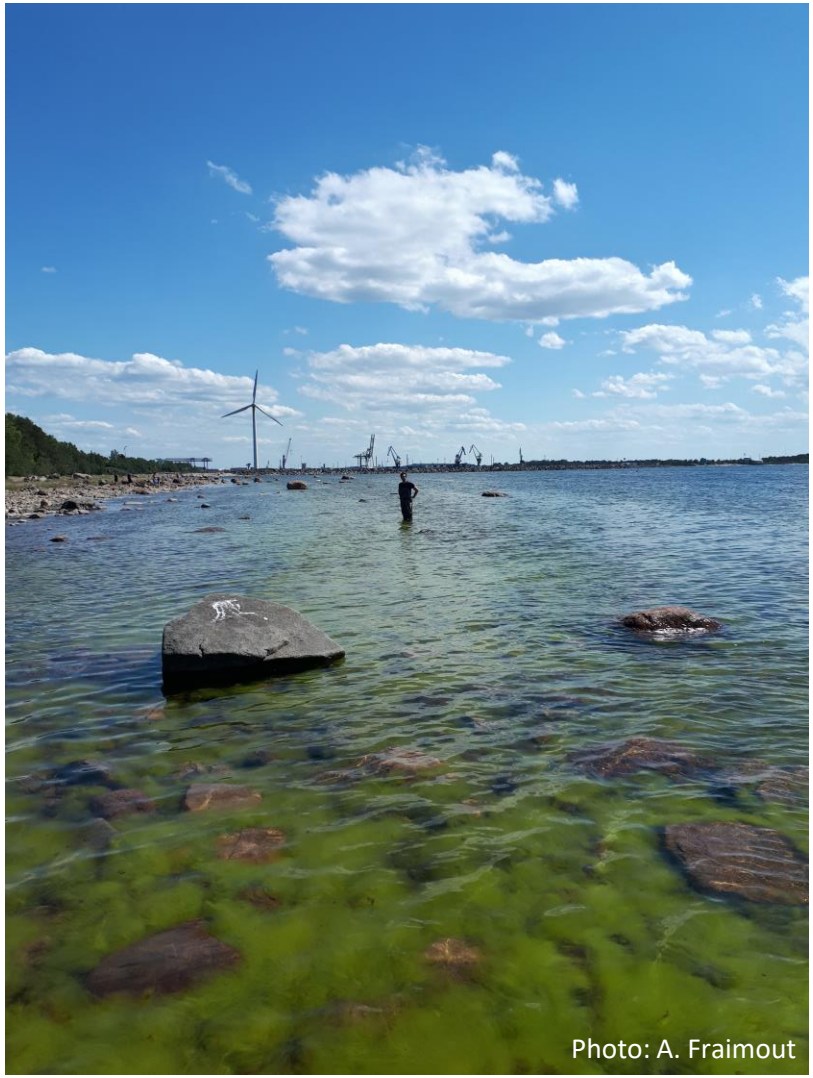


Habitat transitions

Environmental, demographic and selective changes

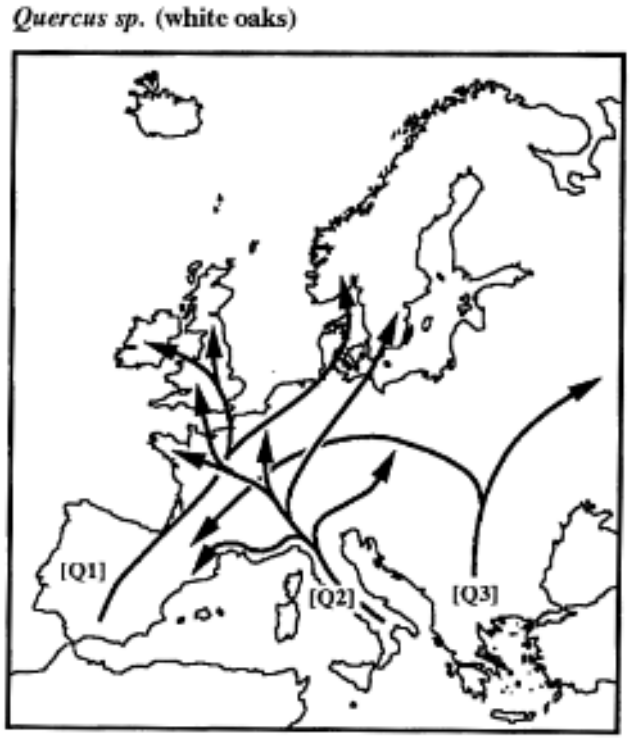


Baltic Sea (Pori, Finland)

Oulanka river (Kuusamo, Finland)

Habitat transitions

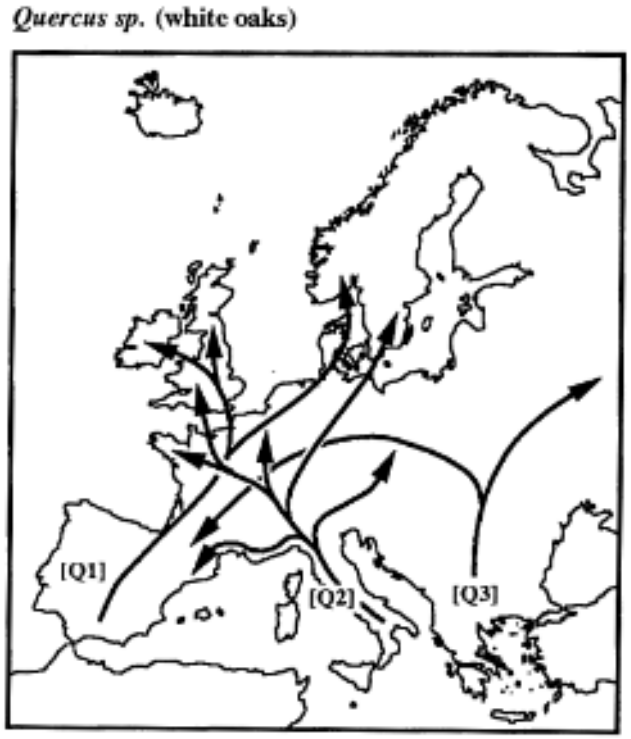
Multiple independent colonization events



Post-glacial colonization
(Taberlet *et al.* 1998)

Habitat transitions

Multiple independent colonization events



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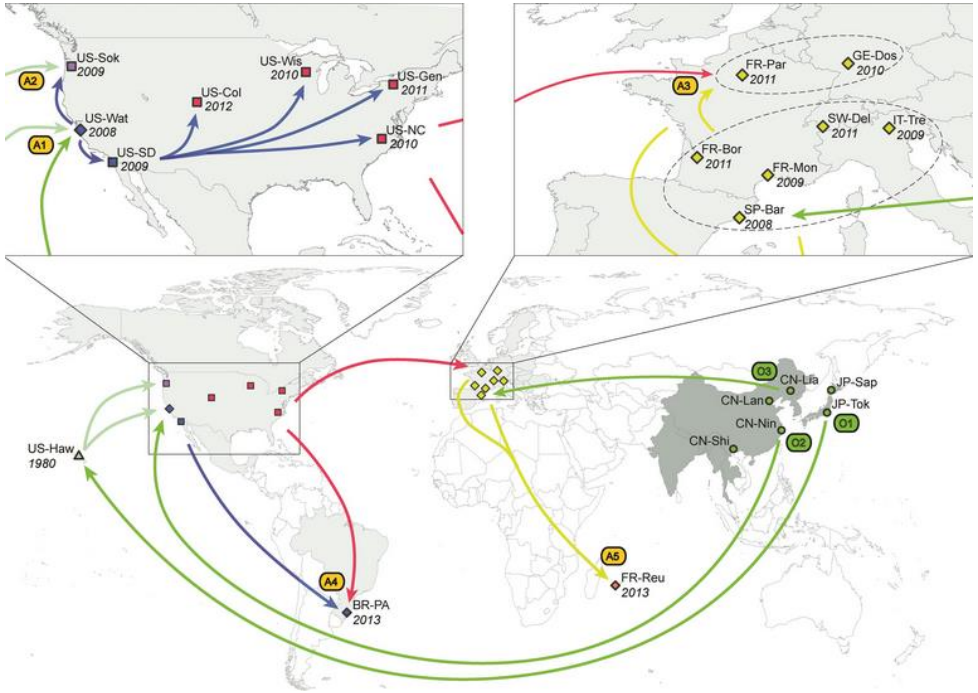
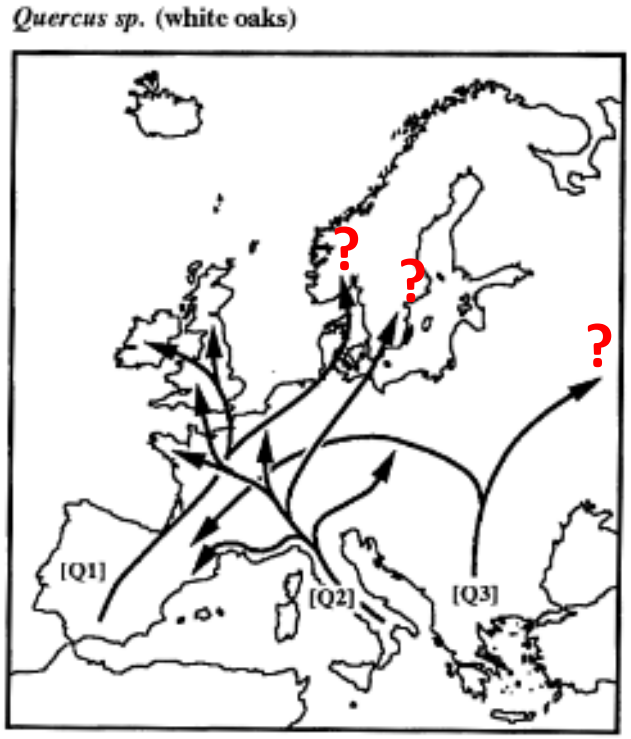


Biological invasions
(Fraimout *et al.* 2017)

Habitat transitions

Multiple independent colonization events



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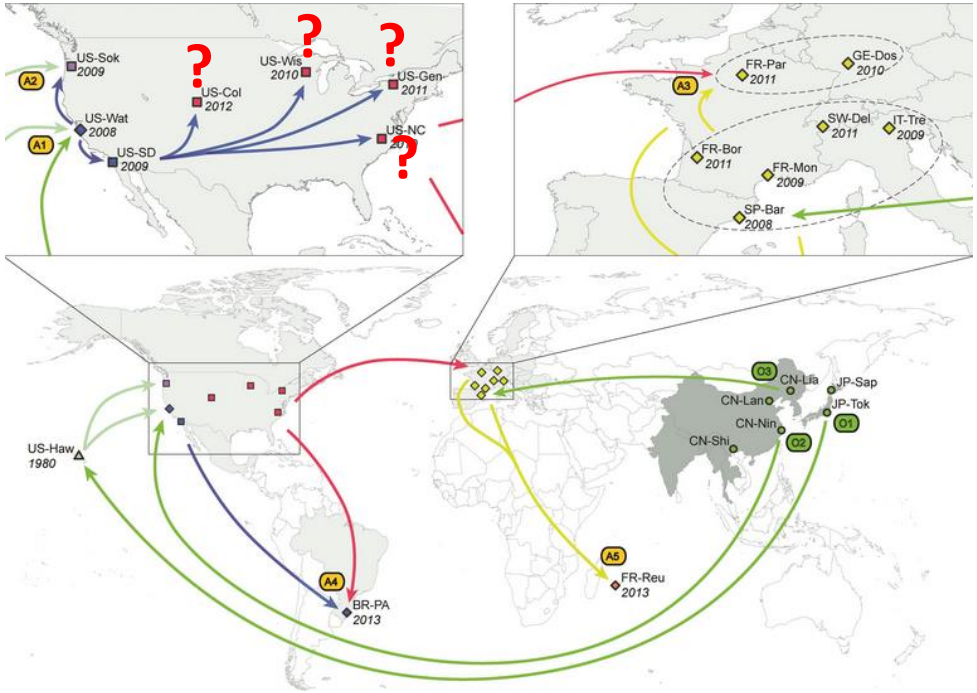


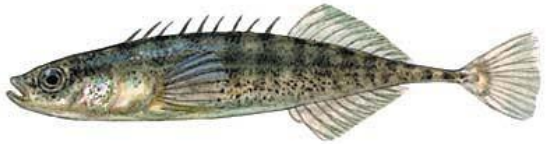
Biological invasions
(Fraimout *et al.* 2017)

Outline

Part I : Repeated evolution following post-glacial colonization of freshwater by nine-spined sticklebacks

– Parallel evolution of behaviour

– (non)Parallel evolution?



Pungitius pungitius

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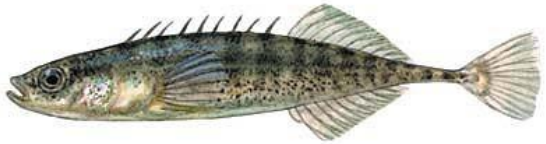

Pungitius pungitius

Part II : Repeated evolution following multiple invasions of freshwater by copepods

– Genetic bases of salinity adaptation

Eurytemora affinis

Glossary

Repeated evolution: same evolutionary output occuring multiple times

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Parallel phenotypic evolution: evolution of similar phenotypes between multiple populations **of the same species**

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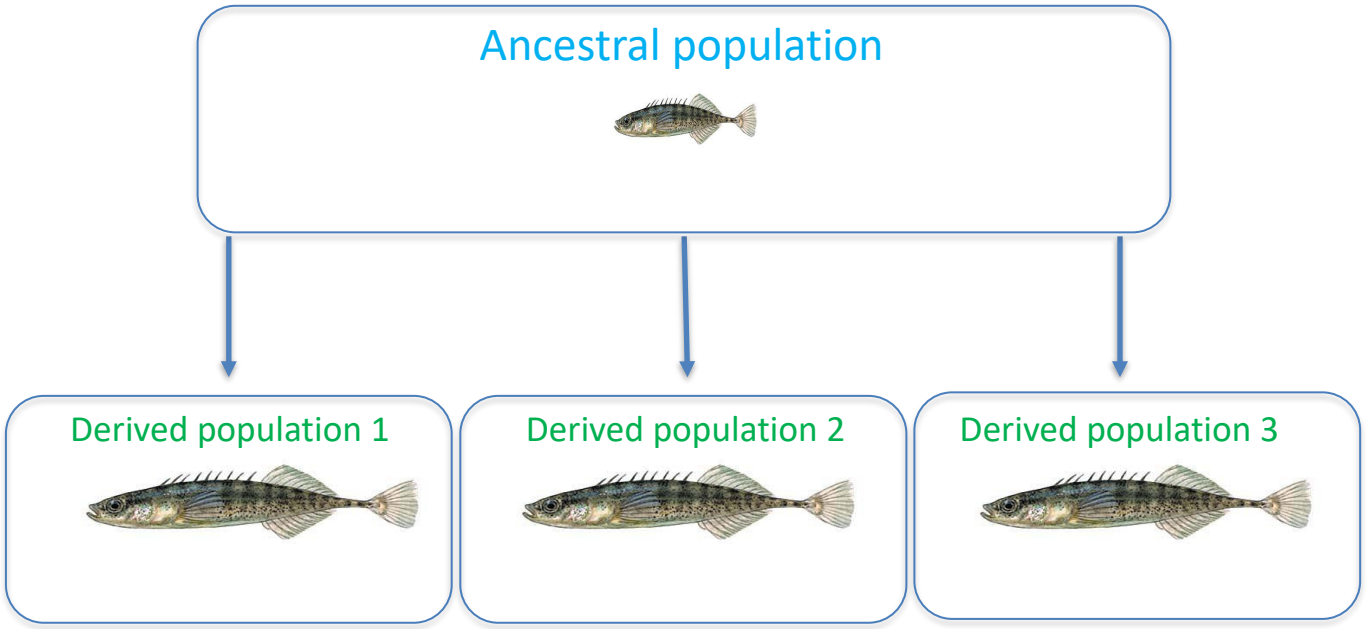
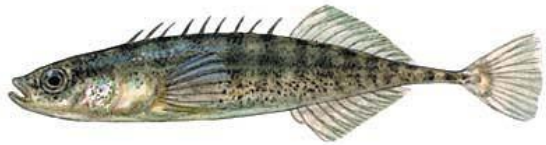


Part I : Repeated evolution following post-glacial colonization of freshwater by nine-spined sticklebacks



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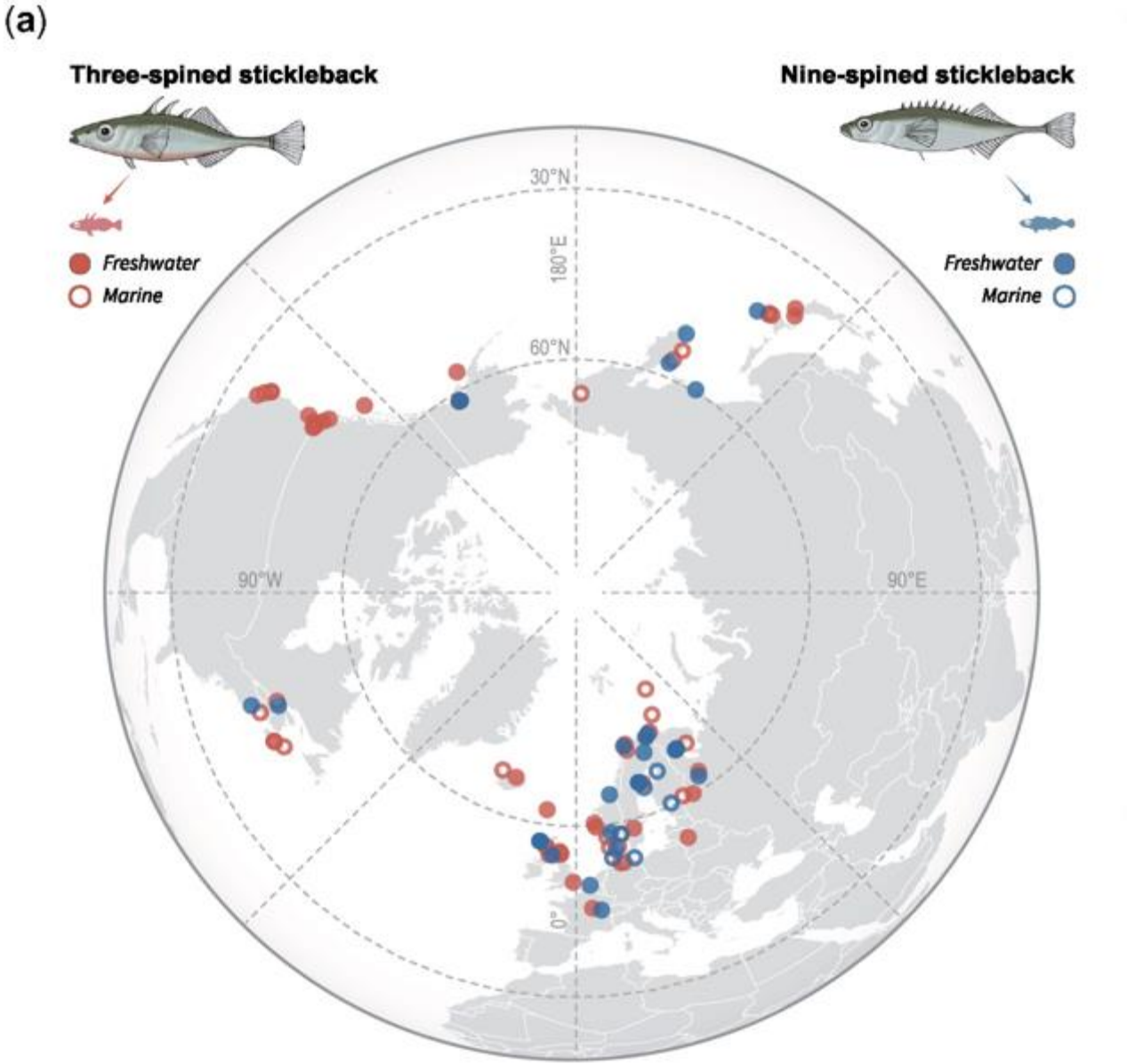
I – The nine-spined stickleback



Fang *et al.* 2021

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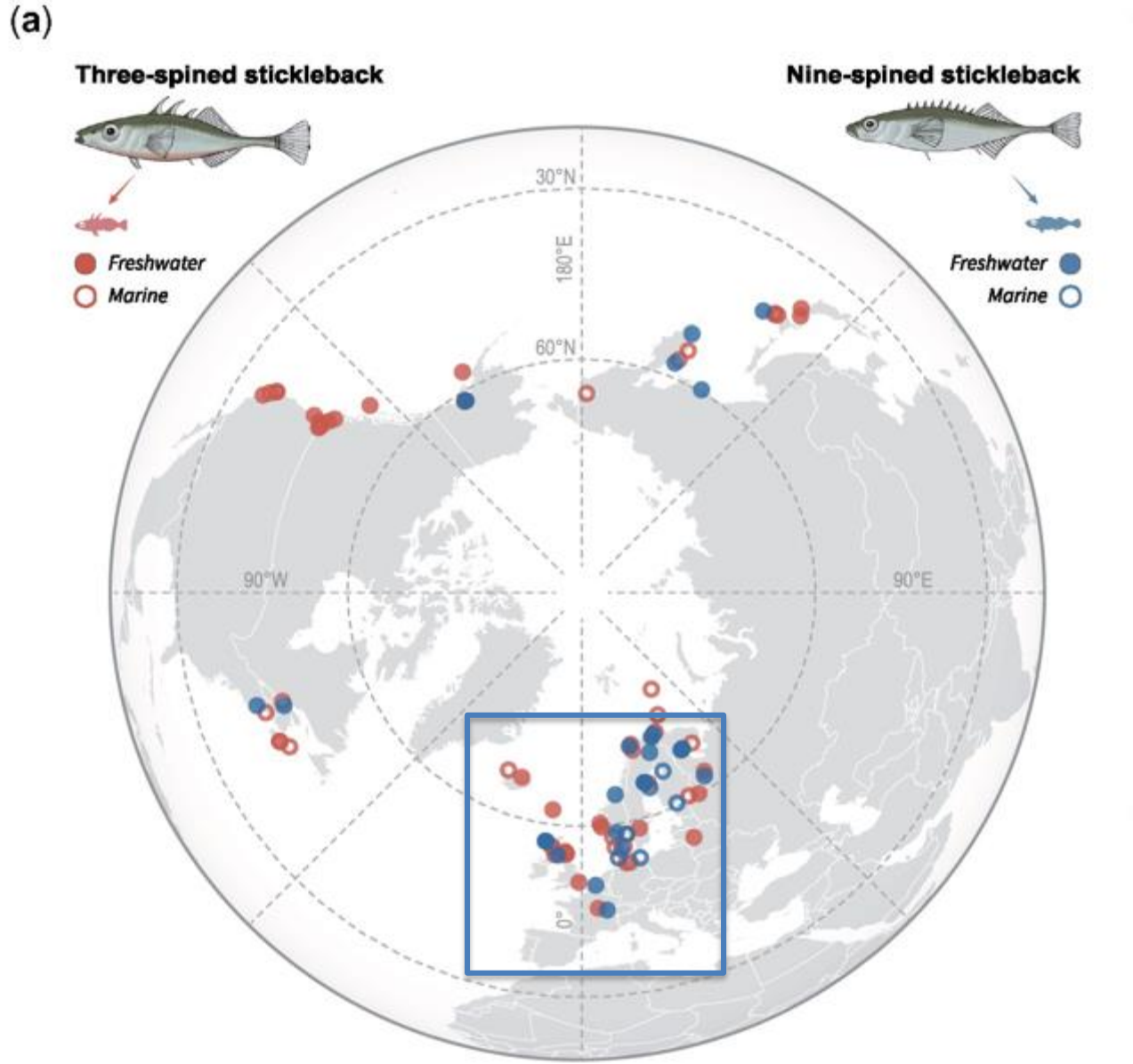

Fang *et al.* 2021

I – The nine-spined stickleback

Pungitius pungitius

Teacher *et al.* 2011

I – Habitat transition

Pungitius pungitius

Marine habitat

Photo: A. Fraimout

Teacher *et al.* 2011

I – Habitat transition

Pungitius pungitius

Freshwater pond

Marine habitat

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I – Repeated phenotypic evolution

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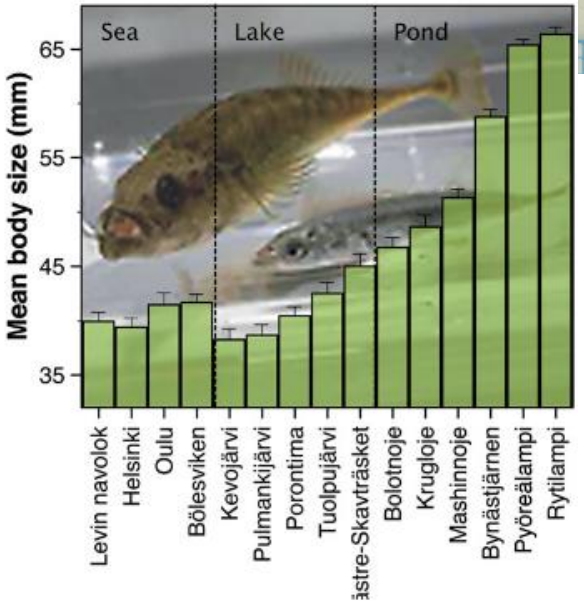

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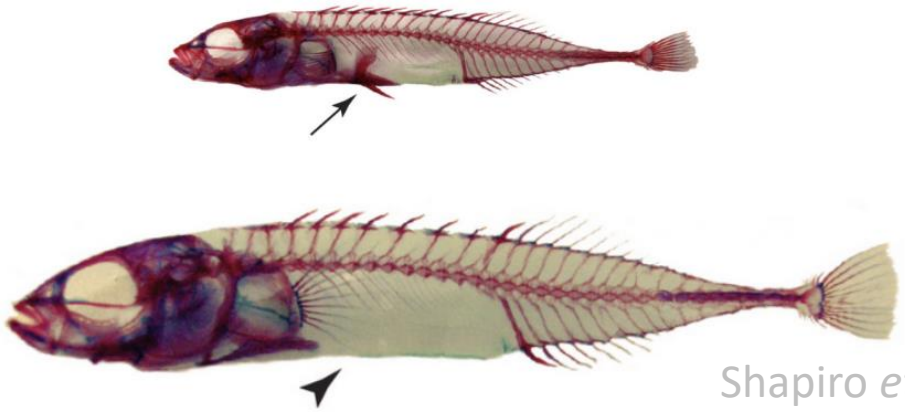
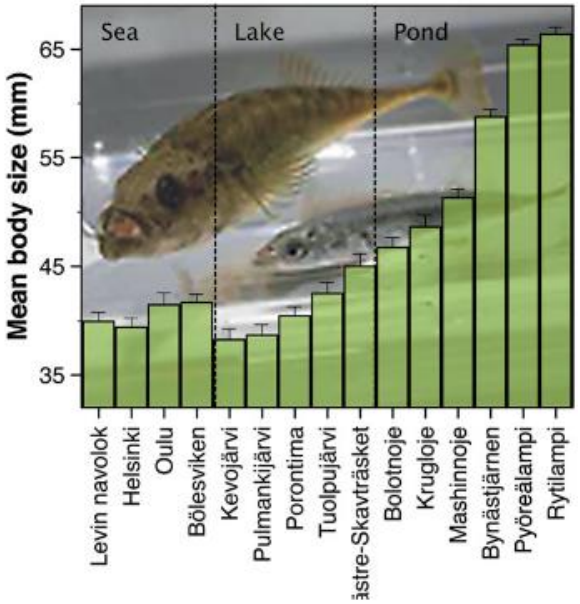
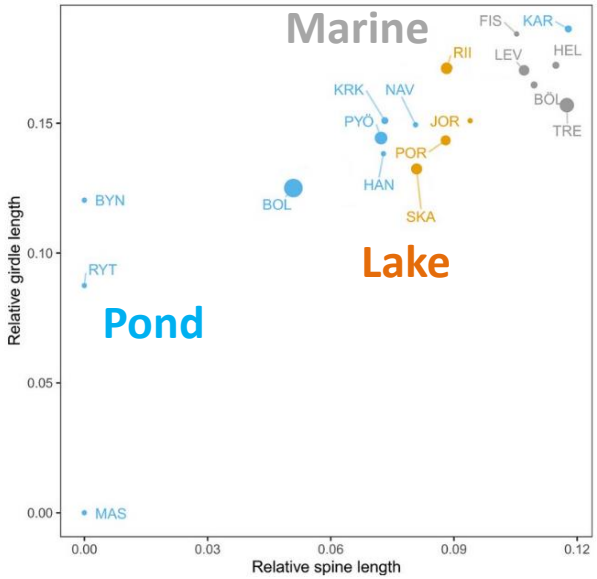


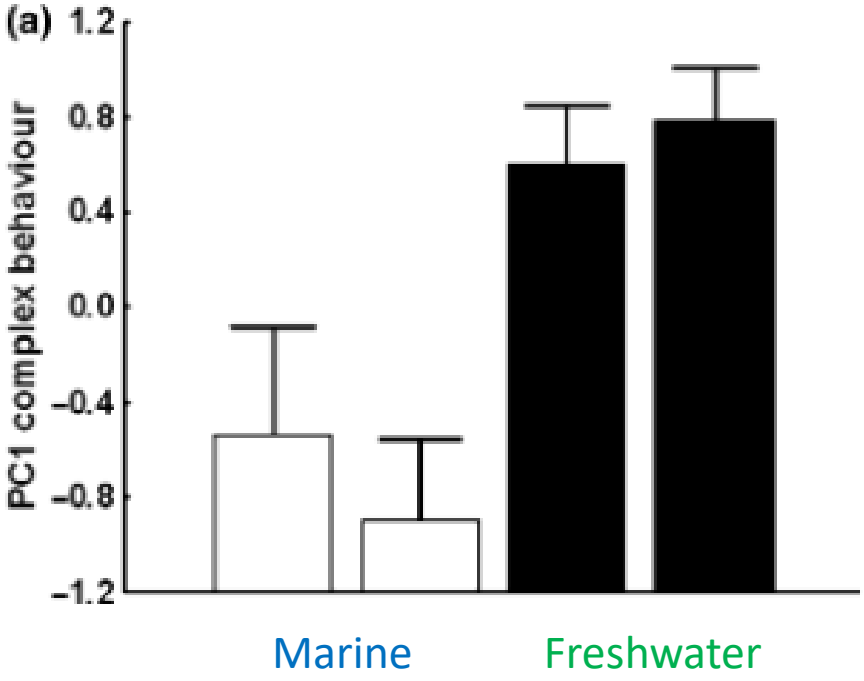
Shapiro *et al.* (2009)





Kemppainen *et al.* 2021

I – Repeated phenotypic evolution



Common garden experiment showed **marine** individuals are **shy and peaceful**, while **pond** individuals are **bold and aggressive**

Herczeg *et al.* (2009)

What drove behaviour evolution in freshwater *P. pungitius*?

I – Habitat differentiation

Pungitius pungitius

Freshwater pond

Marine habitat

Teacher *et al.* 2011

I – Habitat differentiation

Pungitius pungitius

Freshwater pond

Marine habitat

Teacher *et al.* 2011

I – Research question

Did predation release drive repeated evolution of behaviour in *P. pungitius*?

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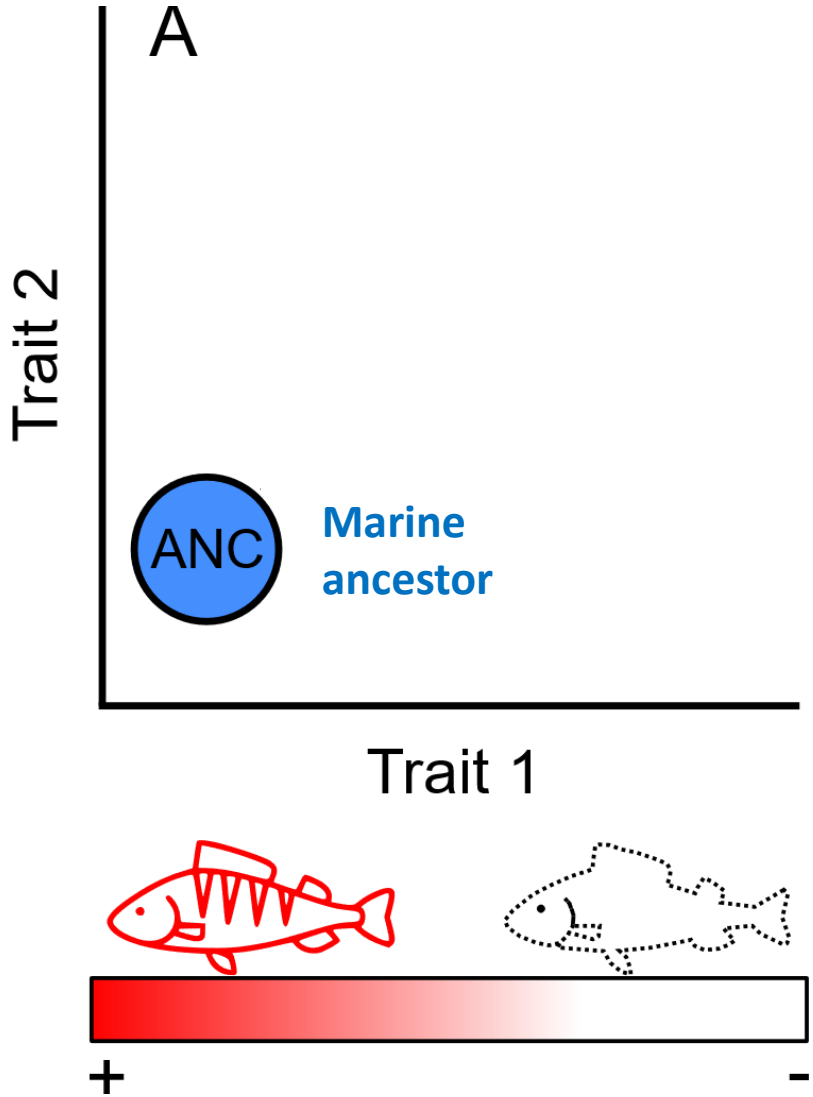
Did predation release drive repeated evolution of behaviour in *P. pungitius*?

Did behaviour evolve in parallel among freshwater populations?

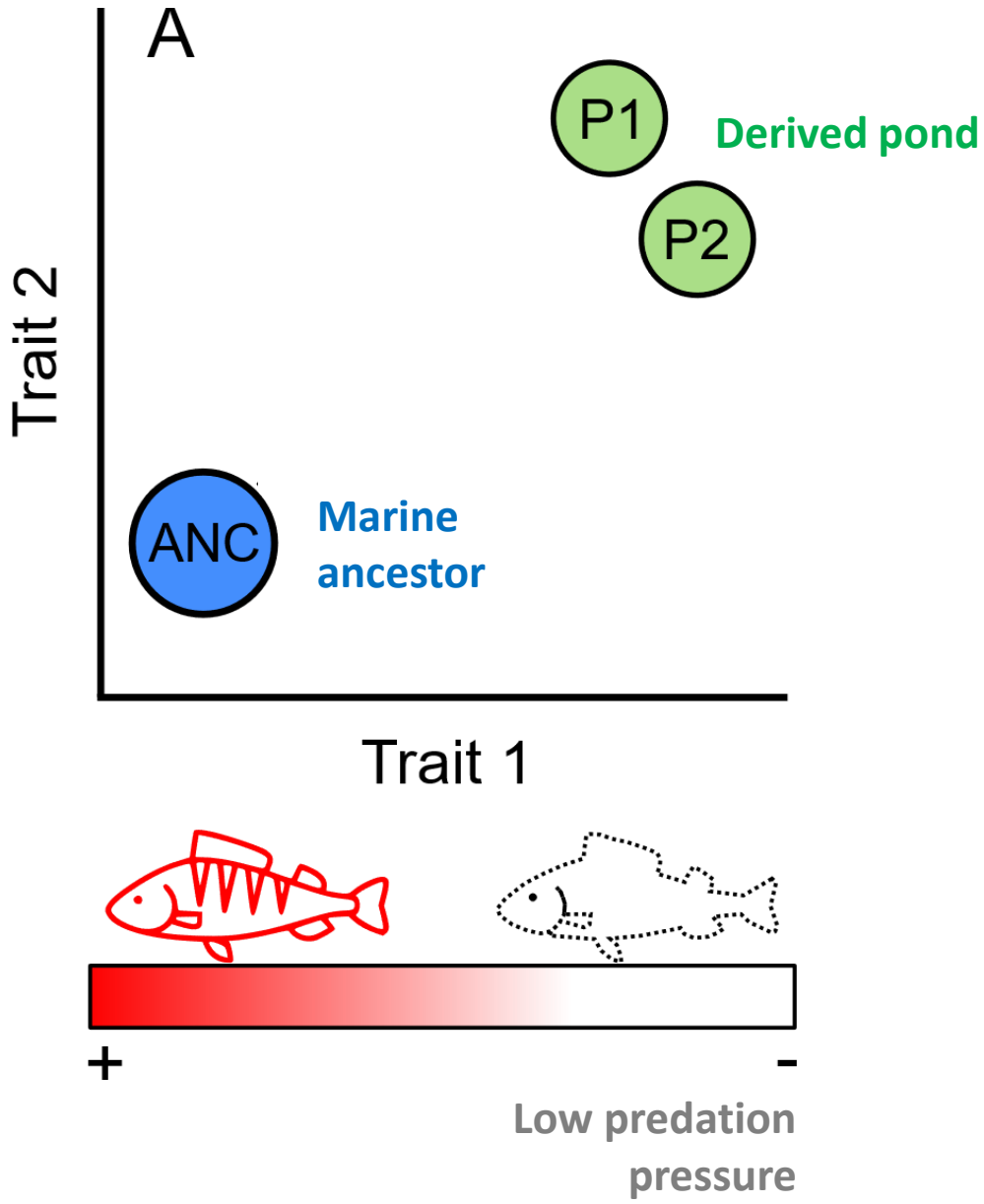
I – A geometric approach to parallel evolution

I – Theory



Fraimout, Päiviö & Merilä 2022

I – Theory



Fraimout, Päiviö & Merilä 2022

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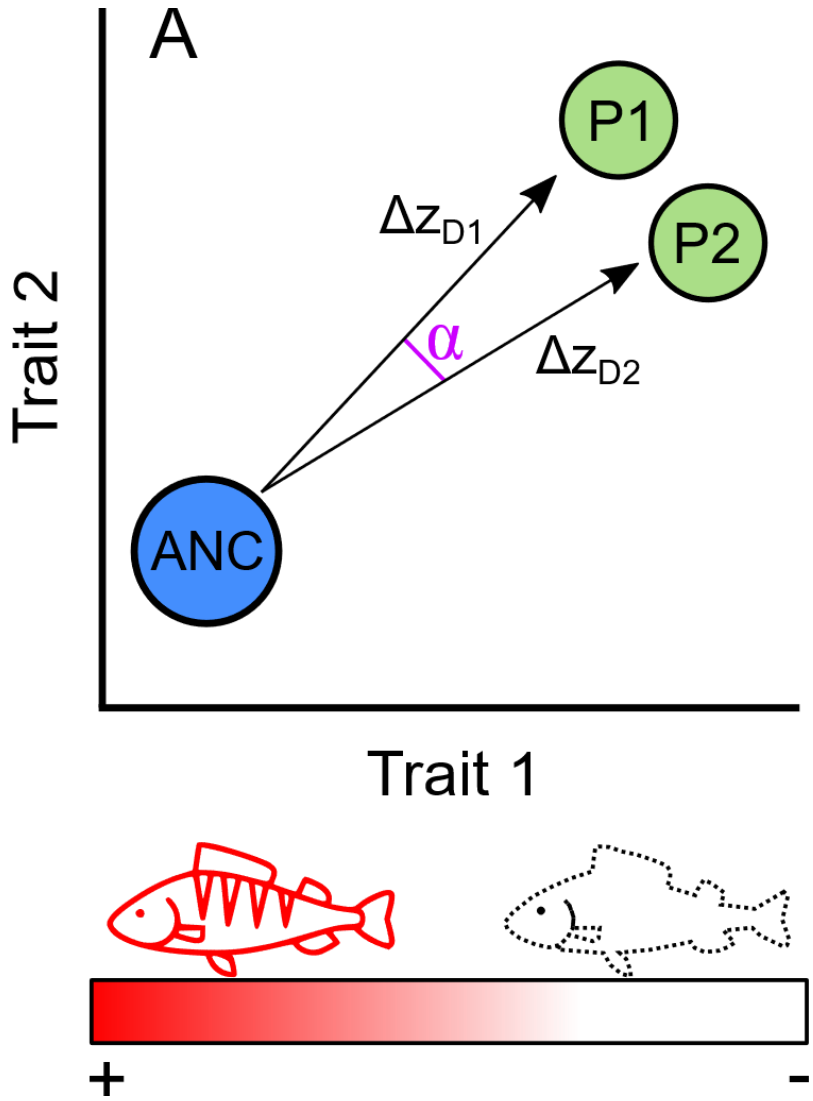
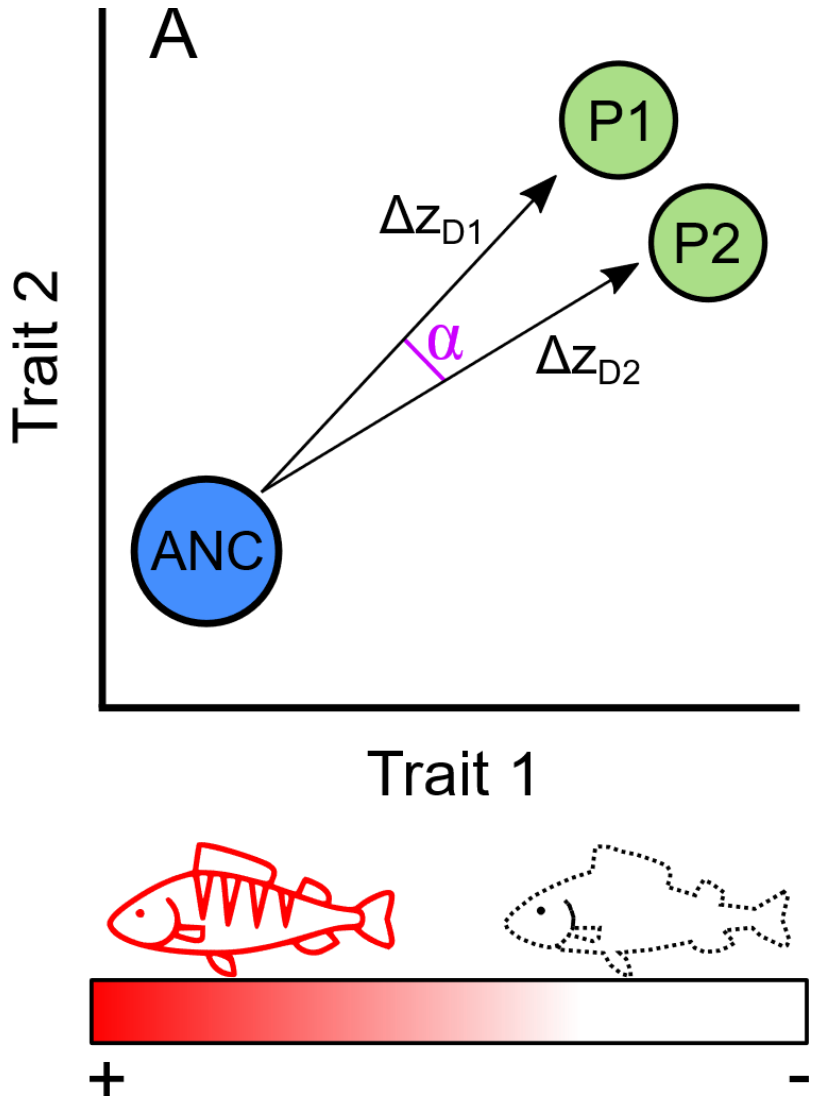


Δz_D = vector of phenotypic divergence

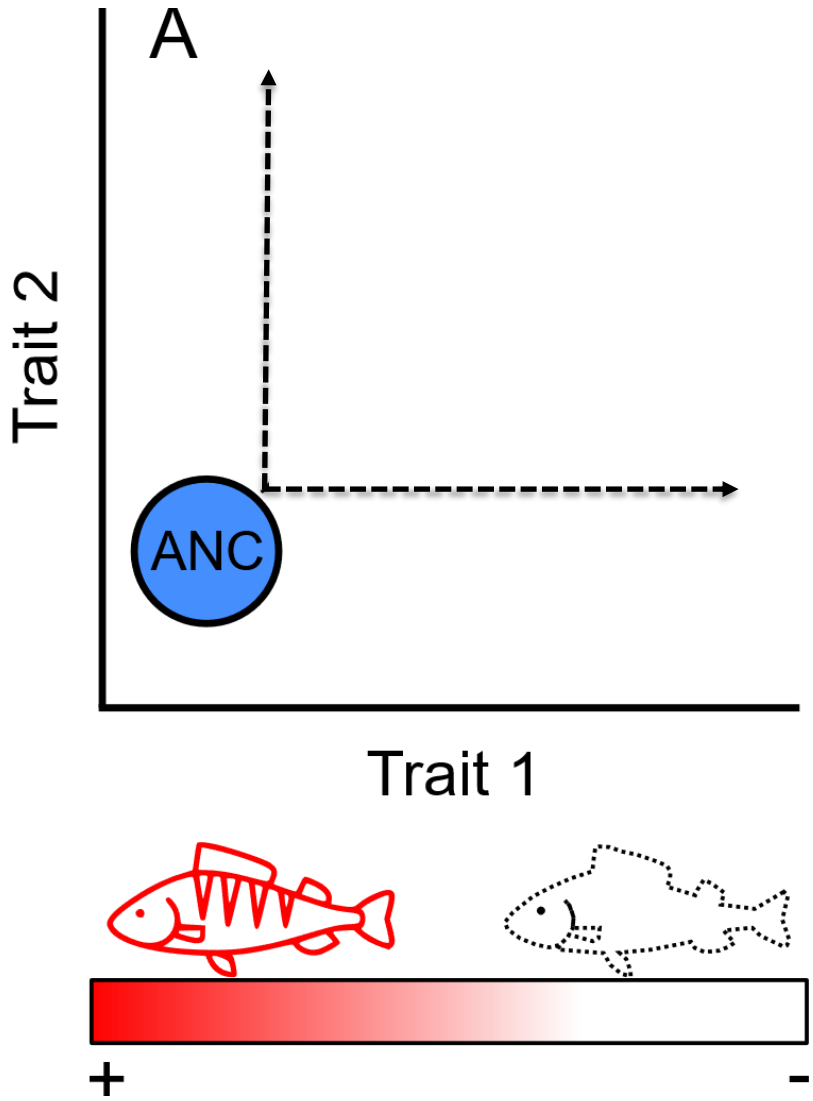
I – Theory



Δz_D = vector of phenotypic divergence

α = angle between divergence vectors

I – Theory

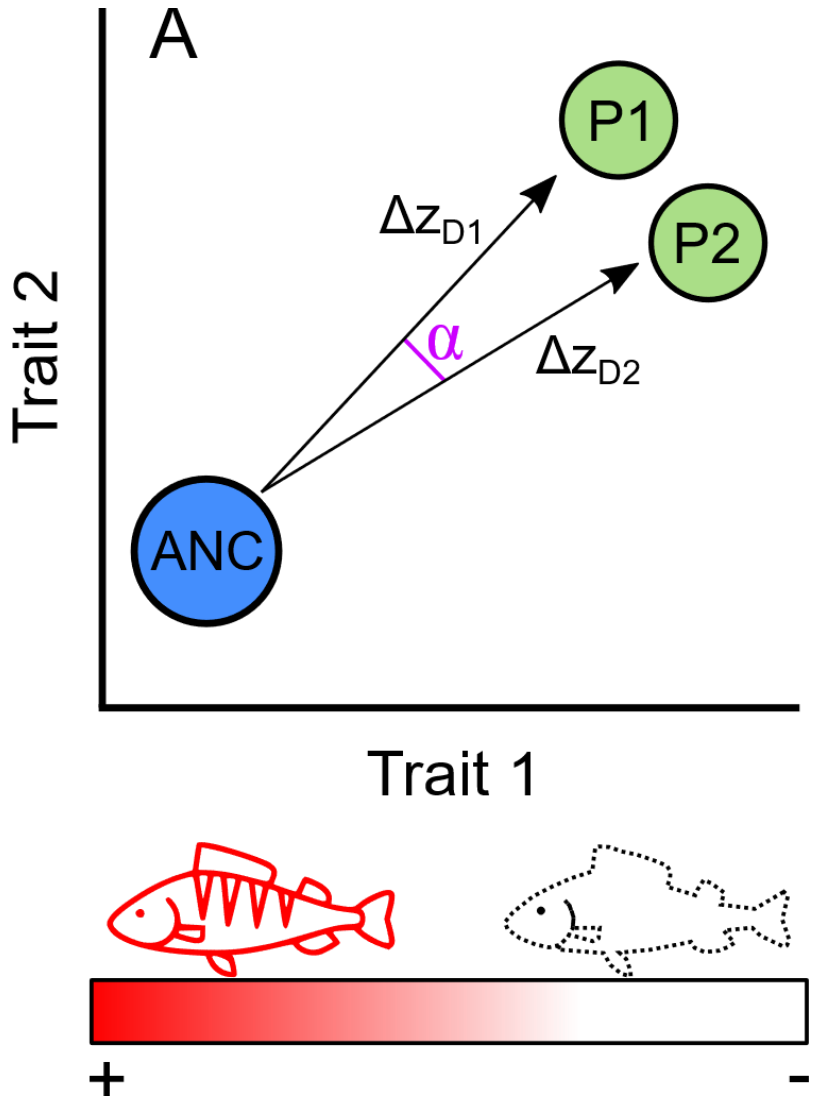


Δz_D = vector of phenotypic divergence

α = angle between divergence vectors

H_0: α = 90° → phenotypic evolution in random directions

I – Theory



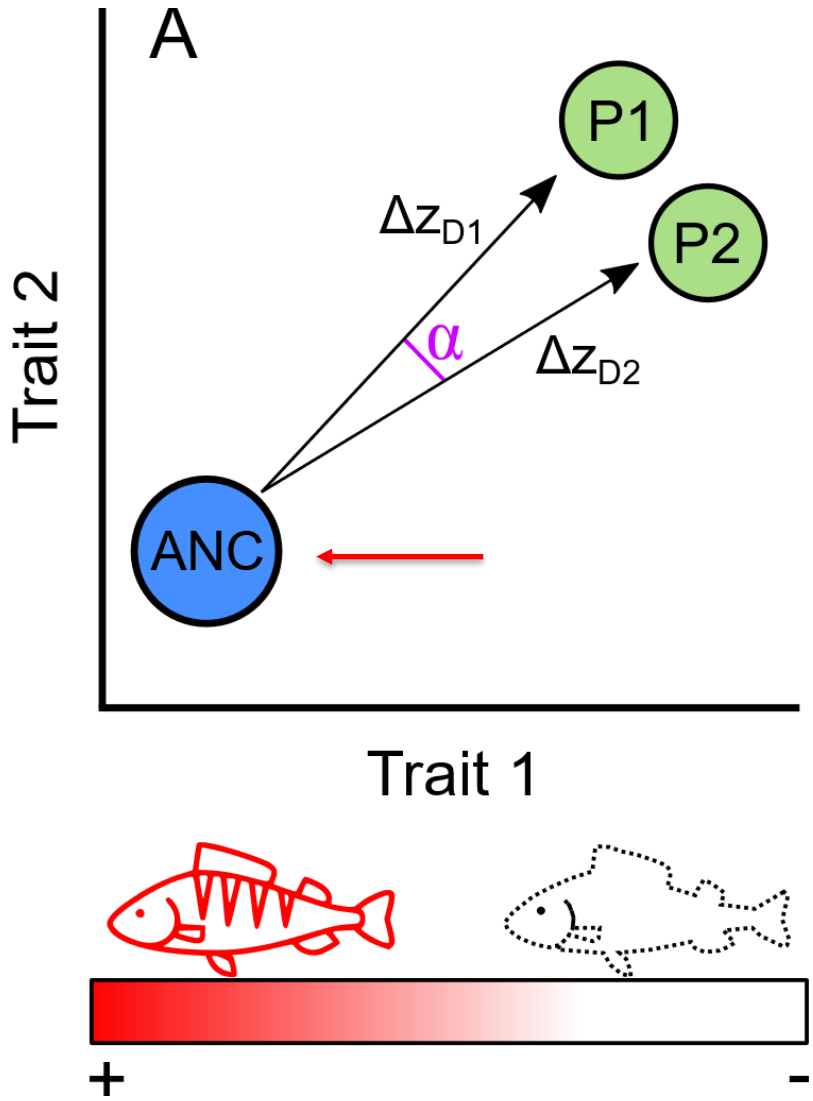
Δz_D = vector of phenotypic divergence

α = angle between divergence vectors

H_0: α = 90° → phenotypic evolution in random directions

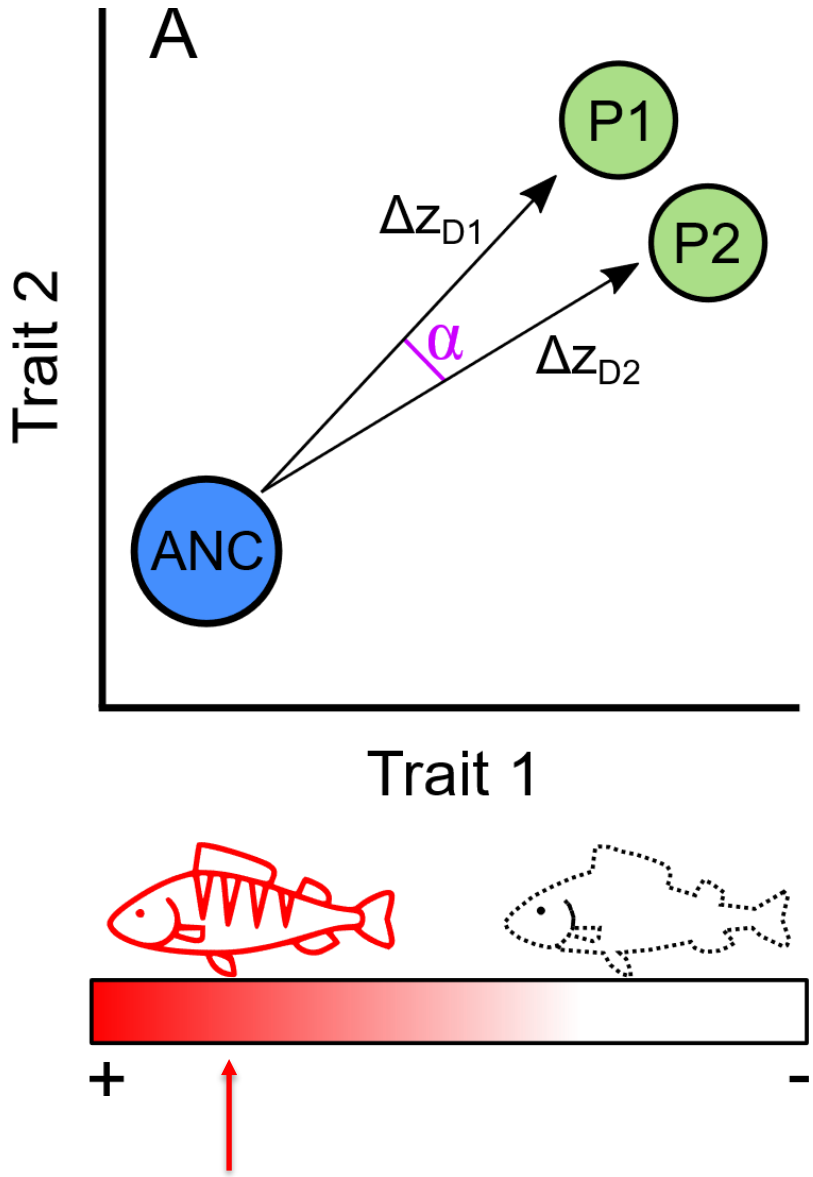
H_1: α = 0° → parallel evolution

I – Practice



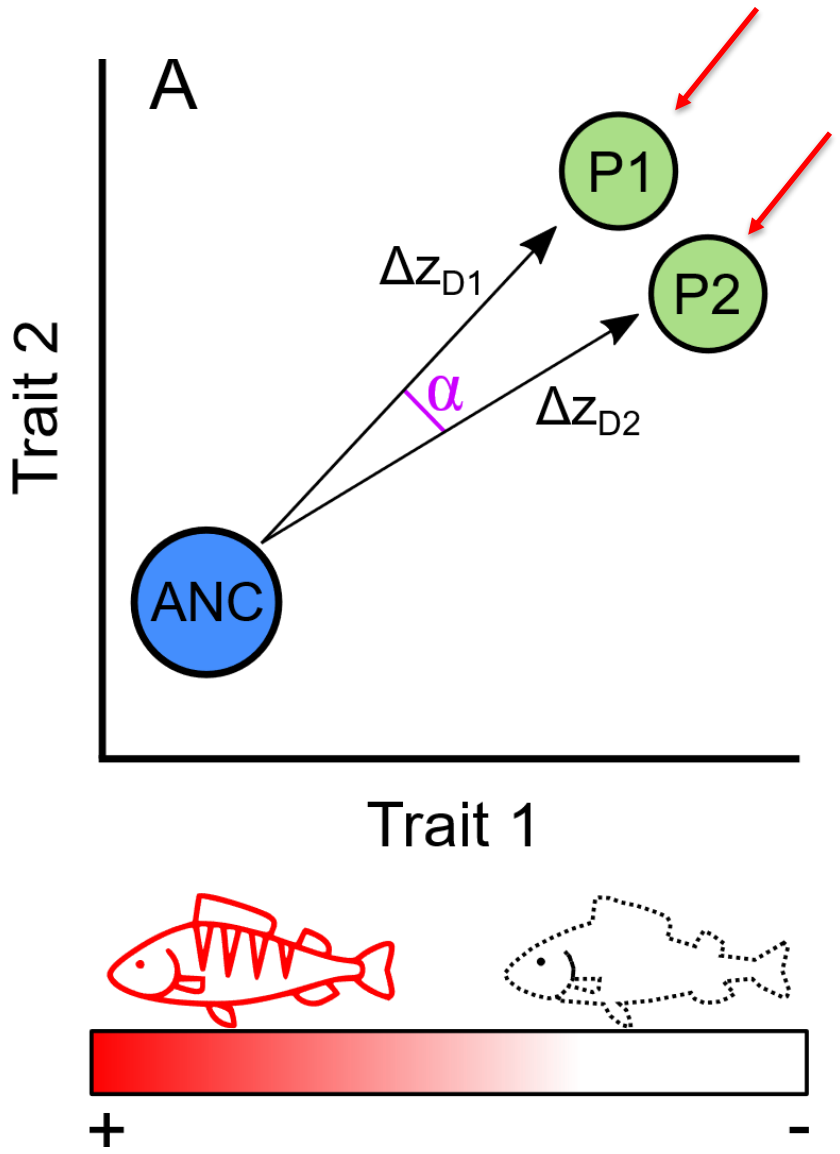
Sample marine ancestors

I – Practice



Sample marine ancestors
Experimental tests of behaviour
under predation risk

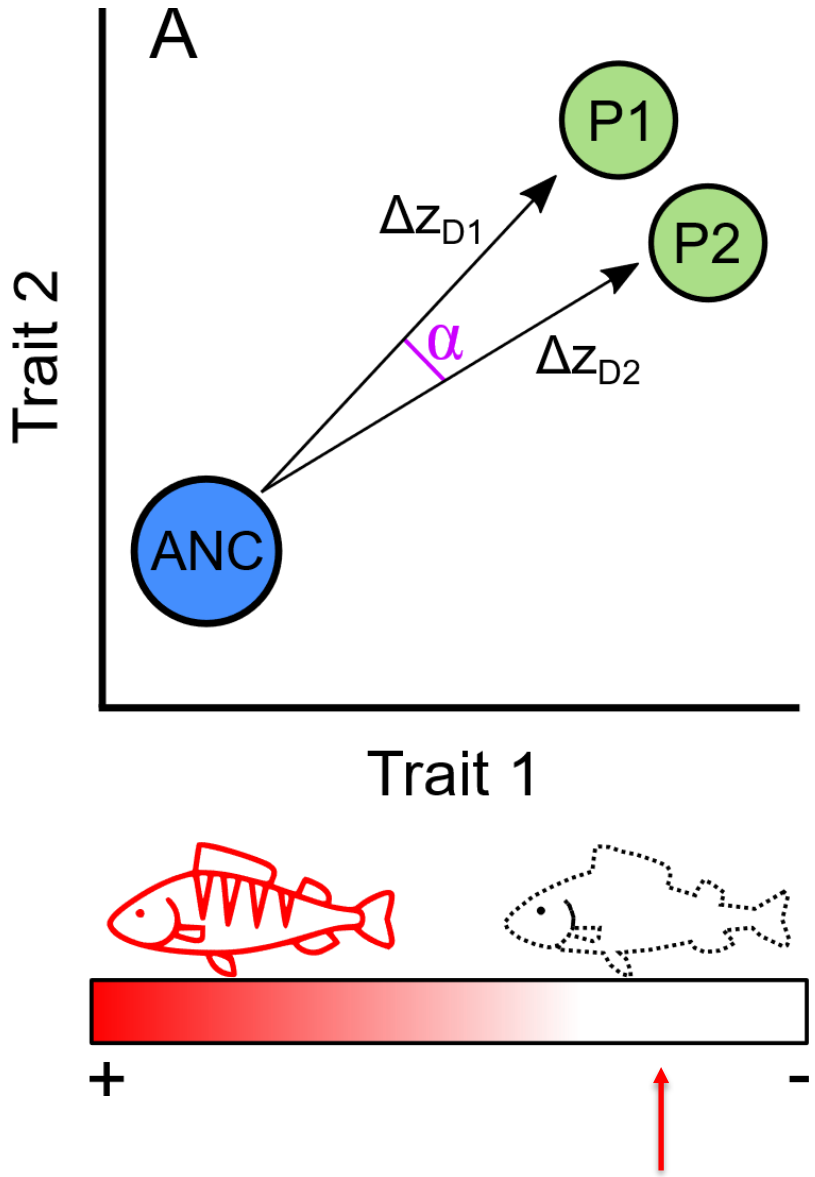
I – Practice



Sample marine ancestors
Experimental tests of behaviour
under predation risk

Sample replicate freshwater populations

I – Practice

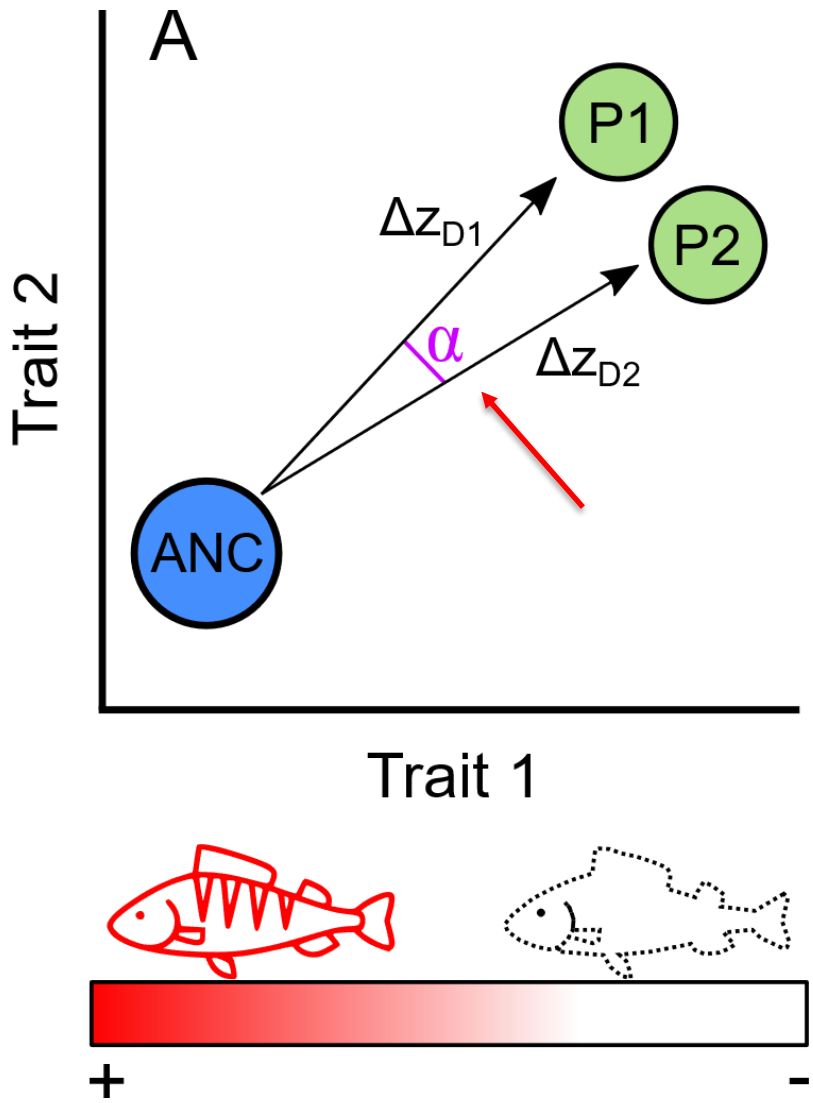


Sample marine ancestors
Experimental tests of behaviour
under predation risk

Sample replicate freshwater populations
Experimental tests of behaviour
without predation

Fraimout, Päiviö & Merilä 2022

I – Practice



Sample marine ancestors
Experimental tests of behaviour
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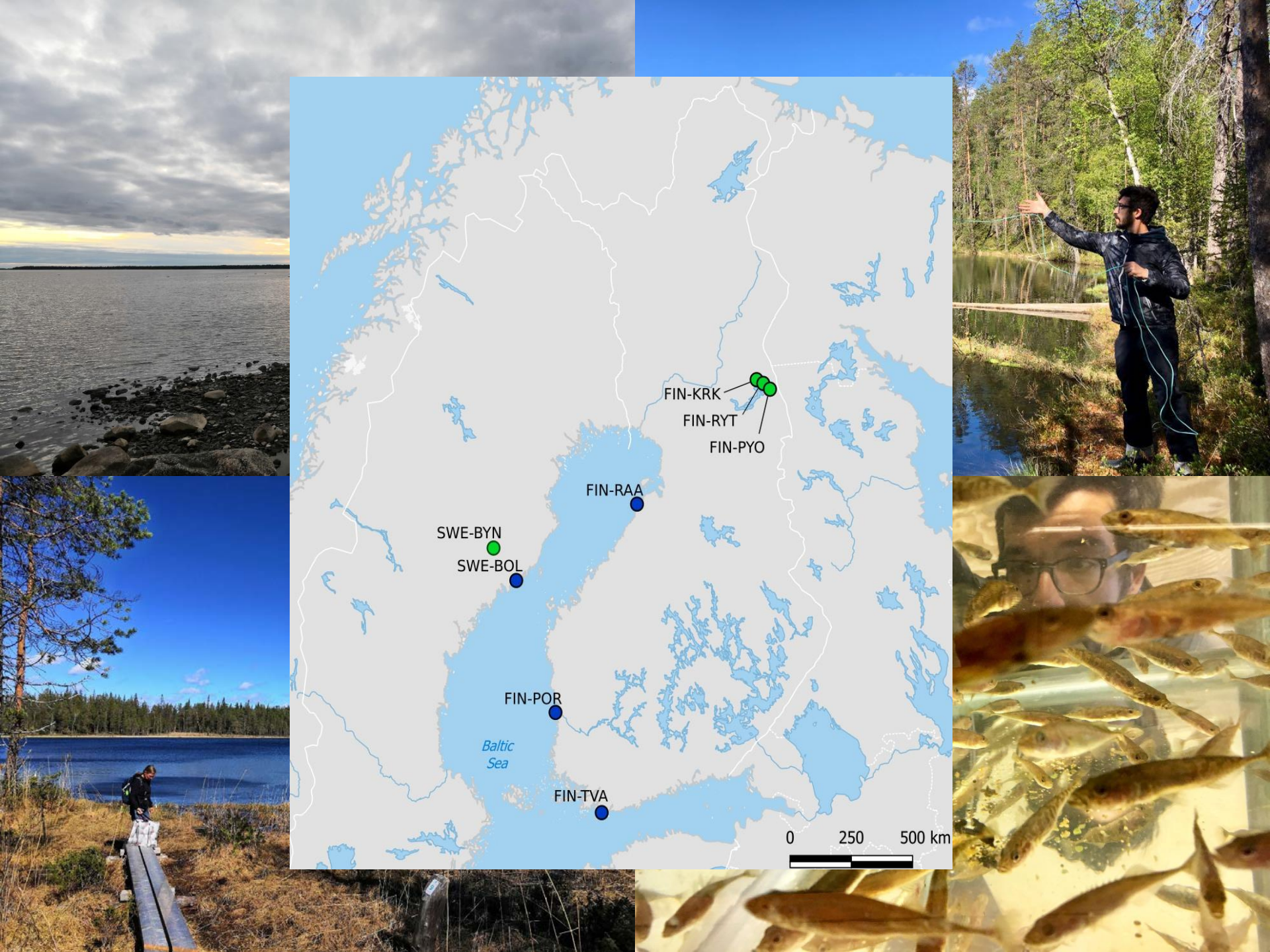
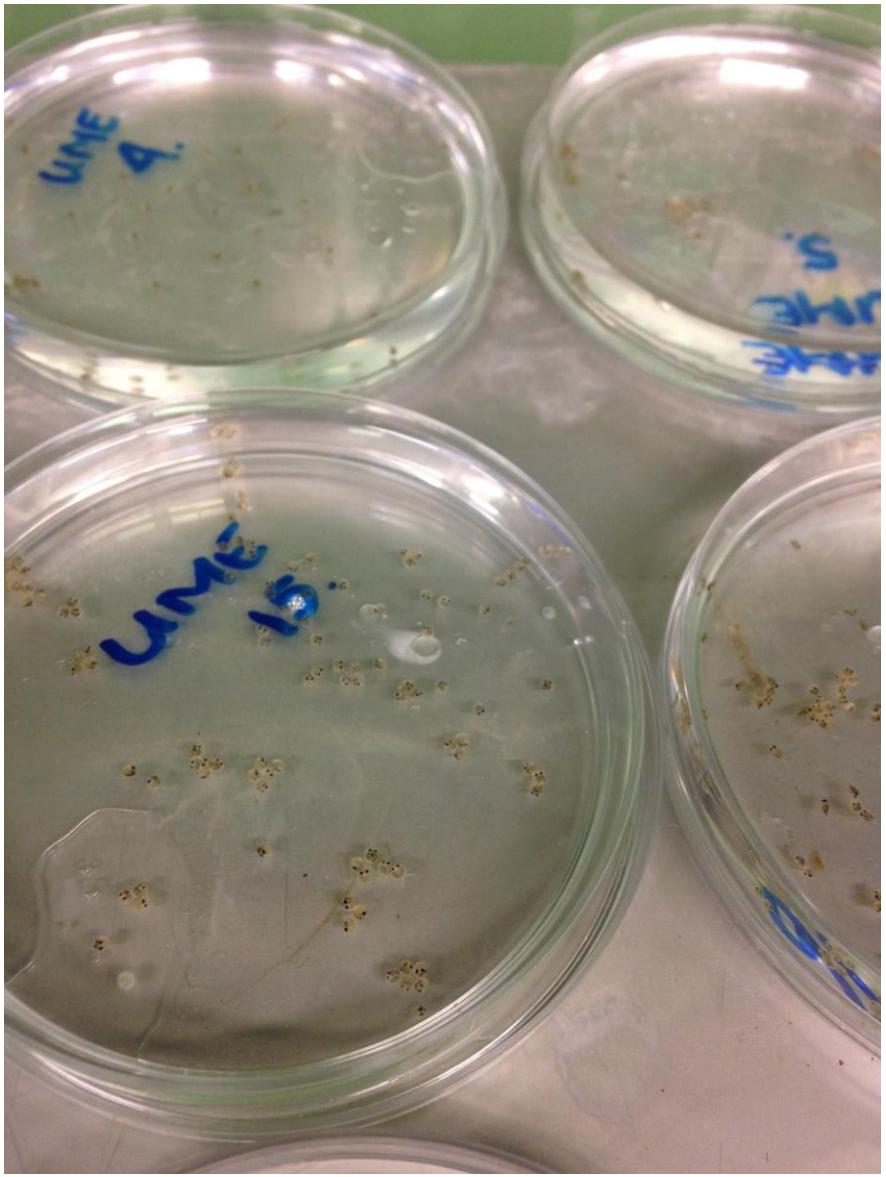
Sample replicate freshwater populations
Experimental tests of behaviour
without predation

Calculate **α** between phenotypic divergence vectors





FIN-KRK
FIN-RYT
FIN-PYO
FIN-RAA
SWE-BYN
SWE-BOL
FIN-POR
Baltic
Sea
FIN-TVA
0
250
500 km

I – Common garden rearing



In vitro fertilization

Rearing in controlled tanks

I – Common garden rearing

Reduced effects of environmental variance on phenotypic variance

Rearing in controlled tanks

I – Common garden rearing

Reduced effects of environmental variance on phenotypic variance

Measure genetically based differences among populations

Rearing in controlled tanks

I – Common garden rearing

Reduced effects of environmental variance on phenotypic variance

Measure genetically based differences among populations

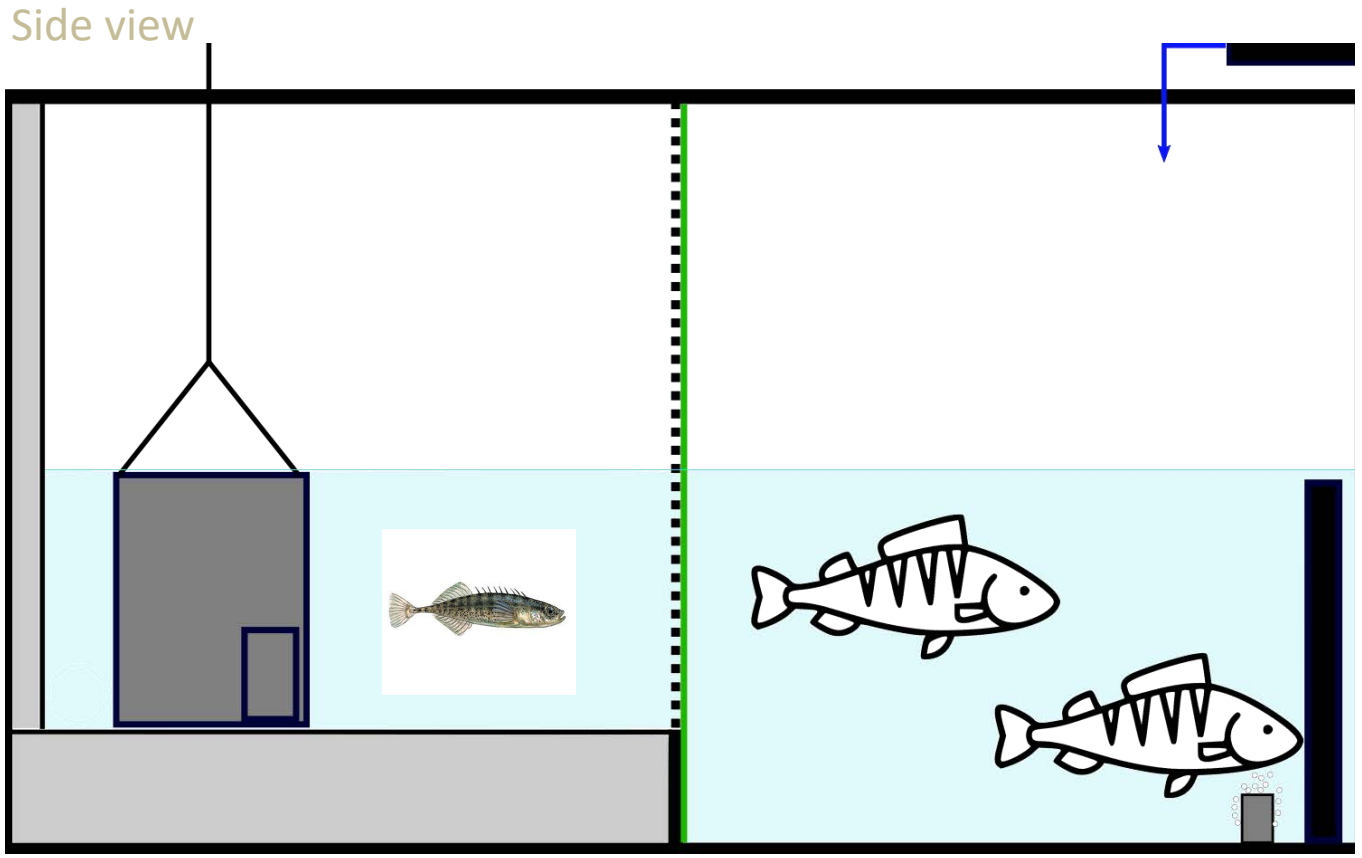
Individuals phenotyped at the same age

Rearing in controlled tanks

I – Experimental setup

Elisa Päiviö, MSc

I – Experimental setup



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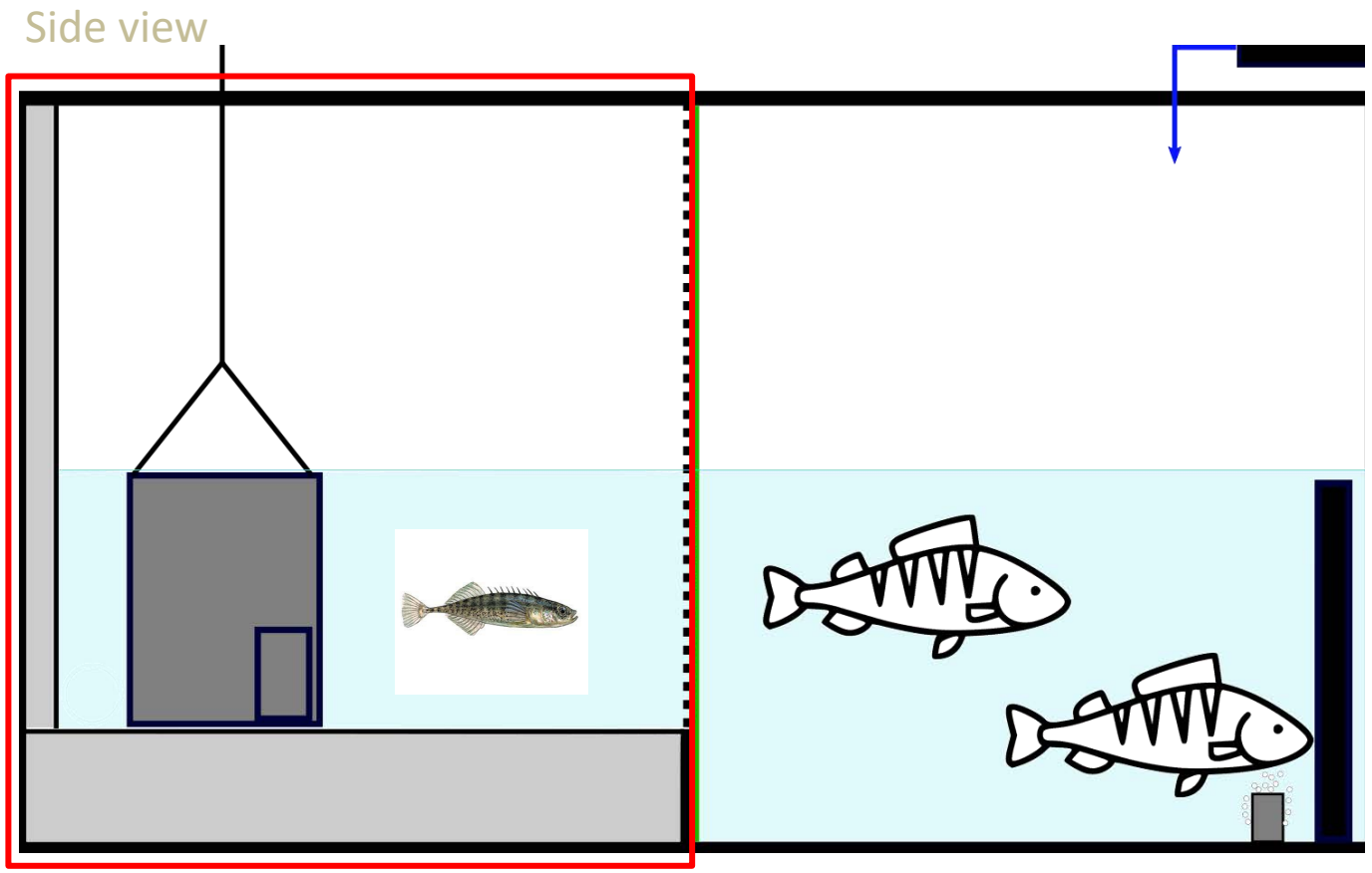

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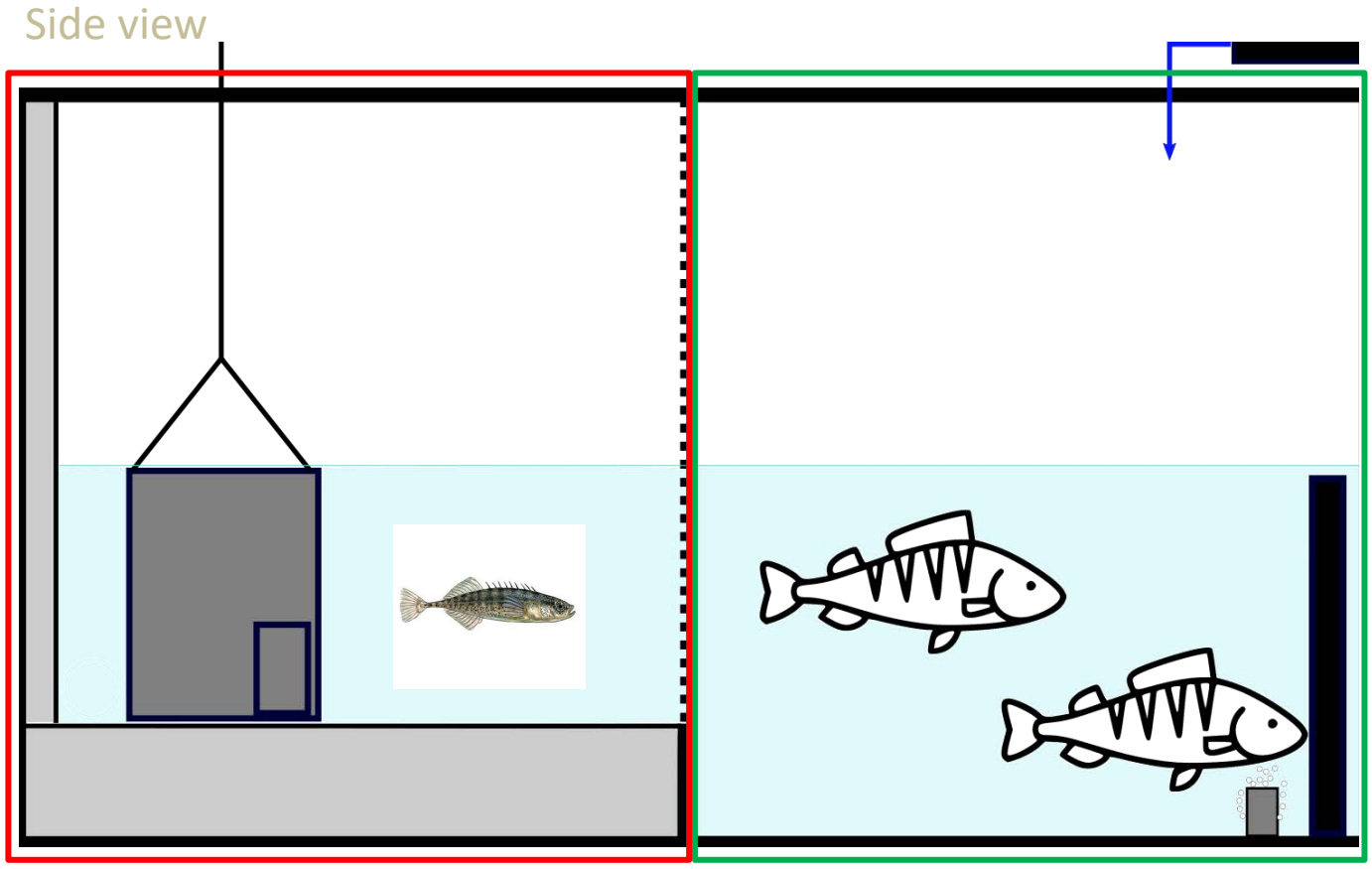

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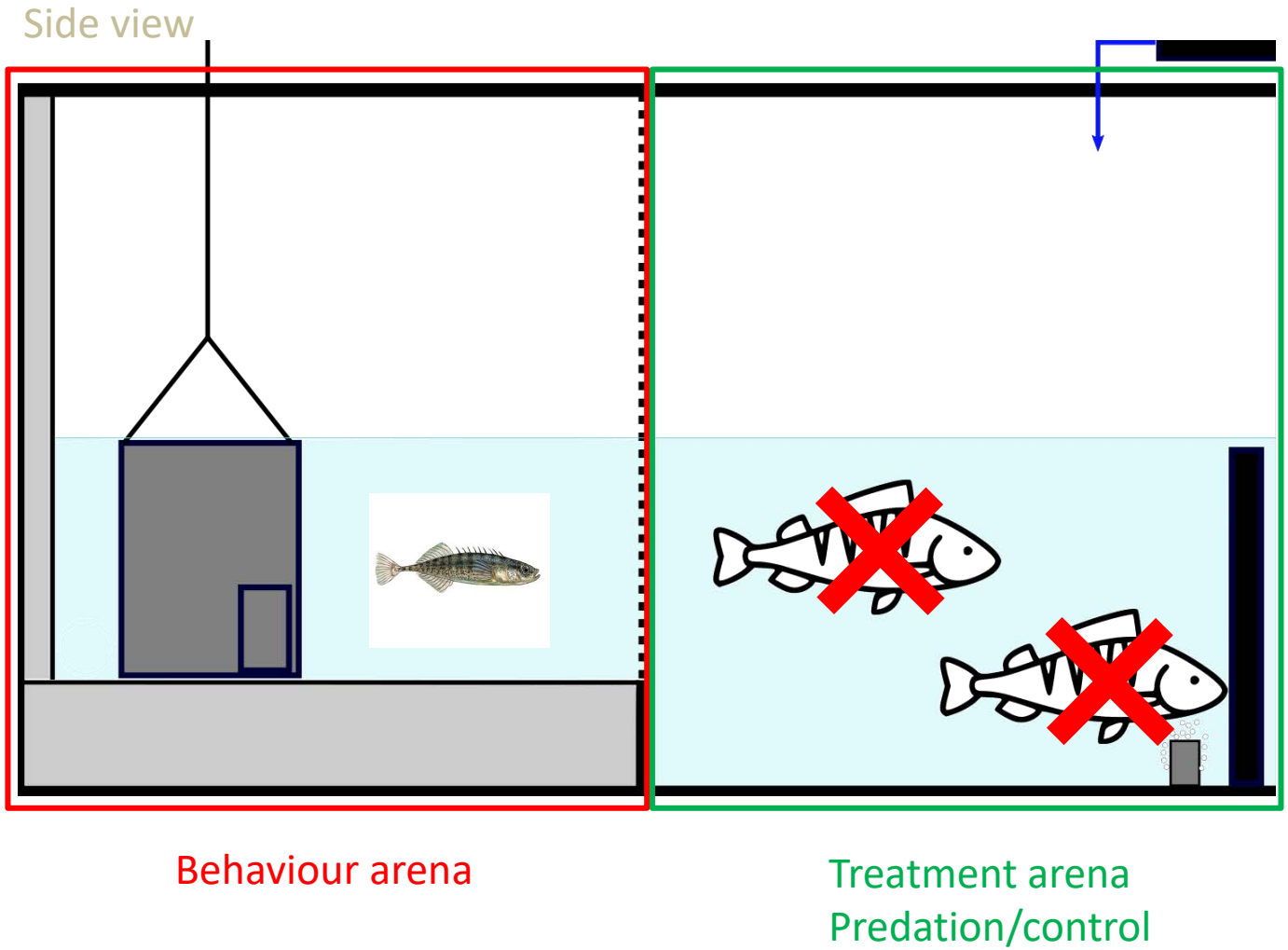

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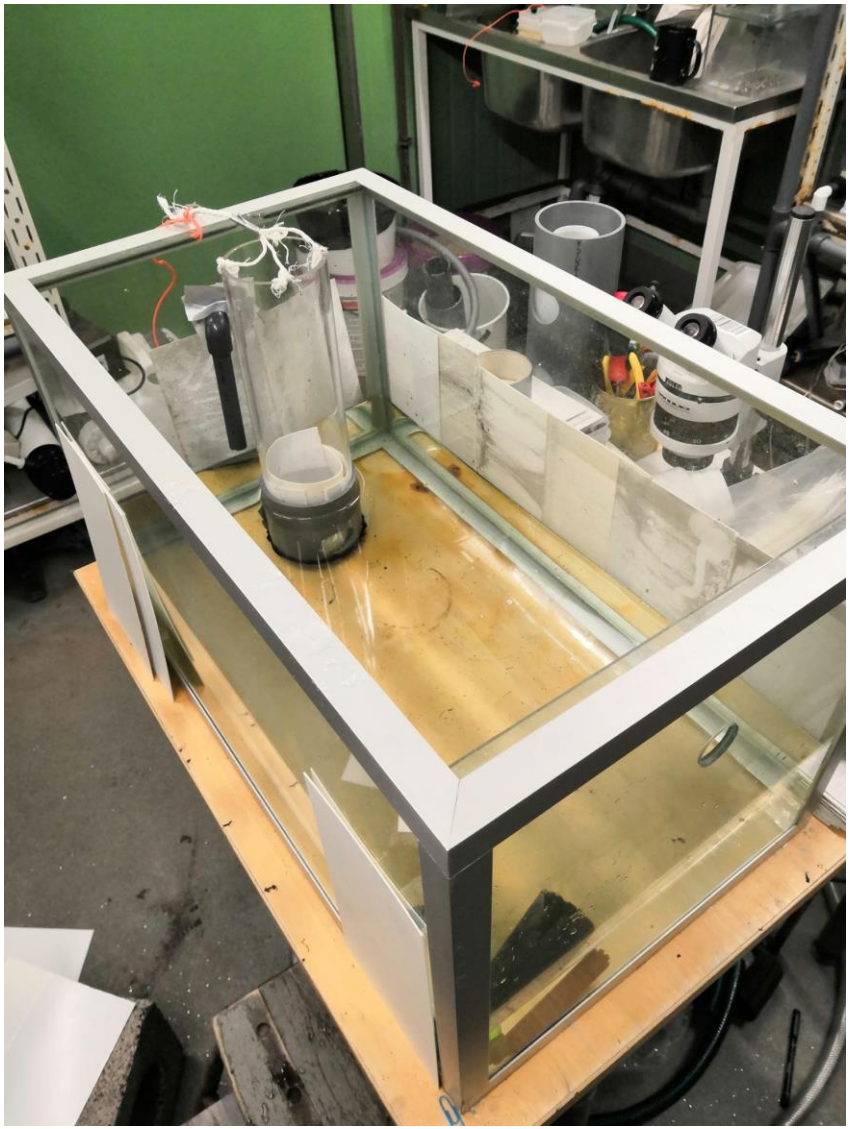
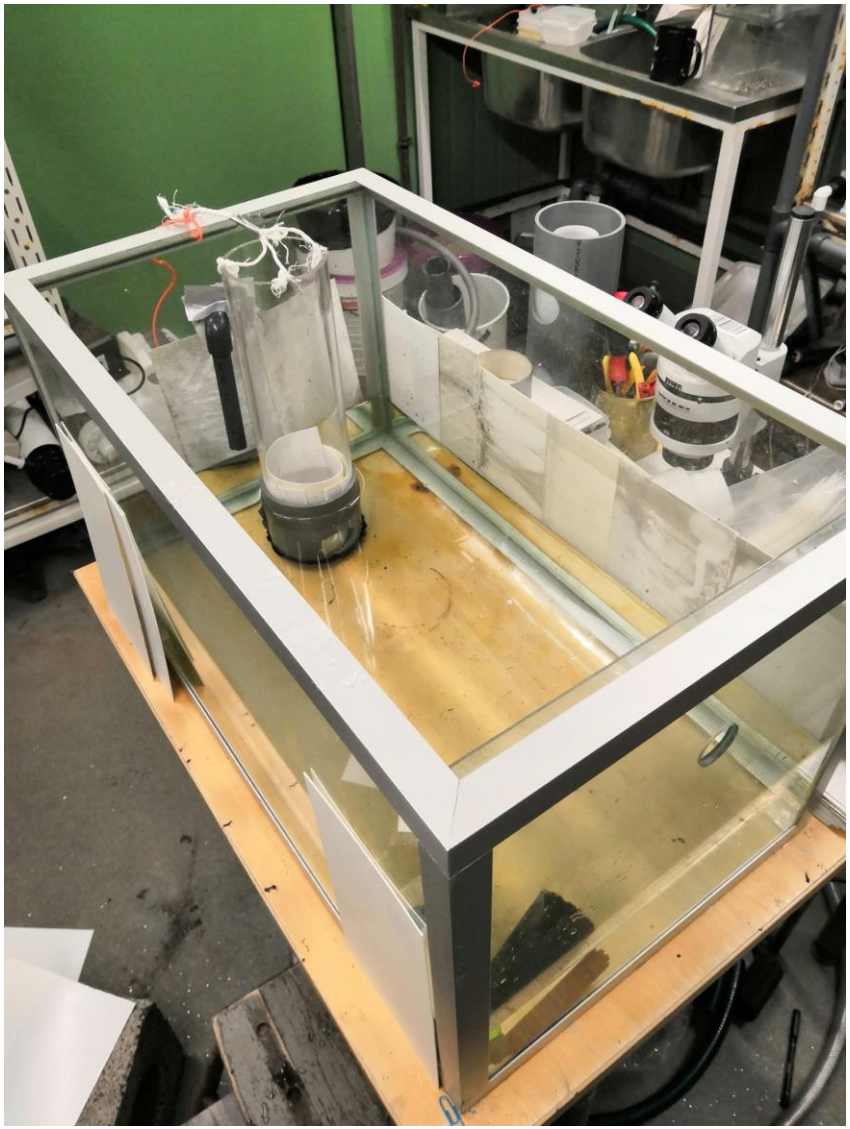


Strictly identical between treatments

I – Experimental setup

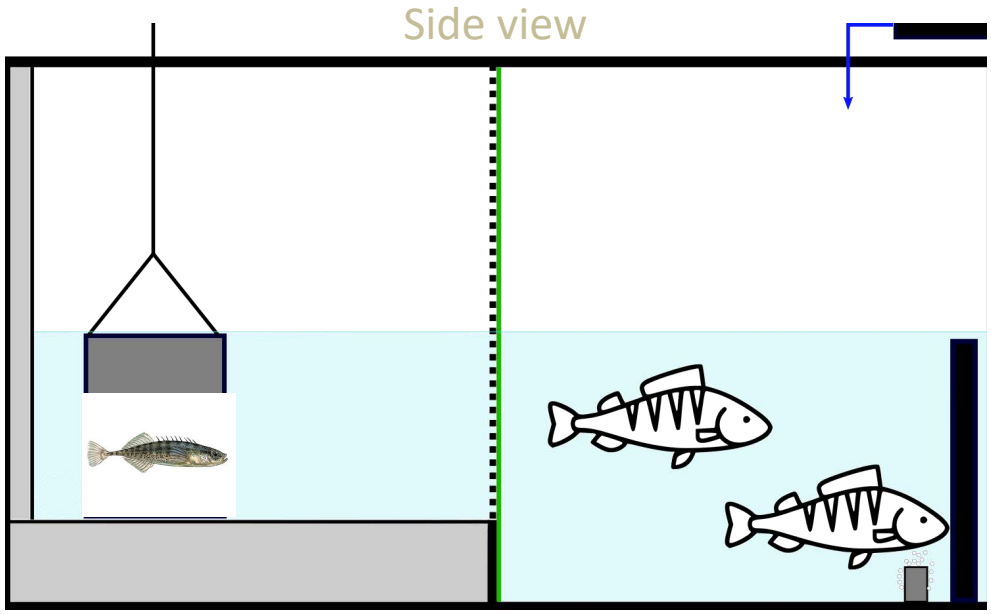


Strictly identical between treatments

I – Behavioural tests: exploration and foraging

Exploration

Latency to exit refuge and start exploring



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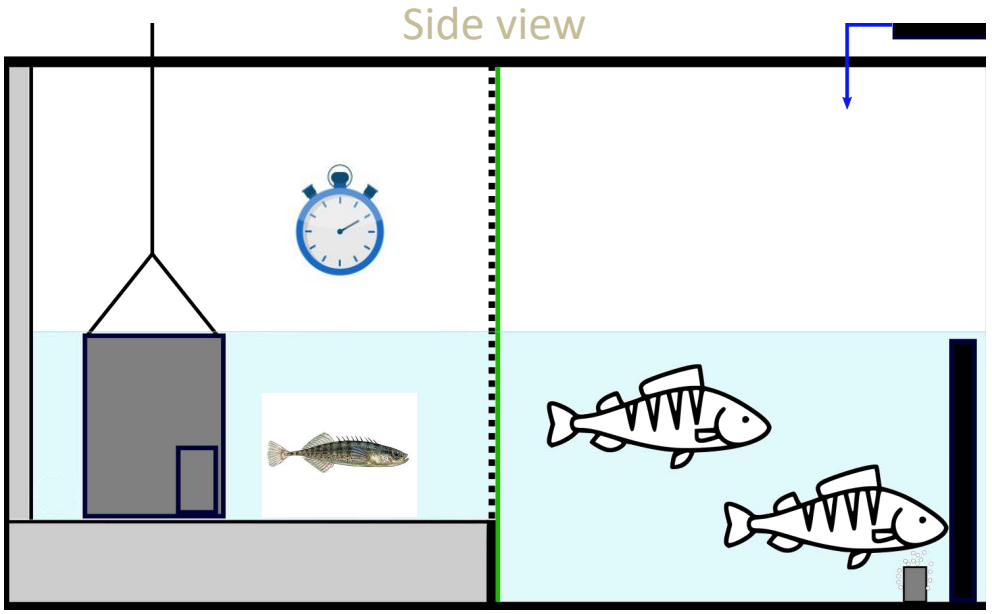
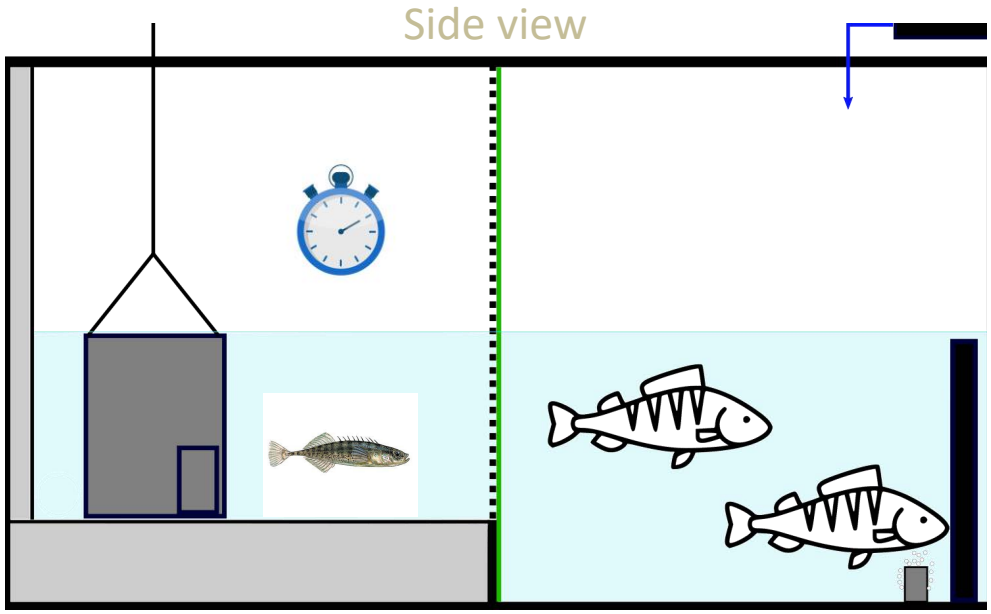


I – Behavioural tests: exploration and foraging

Exploration
Latency to exit refuge and start exploring

Time spent in the open area (activity time)



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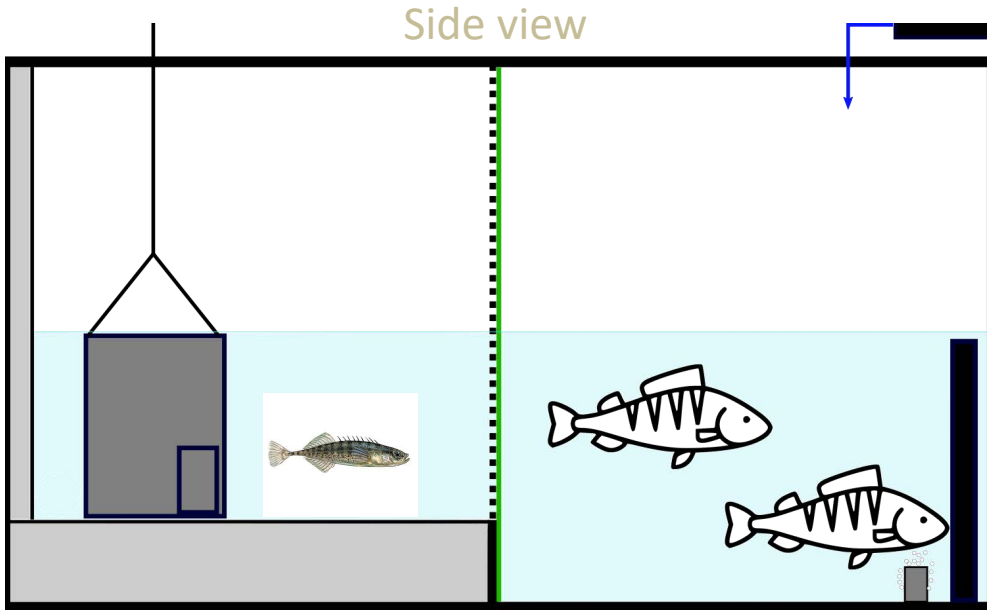
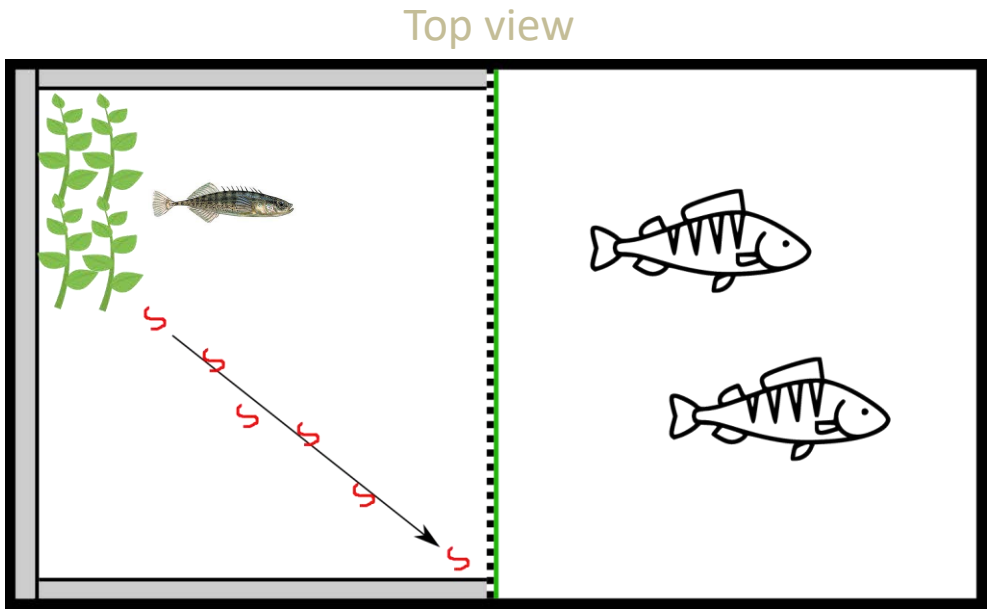


Foraging
Latency to start feeding



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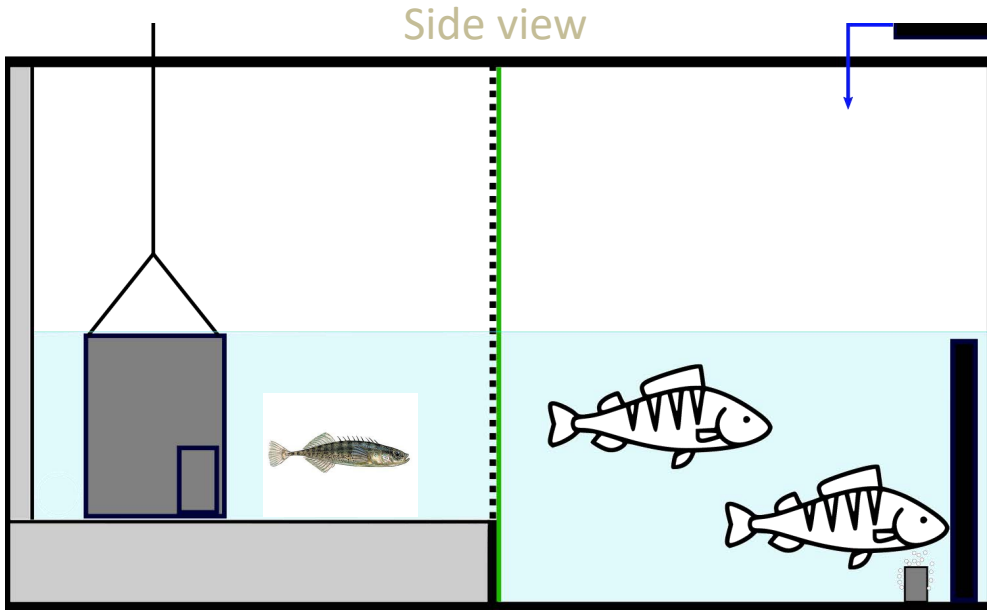
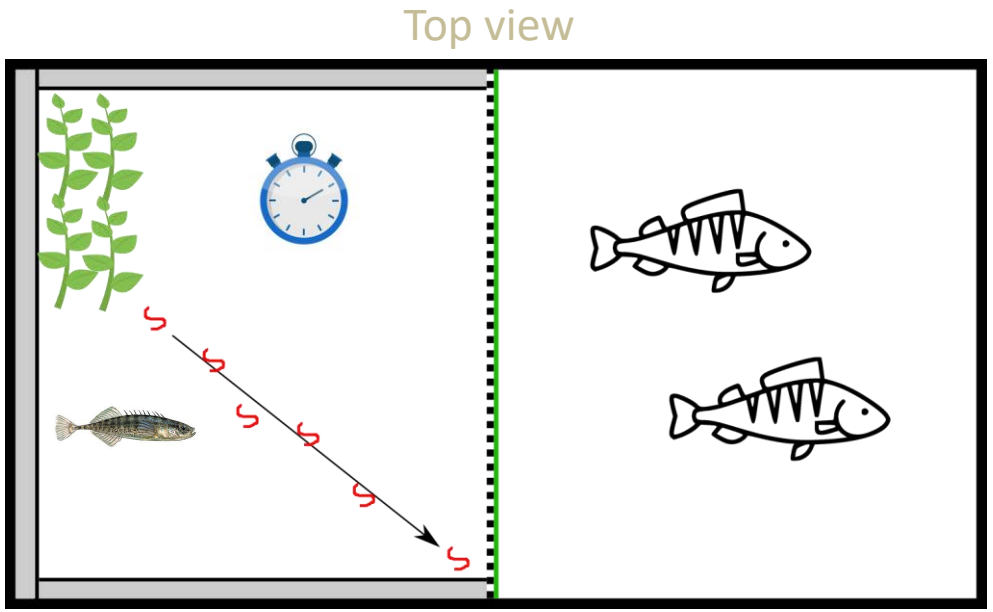


Foraging
Latency to start feeding



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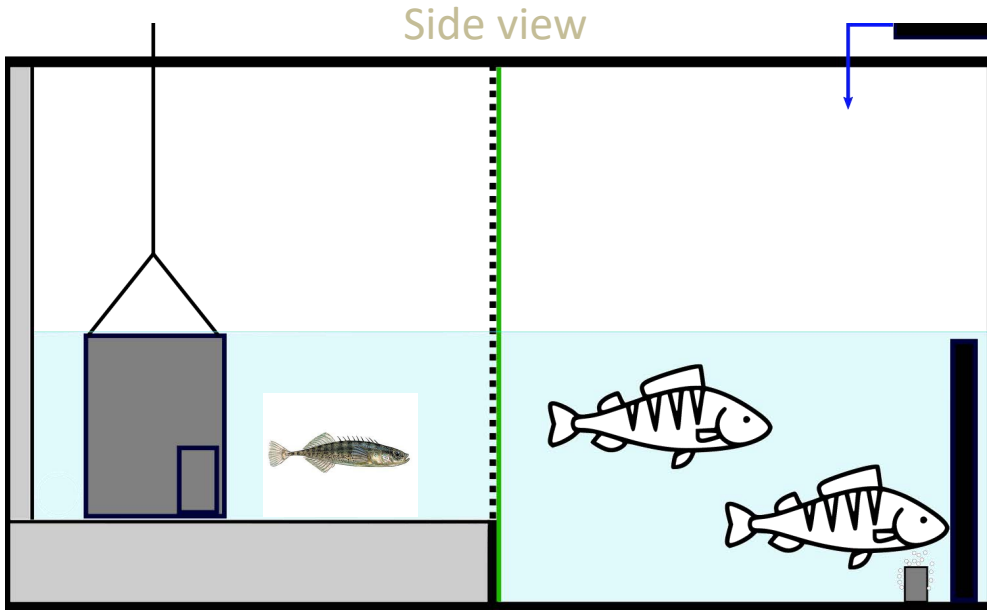
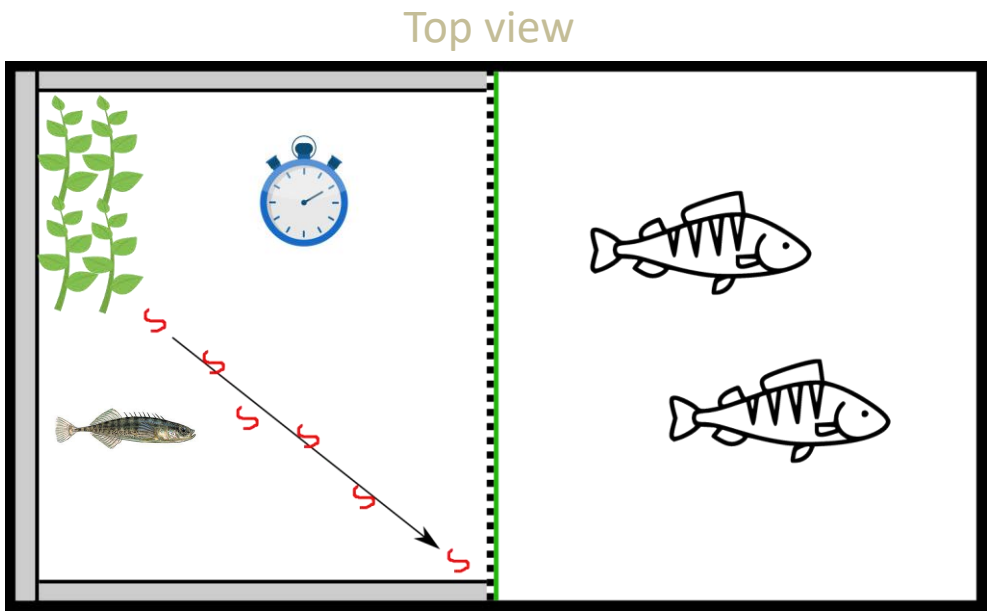


Foraging
Latency to start feeding

Number of food intakes



I – Data summary

8 populations (4 ponds/4 marine)

I – Data summary

8 populations (4 ponds/4 marine)

5-10 F1 full-sib family per population

I – Data summary

8 populations (4 ponds/4 marine)

5-10 F1 full-sib family per population

465 individuals

I – Data summary

8 populations (4 ponds/4 marine)

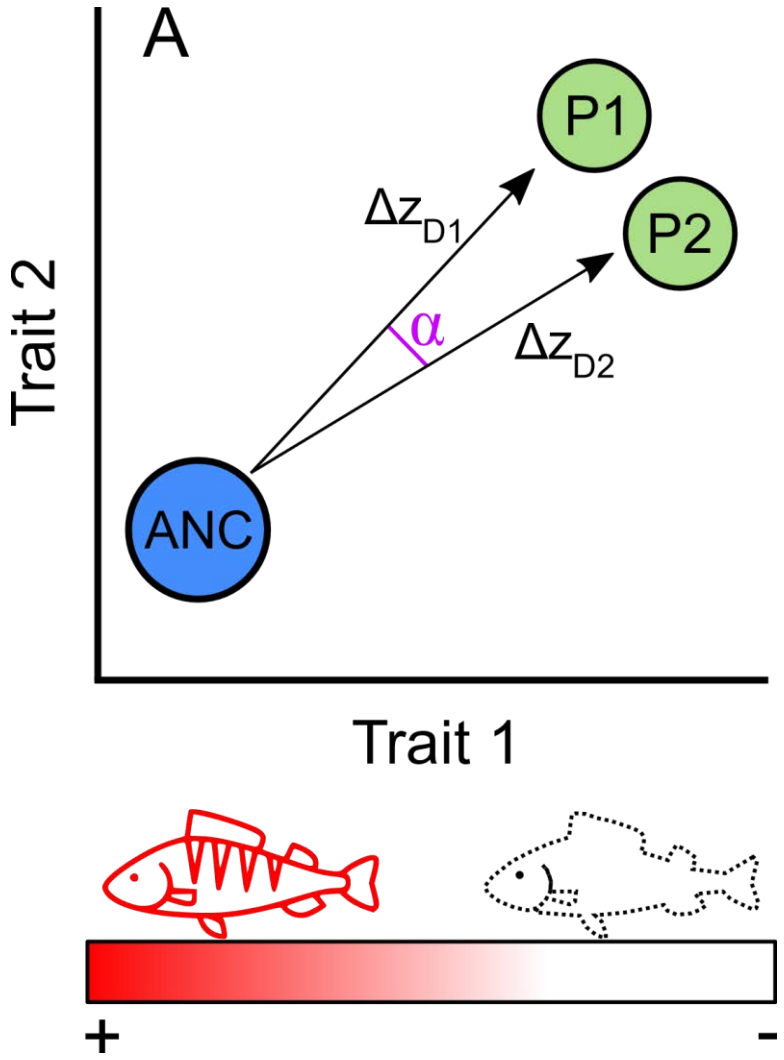
5-10 F1 full-sib family per population

465 individuals

4 behaviour traits

I – Analyses

Phenotypic vectors of evolutionary **divergence (Z_D)** estimated from the **difference** in **mean multivariate phenotype** between **ancestral** and **derived** populations

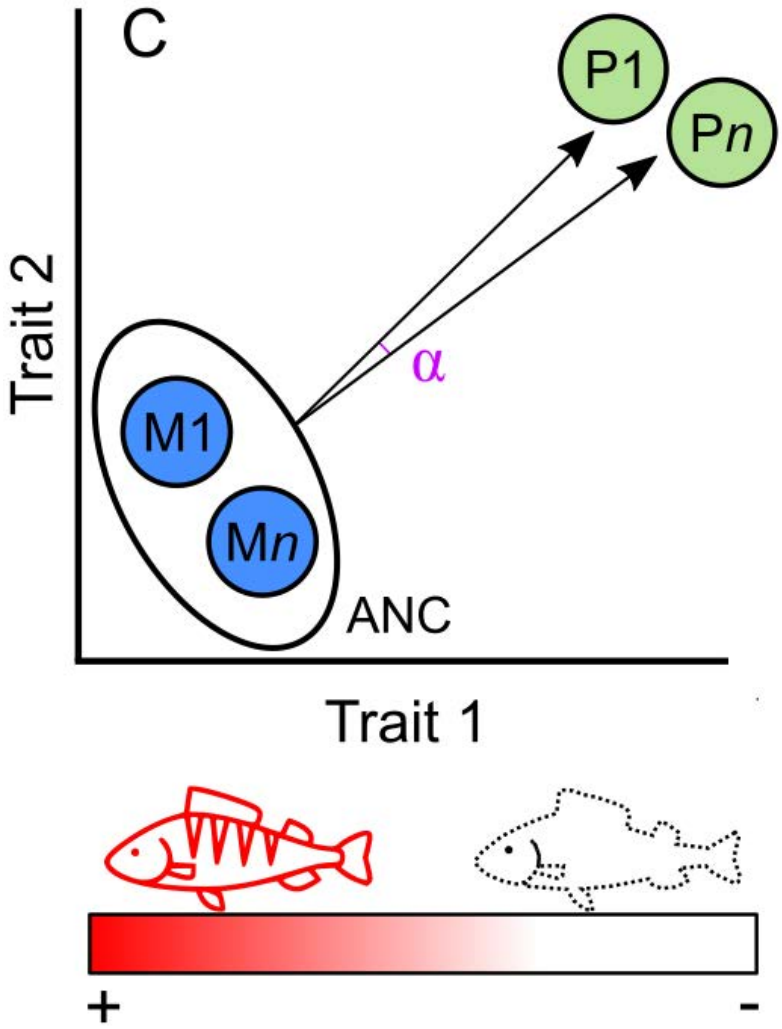


Fraimout, Päiviö & Merilä 2022

I – Analyses

Ancestor = marine populations in predation treatment

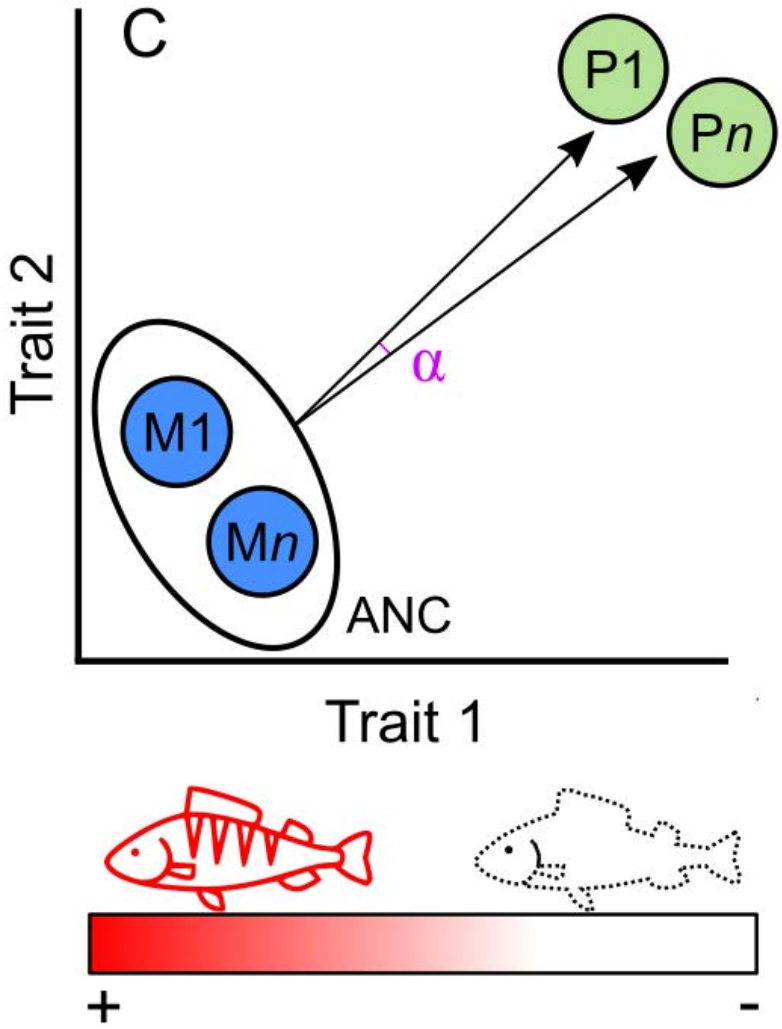
Derived = pond populations in control treatment



Fraimout, Päiviö & Merilä 2022

I – Analyses

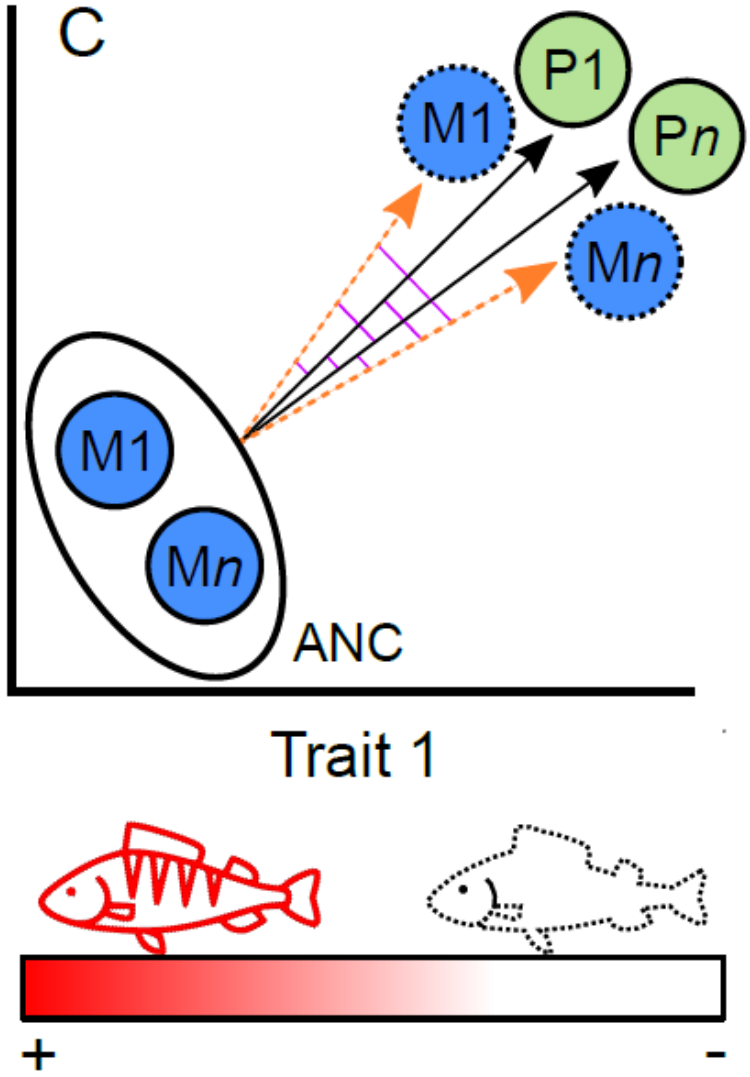
Estimation of **angles** between vectors to determine whether **evolution** occurred in **parallel**



Fraimout, Päiviö & Merilä 2022

I – Analyses

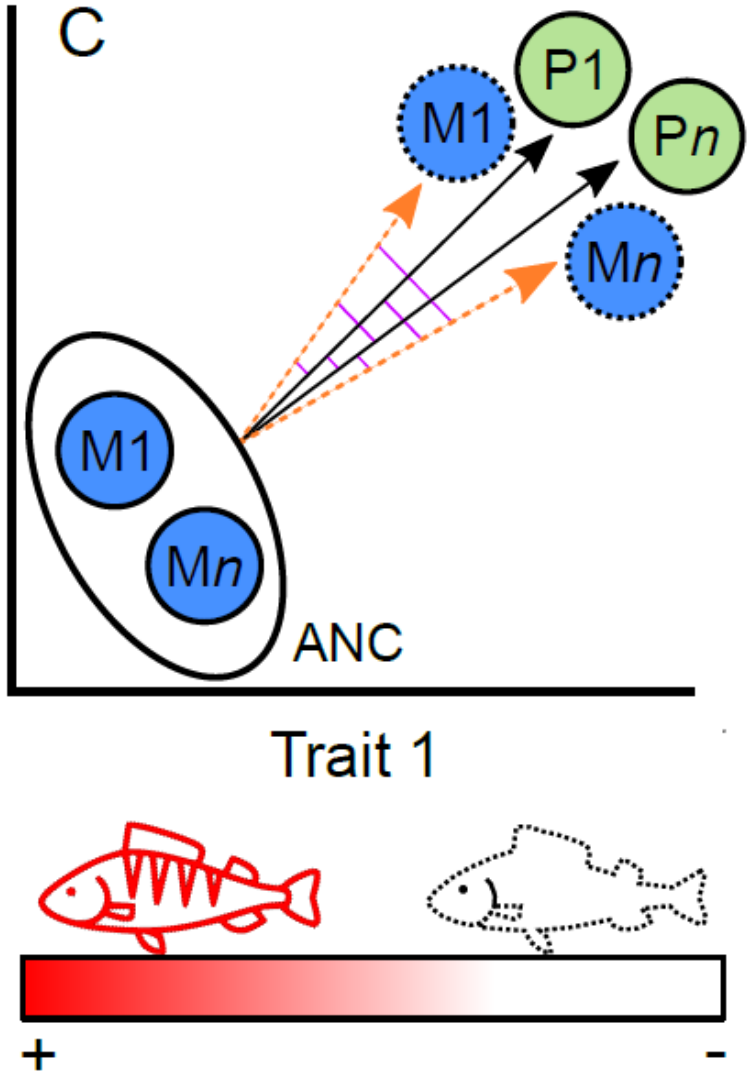
Phenotypic **vectors of plasticity** estimated from the **difference** in **mean phenotype** between **hypothetical ancestor** and **marine** populations in **control** treatment



Fraimout, Päiviö & Merilä 2022

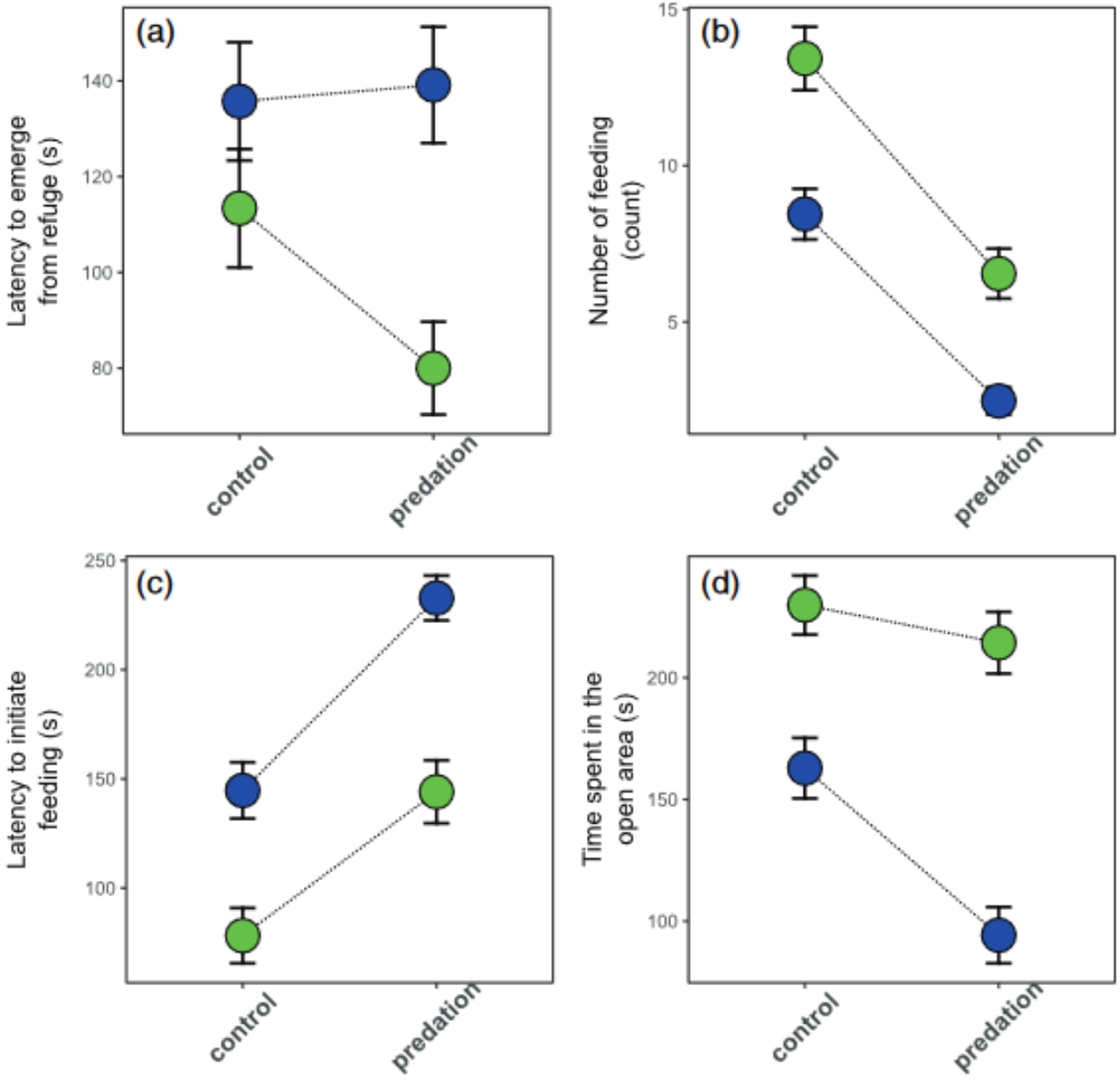
I – Analyses

Estimation of **angles** between **divergence** and **plasticity** vectors to determine whether **plasticity to relaxed predation drove evolution of behaviour**



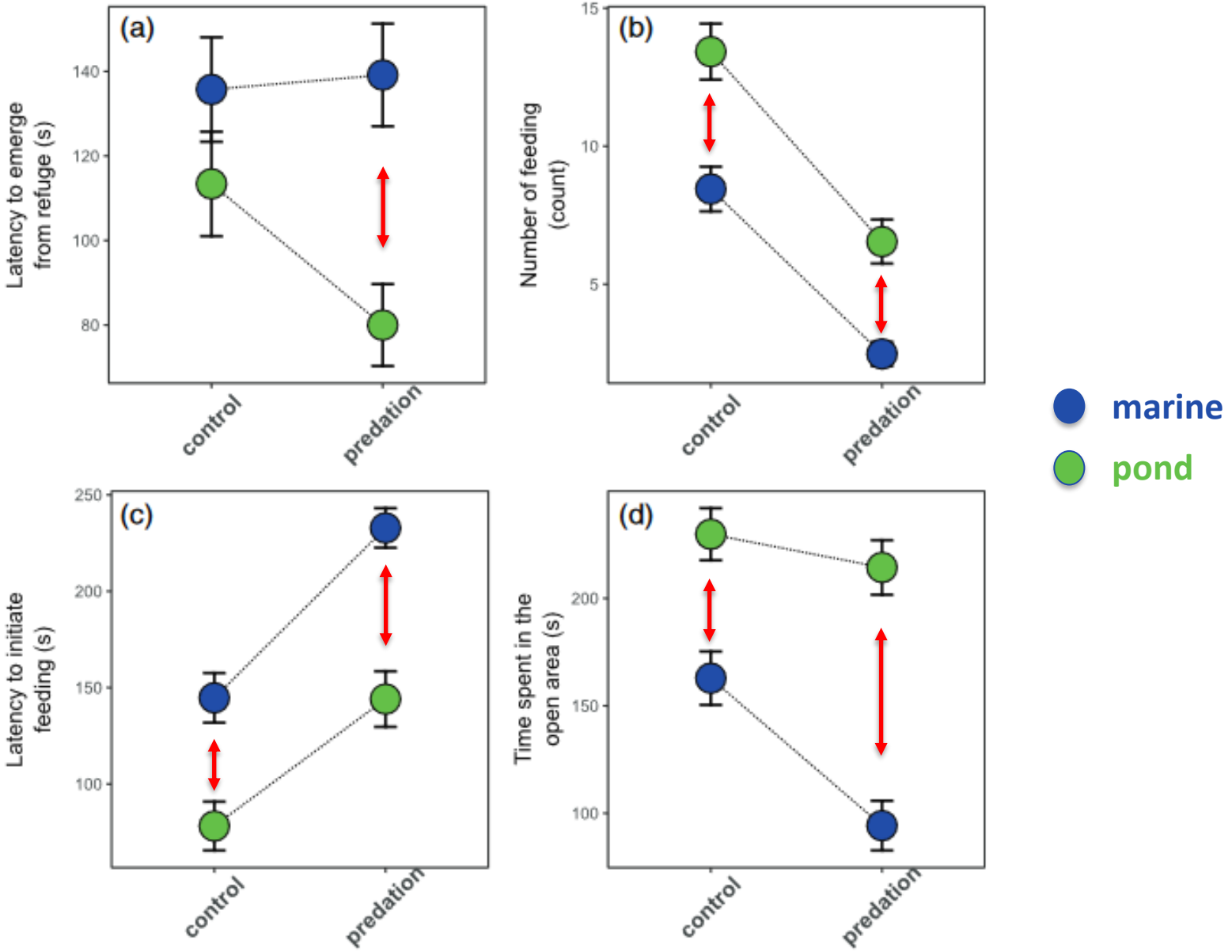
Fraimout, Päiviö & Merilä 2022

I – Results



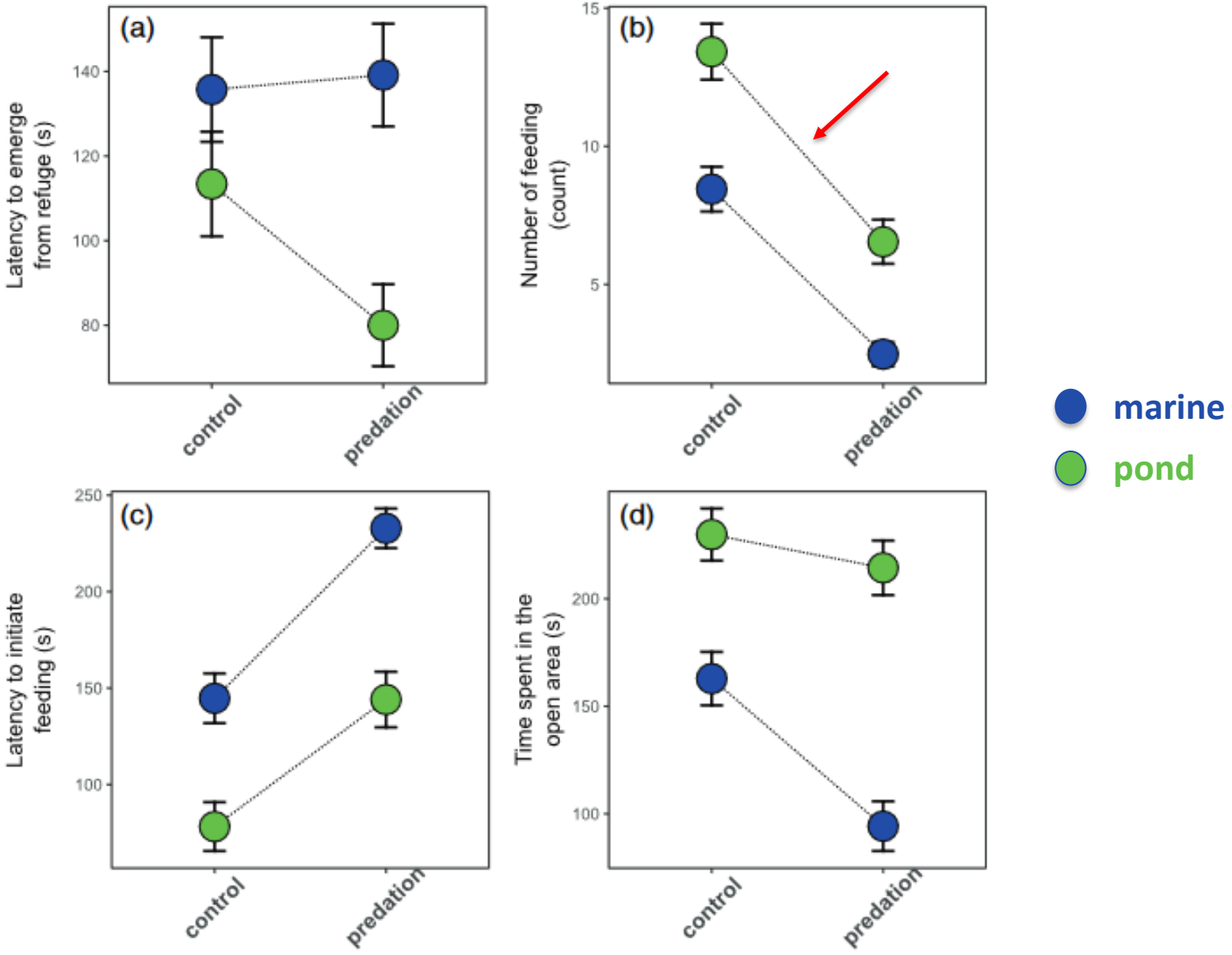
Fraimout, Päiviö & Merilä 2022

I – Results: habitat effect



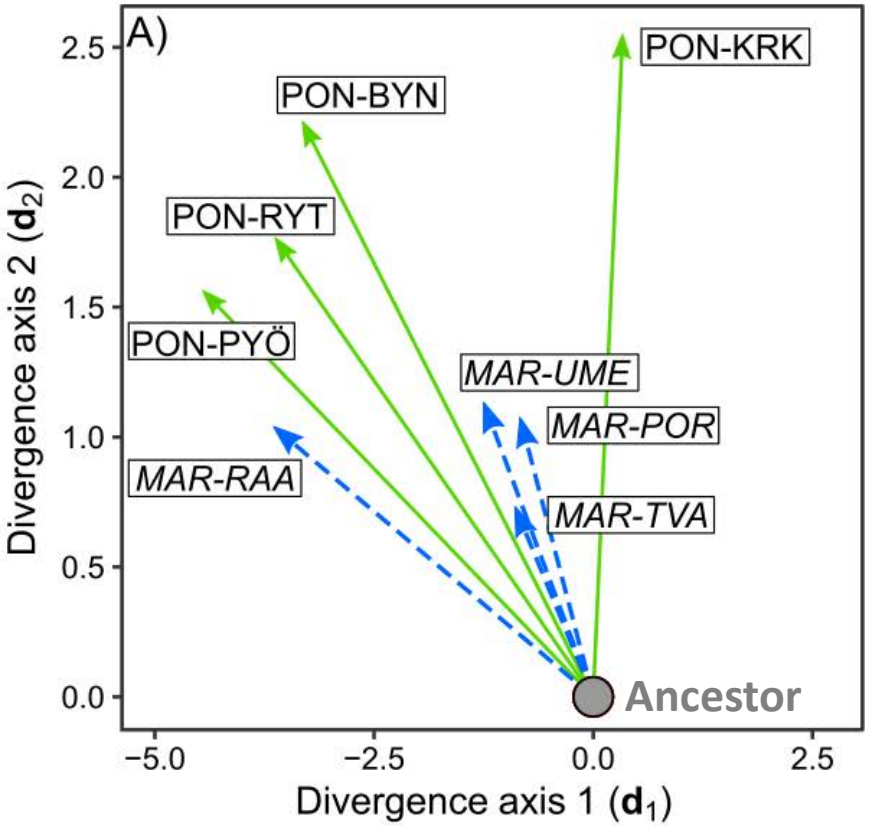
Fraimout, Päiviö & Merilä 2022

I – Results: treatment effect



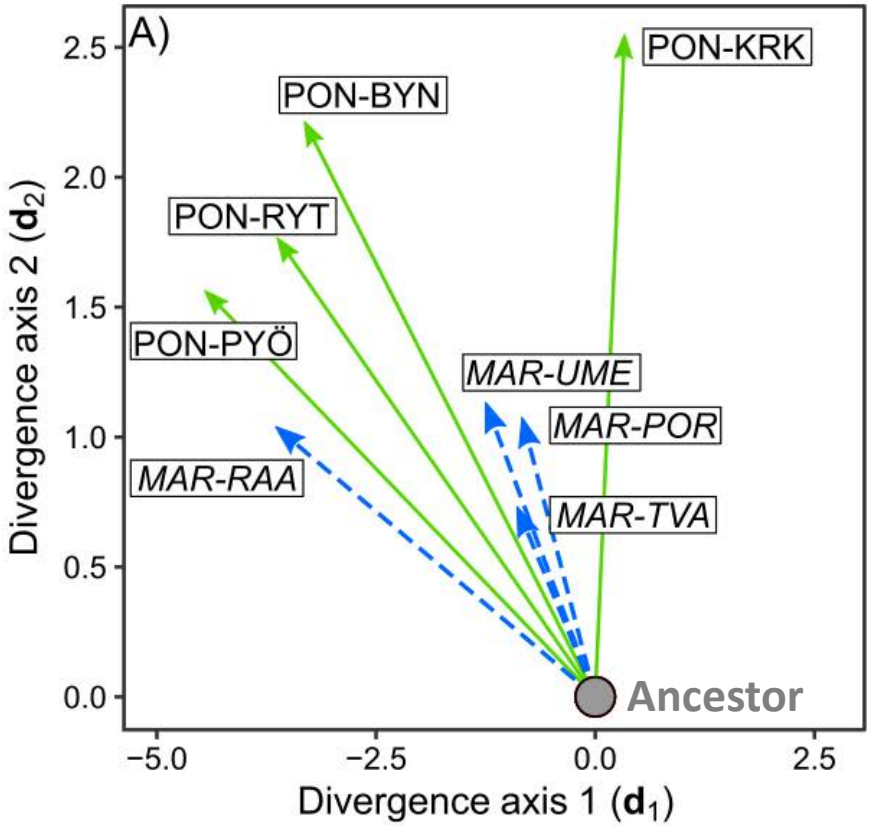
Fraimout, Päiviö & Merilä 2022

I – Results



Fraimout, Päiviö & Merilä 2022

I – Results

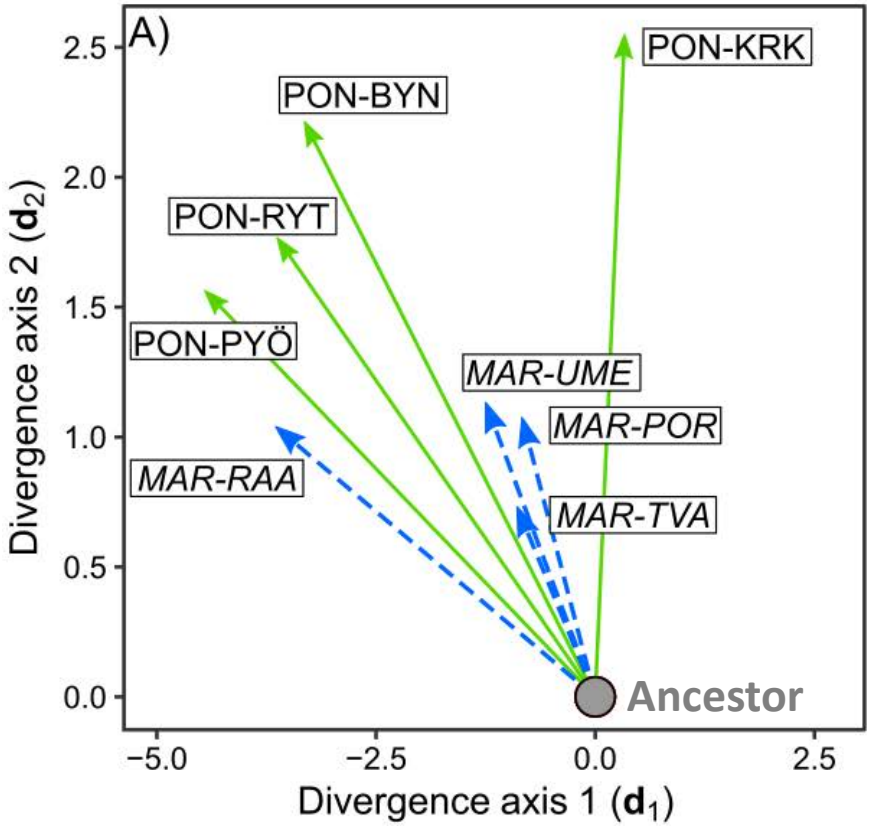


Divergence vectors

- > difference between pond and ancestral marine

Fraimout, Päiviö & Merilä 2022

I – Results



Divergence vectors

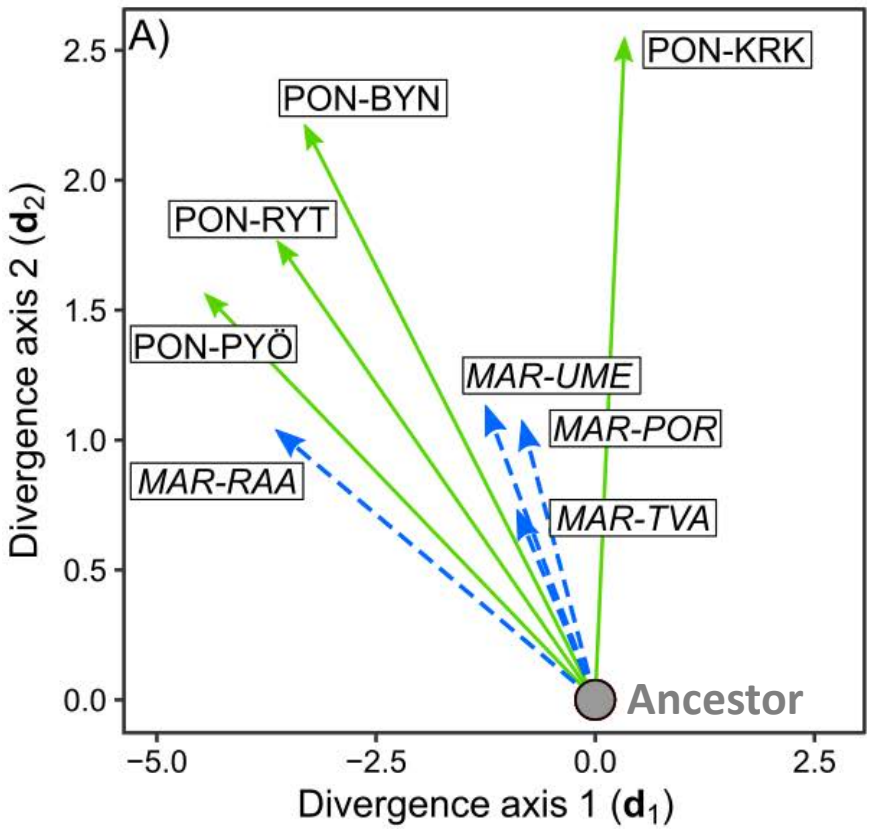
- > difference between pond and ancestral marine

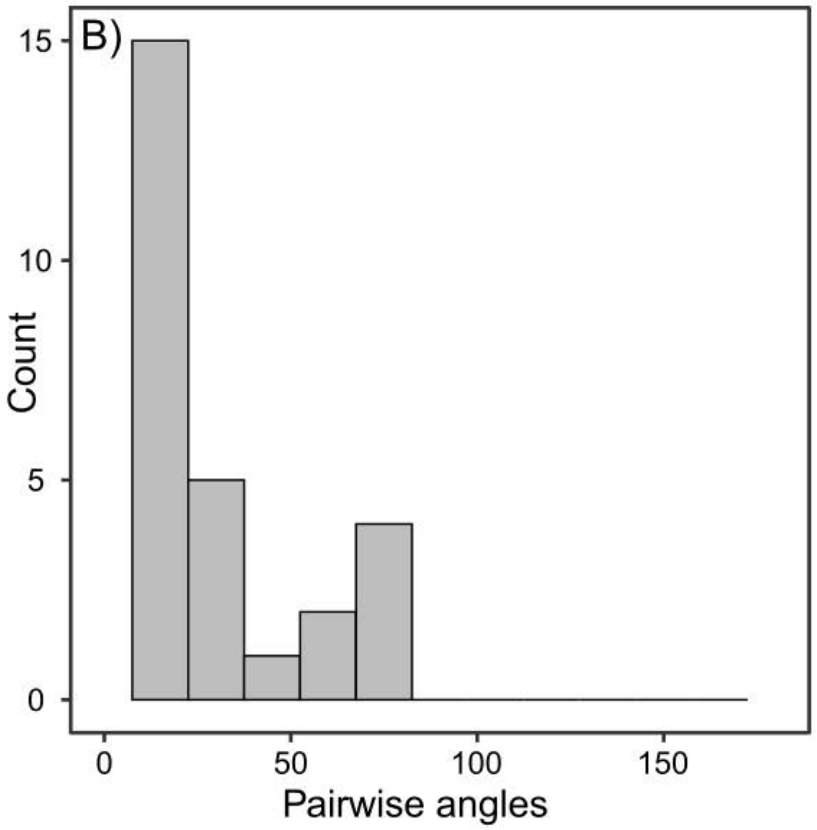
Plasticity vectors

- > difference between marine in control and ancestral marine

Fraimout, Päiviö & Merilä 2022

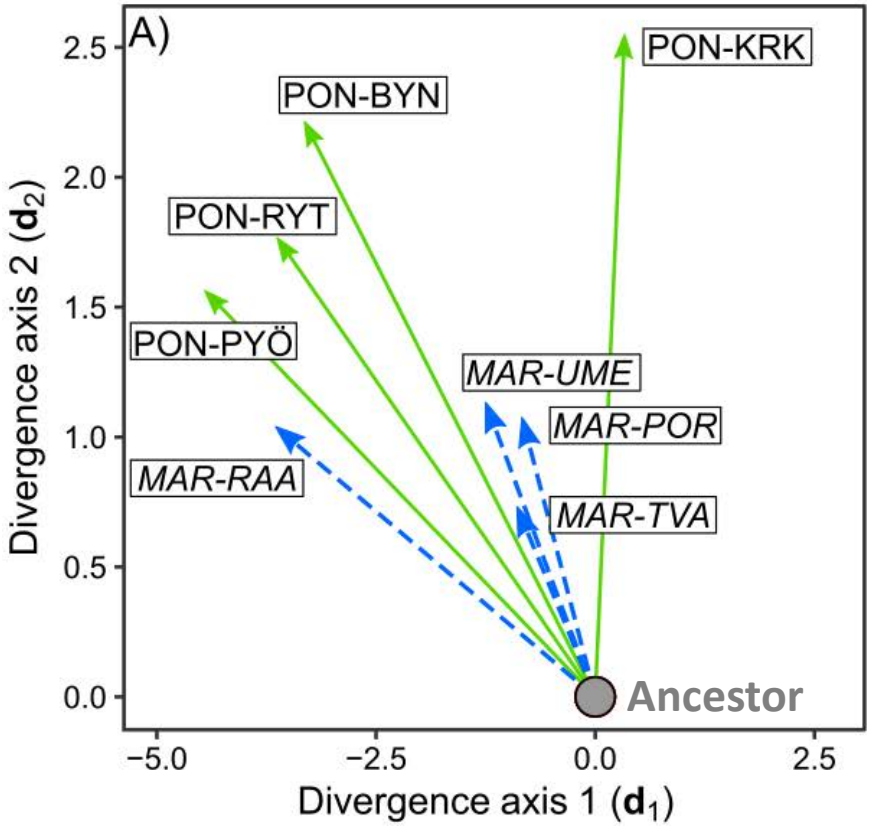
I – Results

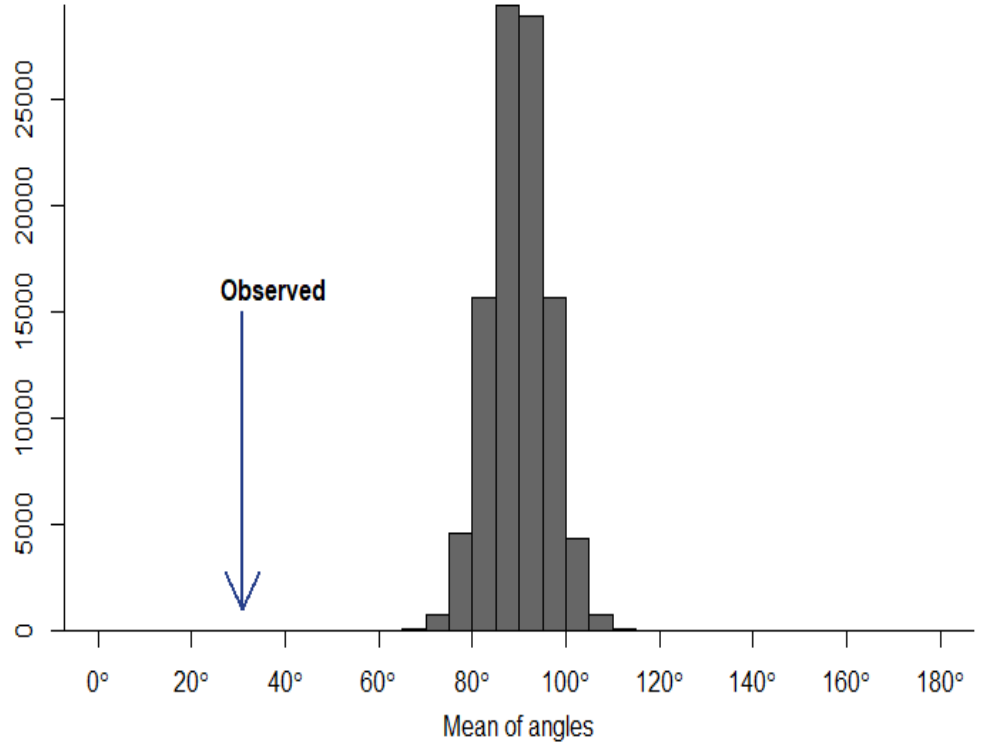




Fraimout, Päiviö & Merilä 2022

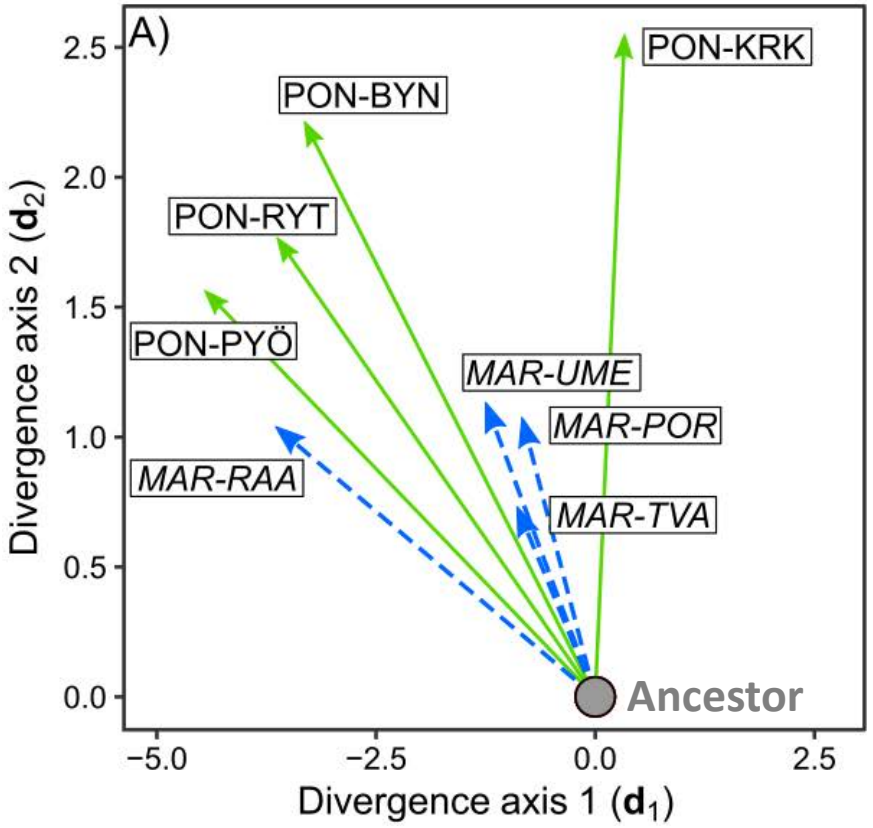
I – Results





Fraimout, Päiviö & Merilä 2022

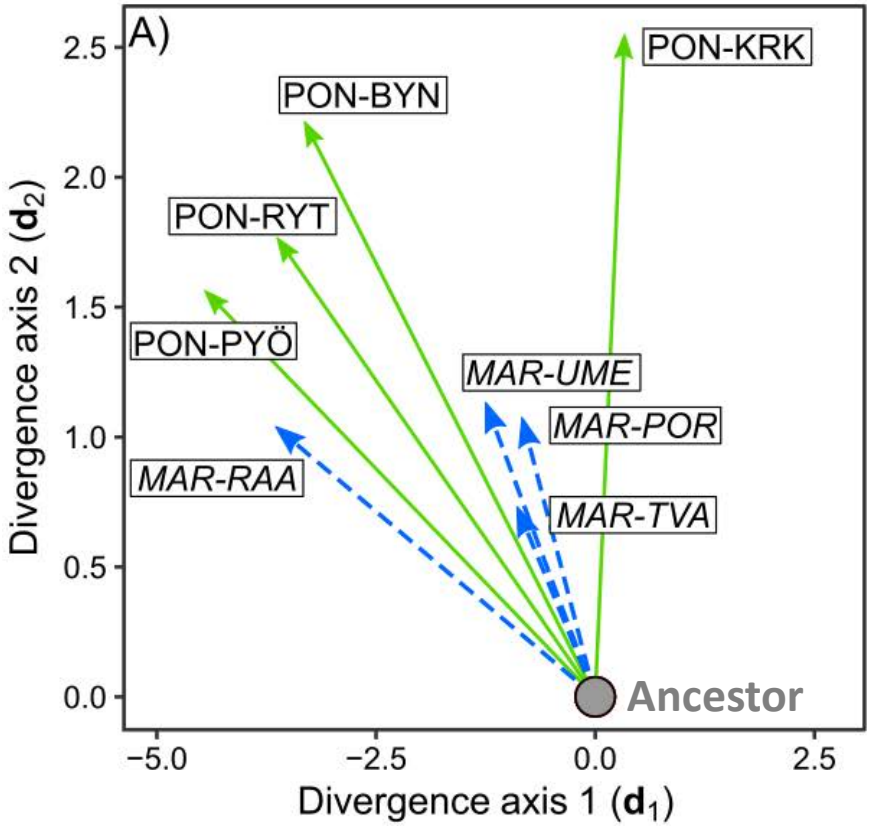
I – Results



Alignment between divergence vectors

Fraimout, Päiviö & Merilä 2022

I – Results

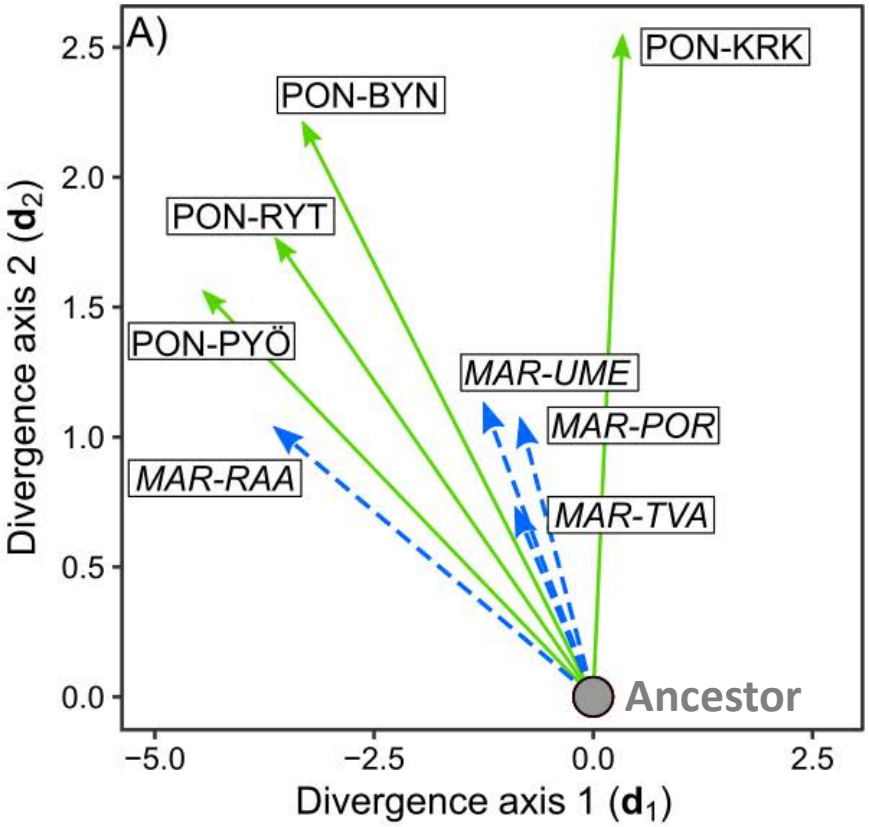


Alignment between divergence vectors

Parallel evolution of complex behavior

Fraimout, Päiviö & Merilä 2022

I – Results



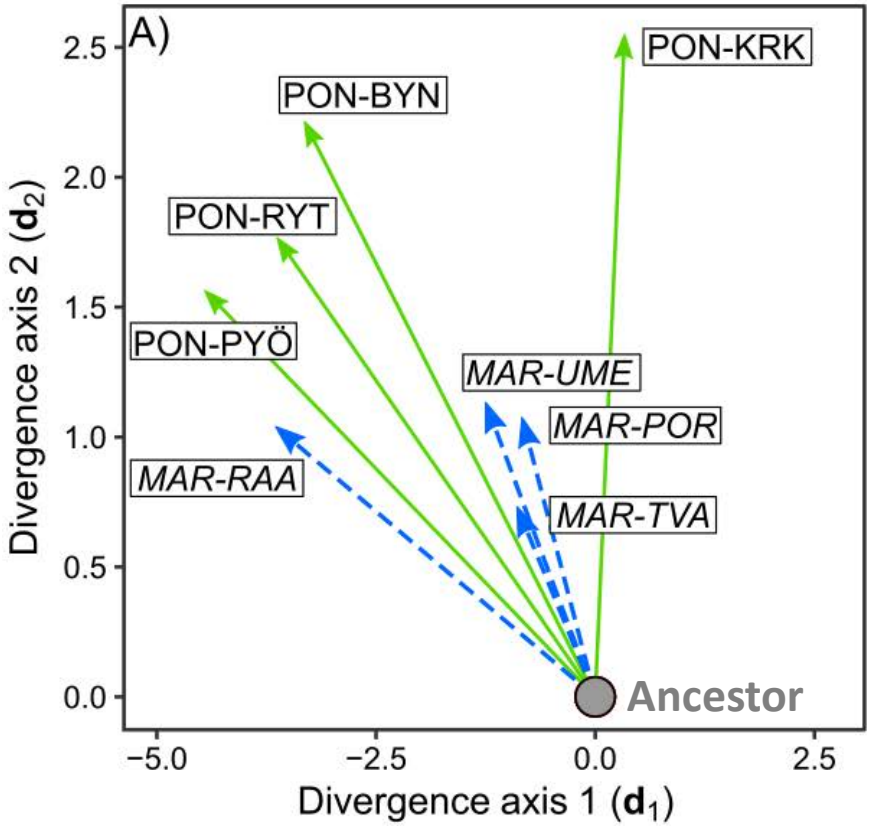
Alignment between divergence vectors

Parallel evolution of complex behavior

Alignment between plasticity vectors

Fraimout, Päiviö & Merilä 2022

I – Results



Alignment between divergence vectors

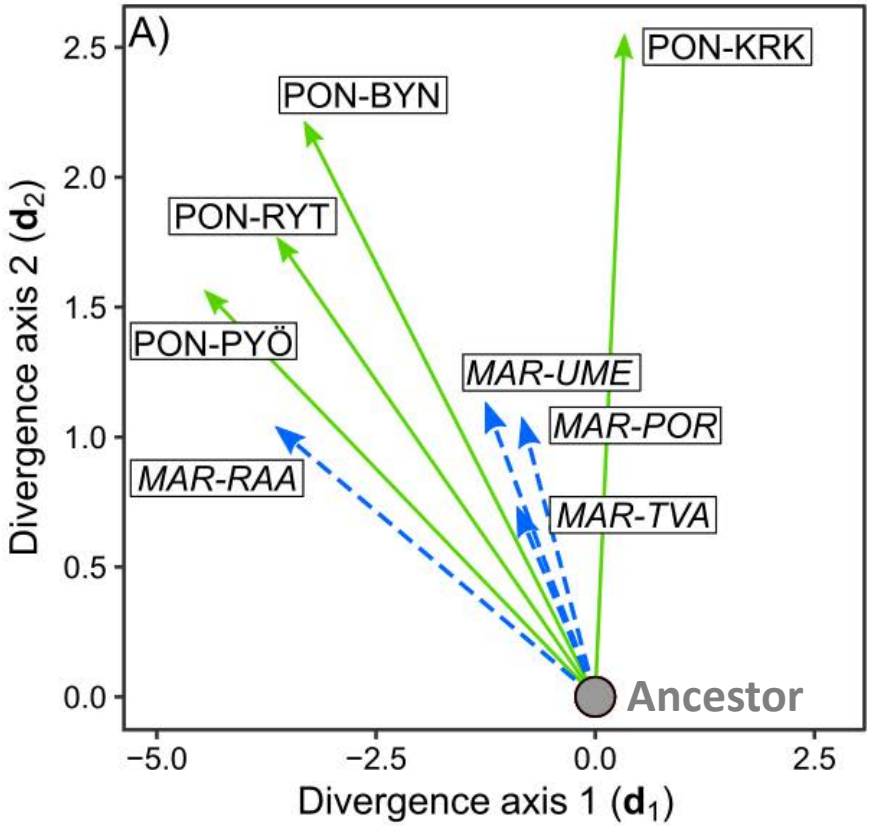
Parallel evolution of complex behavior

Alignment between plasticity vectors

Shared plastic response to predation release

Fraimout, Päiviö & Merilä 2022

I – Results



Alignment between divergence vectors

Parallel evolution of complex behavior

Alignment between plasticity vectors

Shared plastic response to predation release

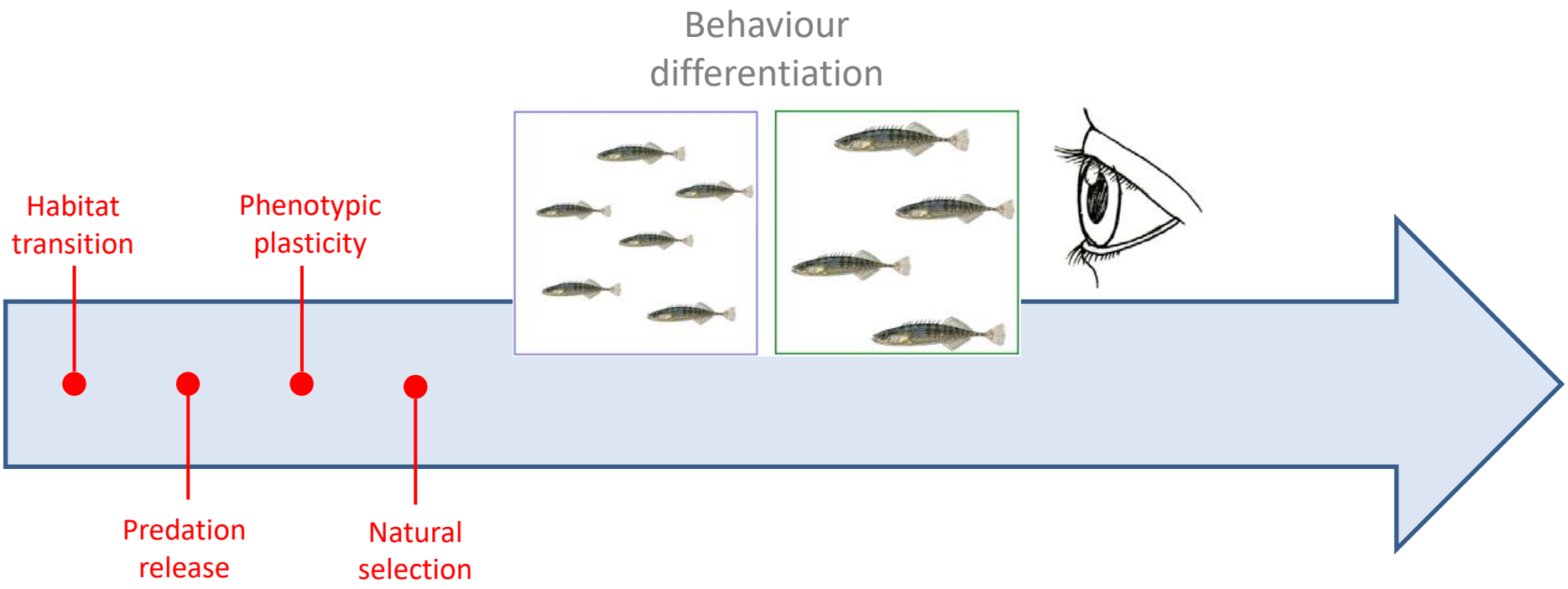
Alignment between divergence and plasticity vectors

Predation is the ecological driver of repeated evolution

Fraimout, Päiviö & Merilä 2022

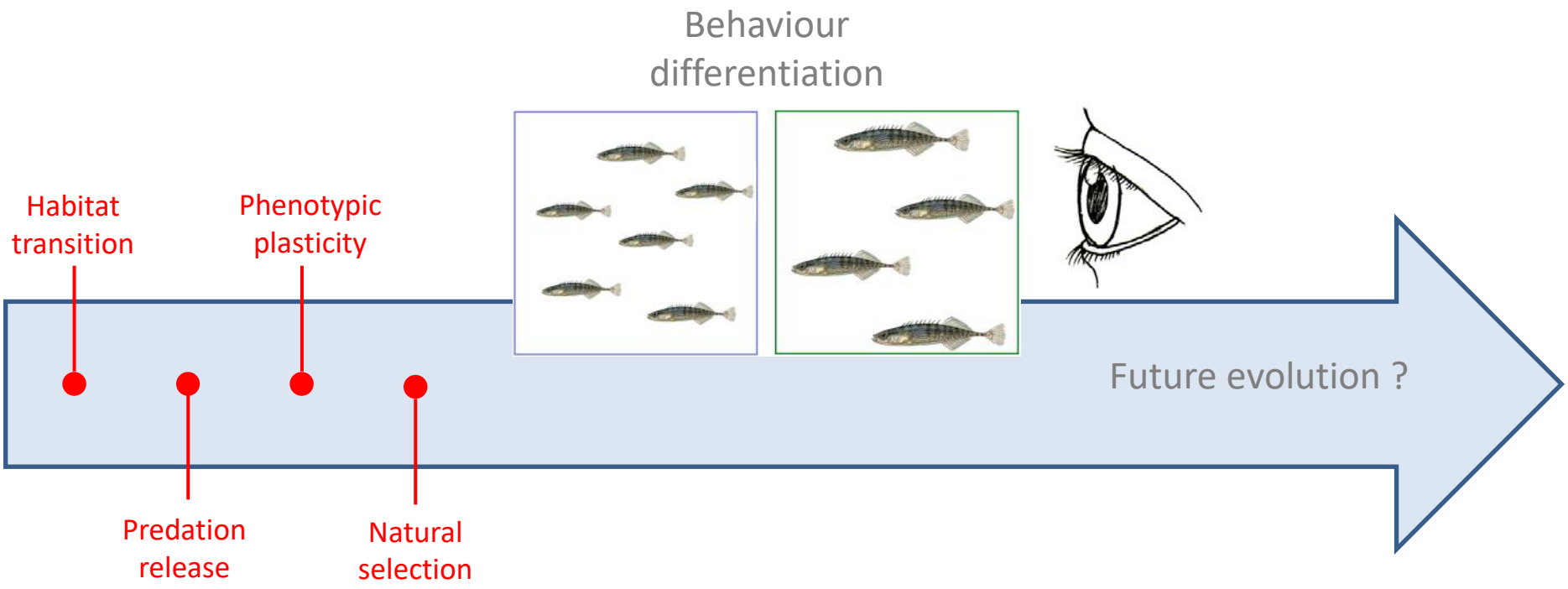
I – Conclusions

Relaxed risk of predation drove parallel evolution of nine-spined stickleback behavior



I – Conclusions

Relaxed risk of predation drove parallel evolution of nine-spined stickleback behavior



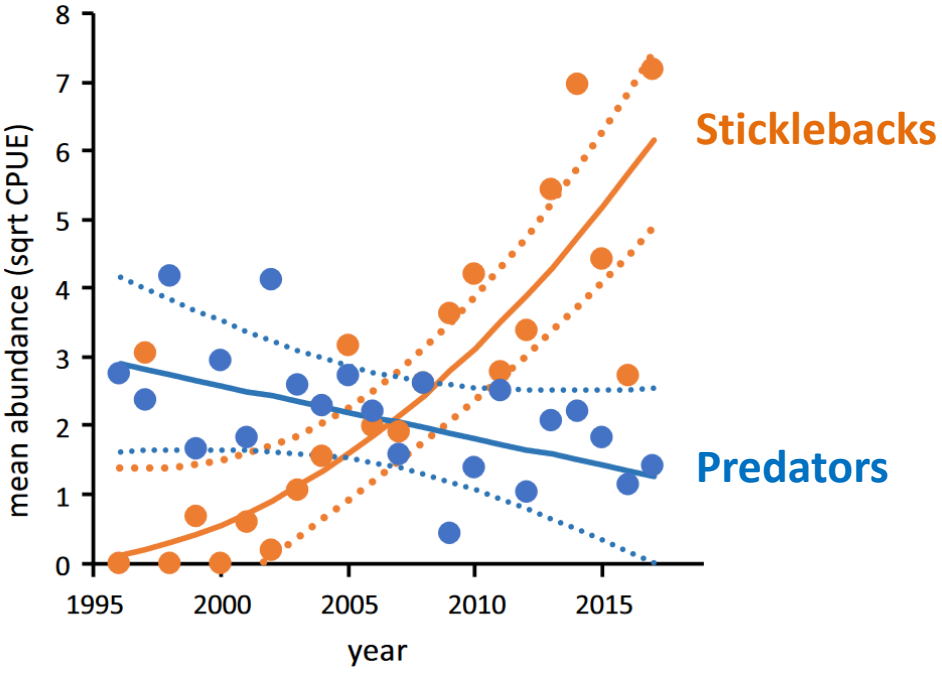
I – Future evolution?

Review

Past and Current Trends of Coastal Predatory Fish in the Baltic Sea with a Focus on Perch, Pike, and Pikeperch

Jens Olsson

Swedish University of Agricultural Sciences, Department of Aquatic Resources, Institute of Coastal Research
Skolgatan 6, 74242 Öregrund, Sweden; Jens.Olsson@slu.se; Tel.: +46-(0)104784144



Eriksson *et al.* 2021

I – Future evolution?

Review

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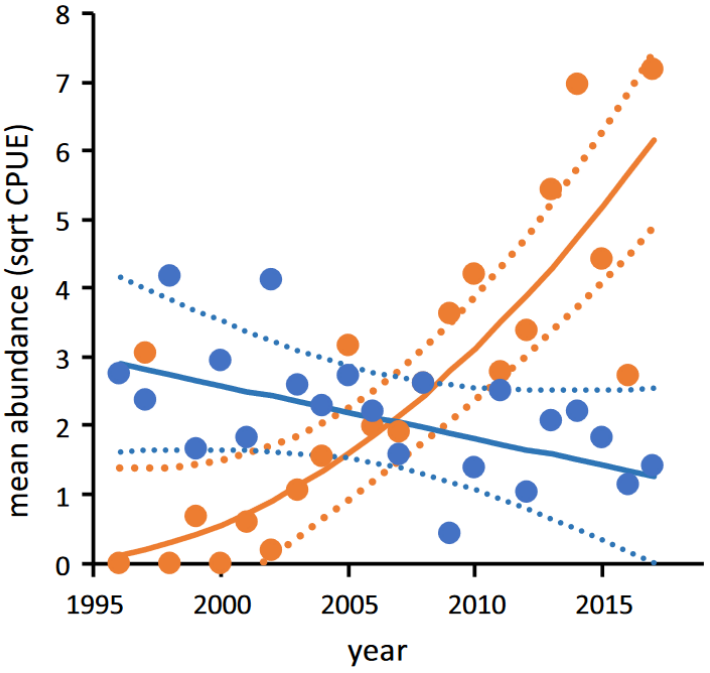


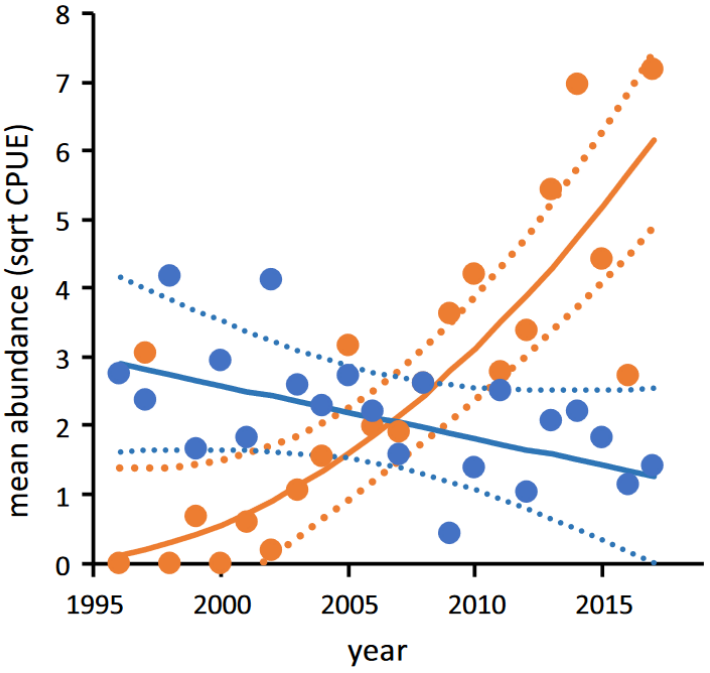
Emergence of freshwater phenotypes in the sea?

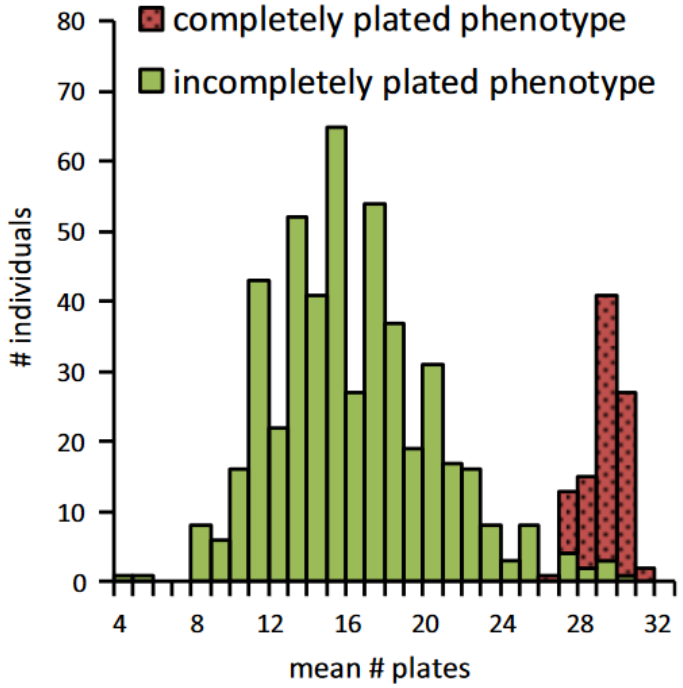
Eriksson *et al.* 2021

I – Future evolution?

Habitat segregation of plate phenotypes in a rapidly expanding population of three-spined stickleback

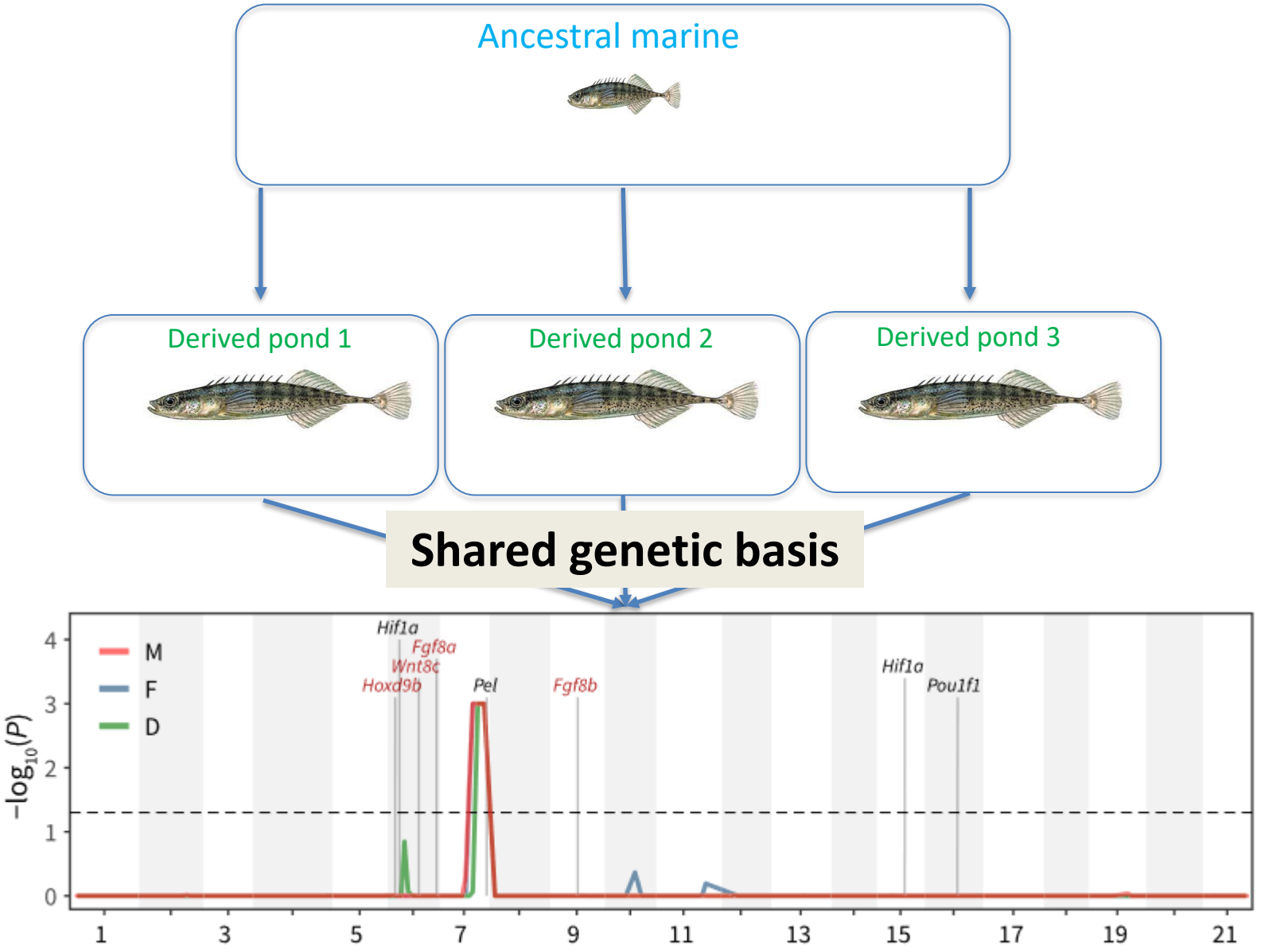
Britas Klemens Eriksson[1,†] Casey Yanos,[1] Sarah J. Bourlat,[2] Serena Donadi[3] Michael C. Fontaine,[4,5] Joakim P. Hansen,[6] Eglė Jakubavičiūtė,[7] Karine Kiragosyan,[1] Martine E. Maan,[1] Juha Merilä,[8,9] Åsa N. Austin,[10] Jens Olsson,[3] Katrin Reiss,[11] Göran Sundblad,[3] Ulf Bergström,[3] and Johan S. Eklöf[10]





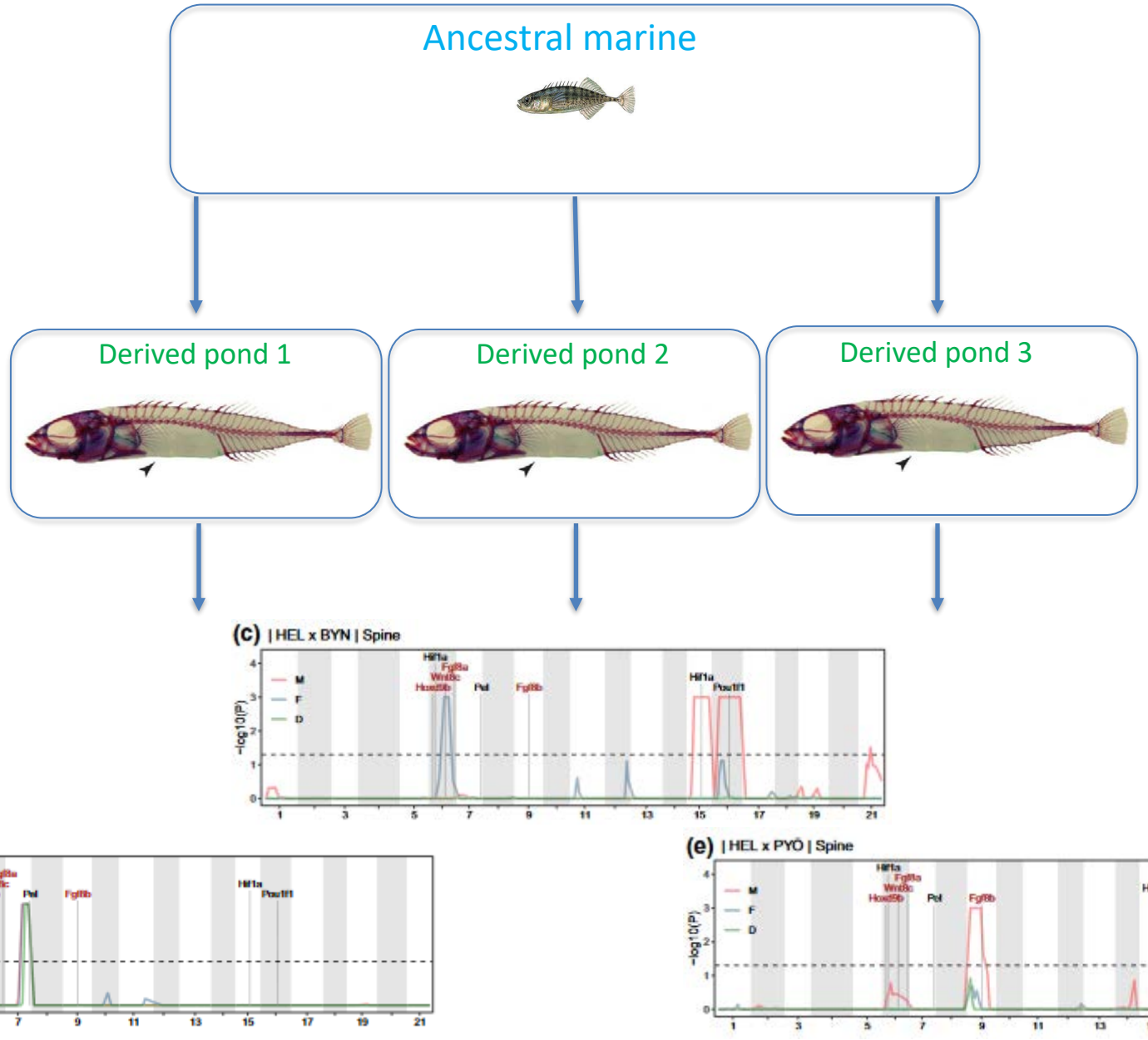
Is evolution predictable?

Is evolution always predictable?


Ancestral marine
Derived pond 1
Derived pond 2
Derived pond 3
Shared genetic basis
M
F
D
Hif1a
Fgf8a
Wnt8c
Hoxd9b
Pel
Fgf8b
Hif1a
Pou1f1
−log10(P)
0
1
2
3
4
1
3
5
7
9
11
13
15
17
19
21

(non)parallel genetic evolution

Kemppainen *et al.* 2021



(non) parallel genetic evolution

« Multiple paths to the same destination »
- Yamakasi & Kitano 2021

(non) parallel genetic evolution

ARTICLE

Received 2 Jun 2014 | Accepted 8 Sep 2014 | Published 27 Oct 2014

DOI: 10.1038/ncomms6168

Parallel evolution of Nicaraguan crater lake cichlid fishes via non-parallel routes

Kathryn R. Elmer[1,2], Shaohua Fan[1], Henrik Kusche[1,3], Maria Luise Spreitzer[1,3], Andreas F. Kautt[1,3], Paolo Franchini[1] & Axel Meyer[1,3]

Genetic population structure constrains local adaptation in sticklebacks

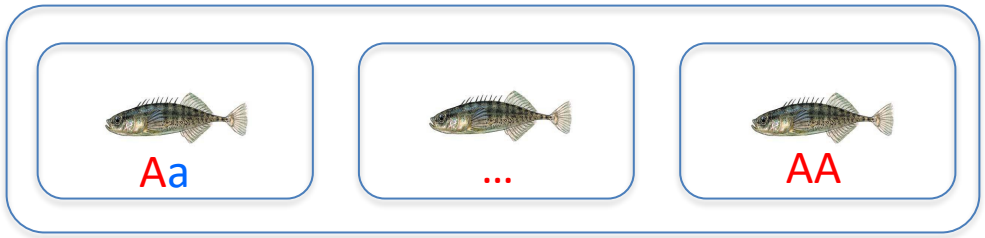
Petri Kemppainen[1] | Zitong Li[1,2] | Pasi Rastas[1,3] | Ari Löytynoja[3] | Bohao Fang[1] | Jing Yang[1,4] | Baocheng Guo[5] | Takahito Shikano[1] | Juha Merilä[1,6]

Distinct Patterns of Selective Sweep and Polygenic Adaptation in Evolve and Resequence Studies

Neda Barghi, Christian Schlötterer

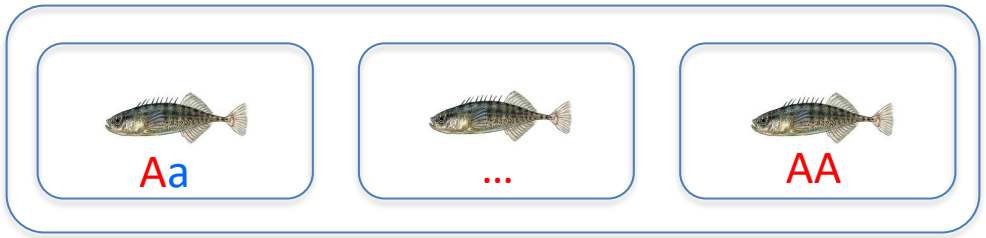
When is evolution predictable?

Genetic population structure in the sea



Fang *et al.* 2021; Kemppainen *et al.* 2021

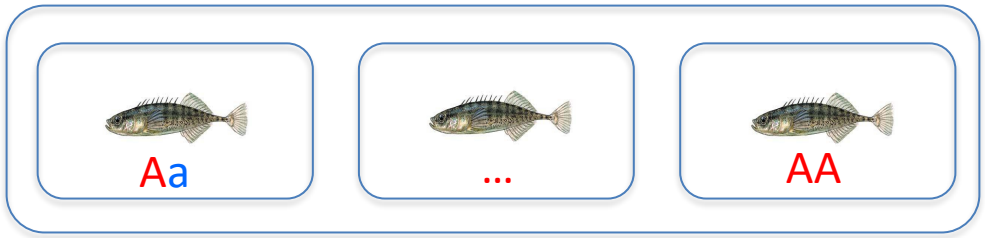
Genetic population structure in the sea



Selection on heterogeneous pool of standing genetic variation

Fang *et al.* 2021; Kemppainen *et al.* 2021

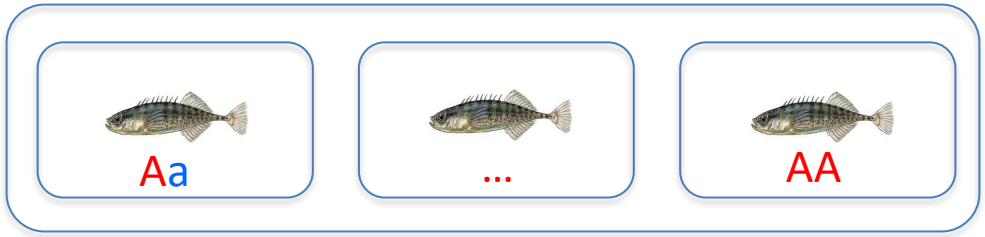
Genetic population structure in the sea



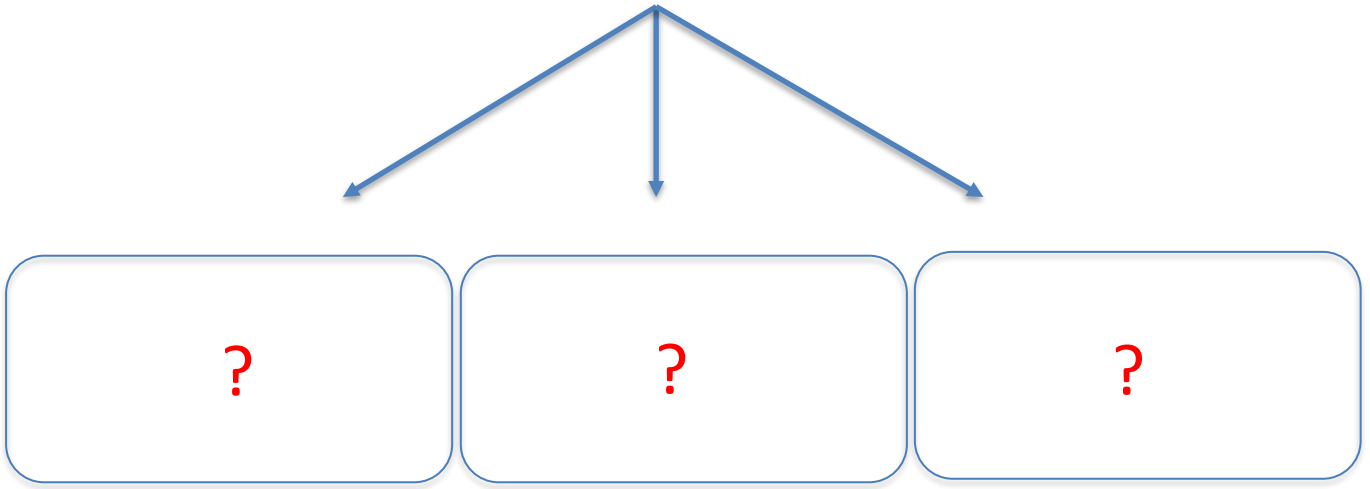
Selection on heterogeneous pool of standing genetic variation

Fang *et al.* 2021; Kemppainen *et al.* 2021

Genetic heterogeneity in the ancestral population



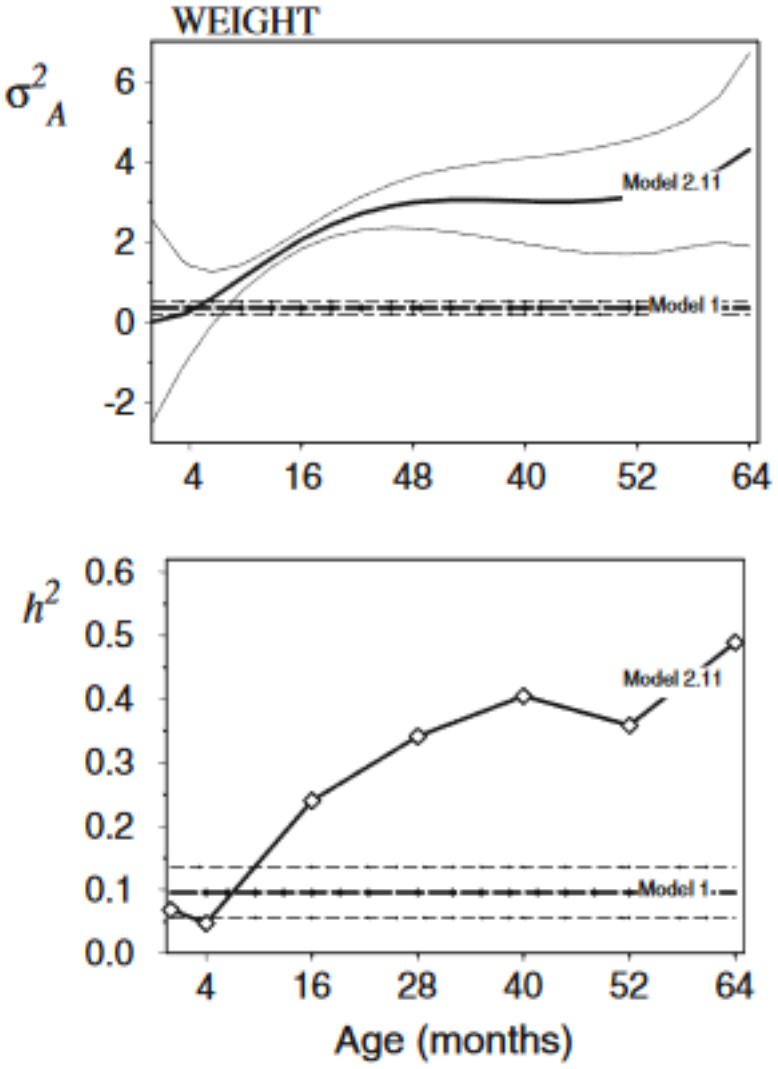
Selection on heterogeneous pool of standing genetic variation



Heterogeneous genetic variation decreases likelihood of parallel evolution

II - Investigating sources of non parallel evolution

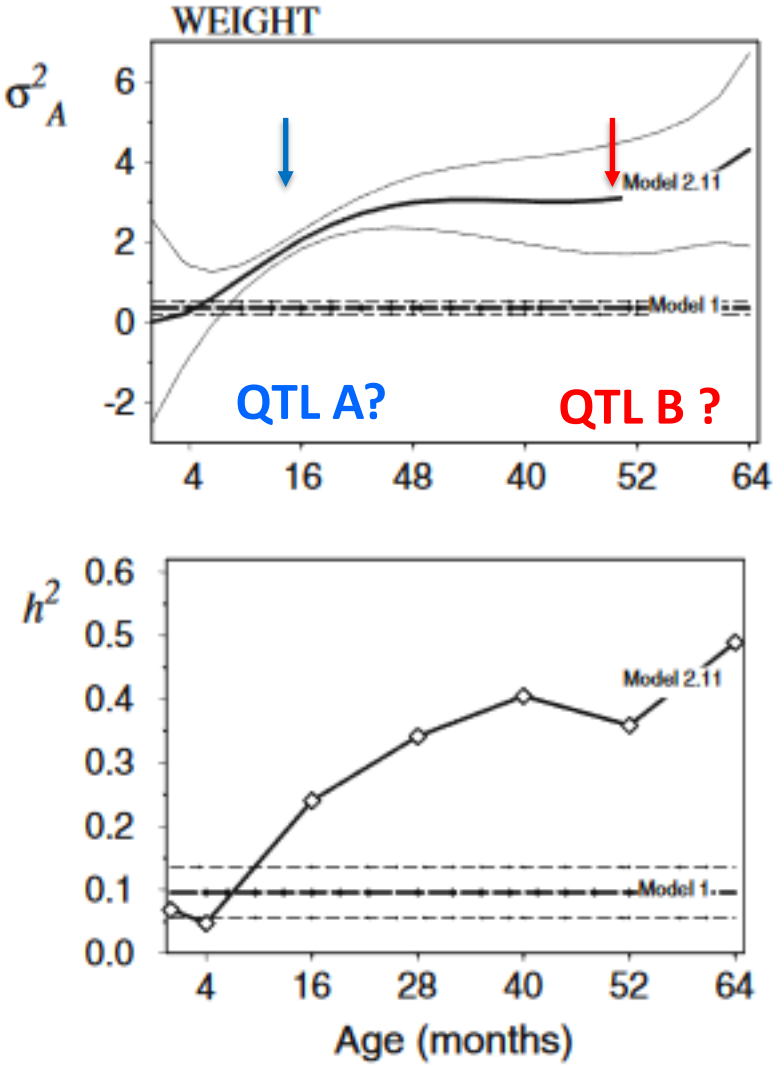
II - Investigating sources of non parallel evolution



Quantitative genetic variance changes with time

Wilson *et al.* 2007

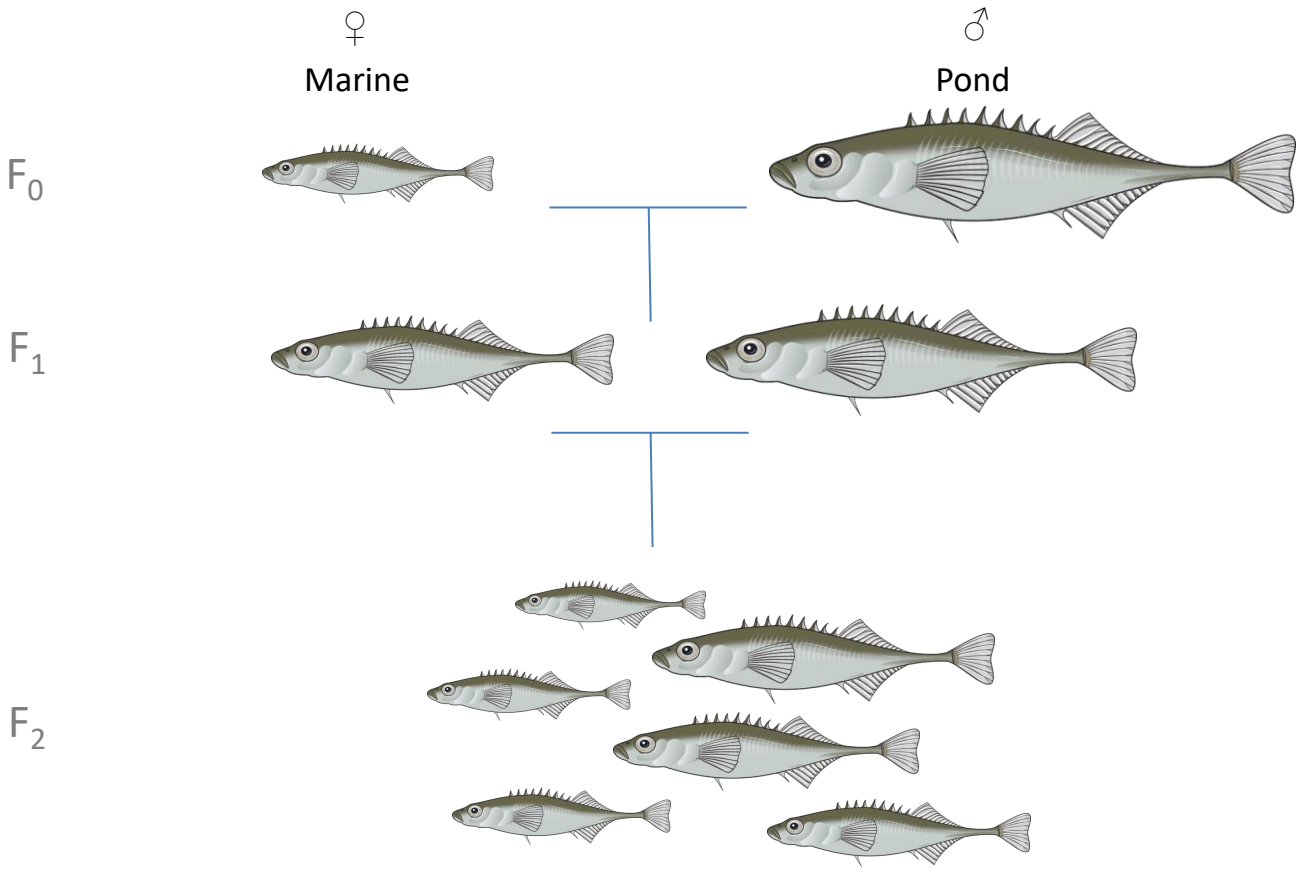
II - Investigating sources of non parallel evolution



Change in actual QTL?

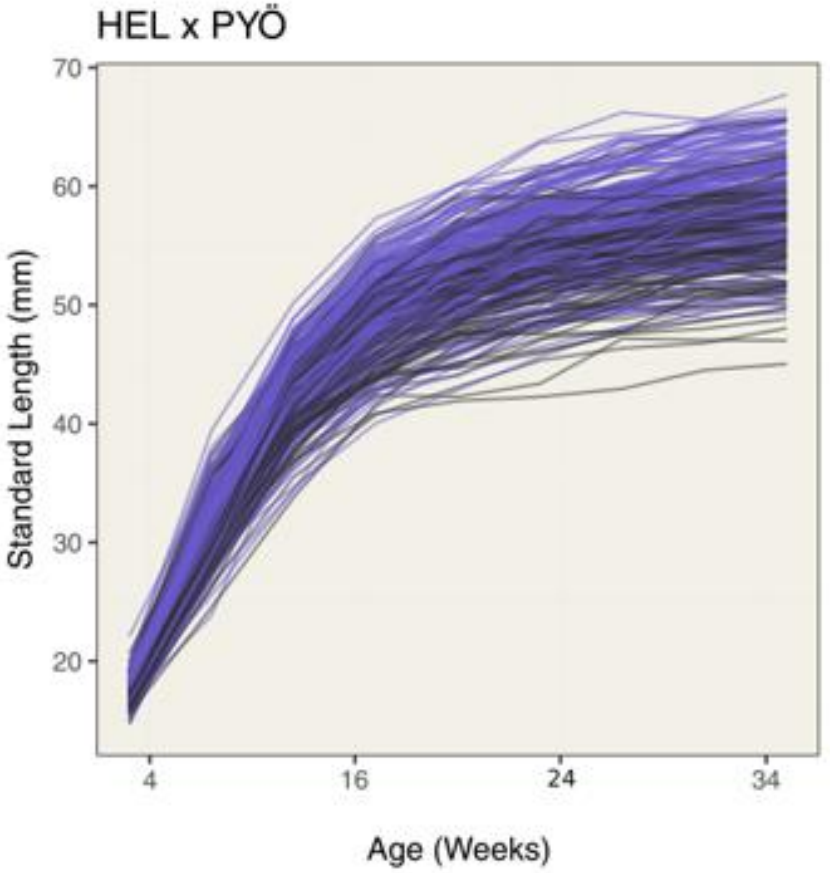
Wilson *et al.* 2007

II – Quantitative genetics of body size: QTL mapping



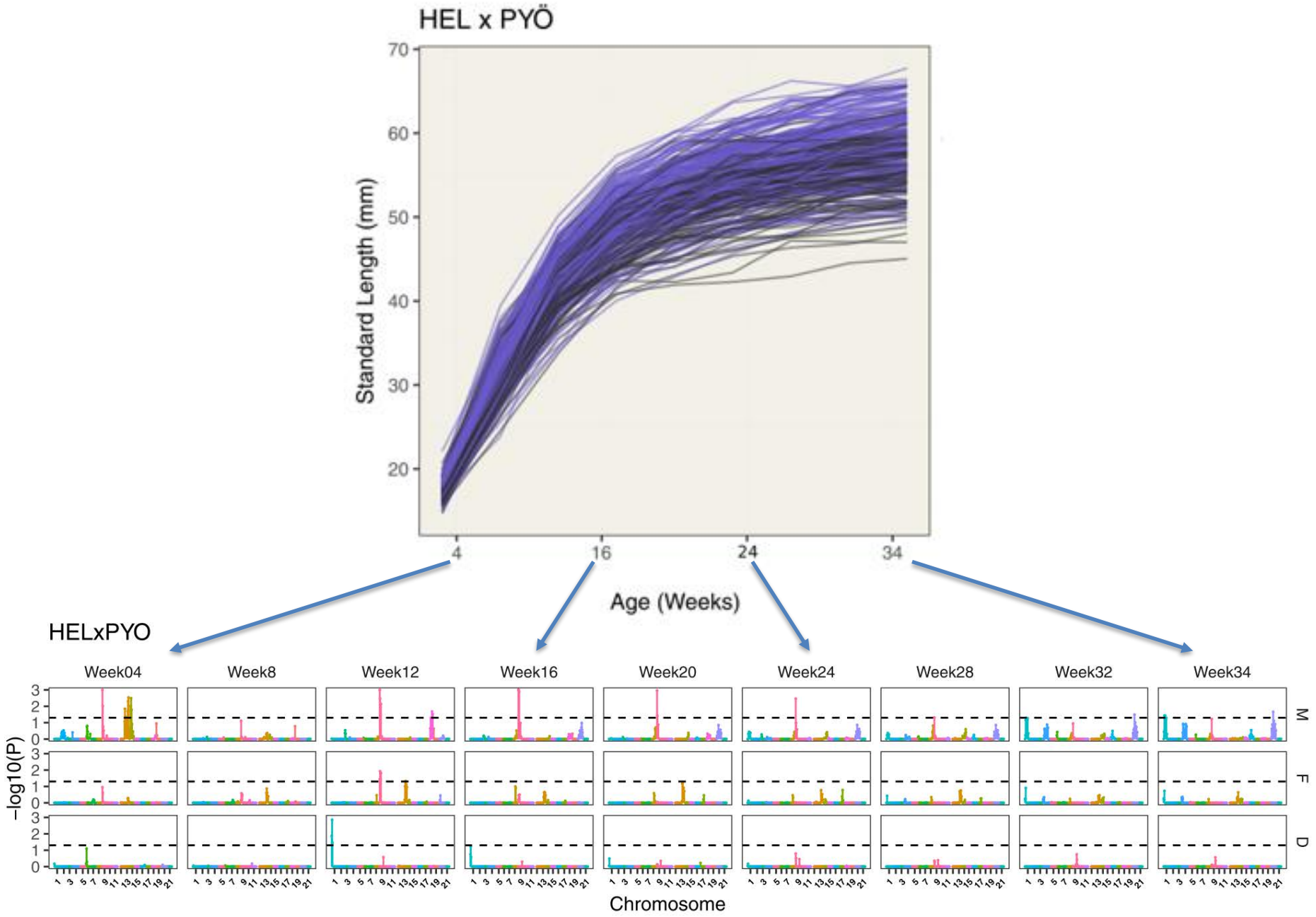
Inter-population F2 QTL cross

II – Quantitative genetics of body size: QTL mapping

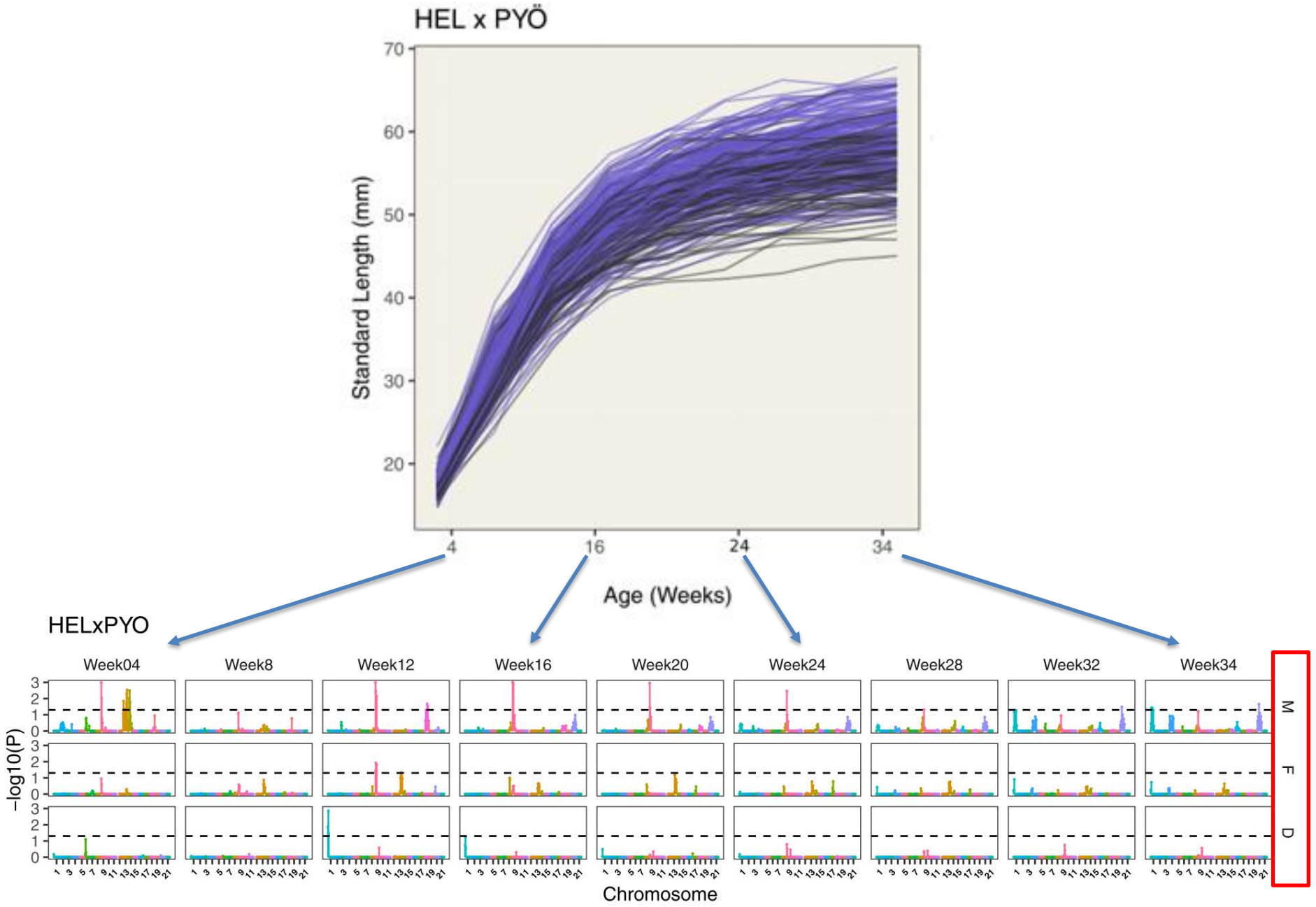


Fraimout *et al.* 2022a

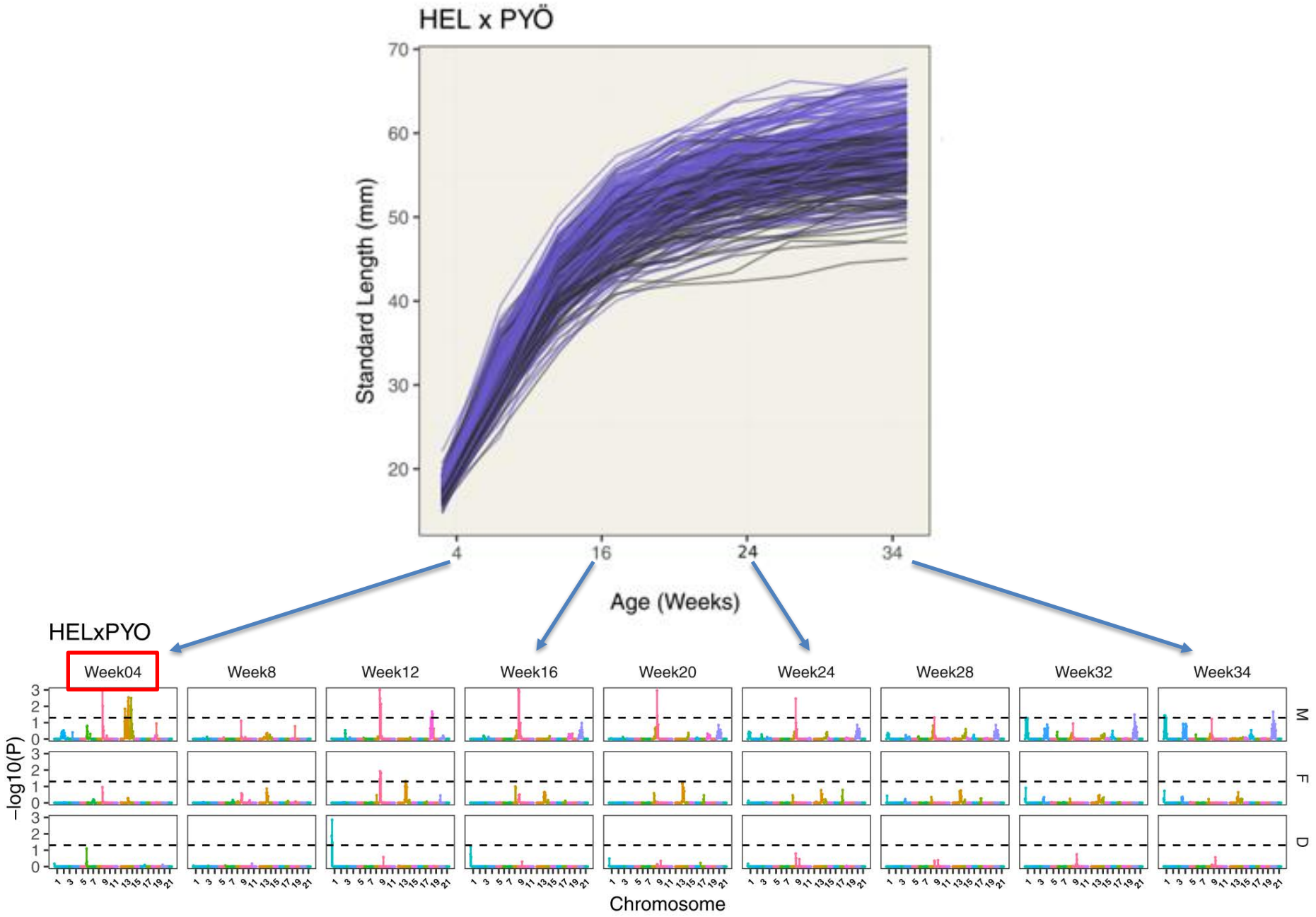
II – Quantitative genetics of body size: QTL mapping



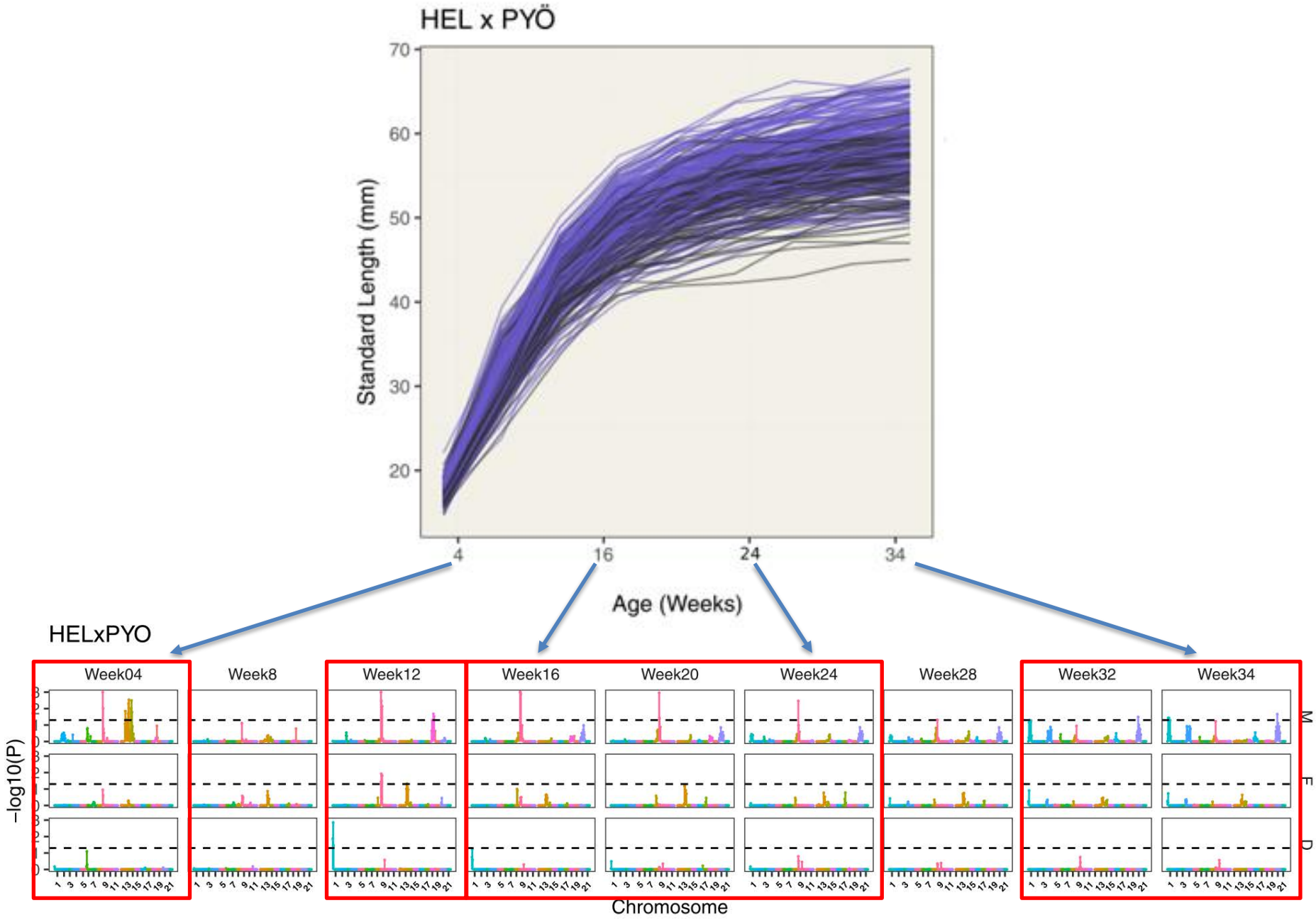
II – Quantitative genetics of body size: QTL mapping



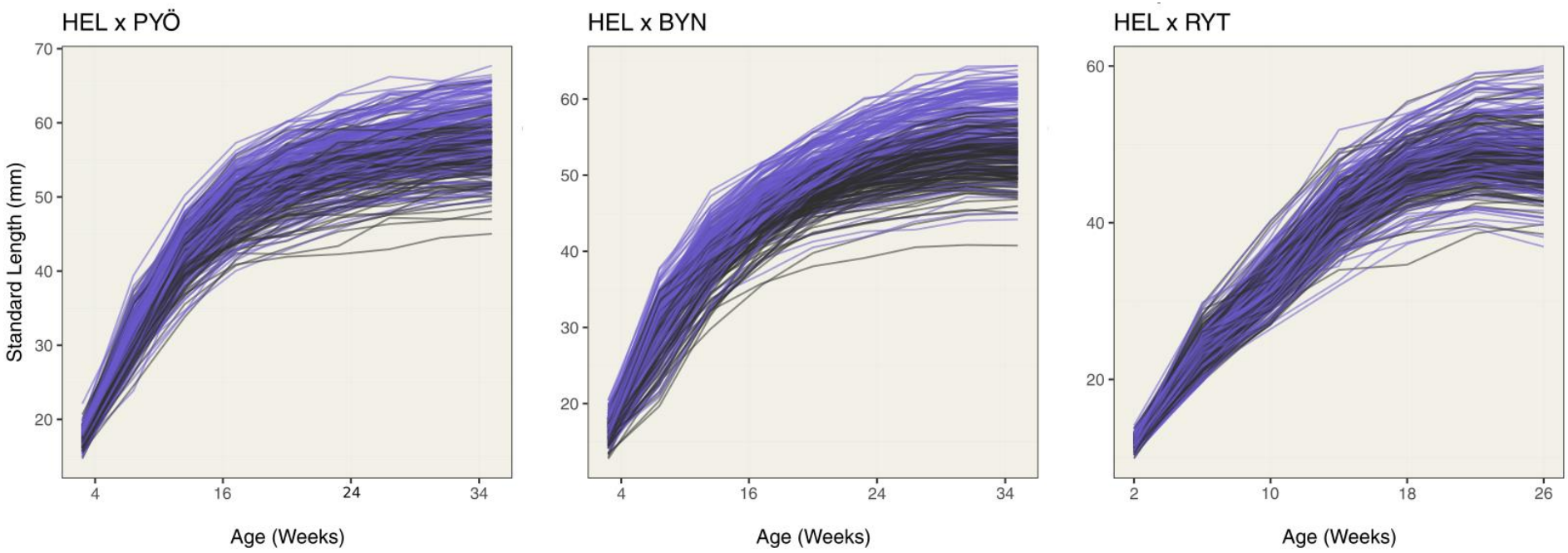
II – Quantitative genetics of body size: QTL mapping



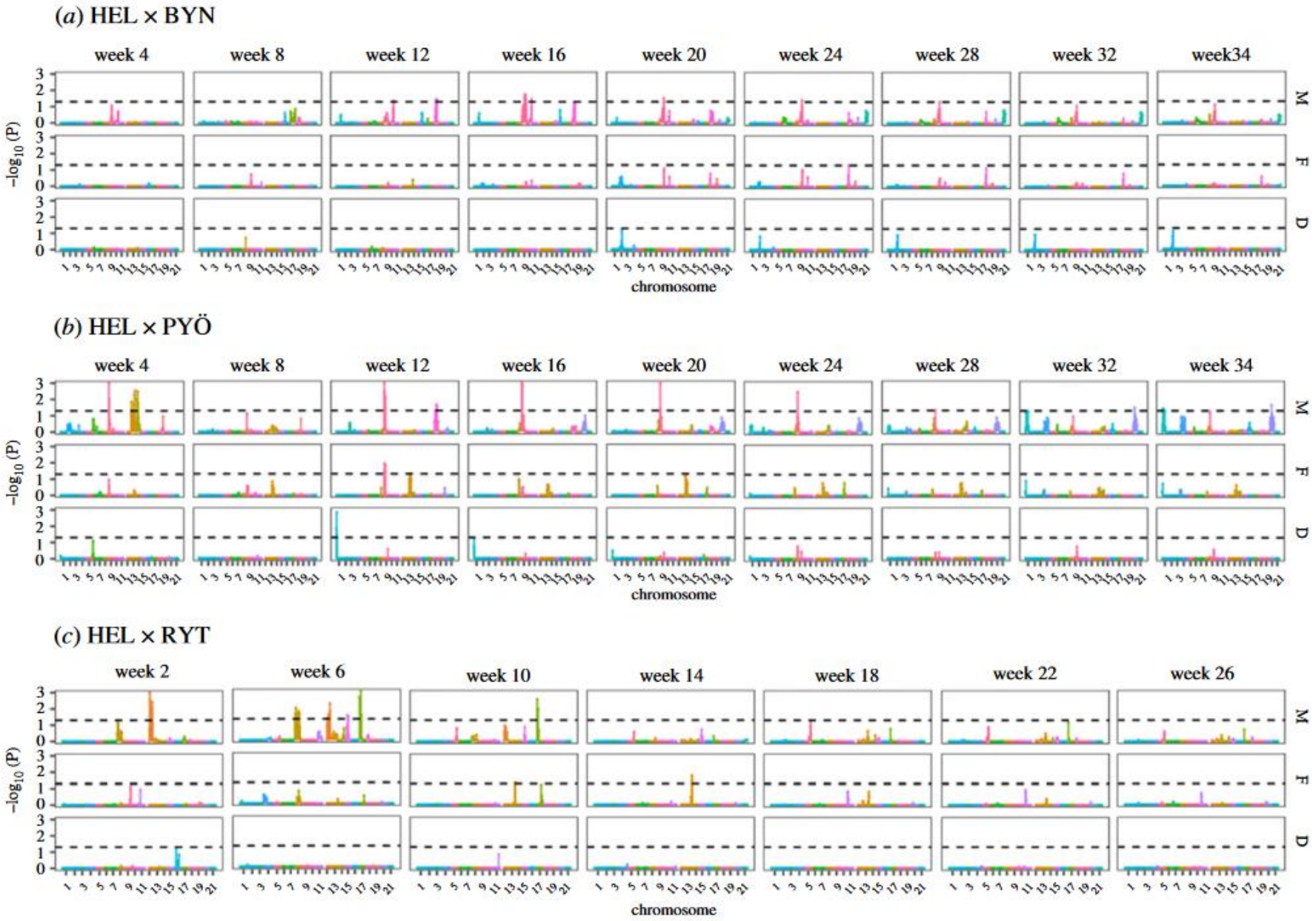
II – Quantitative genetics of body size: QTL mapping



II – Quantitative genetics of body size: QTL mapping

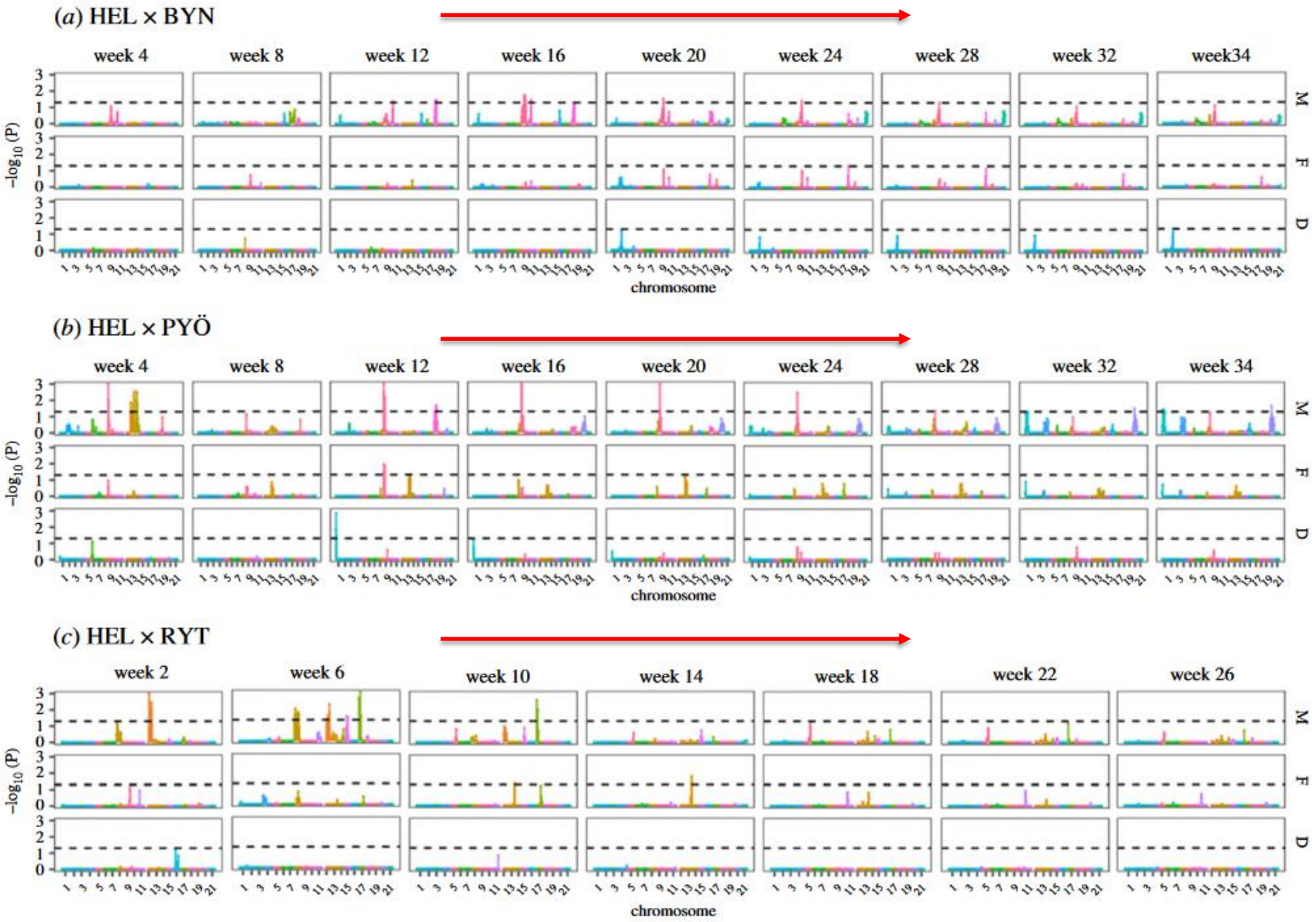


Fraimout *et al.* 2022a



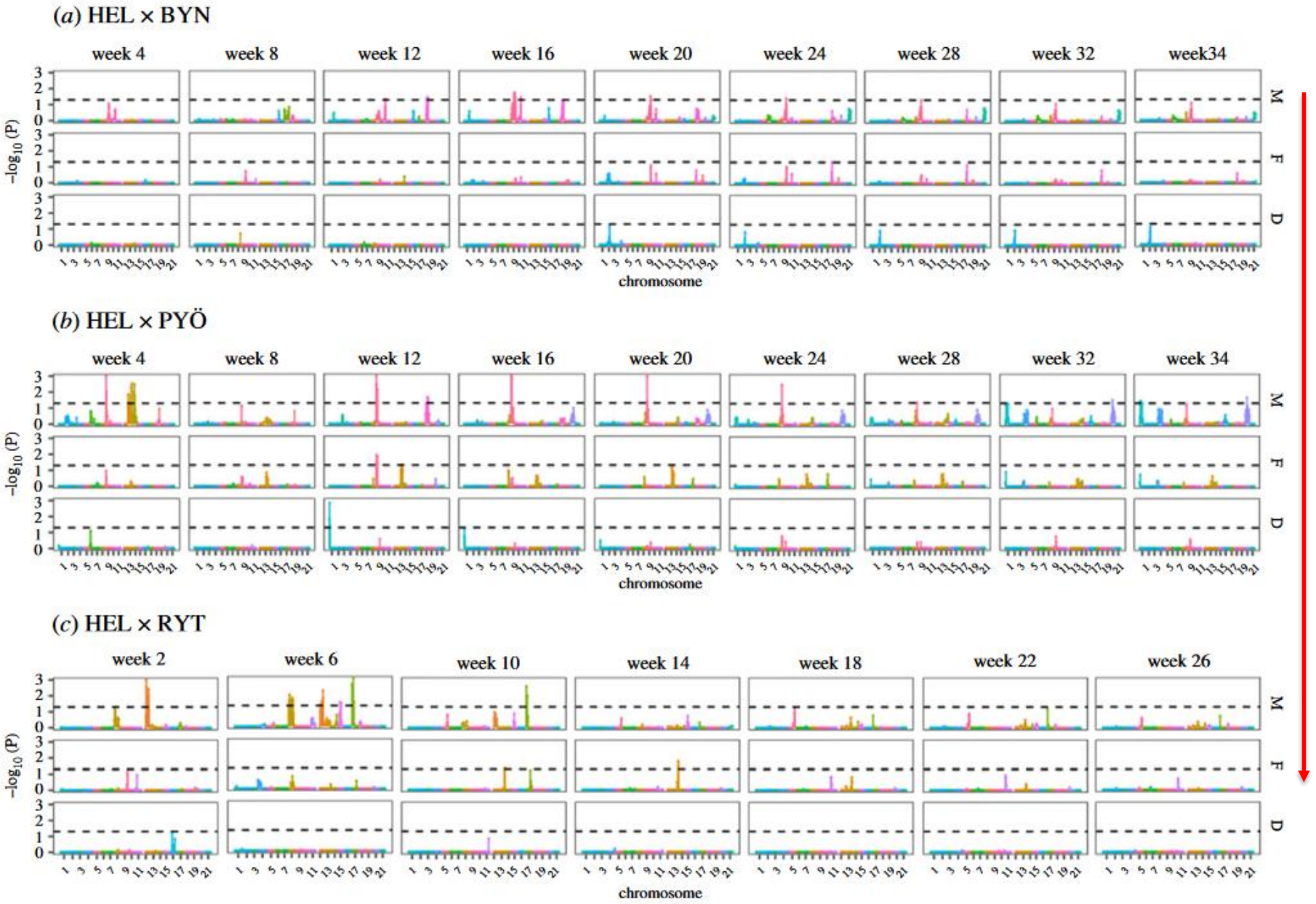
Fraimout *et al.* 2022a

Age-specific genetic architecture



Fraimout *et al.* 2022a

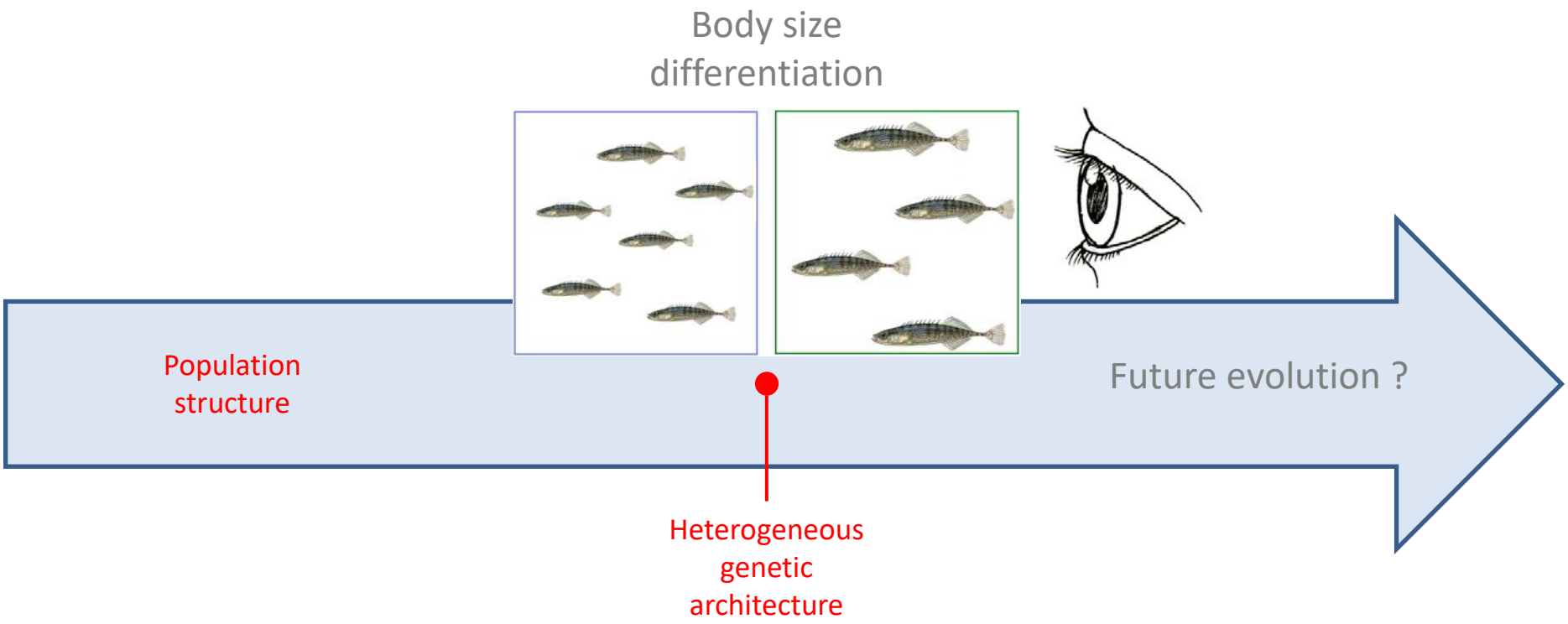
Population specific genetic architecture



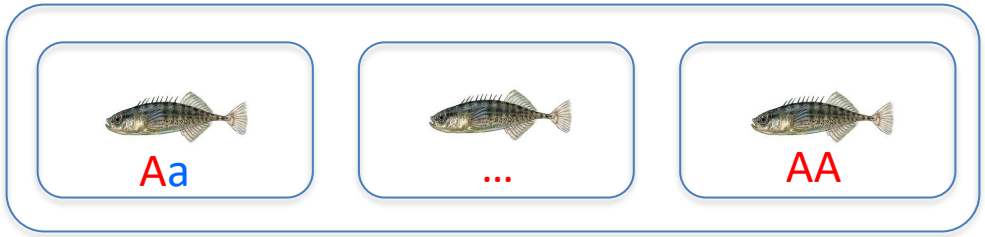
Fraimout *et al.* 2022a

II – Conclusions

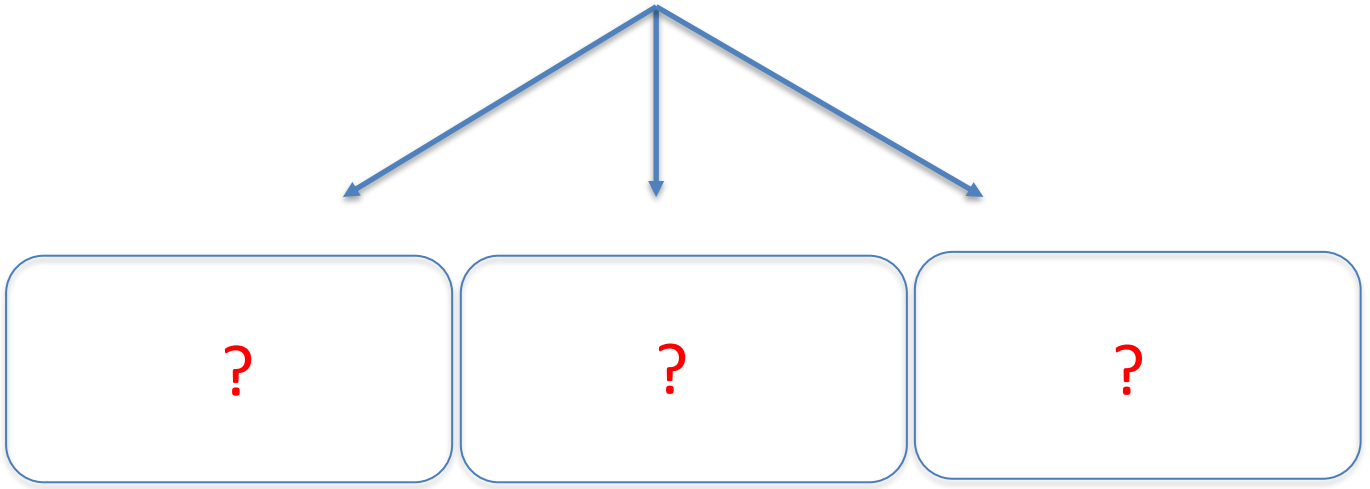
Age-specific genetic architecture of body size throughout ontogeny in nine-spined sticklebacks

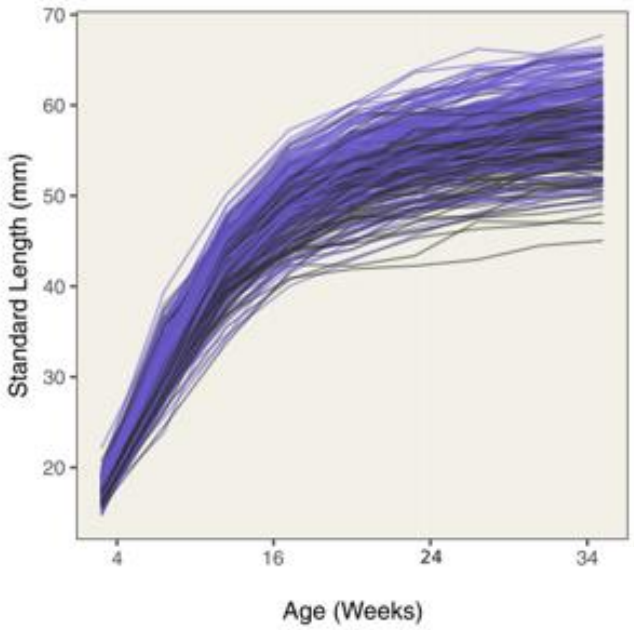


Genetic heterogeneity in the ancestral population



Selection on heterogeneous pool of standing genetic variation





Age-specific selection

?

?

?

II – Conclusions

Fisheries-Induced Evolution

Mikko Heino,[1,2,3] Beatriz Díaz Pauli,[1]
and Ulf Dieckmann[3]

[1]Department of Biology and Hjort Centre for Marine Ecosystem Dynamics, University of Bergen, N-5020 Bergen, Norway; email: mikko.heino@uib.no

[2]Institute of Marine Research and Hjort Centre for Marine Ecosystem Dynamics, N-5817 Bergen, Norway

[3]Evolution and Ecology Program, International Institute for Applied Systems Analysis, A-2361 Laxenburg, Austria

ORIGINAL ARTICLE

Fisheries-induced neutral and adaptive evolution in exploited fish populations and consequences for their adaptive potential

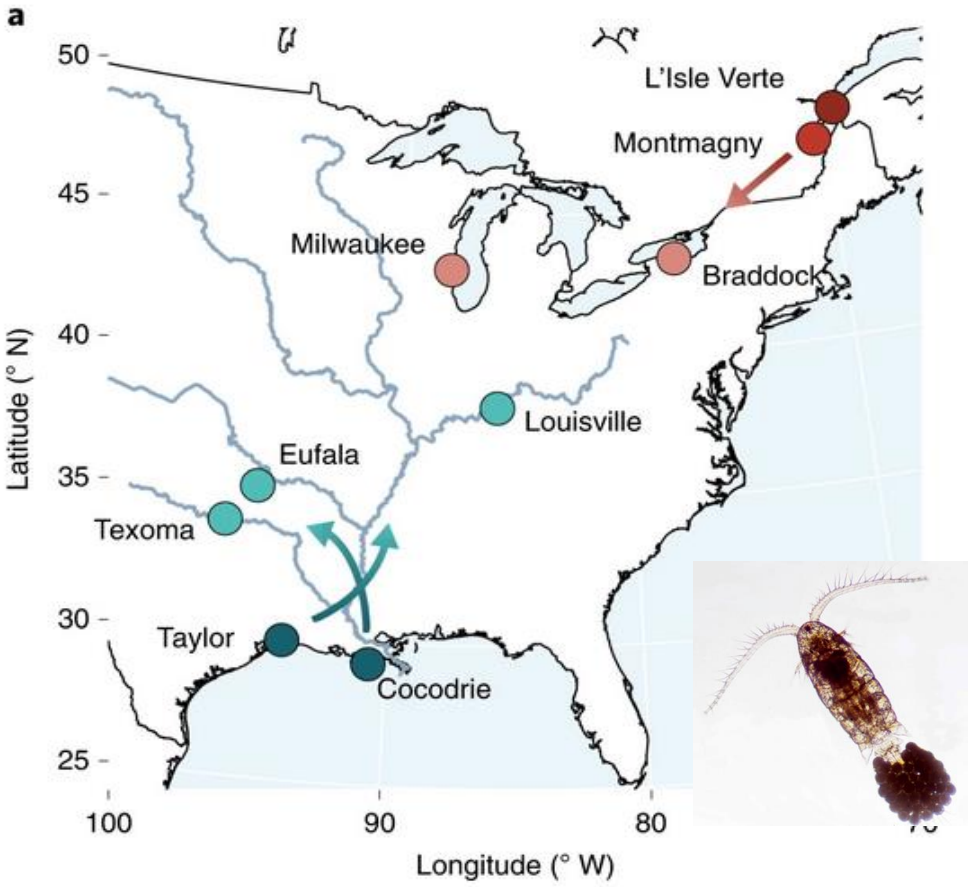
Lise Marty,[1] Ulf Dieckmann[2] and Bruno Ernande[1,2]

1 IFREMER, Laboratoire Ressources Halieutiques, Unité Halieutique Manche-Mer du Nord, Boulogne-sur-mer, France
2 IIASA, Evolution and Ecology Program, Laxenburg, Austria

Part II : The genetic bases of repeated freshwater adaptation in copepods

II – Recent transition from marine to freshwater of *E. affinis*

Eurytemora affinis
Abundant marine planktonic species

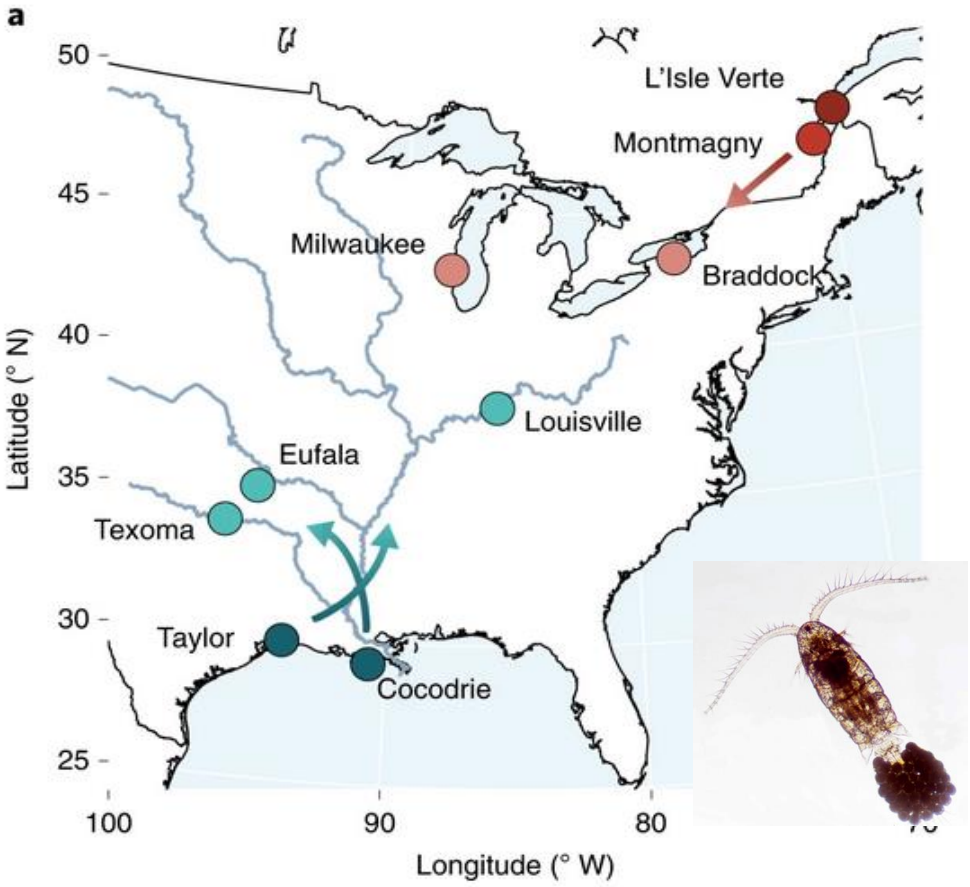


Stern & Lee 2020

II – Recent transition from marine to freshwater of *E. affinis*

Eurytemora affinis
Abundant marine planktonic species

Transported with balast waters to freshwater lakes



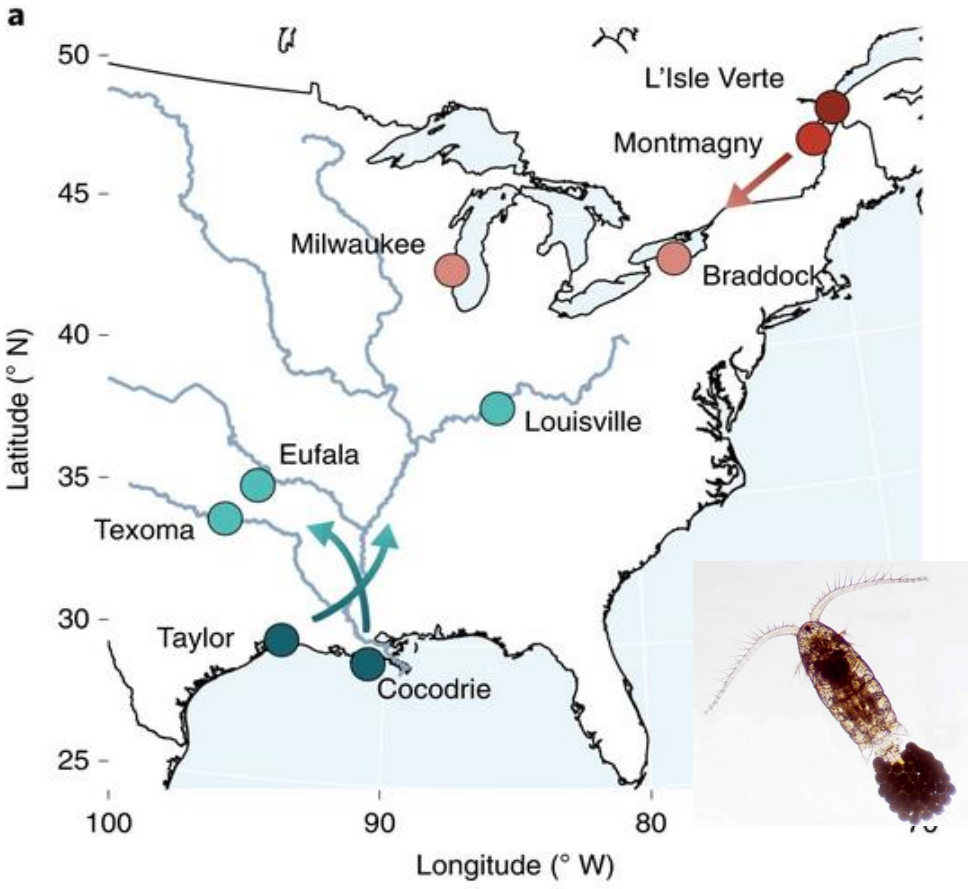
Stern & Lee 2020

II – Recent transition from marine to freshwater of *E. affinis*

Eurytemora affinis
Abundant marine planktonic species

Transported with balast waters to freshwater lakes

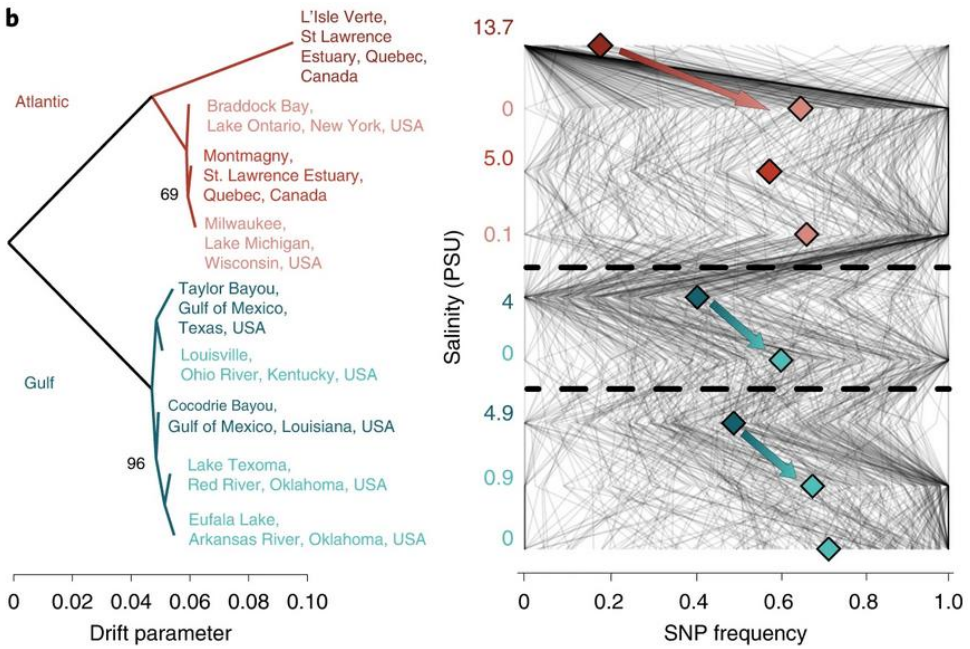
Adapted to freshwater in < 100 years



Stern & Lee 2020

II – Recent transition from marine to freshwater of *E. affinis*

Balancing selection maintains genetic variation in the ancestral population

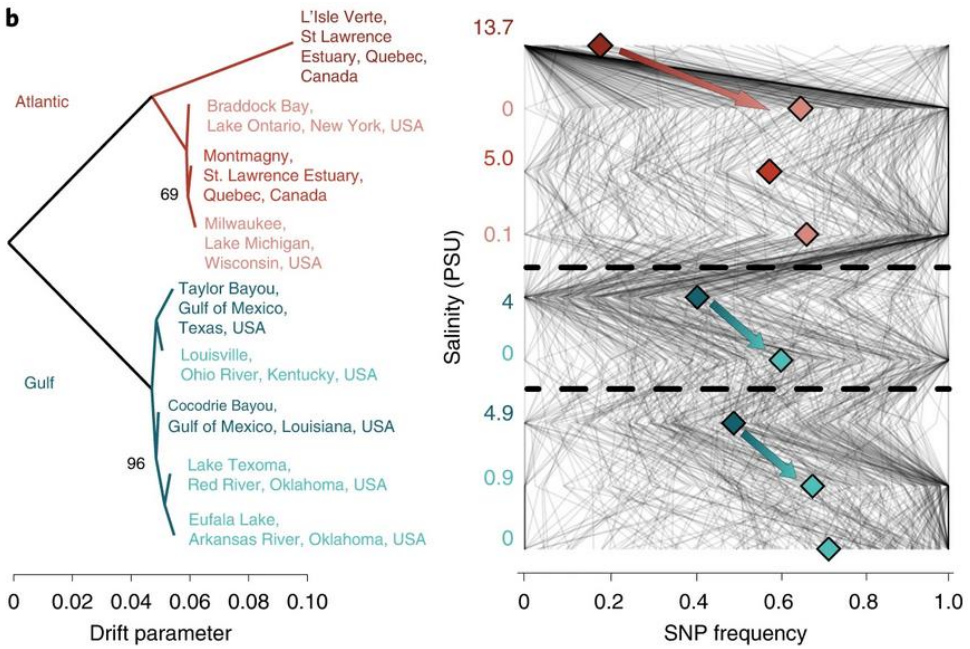


Stern & Lee 2020

II – Recent transition from marine to freshwater of *E. affinis*

Balancing selection maintains genetic variation in the ancestral population

Same SNPs increasing in frequency in parallel across lakes



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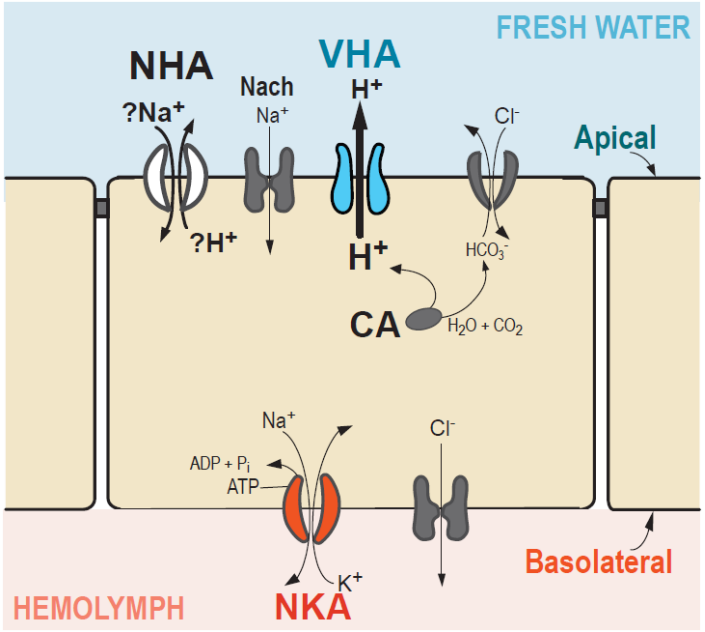
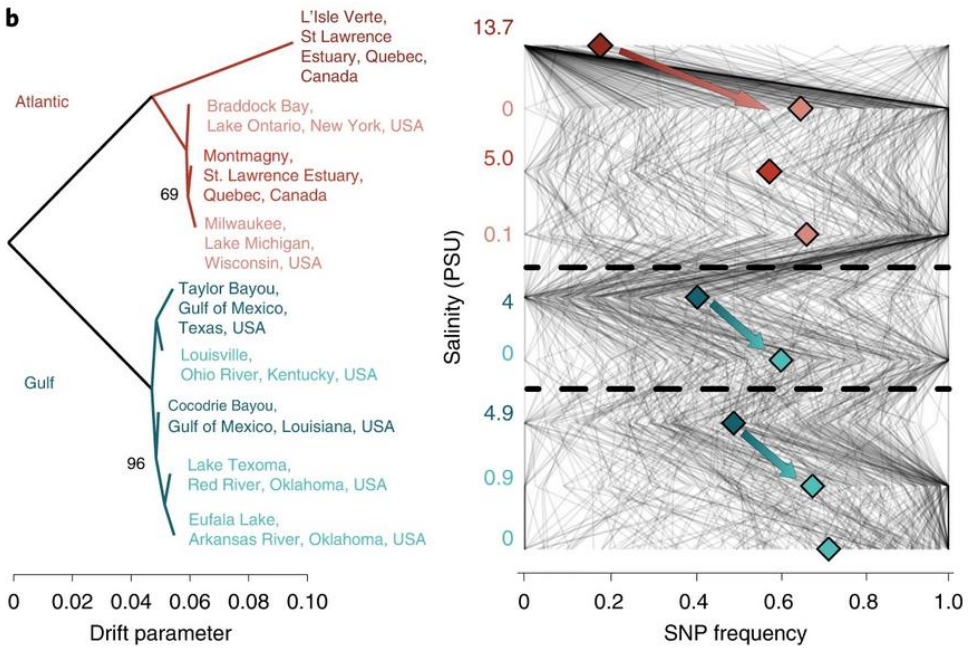




Stern & Lee 2020

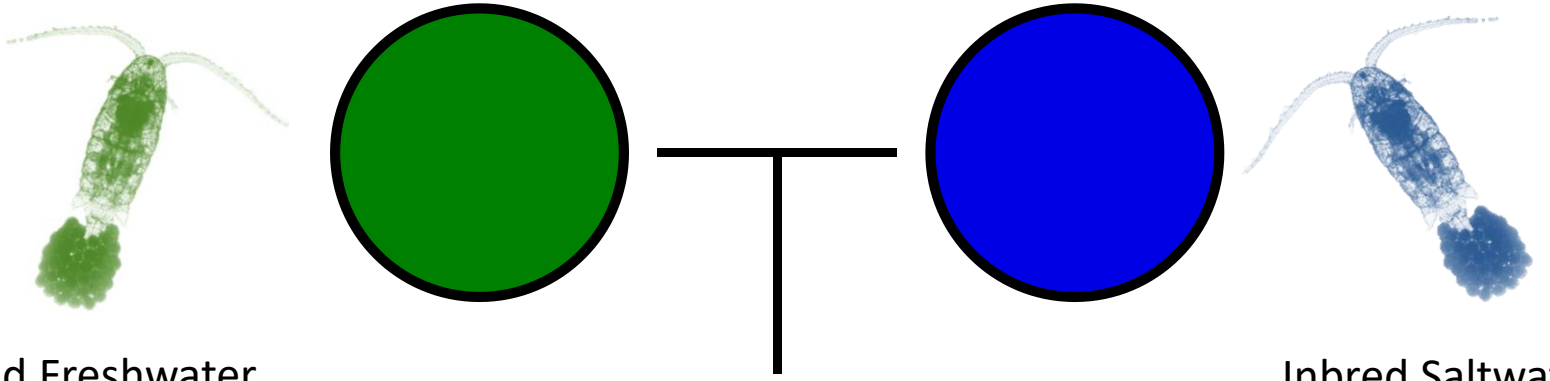
Located at ion-transporter genes

II – Research question

What are the fitness effects of ion-transporter alleles in different salinities ?

II – Experimental approach: genetic association study

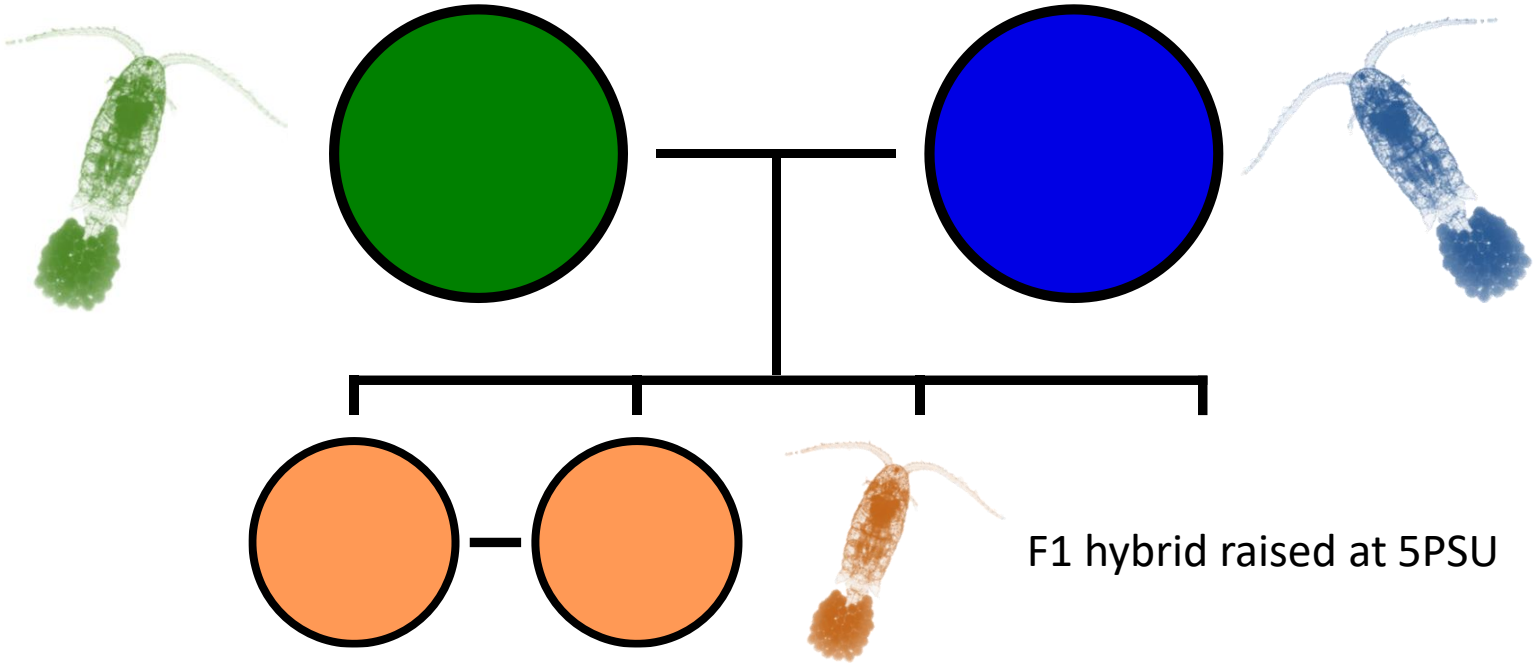
II – A genetic association study



Wild Freshwater Population 0PSU

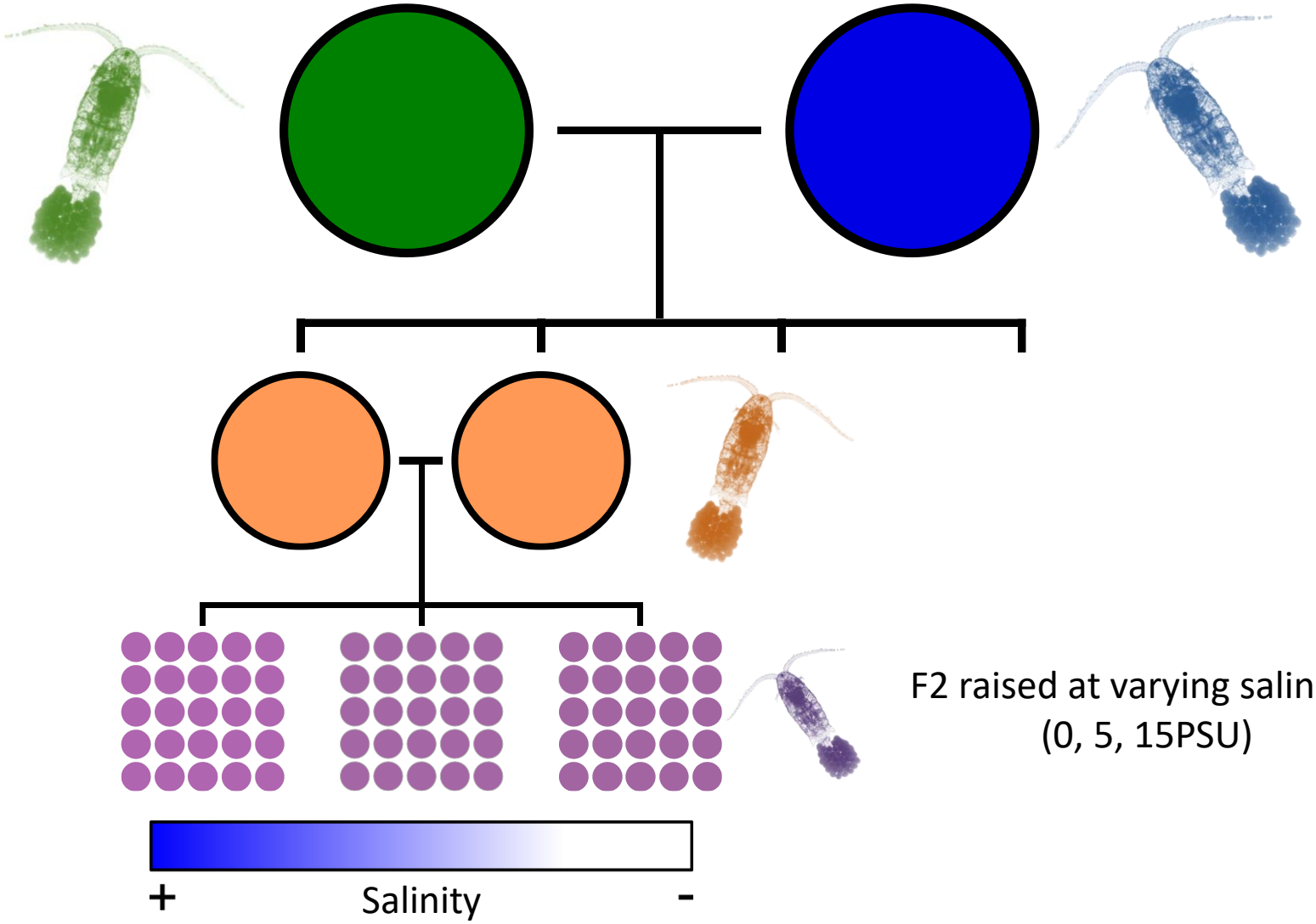
Inbred Saltwater Population 15PSU

II – A genetic association study



F1 hybrid raised at 5PSU

II – A genetic association study



F2 raised at varying salinities
(0, 5, 15PSU)

II – A genetic association study

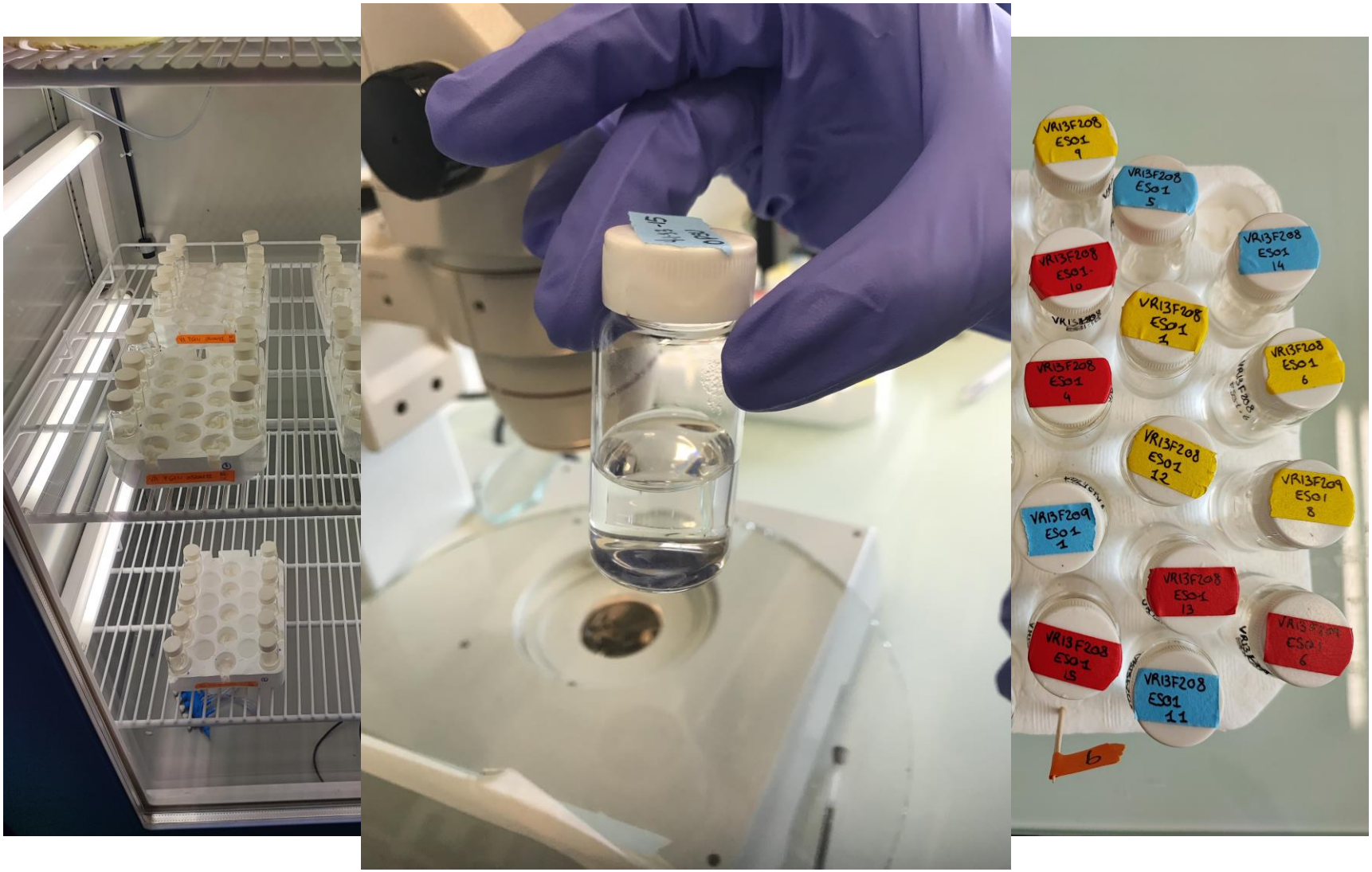
Controlled environment incubators

II – A genetic association study

Controlled environment incubators

Individual level salinity treatments

II – A genetic association study



Daily record: life stage, survival

II – Data summary

Data Block 1

387 F2 individuals

101 survivors

Teresa Popp
PhD candidate

Benjamin Kleinerman
Lab technician

II – Data summary

Data Block 1

387 F2 individuals

101 survivors

Teresa Popp
PhD candidate

Benjamin Kleinerman
Lab technician

Data Block 2

514 F2 individuals

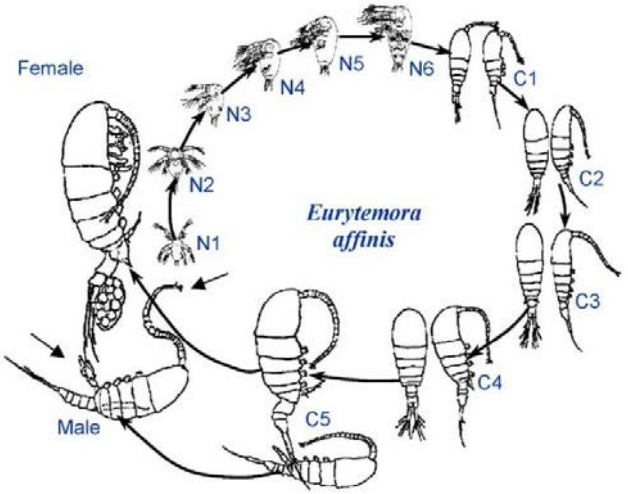
374 survivors

Estelle Dupré (M1) & Dorian Decamus (M2)

II – Data summary

Individual-level data on fitness related traits

Development time

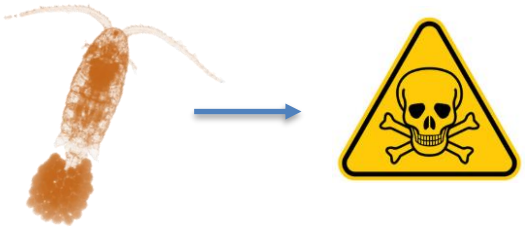


II – Data summary

Individual-level data on fitness related traits

Development time

Survival rate



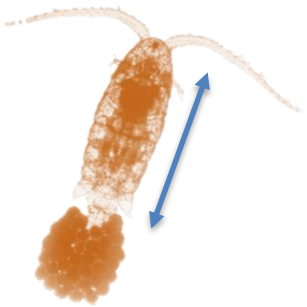
II – Data summary

Individual-level data on fitness related traits

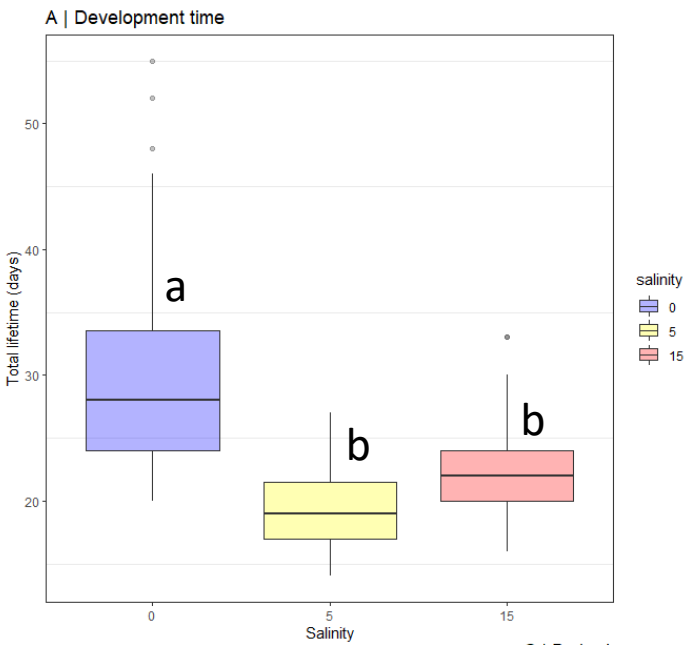
Development time

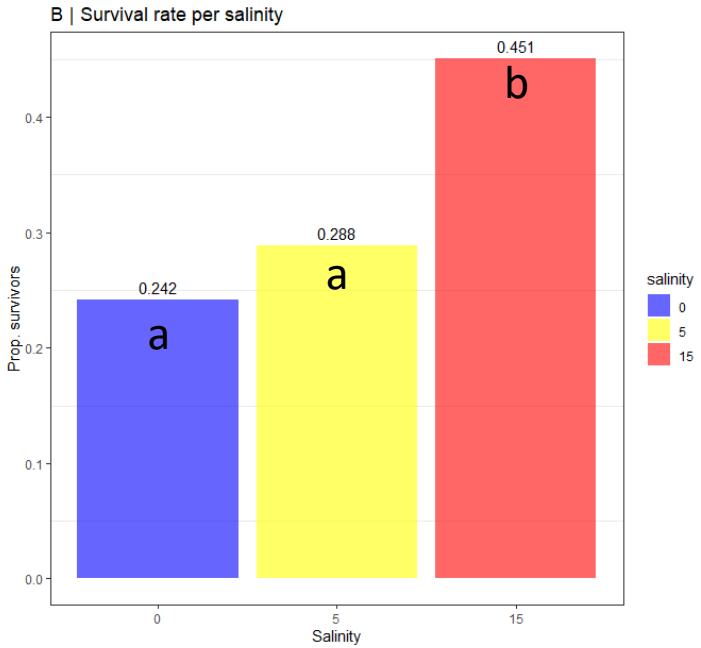
Survival rate

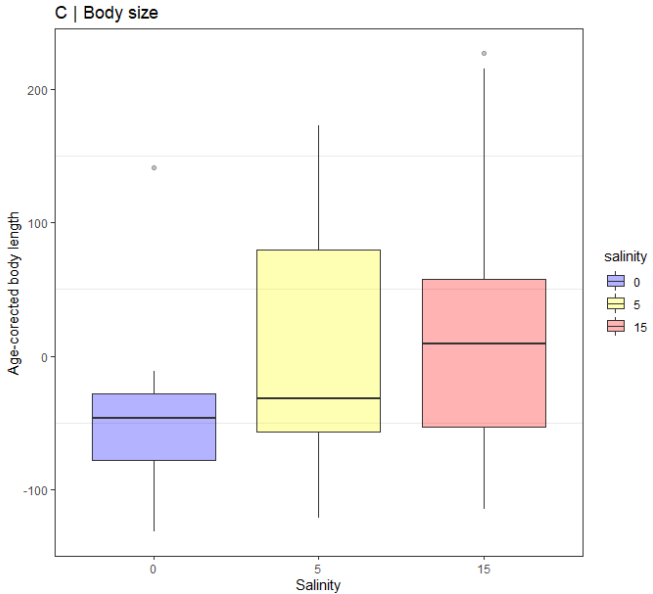
Body size



II – Preliminary results block 1

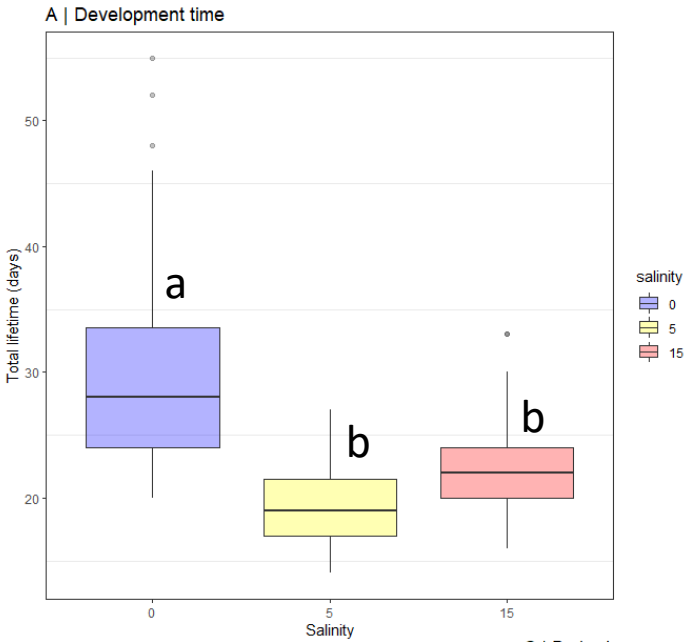


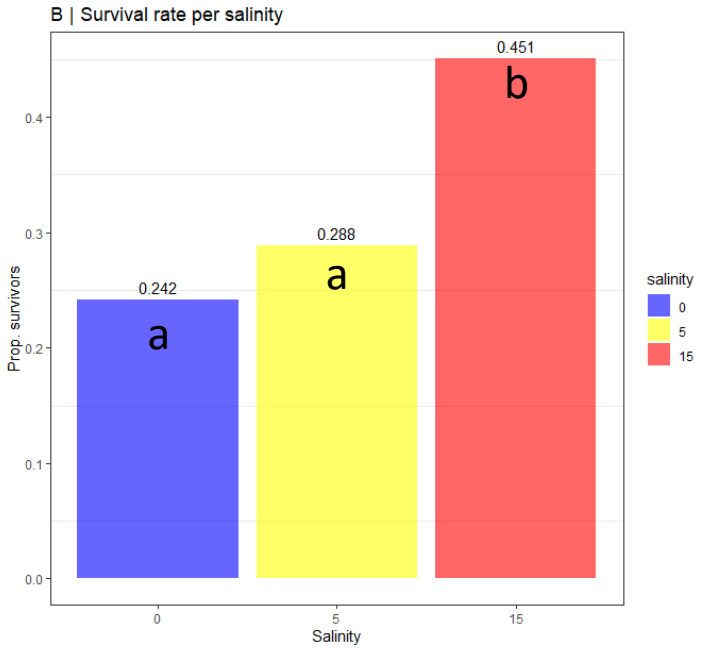


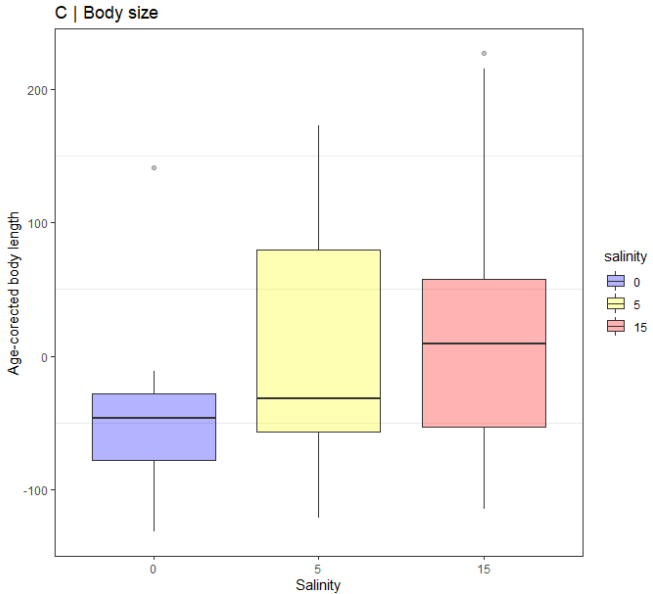


II – Preliminary results block 1

Slower development time in freshwater







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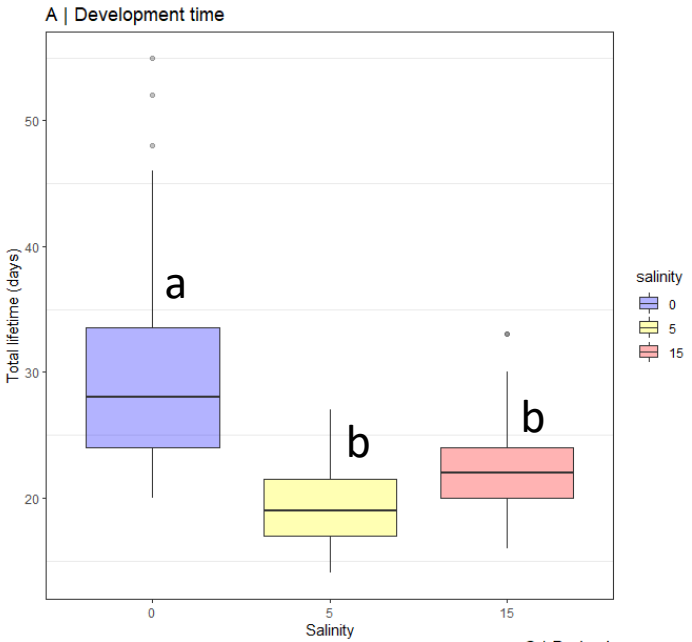
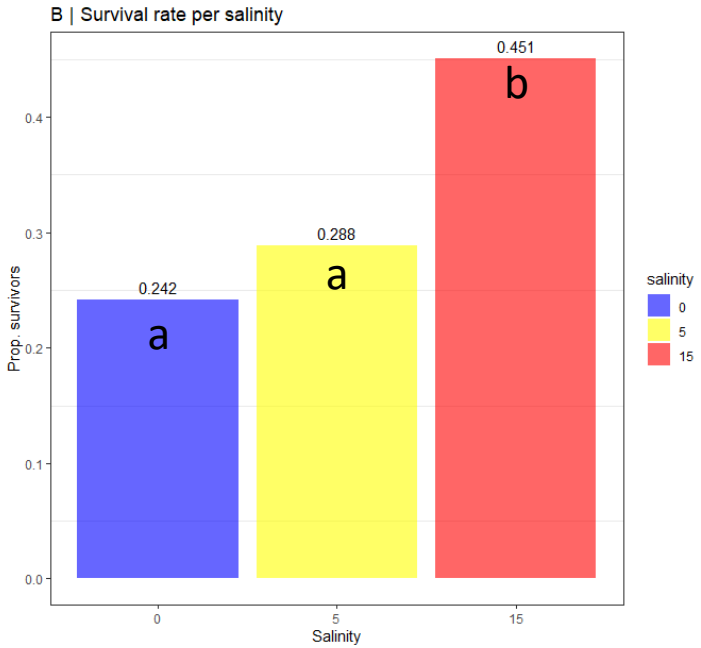
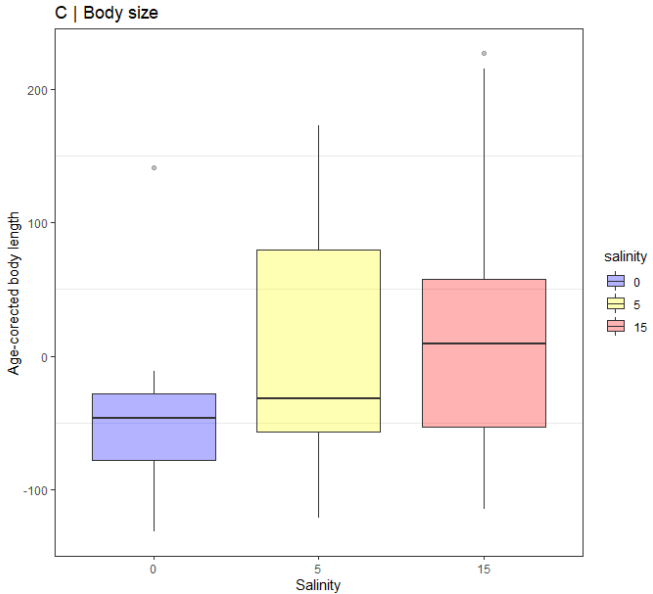
Slower development time in freshwater



Higher mortality rate in freshwater





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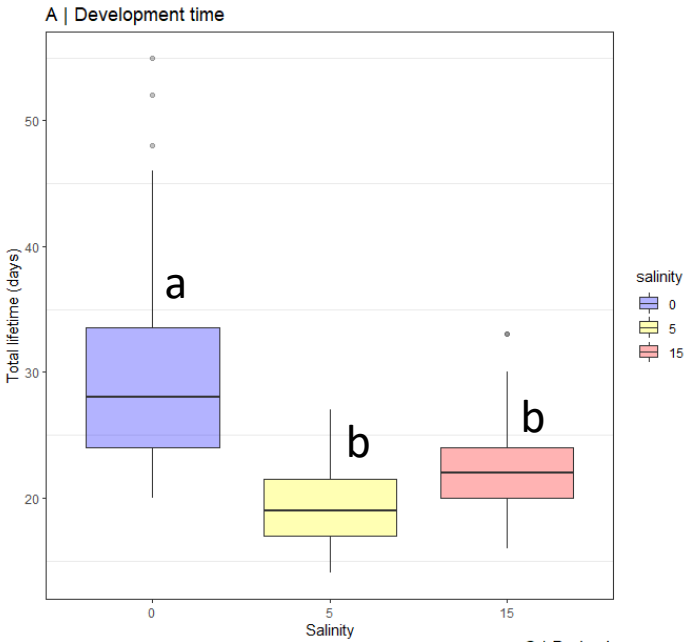
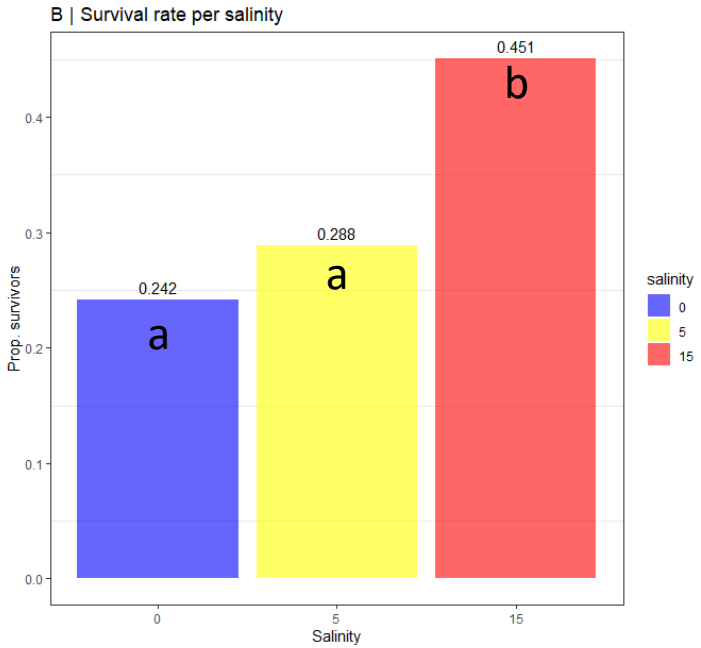
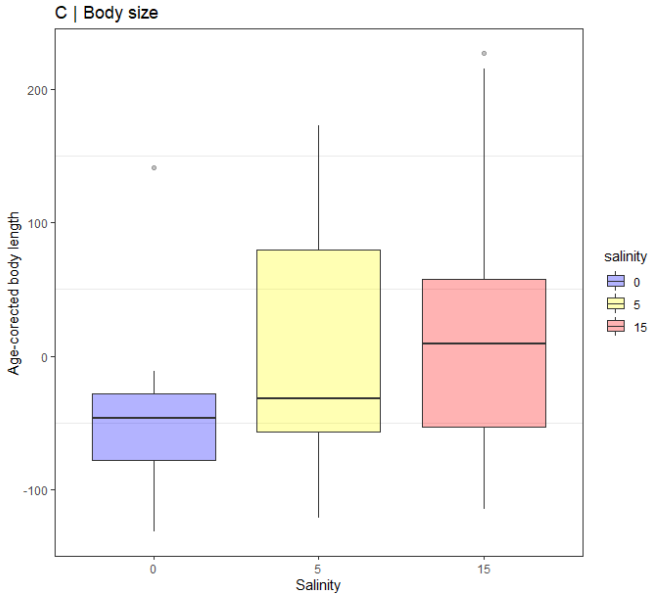
Slower development time in freshwater



Higher mortality rate in freshwater

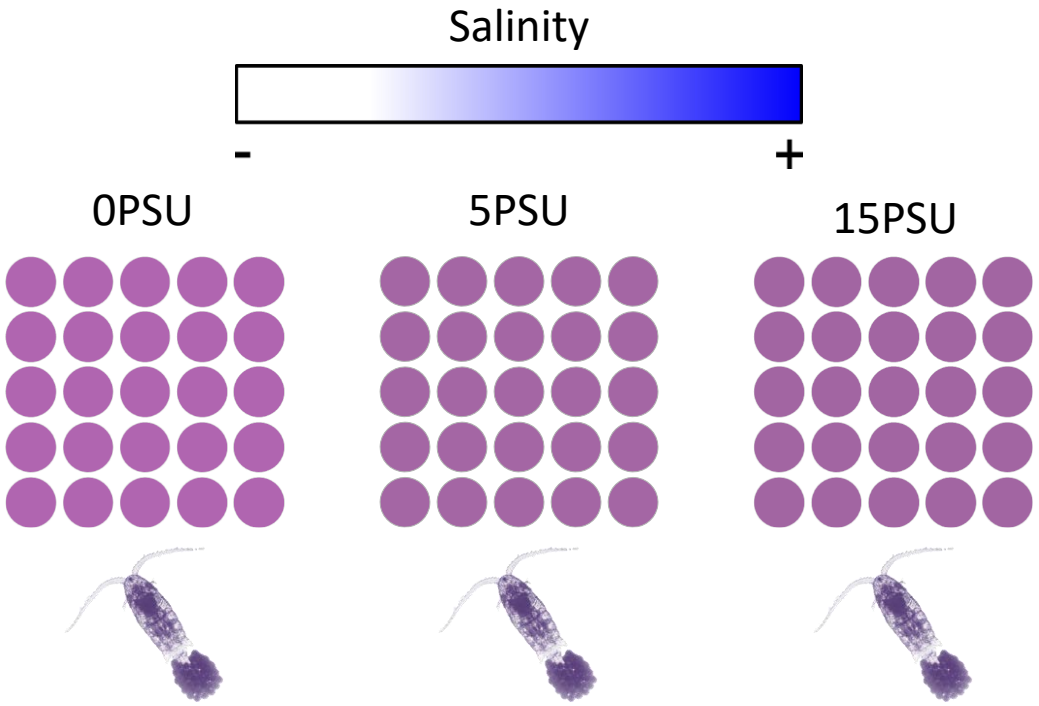




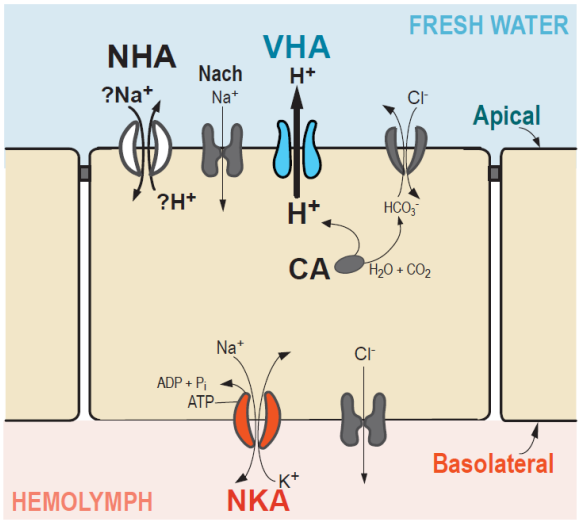
Smaller size in freshwater

(NS)

II – Genotyping at candidate loci



Individual-level data: genotype at candidate genes

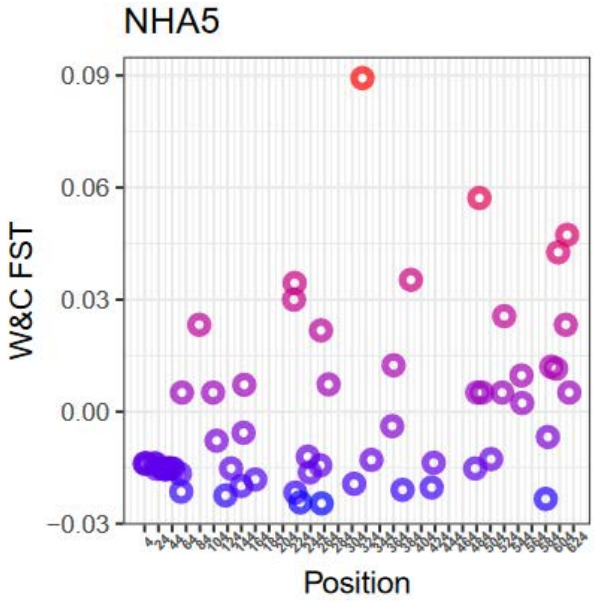


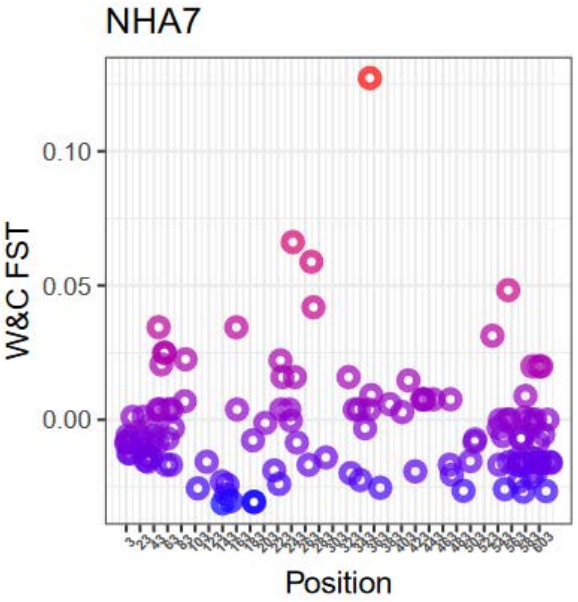
NHA5

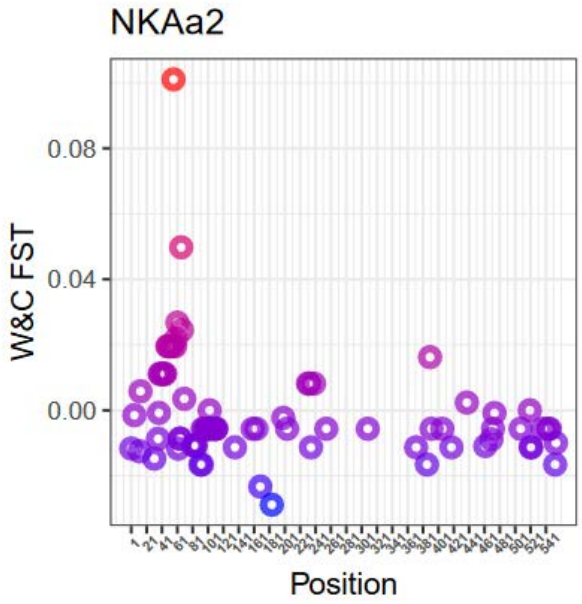
NHA7

NKAa2

II – Preliminary results block 1

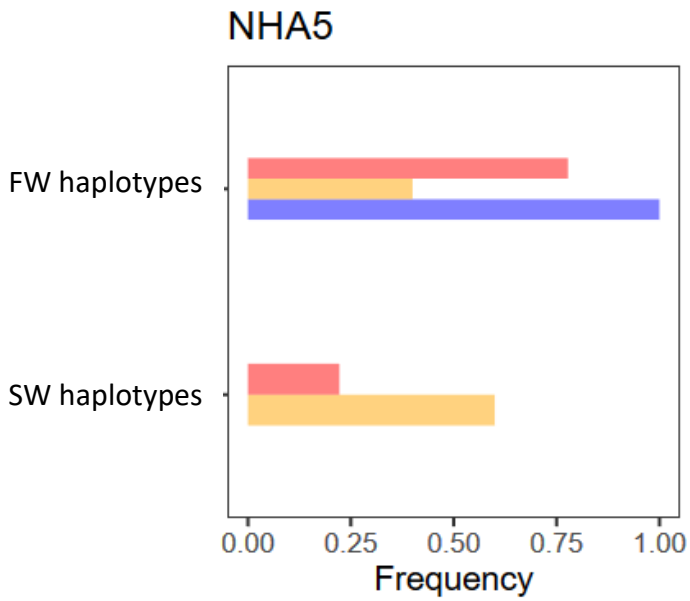


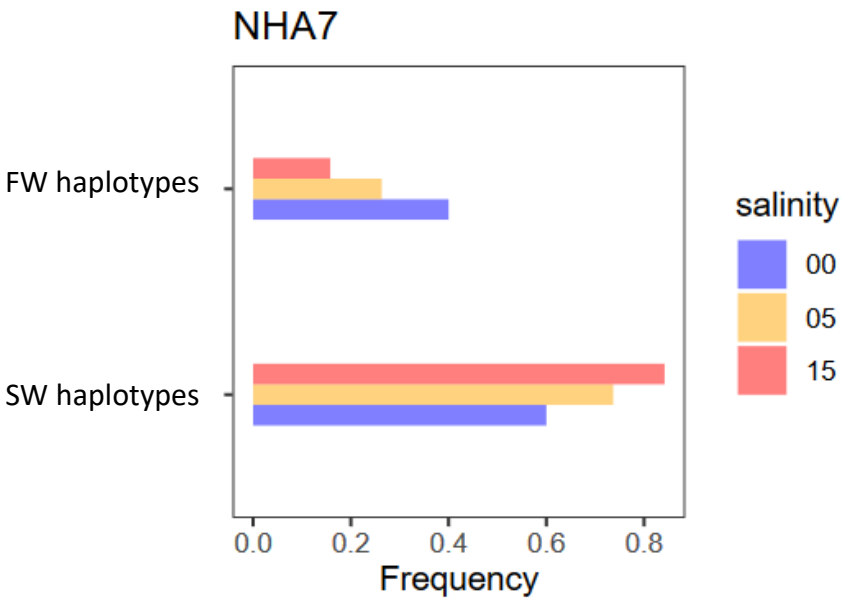


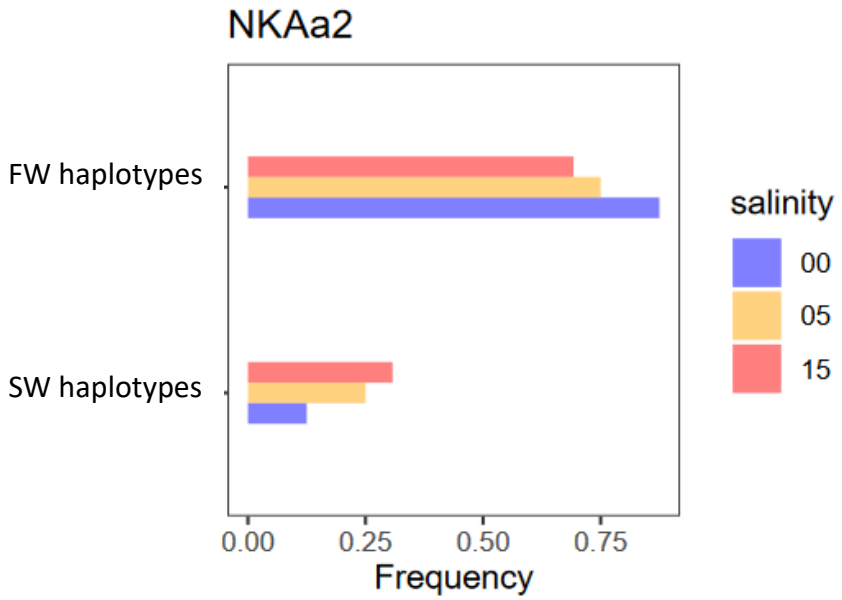


Genetic differentiation between survivors of salt- and fresh-water treatment

II – Preliminary results block 1

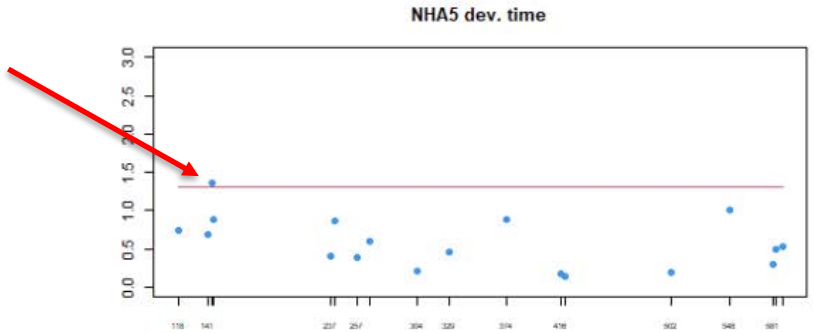


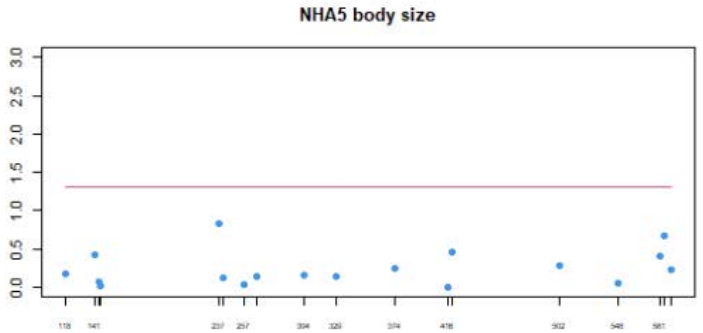


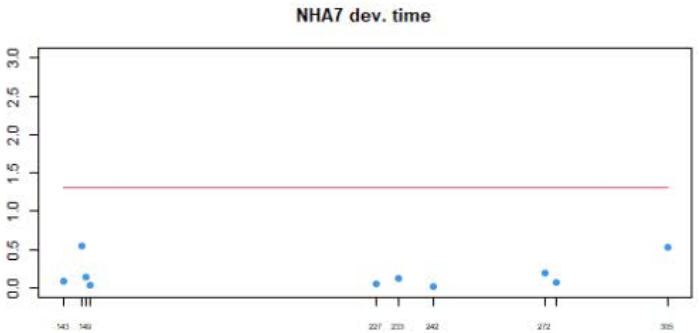


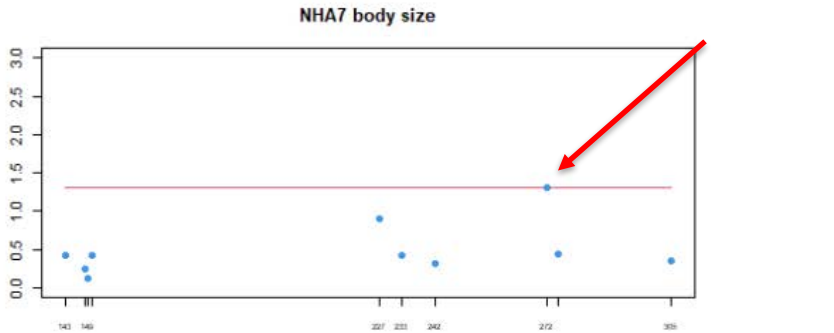
Differential distribution of salt- and freswater haplotypes in salt- and freshwater treatments

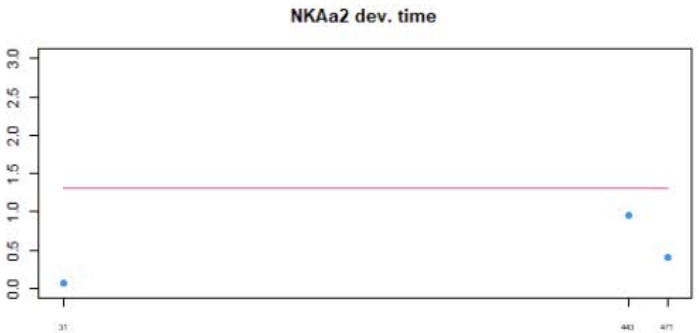
II – Preliminary results block 1

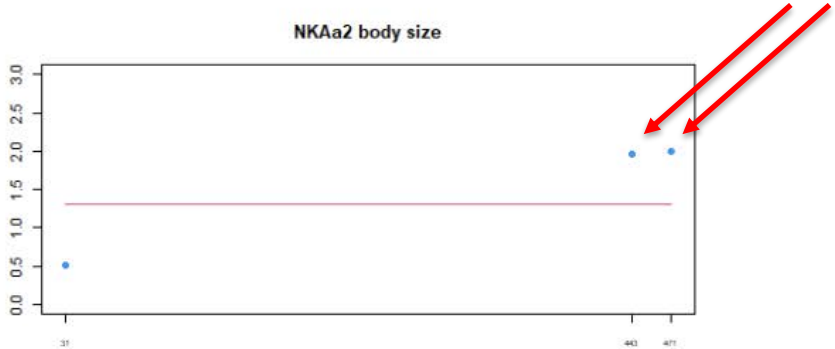










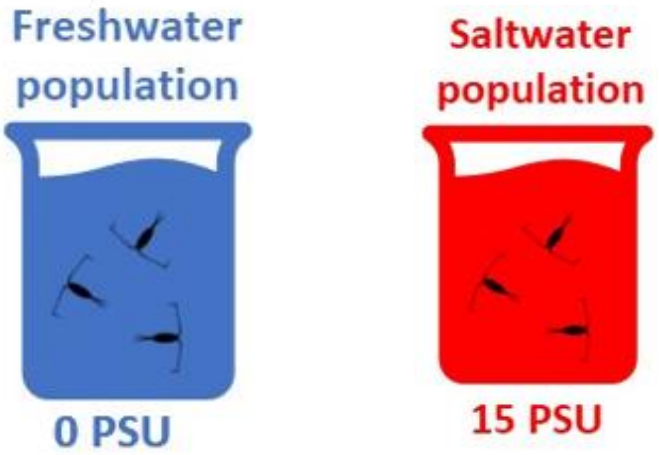


$$Y = \mu + SNP_i + sex + (1|F0)$$

II – Next steps

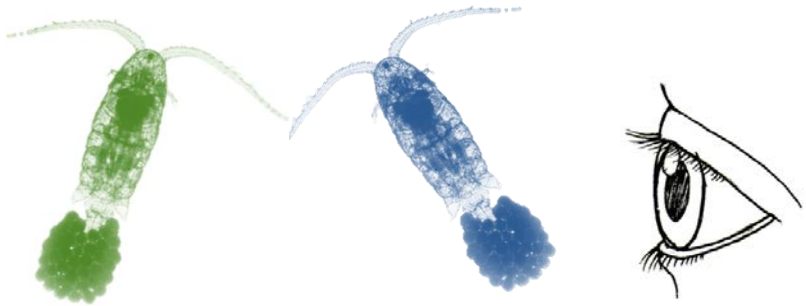
Genotyping block 2
Finer resolution on genetic association

Pool-seq
Shifts in genome-wide allele frequencies between FW and SW



II – Conclusions

Identifying the fitness effects of osmoregulatory genes in freshwater conditions



Balancing selection in the ancestral populations

Future evolution ?

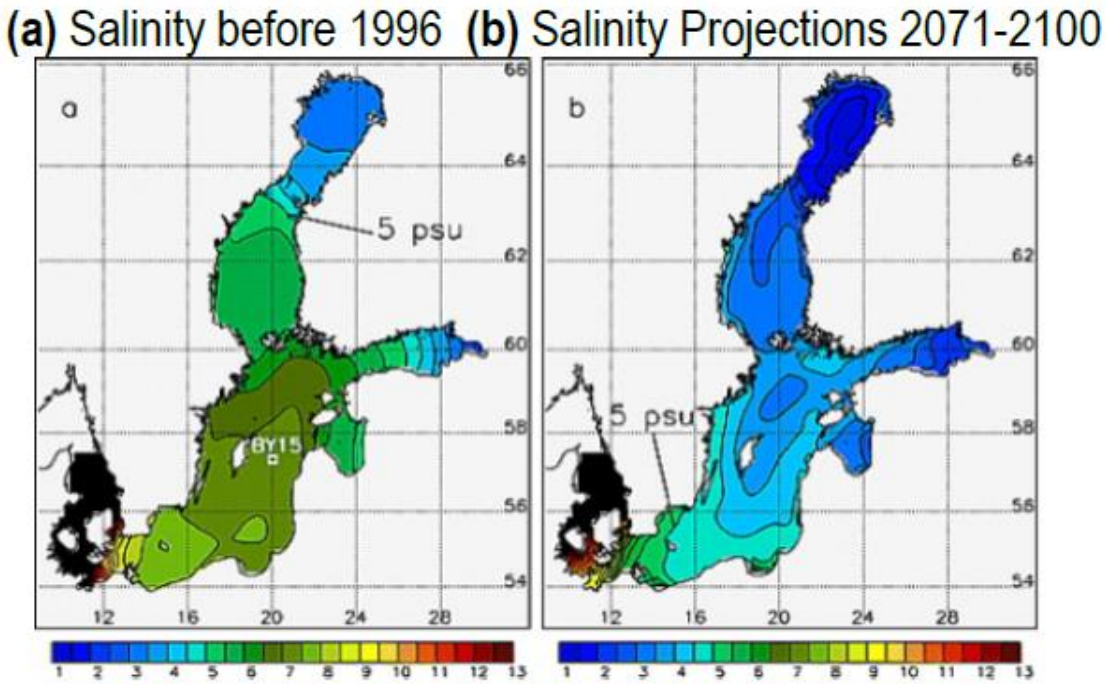
Genetic bases of salinity adaptation

II – Conclusions

Salinity decrease in the Sea

Strong selection pressure on marine populations

Using data from genetic association in predictive models of evolutionary rescue



Meier et al. 2006

Take home messages

Evolution is predictable (sometimes)

Take home messages

Evolution is predictable (sometimes)

Importance of ancestral pop. history, genetic architecture of traits, genomic landscape, etc.

Take home messages

Evolution is predictable (sometimes)

Importance of ancestral pop. history, genetic architecture of traits, genomic landscape, etc.

Important for predicting/modelling response to future selection pressures

Thank you

Relaxed risk of predation drives parallel evolution of stickleback behavior

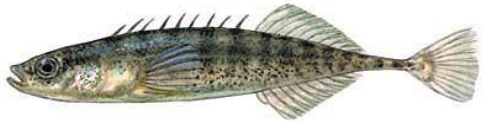
Antoine Fraimout,[1,2,3] Elisa Päiviö,[1] and Juha Merilä[1,2]

Age-dependent genetic architecture across ontogeny of body size in sticklebacks

Antoine Fraimout[1], Zitong Li[1,2], Mikko J. Sillanpää[3] and Juha Merilä[1,4]

Contact: fraimout.antoine@gmail.com

Thank you



Elisa Päiviö
Juha Merilä
Niina Nurmi
Miinastiina Issakainen
Niko Björkell
Nicolas Navarro
Benjamin Weigel
Pierre Nouhaud

Benny Kleinerman
Teresa Popp
Corentin Baumlin
Estelle Dupré
Dorian Decamus
Delphine Bonnet
Catherine Lorin-Nebel
Carol Lee

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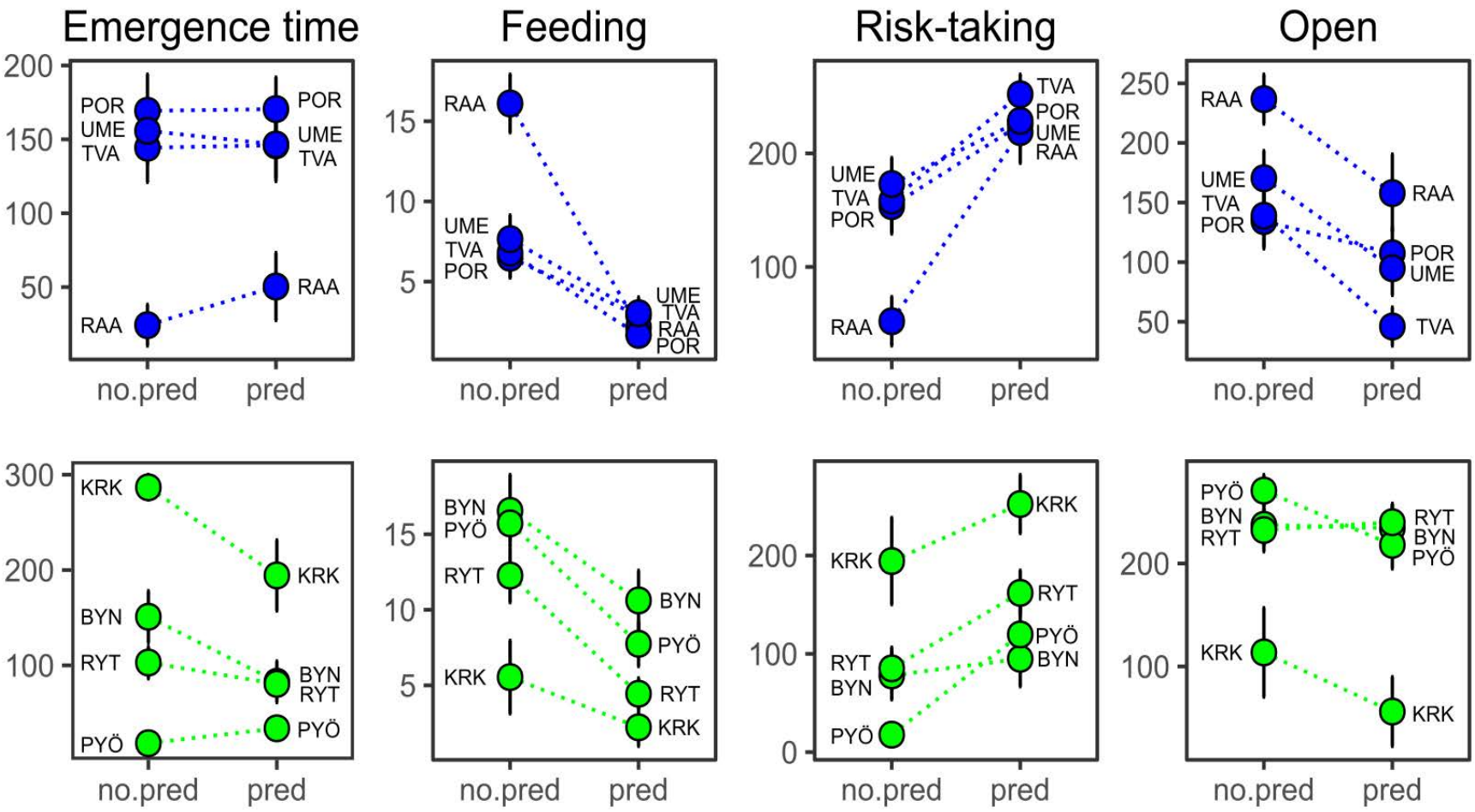
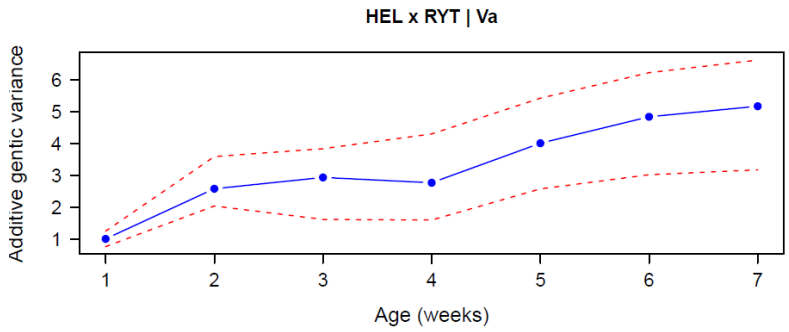
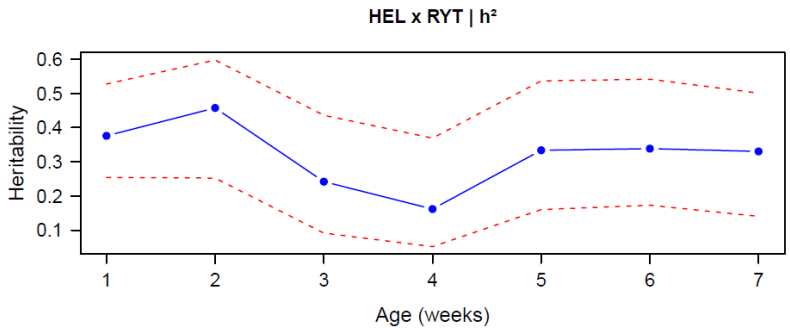
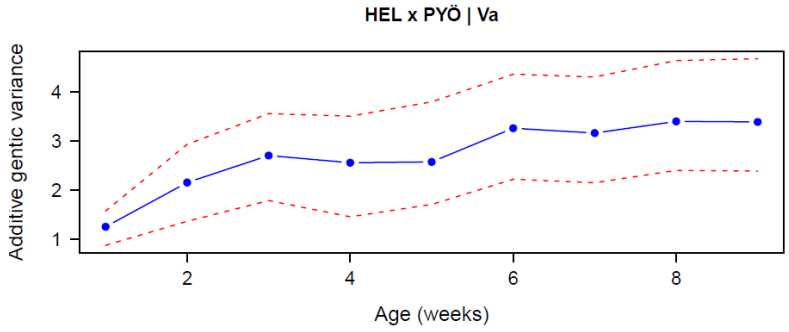
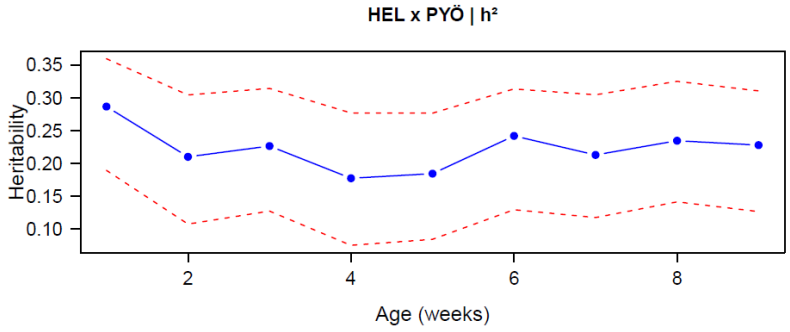
MOPGA

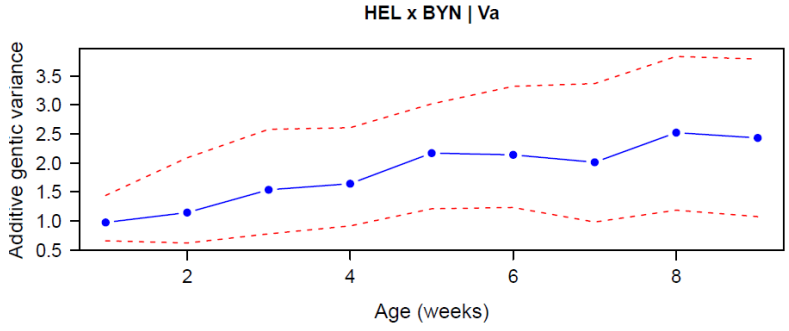

Emergence time
Feeding
Risk-taking
Open
200
150
100
50
POR
UME
TVA
RAA
15
10
5
250
no.pred
pred
300
KRK
BYN
RYT
PYÖ
0

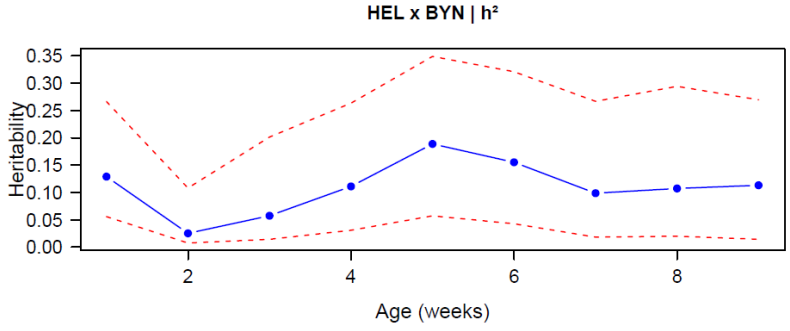

HEL x RYT | Va
Additive gentic variance
1
2
3
4
5
6
1
2
3
4
5
6
7
Age (weeks)


HEL x RYT | h²
Heritability
0.1
0.2
0.3
0.4
0.5
0.6
1
2
3
4
5
6
7
Age (weeks)


HEL x PYÖ | Va
Additive gentic variance
1
2
3
4
2
4
6
8
Age (weeks)


HEL x PYÖ | h²
Heritability
0.10
0.15
0.20
0.25
0.30
0.35
2
4
6
8
Age (weeks)


HEL x BYN | Va
Additive gentic variance
0.5
1.0
1.5
2.0
2.5
3.0
3.5
2
4
6
8
Age (weeks)


HEL x BYN | h²
Heritability
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
2
4
6
8
Age (weeks)