

# Genomic basis of repeated adaptation varies with divergence in *Arabidopsis* (and other species)!

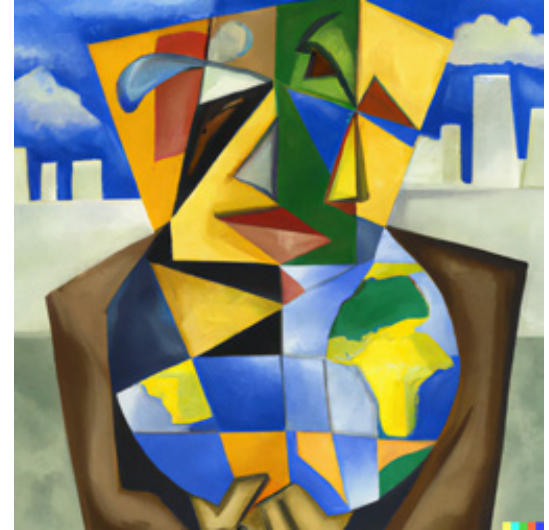


# Is adaptive evolution predictable?

- Determinism or historical contingency?

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- Determinism or historical contingency?
- Predictive evolution of pathogens/pests/in polluted environment?

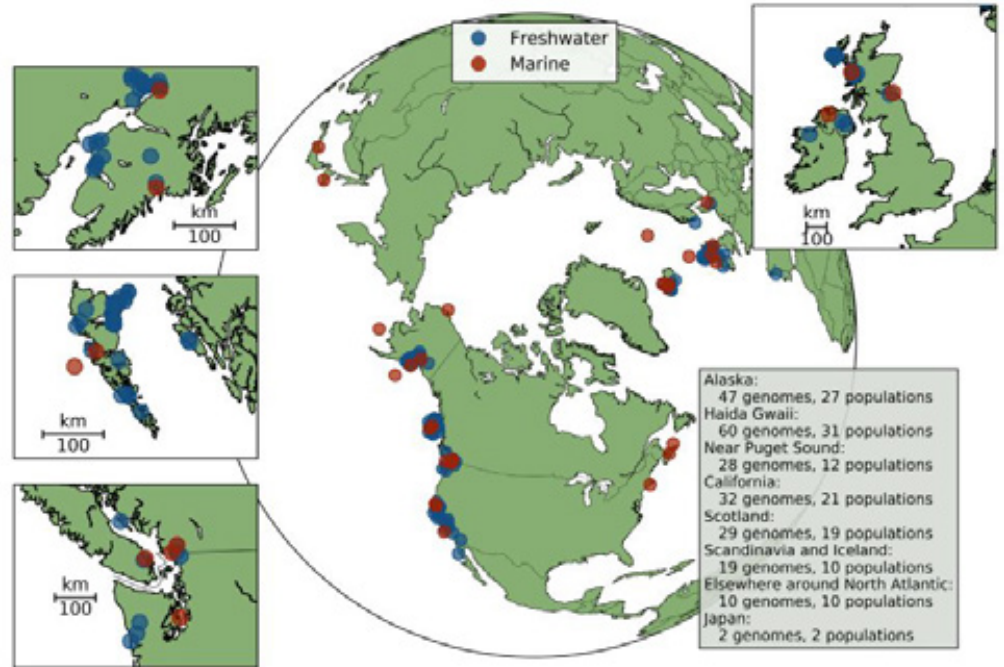


# Predictable adaptation?

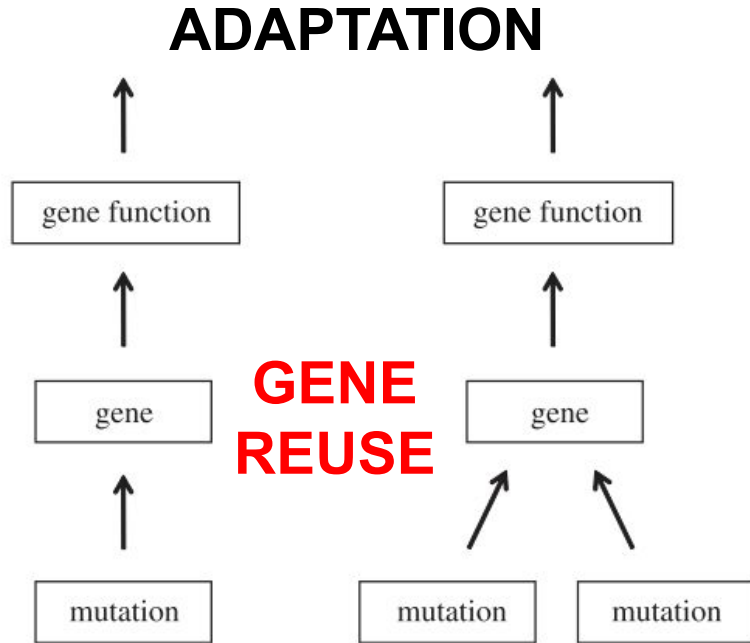
Repeated adaptation in nature - model system to test it



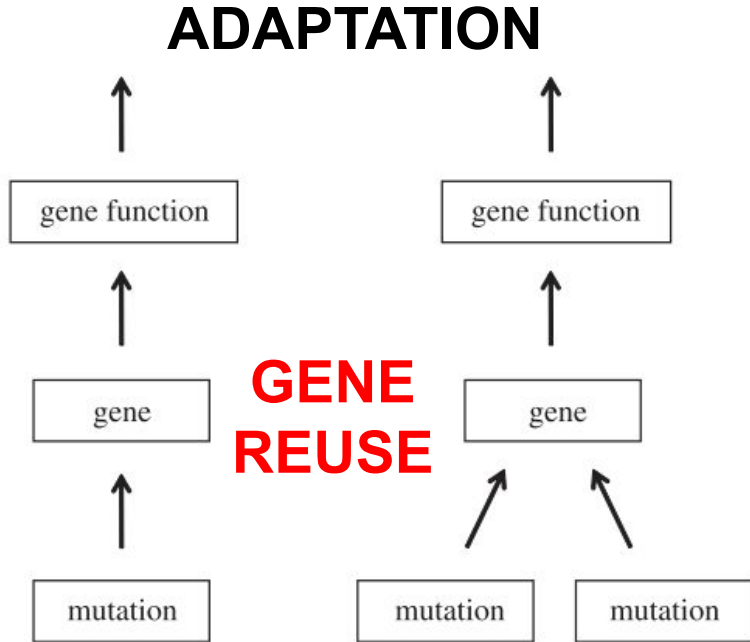
Repeated freshwater adaptation art



# Genetic basis of repeated adaptation



# Genetic basis of repeated adaptation



Freshwater adaptation 1



EDA gene

Freshwater adaptation 2



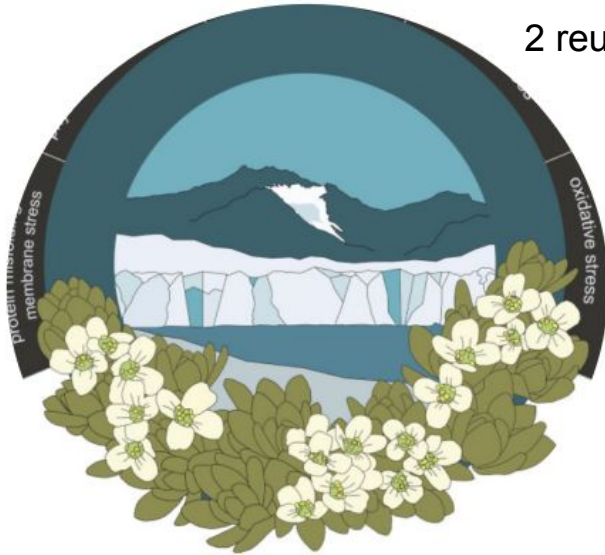
also EDA gene

**GENE REUSE**



# Predictable genetic basis of repeated adaptation?

Variation in the degree of gene reuse!



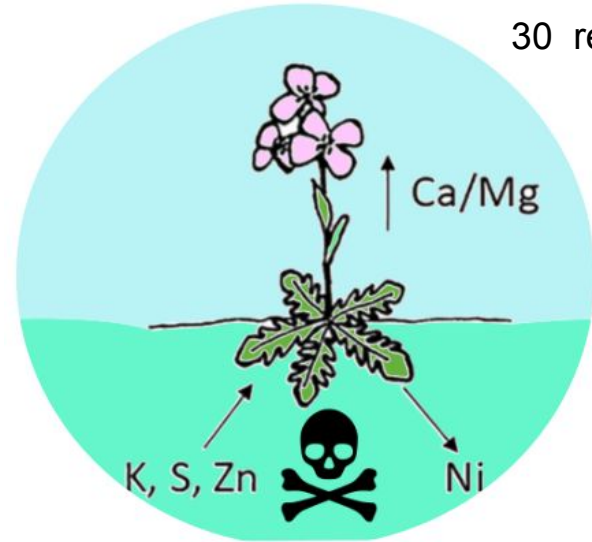
2 reused genes

Arctic adaptation

*Draba* and *Cochlearia* species

**Low gene reuse**

Birkeland et al., 2020



30 reused genes

Serpentine soil adaptation

*Arabidopsis* populations

**High gene reuse**

Konecna et al., 2021

# Predictable genetic basis of repeated adaptation?

**Variation** in the degree of gene reuse!



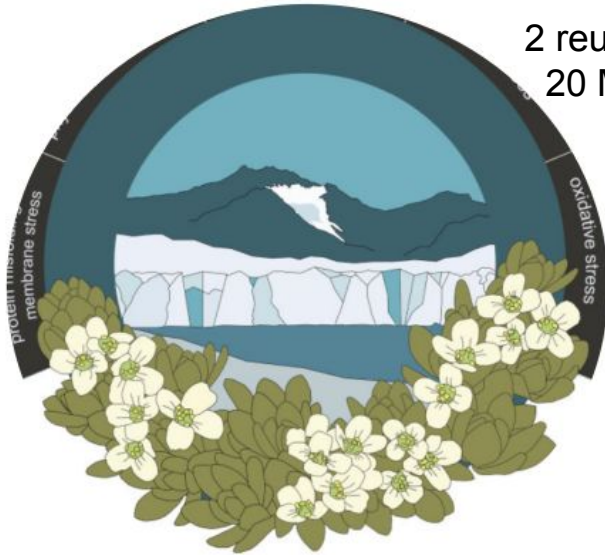
WHY?





# Divergence time?

## Variation in the degree of gene reuse!



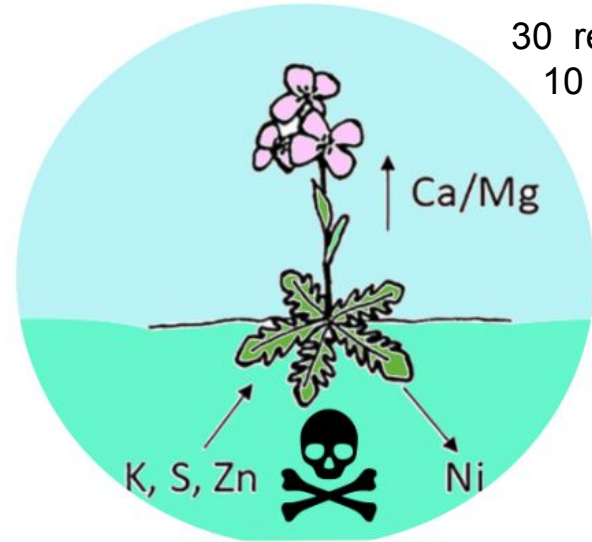
2 reused genes  
20 Mya diverged

**Arctic adaptation**

*Draba* and *Cochlearia* species

**Low gene reuse**

Birkeland et al., 2020



30 reused genes  
10 kya diverged

**Serpentine soil adaptation**

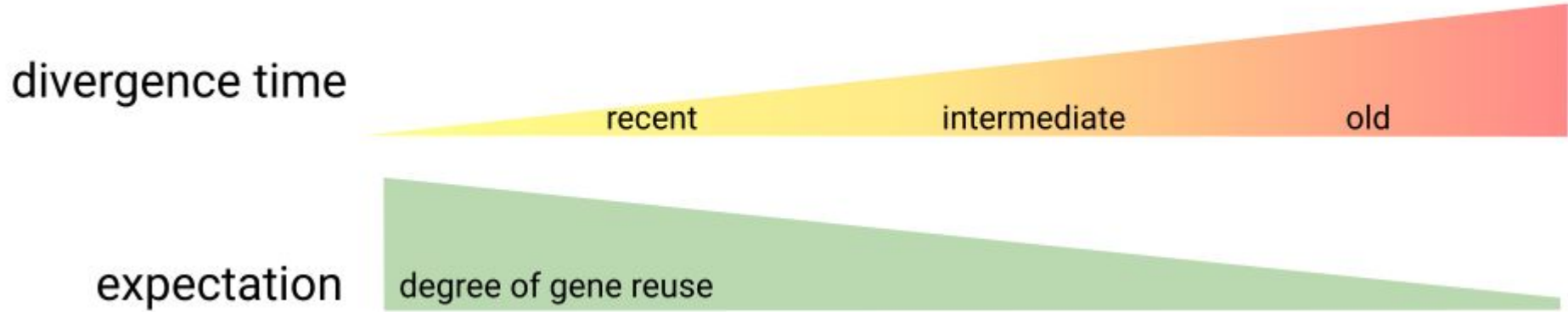
*Arabidopsis* populations

**High gene reuse**

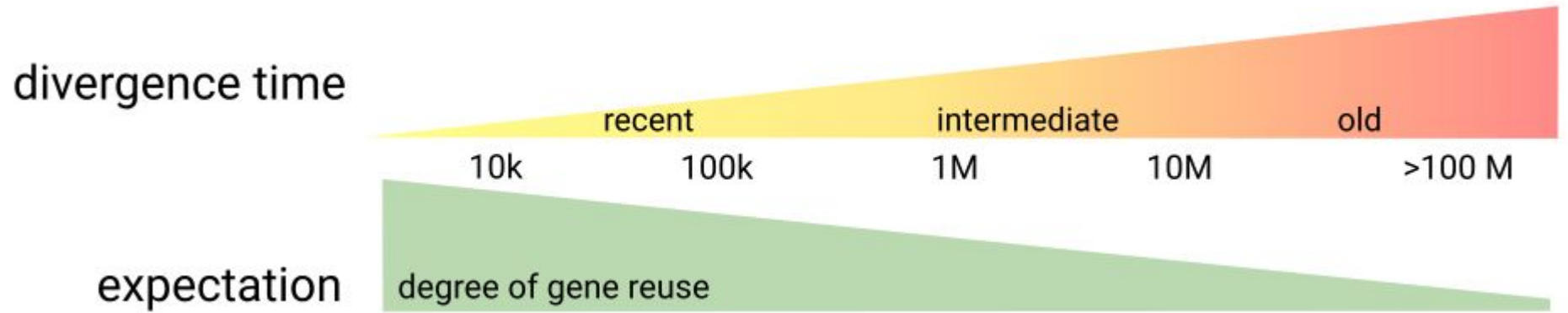
Konecna et al., 2021

# Hypothesis

- **Divergence time**-driven probability of repeated adaptation







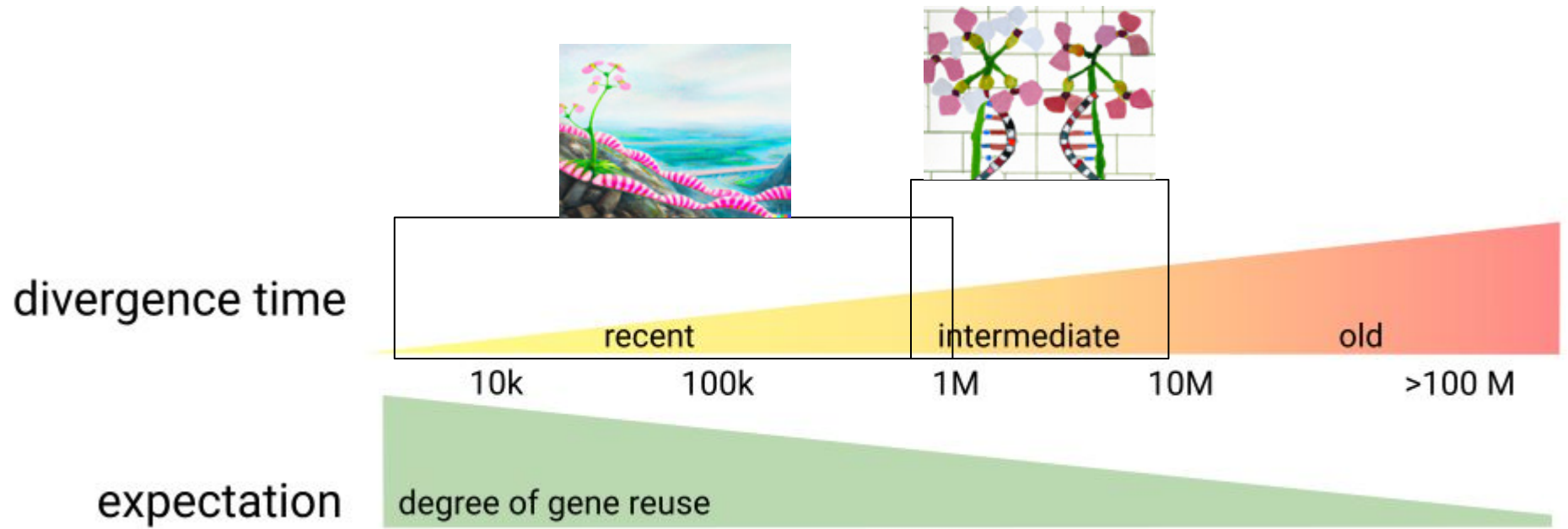
## Questions

- Empirical support in nature?
- If yes, what are the underlying mechanisms?



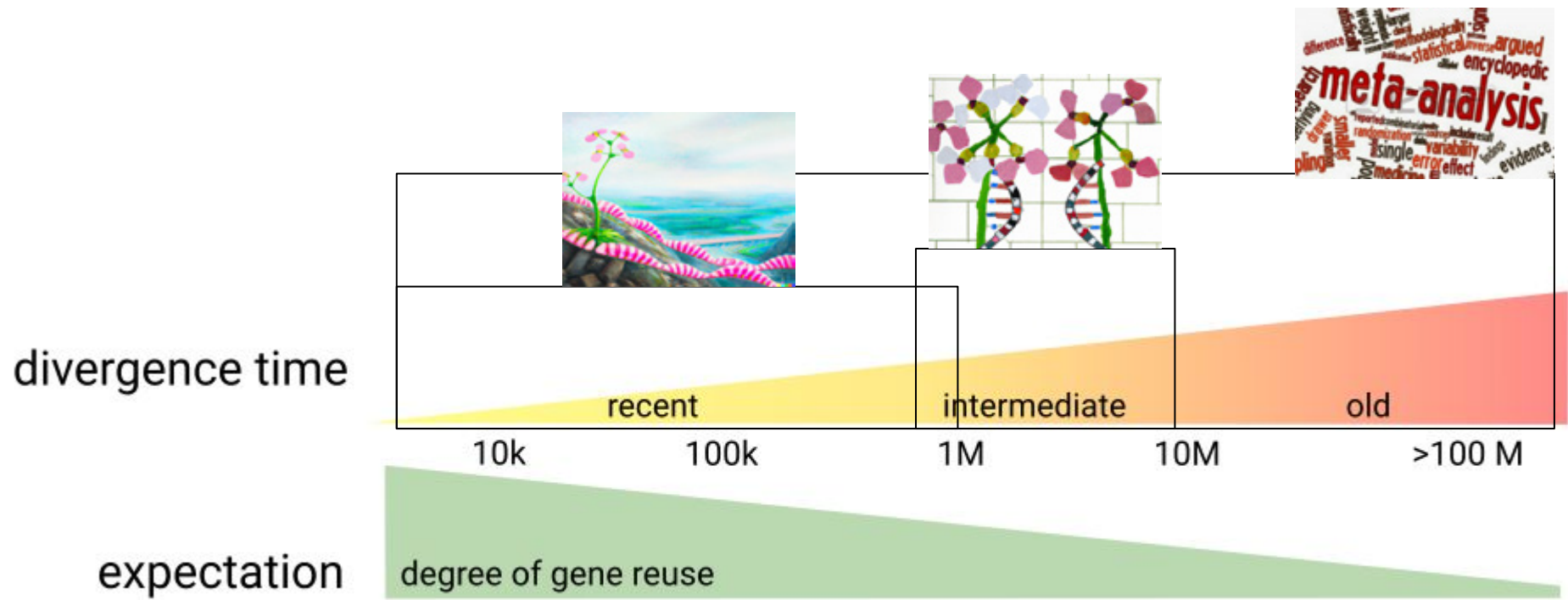
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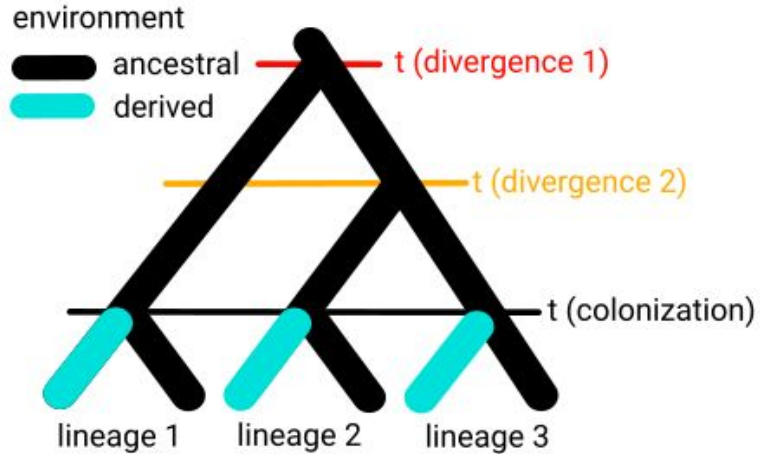
## Questions

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# Methods

## Desired case study design



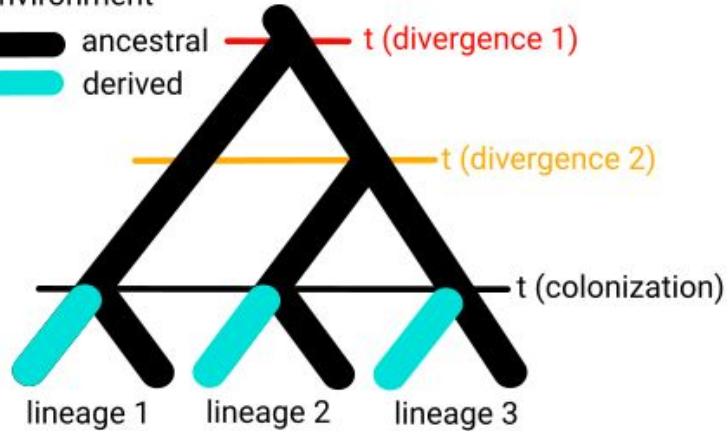
# Methods

## Desired case study design

environment

— ancestral

— derived

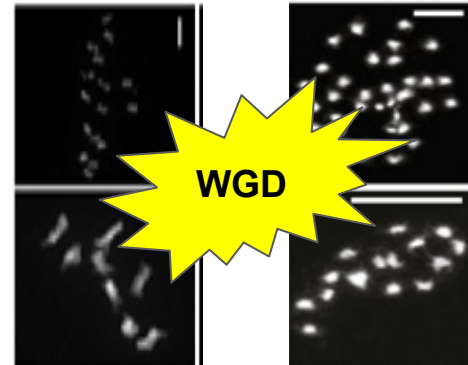


**TETRAPLOID**

**DIPLOID**



Adaptation ↑



Adaptation ↑

# Methods

Candidate genes

genome sequencing

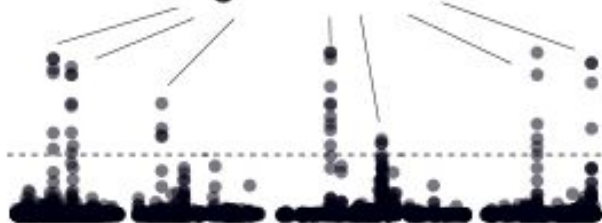


derived

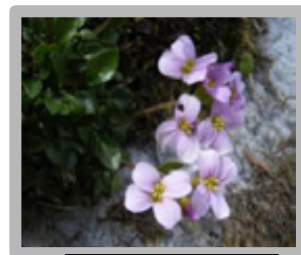
lineage 1

ancestral

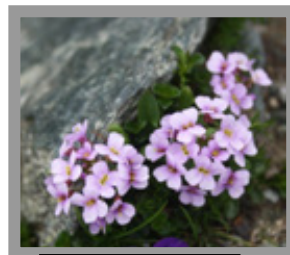
gene set 1



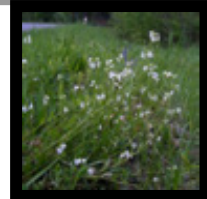
selection scan (derived - ancestral)



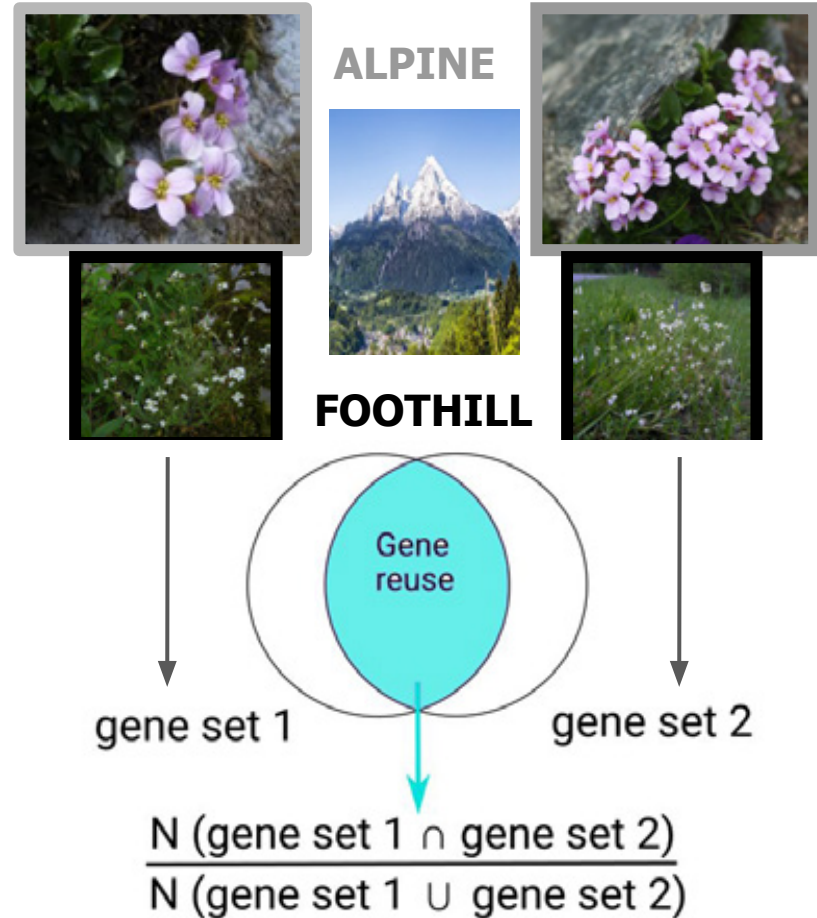
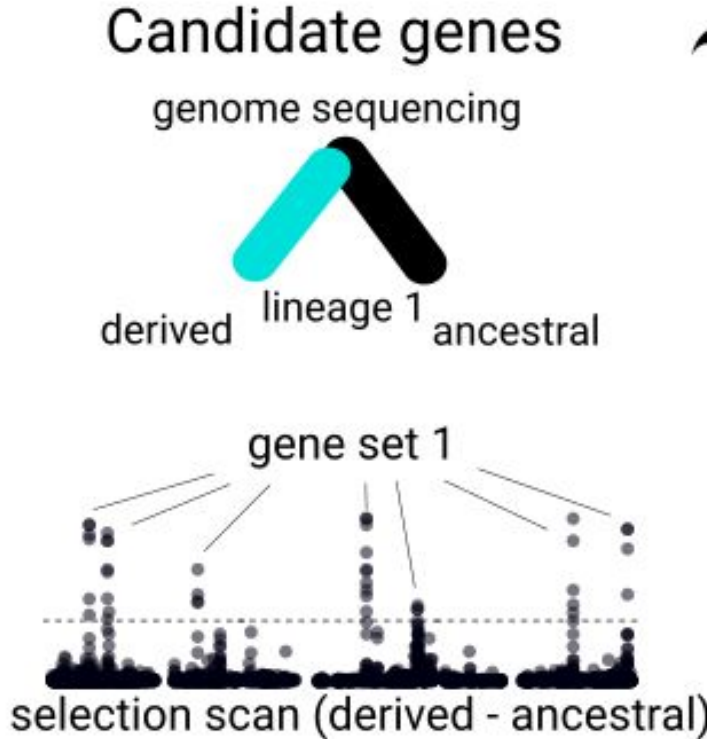
**ALPINE**



**FOOTHILL**



# Methods



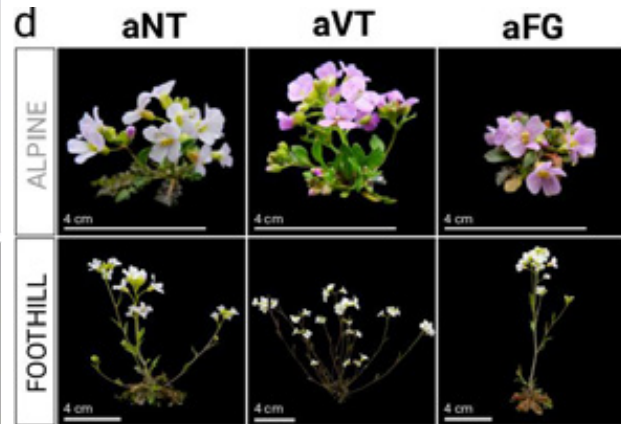
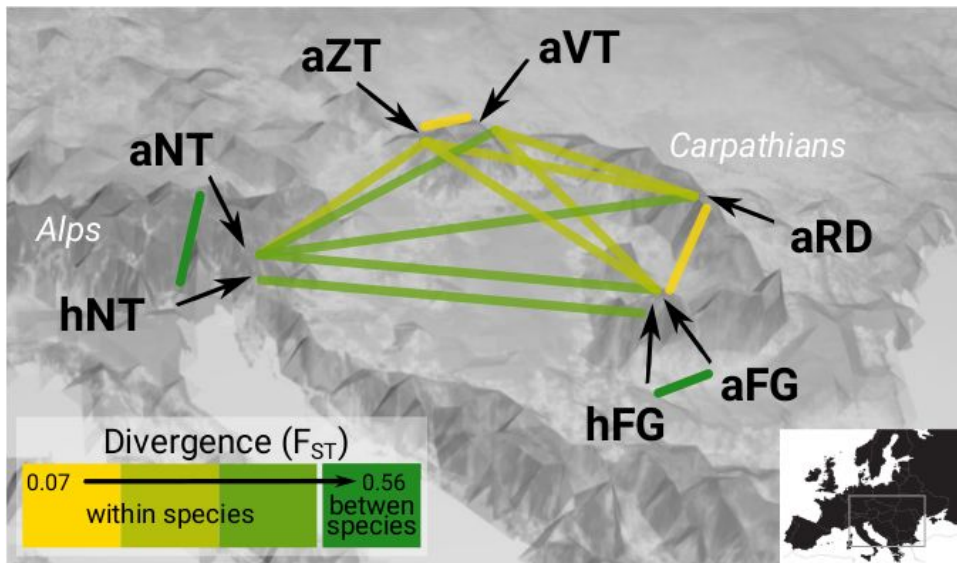
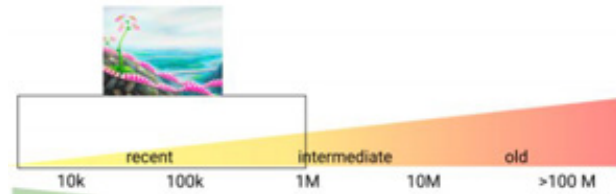
# Results

# 1. Recent divergences

7 alpine lineages

*Arabidopsis arenosa* and *A. halleri*

Bohutínská et al. 2021, PNAS



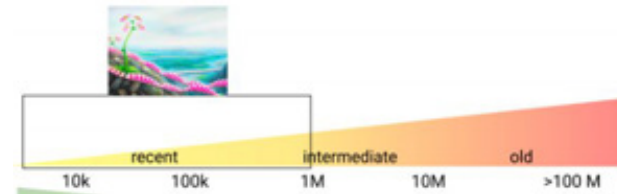


# 1. Recent divergences

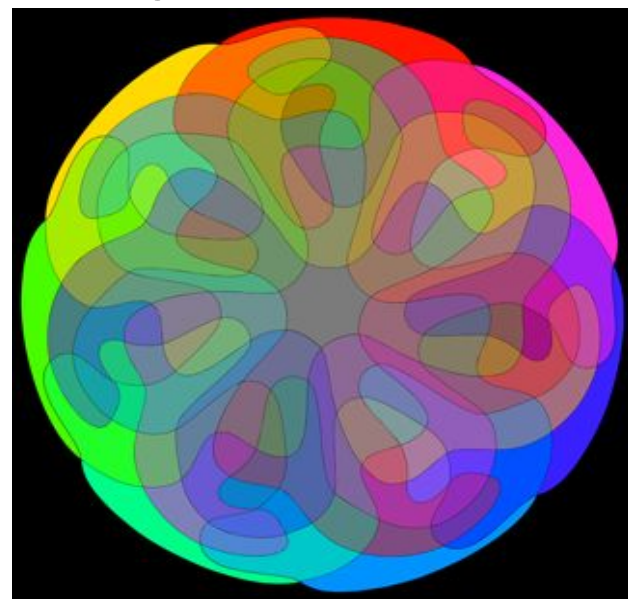
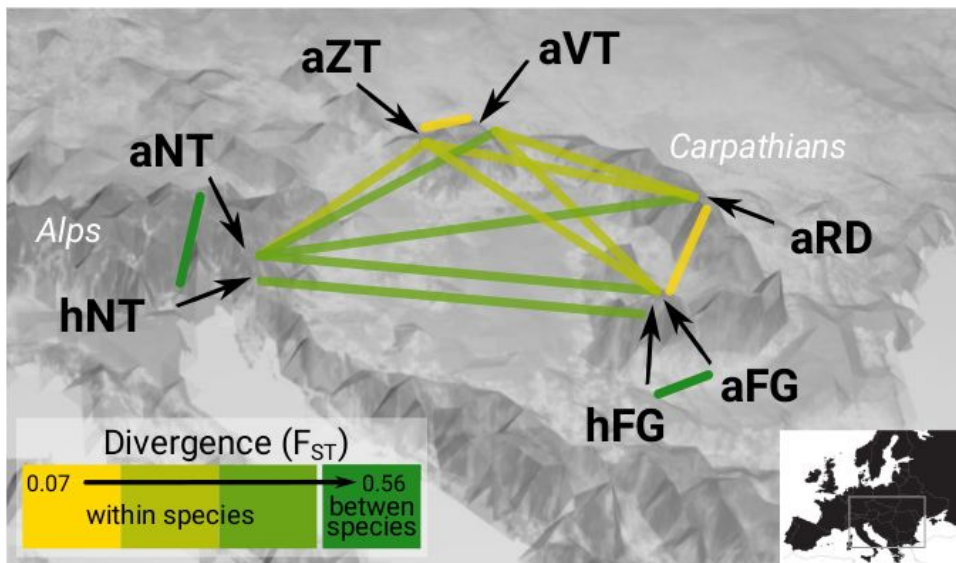
7 independent alpine lineages

*Arabidopsis arenosa* and *A. halleri*

Bohutínská et al. 2021, PNAS



7 lineages = 21 parallel pairs



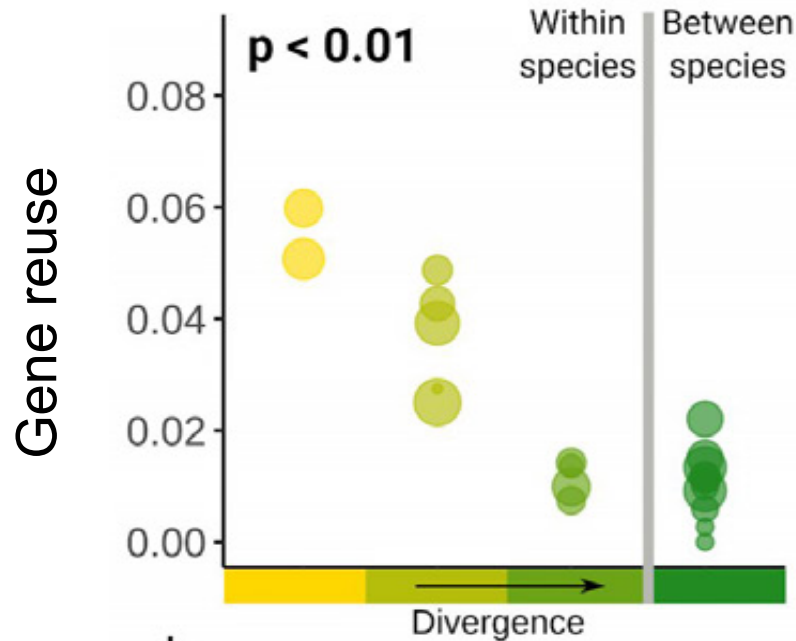
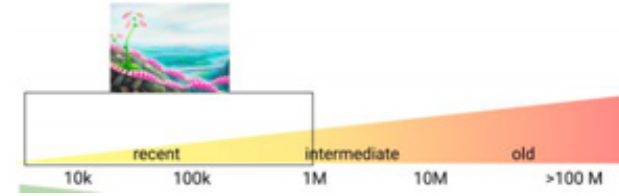


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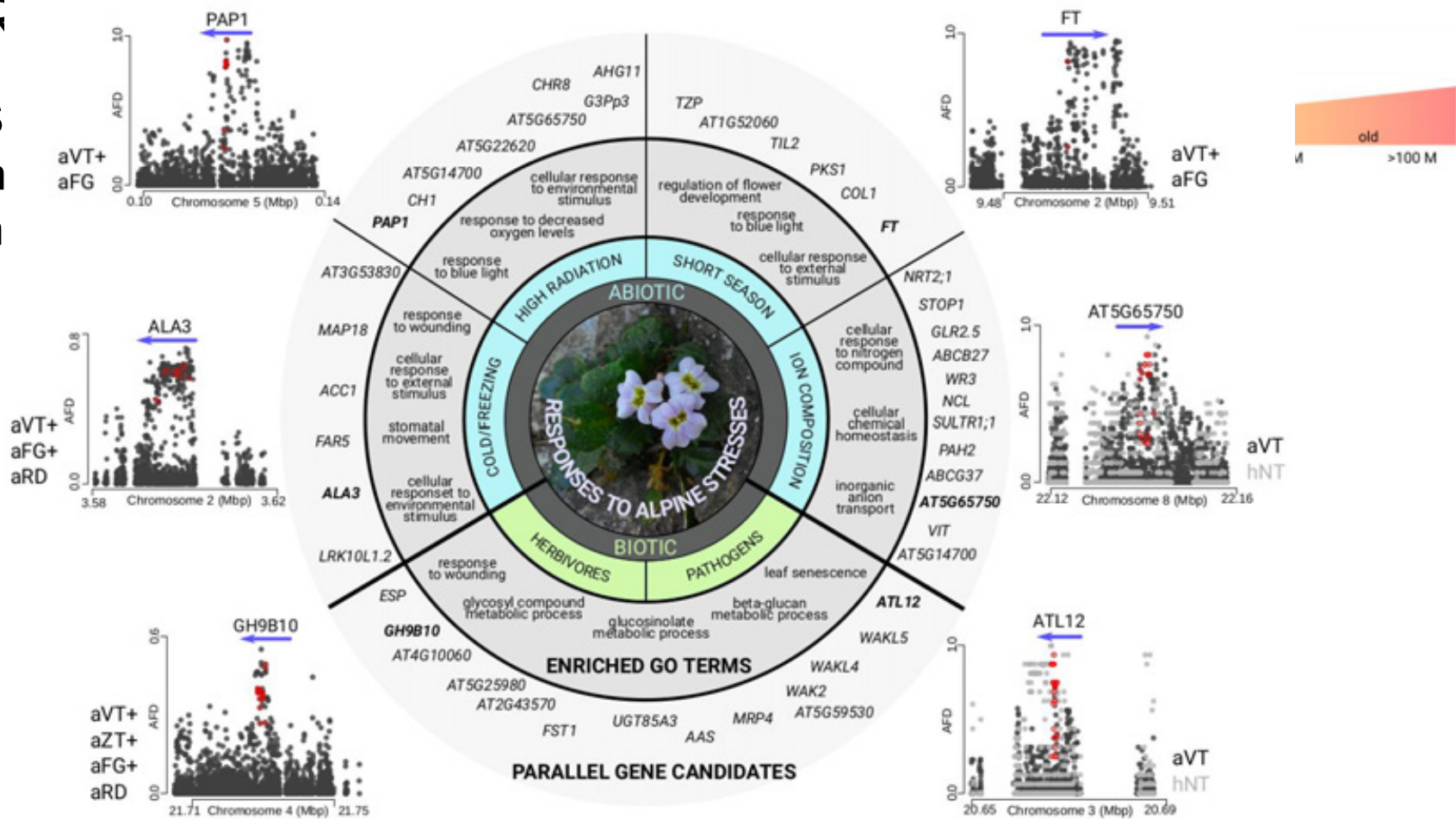
Significant **gene reuse**

↑ genetic divergence

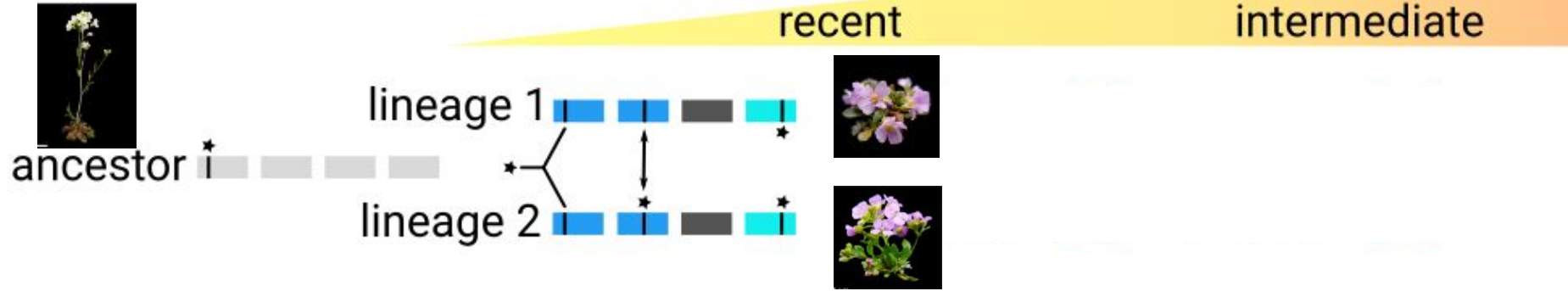
↓ convergent genome evolution



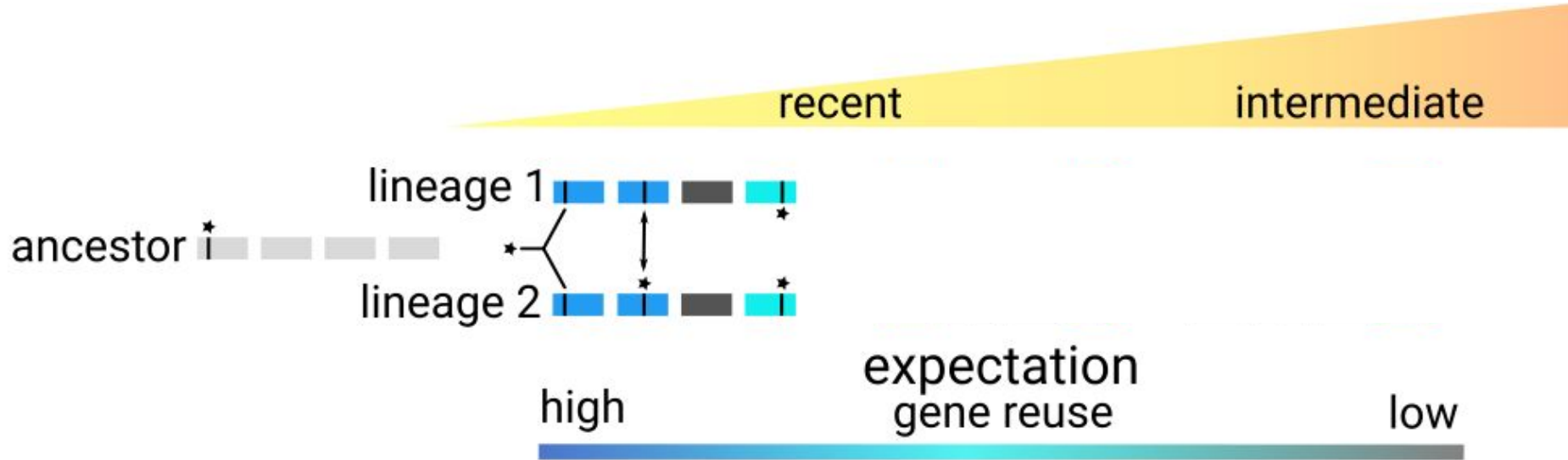
1. F  
S  
↑ gen  
↓ con



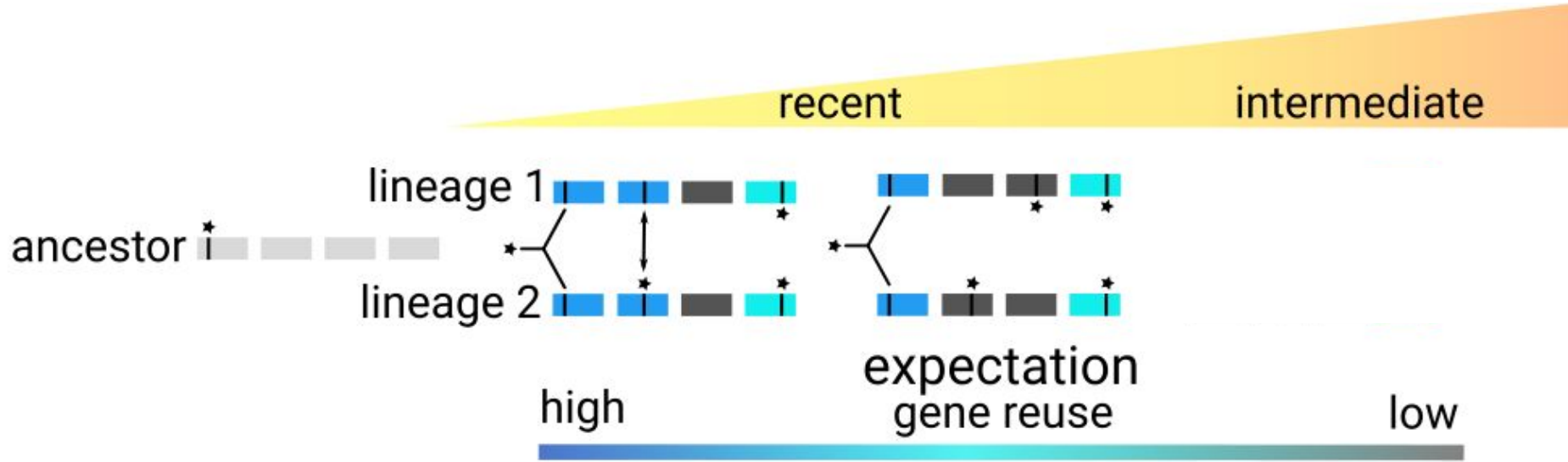
# Mechanism: reduction in allele sharing?



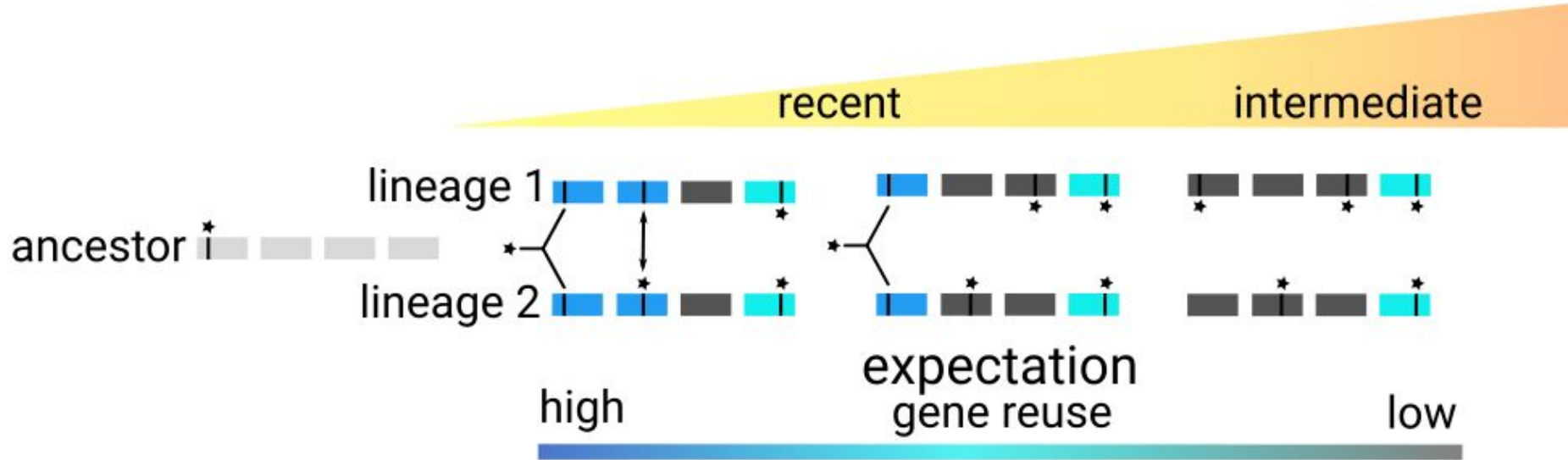
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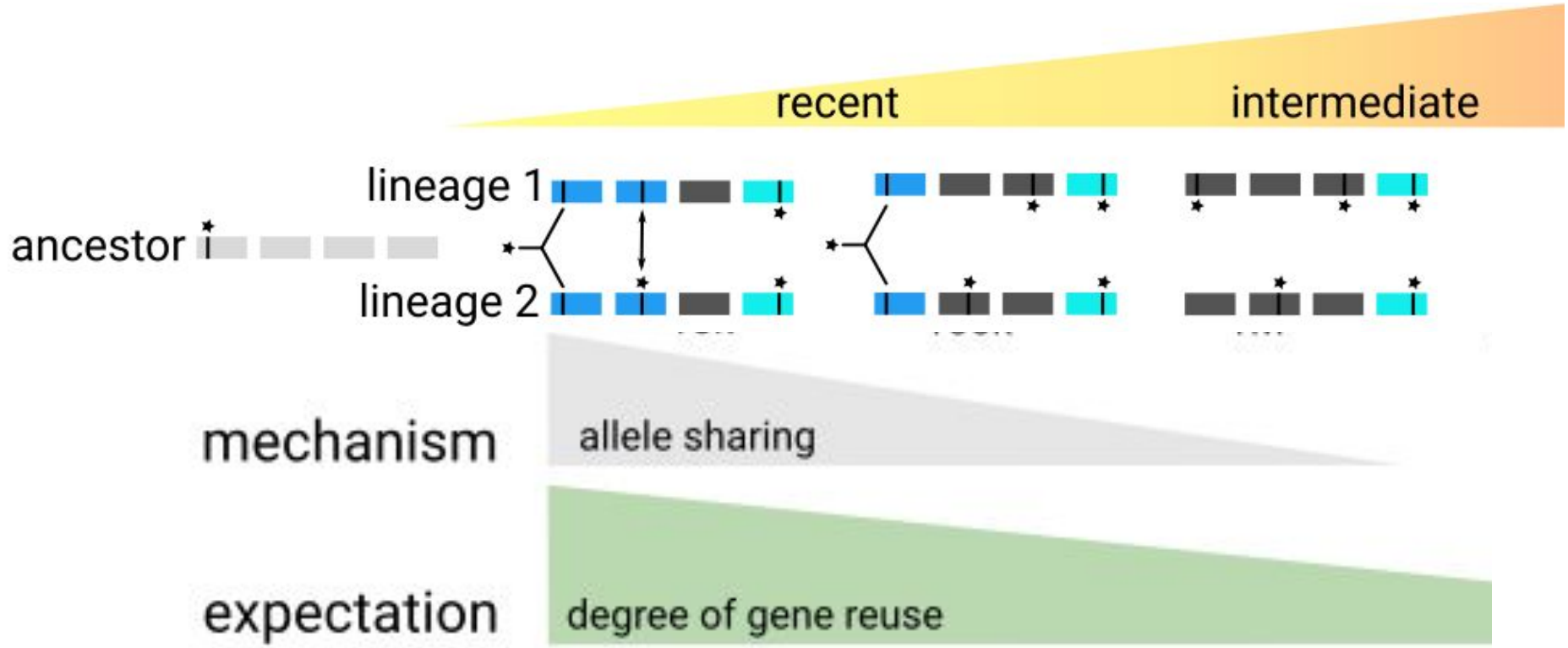
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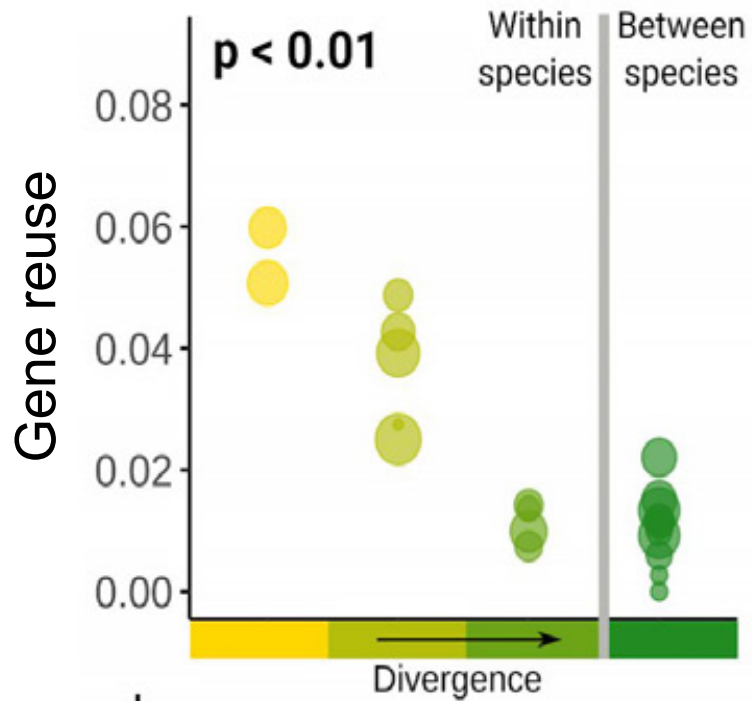
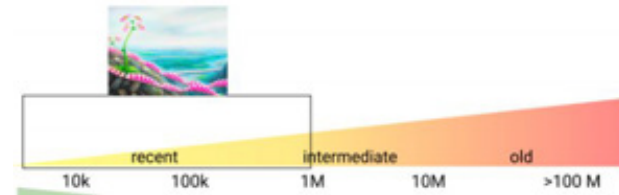


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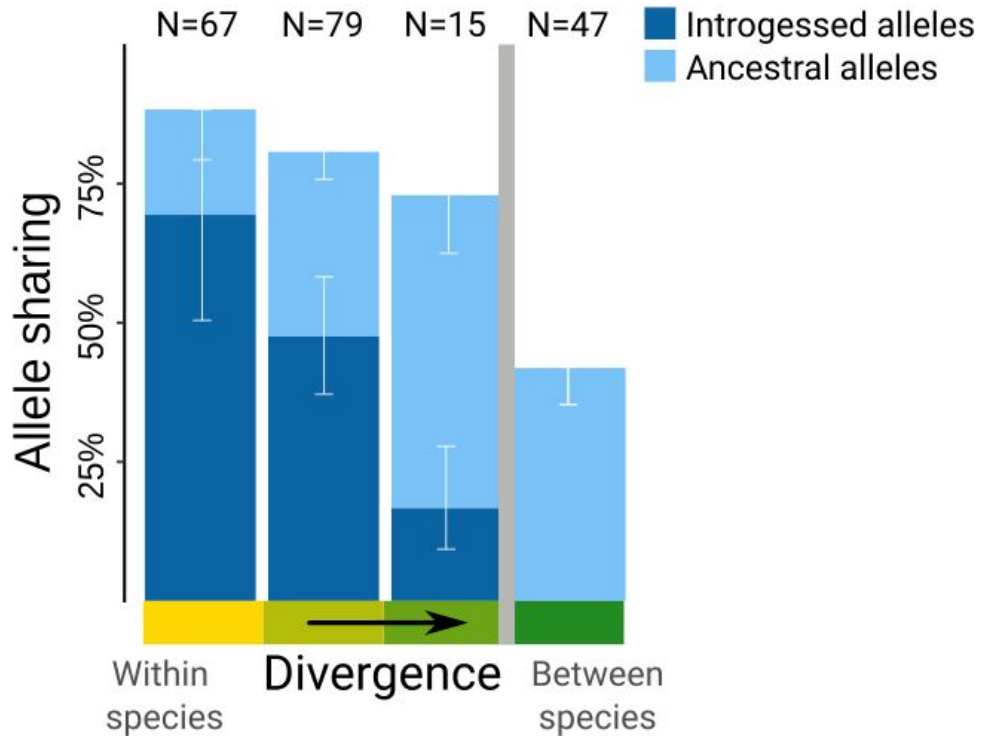
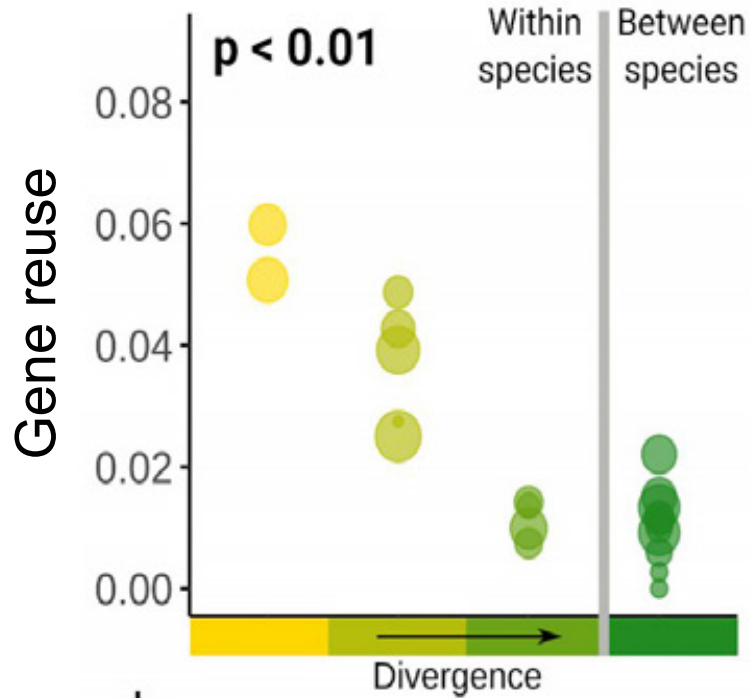
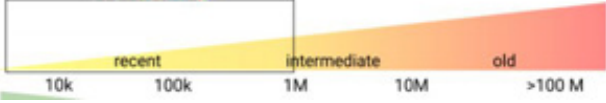




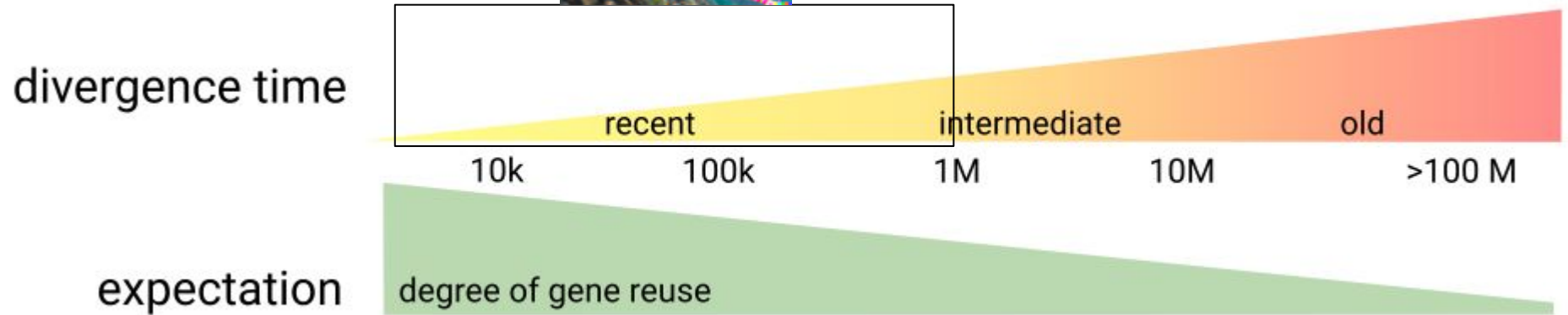
# 1. Recent divergences



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# WRAP-UP 1: alpine adaptation over recent divergences

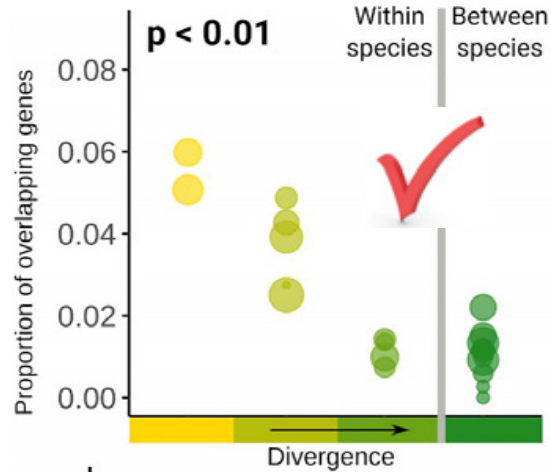


## Questions

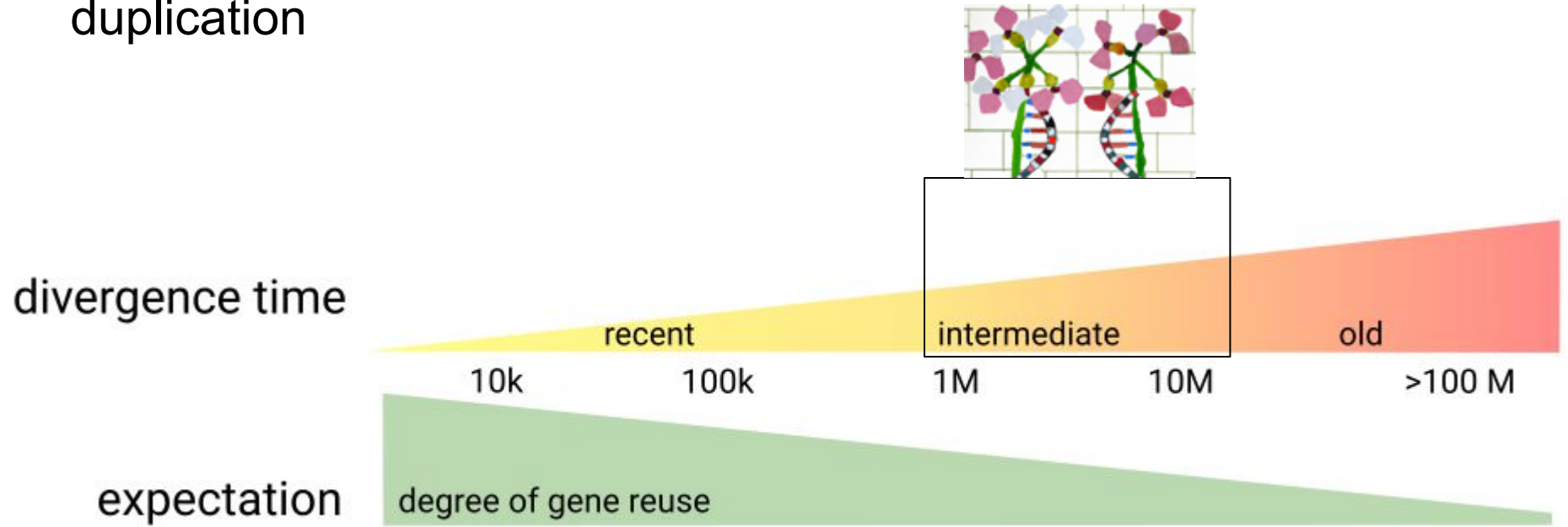
- Empirical support in nature? ✓
- If yes, what are the underlying mechanisms?

**Reduction in allele sharing**

# WRAP-UP 1: alpine adaptation over recent divergences

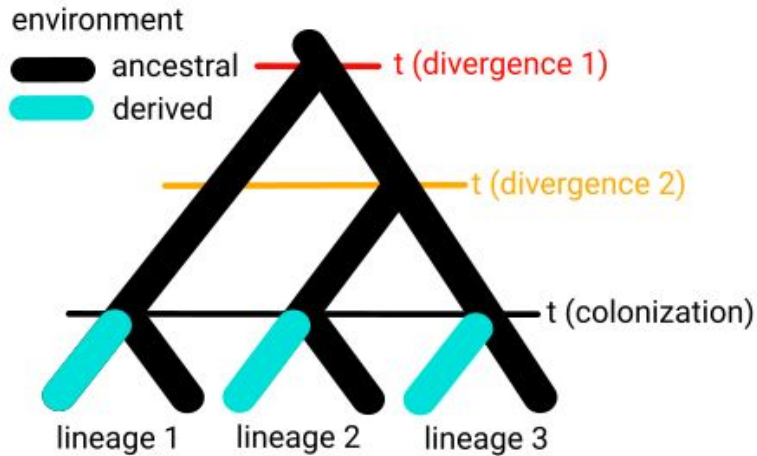


## 2. Intermediate divergences: adaptation to whole genome duplication



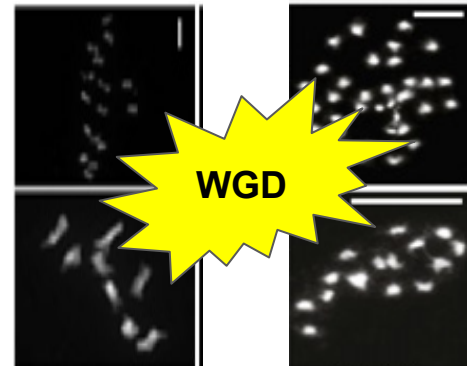
# Methods

## Desired case study design



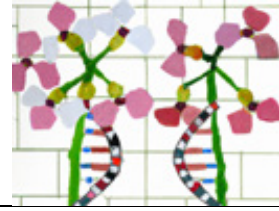
**TETRAPLOID**

**DIPLOID**



Adaptation ↑

## 2. Intermediate divergences: adaptation to whole genome duplication



divergence time

expectation



*Arabidopsis lyrata*

*Arabidopsis arenosa*

*Cardamine amara*



## 2. Intermediate divergences: adaptation to whole genome duplication

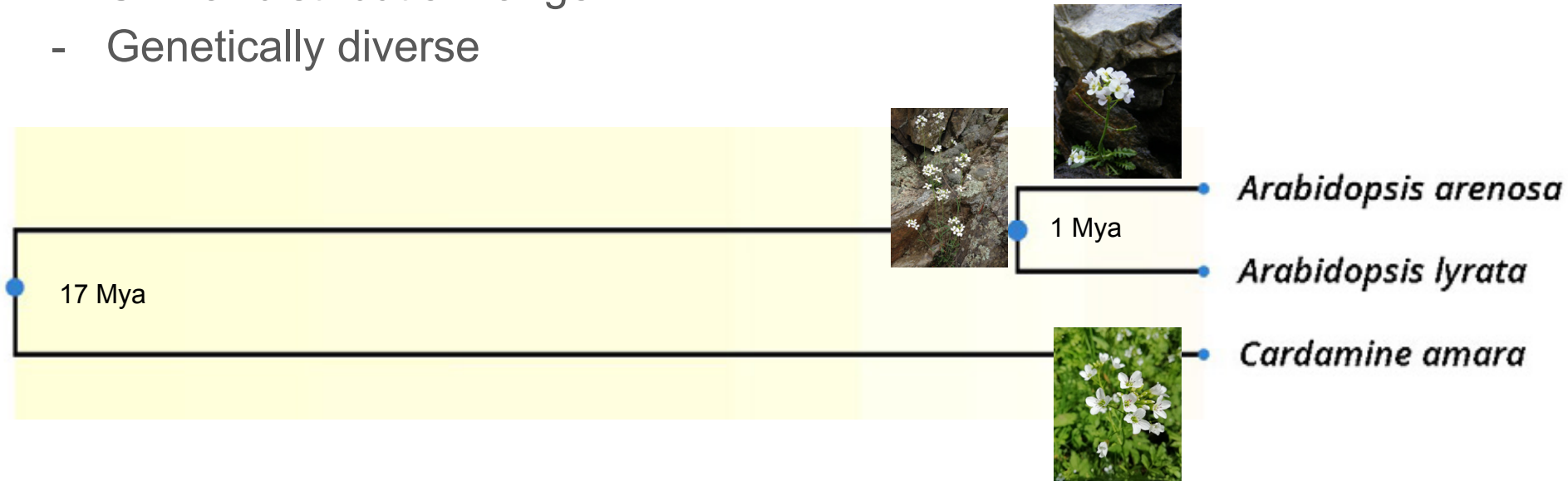
Bohutínská et al. 2021, MBE  
Marburger et al, 2019, Nature Comm



recent

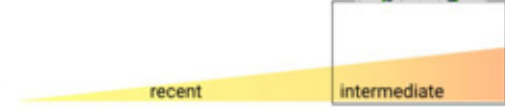
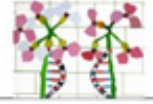
intermediate

- Diploid and tetraploid populations
- Similar distribution range
- Genetically diverse

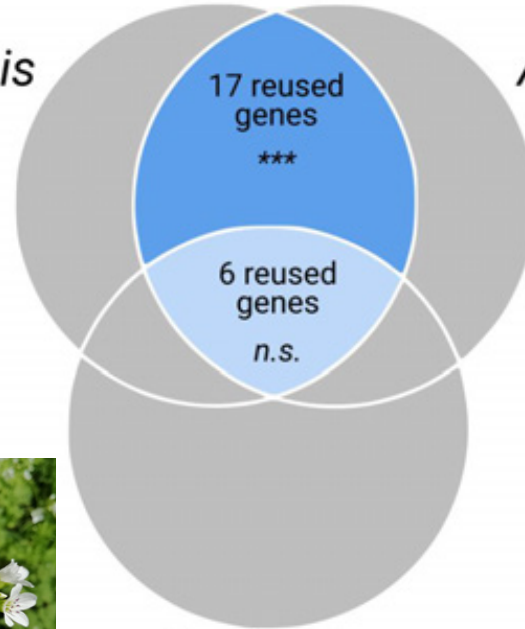


## 2. Intermediate divergences: adaptation to whole genome duplication

Bohutínská et al. 2021, MBE  
Marburger et al, 2019, Nature Comm



*Arabidopsis  
lyrata*



*Arabidopsis  
arenosa*



*Cardamine  
amara*

## 2. Intermediate divergences: adaptation to whole genome duplication

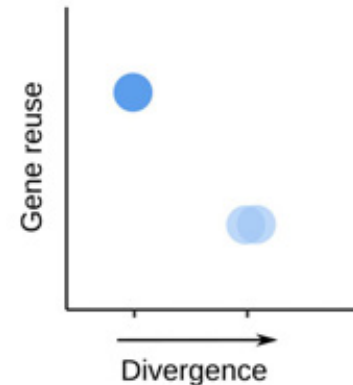
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Marburger et al, 2019, Nature Comm



*Arabidopsis  
lyrata*



*Arabidopsis  
arenosa*

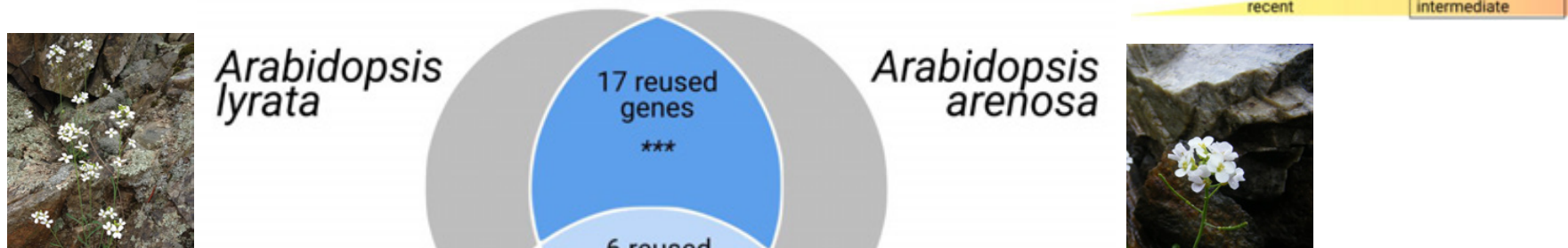


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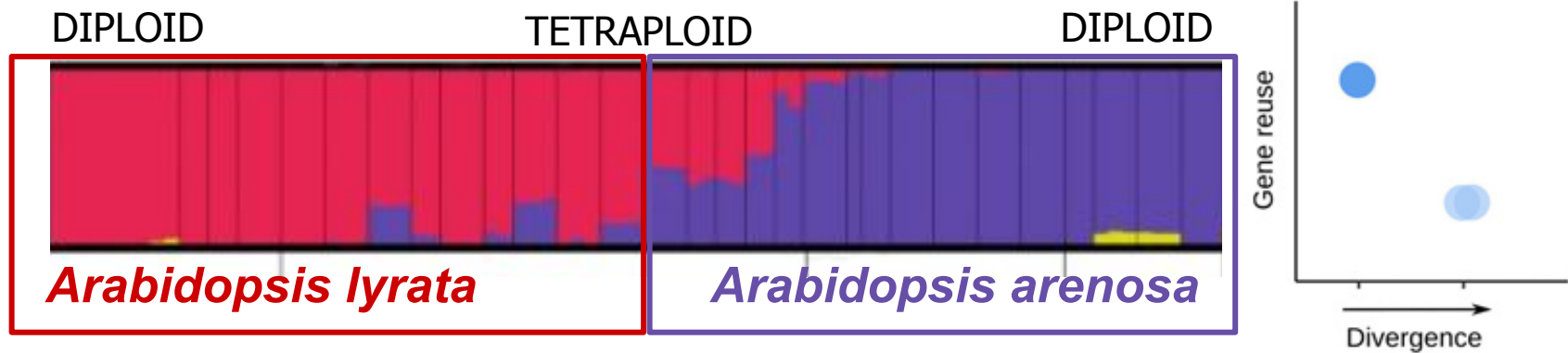
intermediate

## 2. Intermediate divergences: adaptation to whole genome duplication

Bohutínská et al. 2021, MBE  
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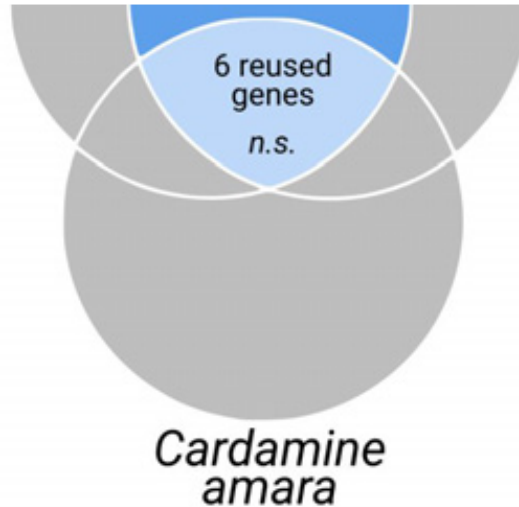
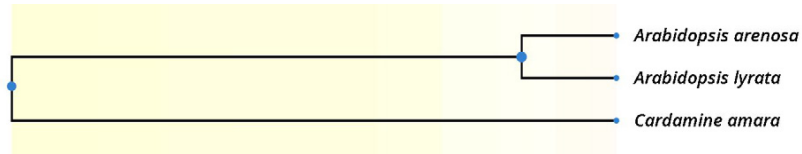


**GENE FLOW -> alleles shared**

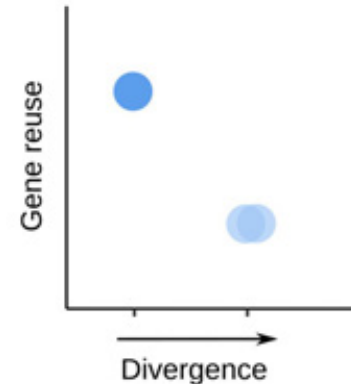
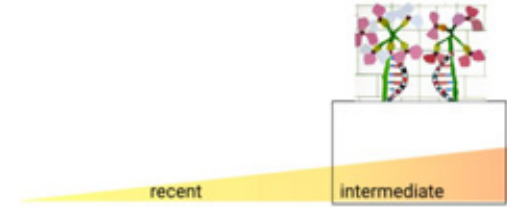


## 2. Intermediate divergences: adaptation to whole genome duplication

Absence of shared alleles ->  
**functional repeatability?**



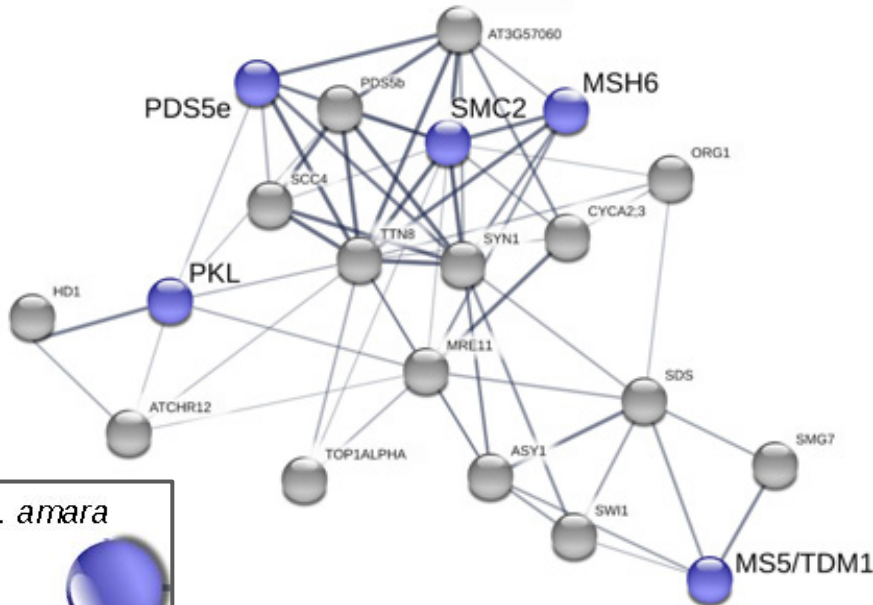
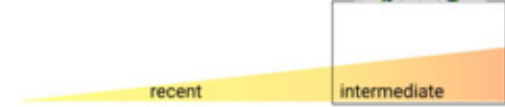
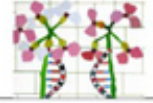
Bohutínská et al. 2021, MBE  
Marburger et al, 2019, Nature Comm



## 2. Intermediate divergences: adaptation to whole genome duplication

Absence of shared alleles ->  
**functional repeatability!**

Bohutínská et al. 2021, MBE  
Marburger et al, 2019, Nature Comm

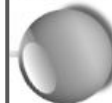


- DNA repair
- exit from meiosis
- ion transport

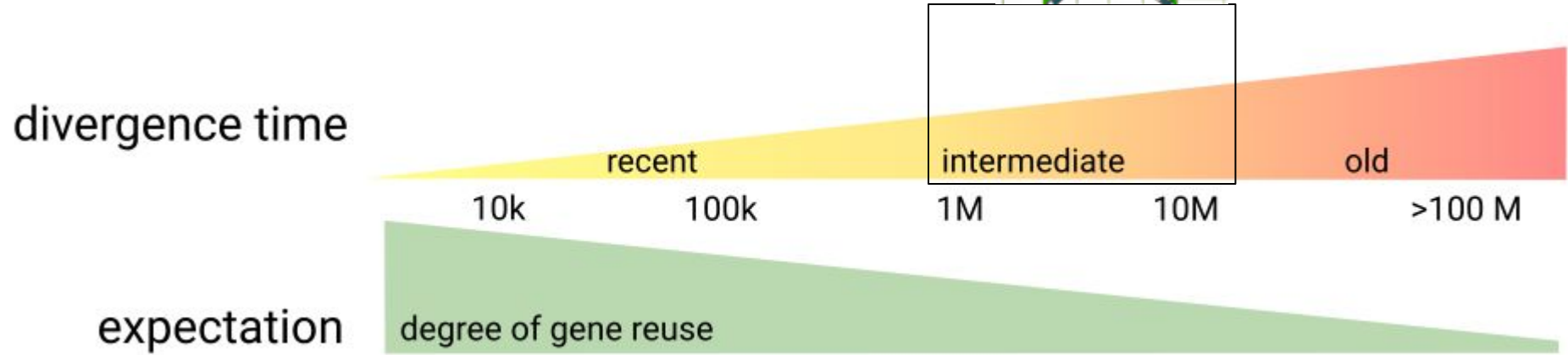
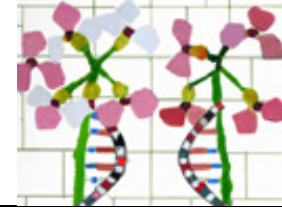
selected in *C. amara*



selected in *A. arenosa*



## WRAP-UP 2: Intermediate divergences: adaptation to whole genome duplication

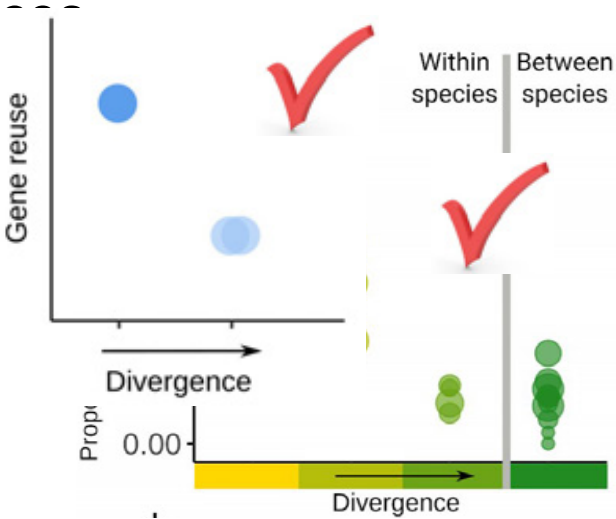


### Questions

- Empirical support in nature? ✓
- If yes, what are the underlying mechanisms?

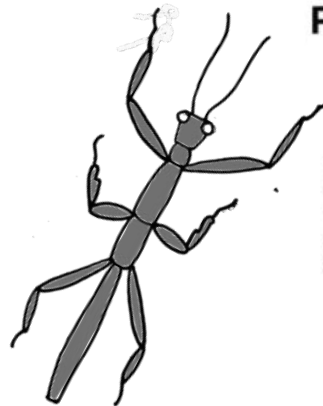
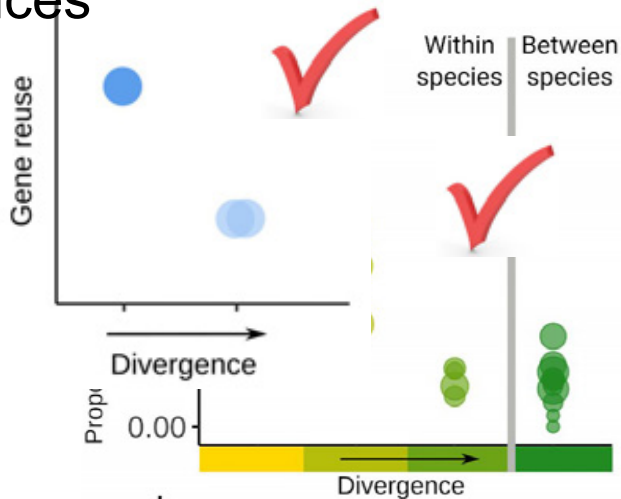
**Reduction in allele sharing + functional repeatability**

# WRAP-UP 2: repeated adaptations over recent + intermediate divergence

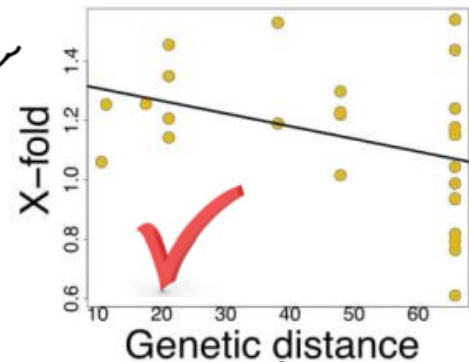




# WRAP-UP 2: repeated adaptations over recent + intermediate divergences

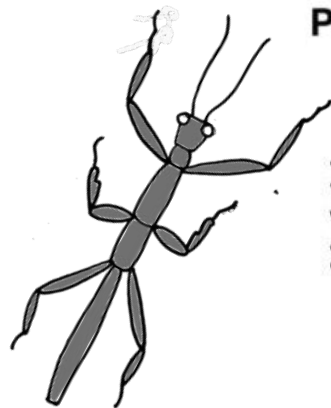
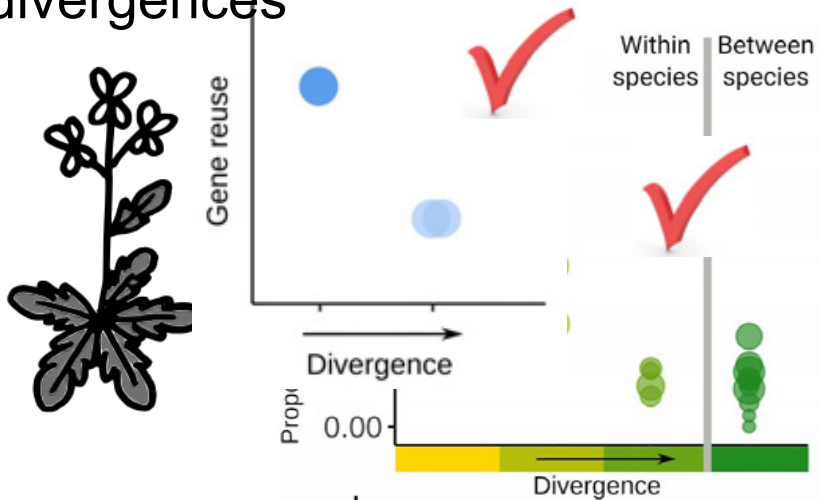


## Parallelism vs. genetic distance

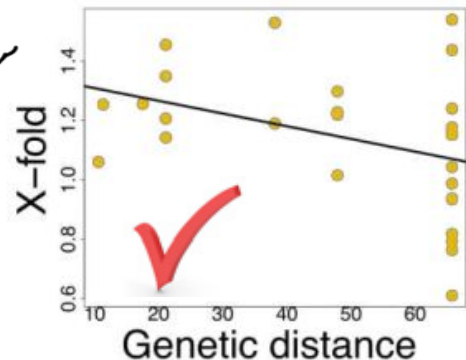


Chaturvedi et al, 2022

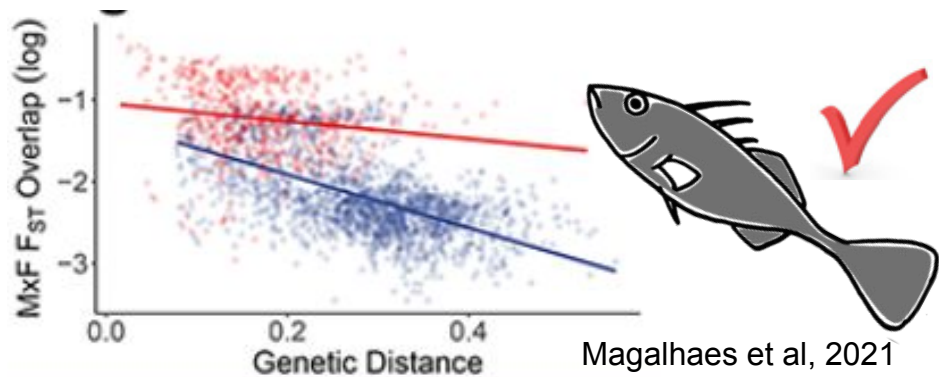
# WRAP-UP 2: repeated adaptations over recent + intermediate divergences



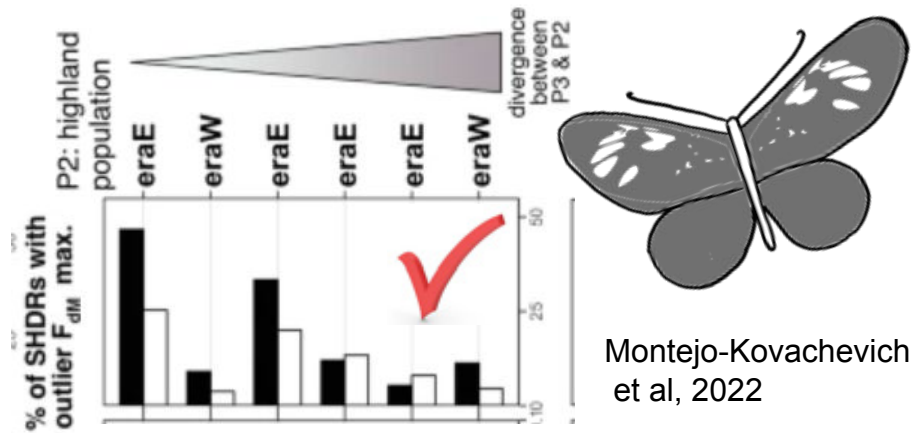
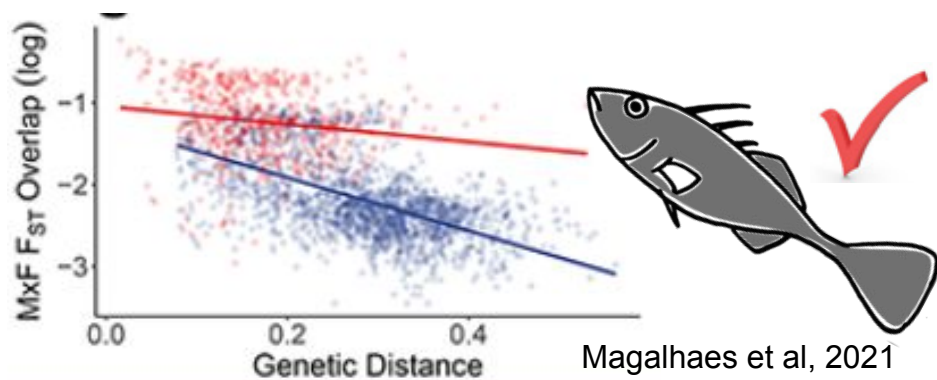
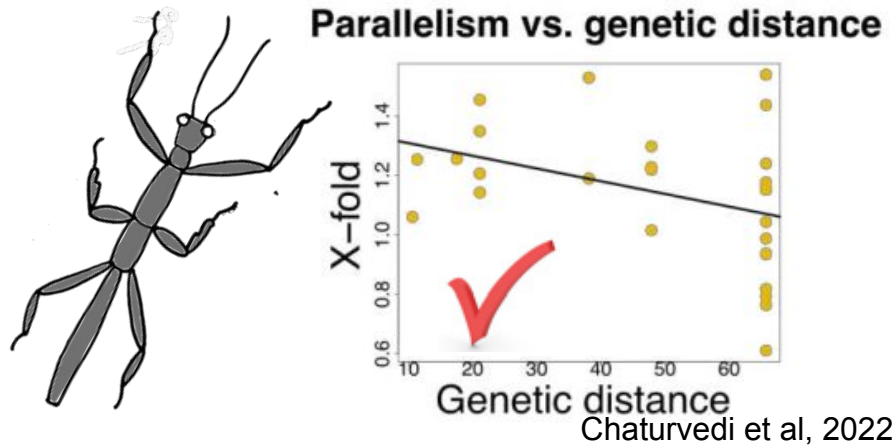
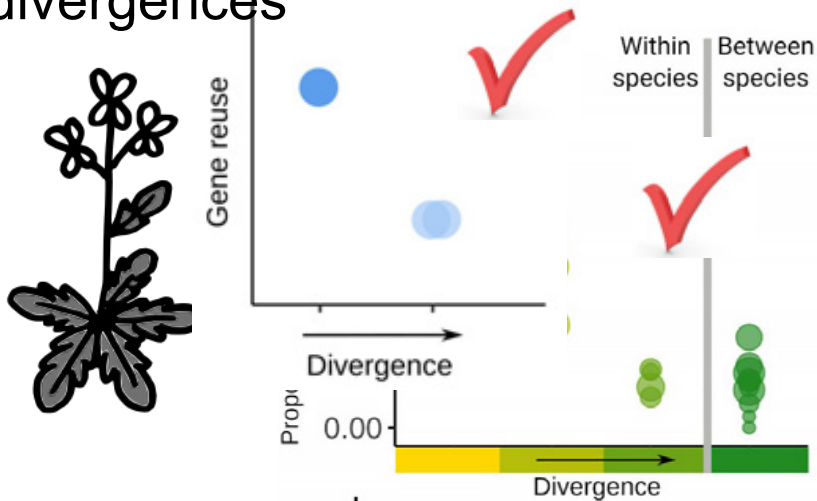
## Parallelism vs. genetic distance



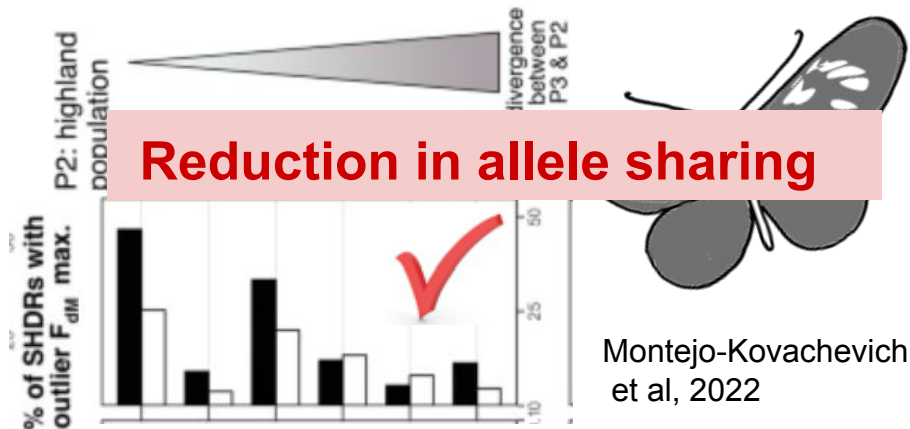
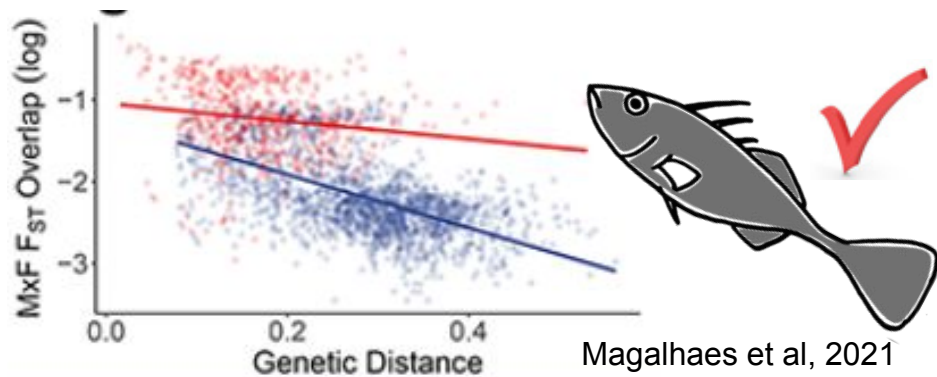
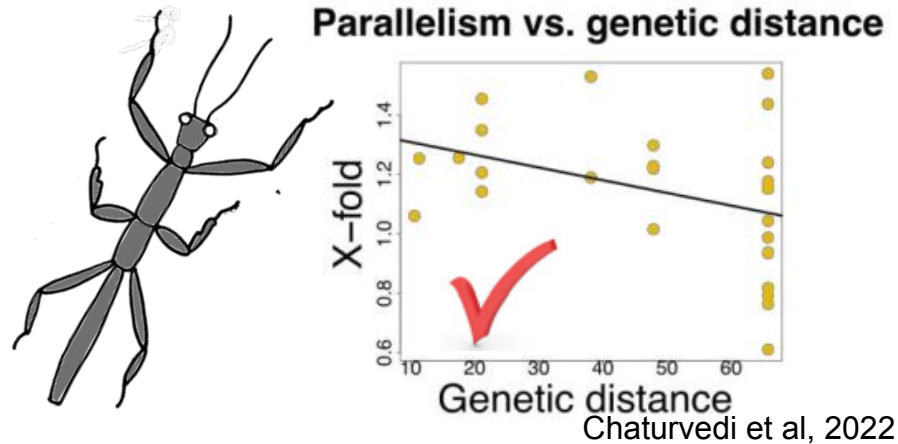
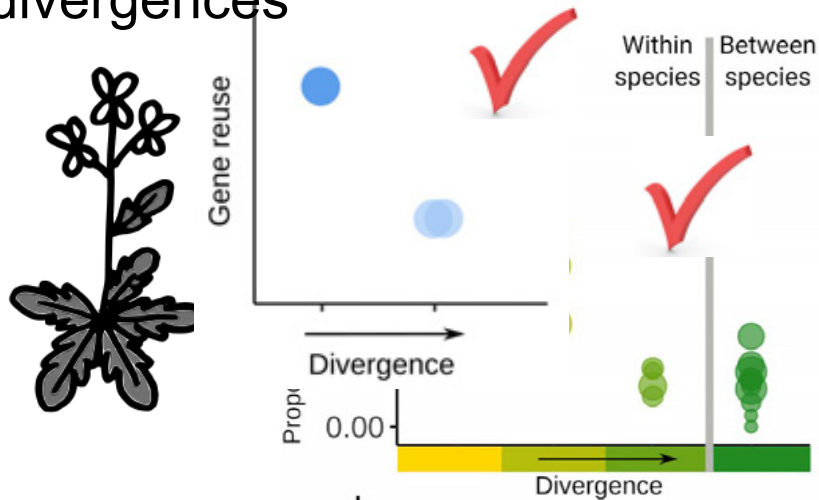
Chaturvedi et al, 2022



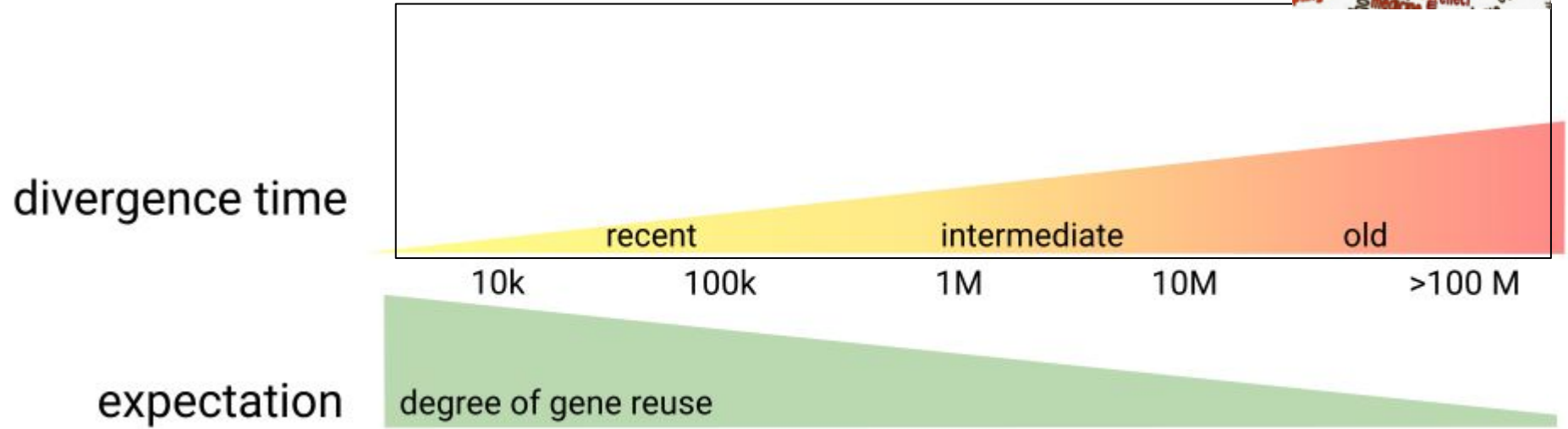
# WRAP-UP 2: repeated adaptations over recent + intermediate divergences



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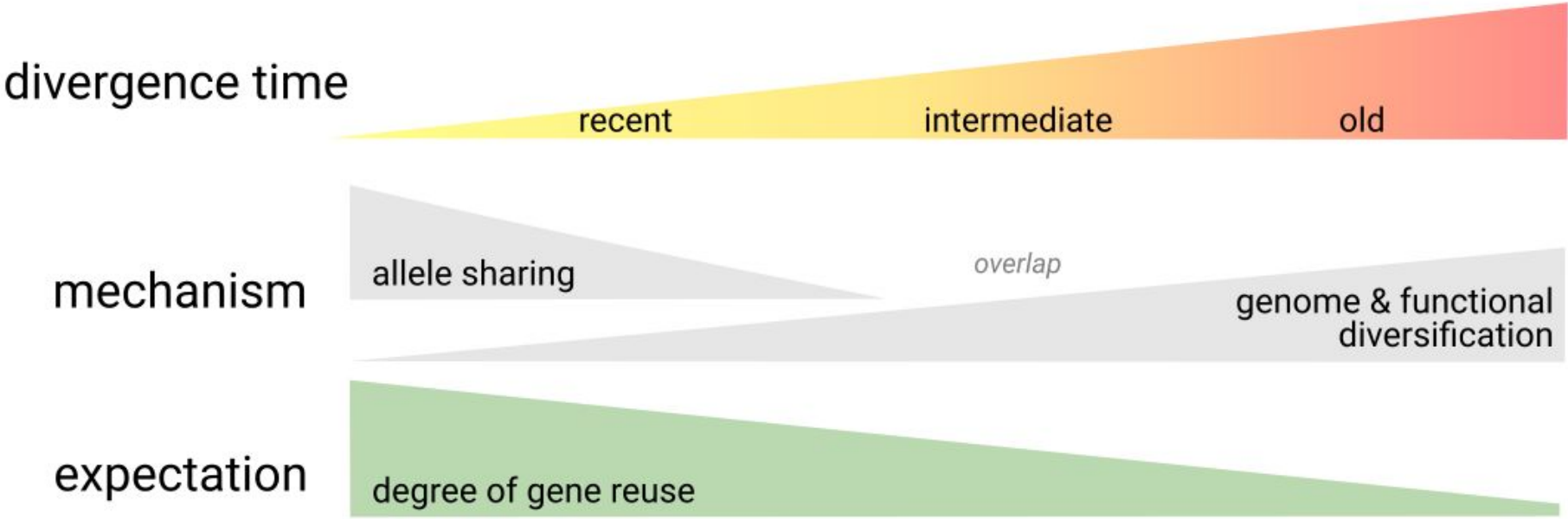
### 3. All divergences: a metaanalysis



#### Questions

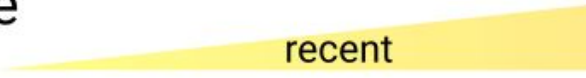
- Empirical support in nature?
- If yes, what are the underlying mechanisms?

# 3. All divergences: expectation



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divergence time



mechanism



expectation

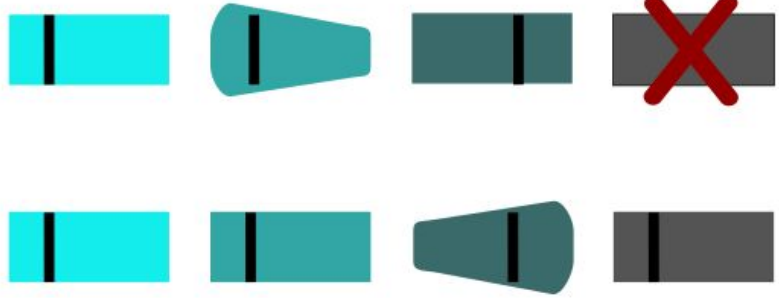


orthologous genes

*functions similar*

*functions diversifying*

*orthologs absent*



### 3. All divergences: data

Bohutinska & Peichel  
in prep.



divergence  
(generations)

10k

100k

1M

10M

>100 M

~populations

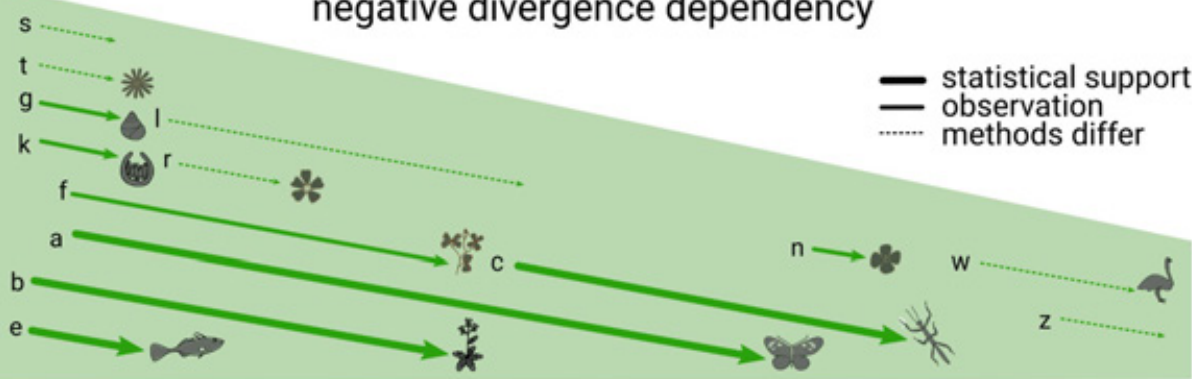
~species

~genera

higher clades

Bohutinska & Peichel  
in prep.

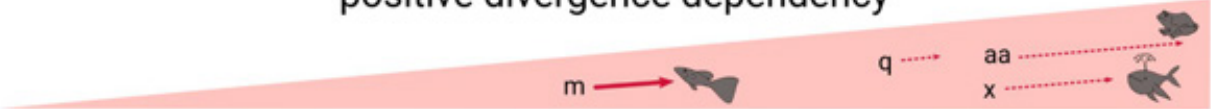
negative divergence dependency



no relationship



positive divergence dependency



case studies of gene reuse

divergence  
(generations)

10k

100k

1M

10M

>100 M

~populations

~species

~genera

higher clades

negative divergence dependency

s

t

g

k

f

a

b

e

d

h

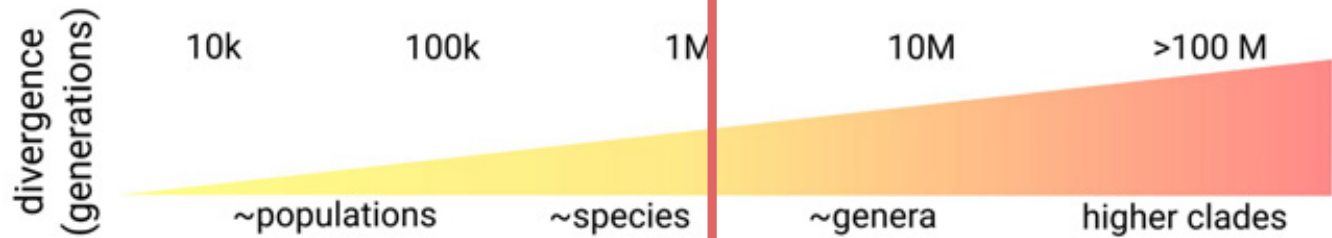
i

j

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l

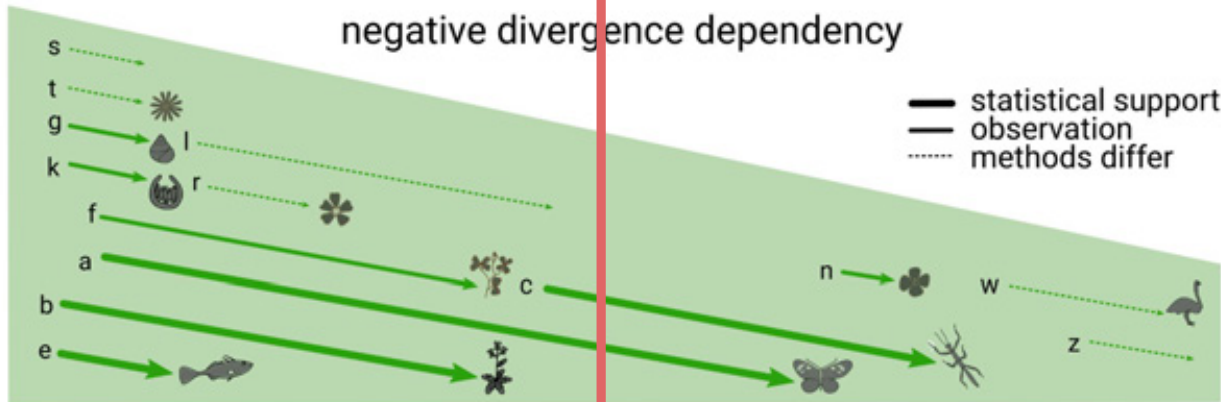
r



Bohutinska & Peichel  
in prep.

case studies of gene reuse

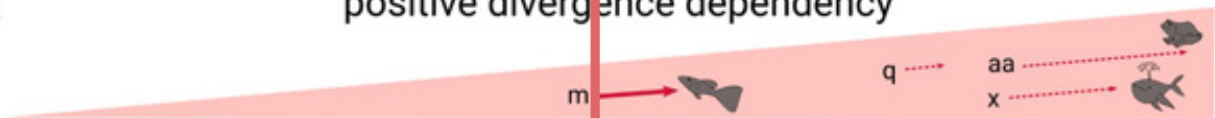
negative divergence dependency



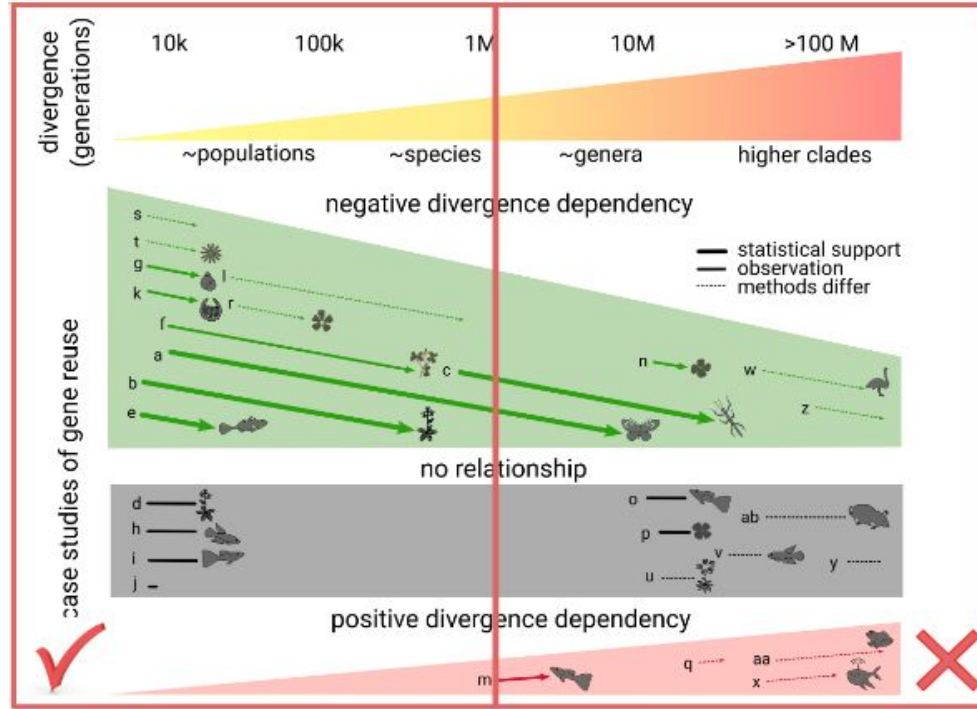
no relationship



positive divergence dependency



# WRAP-UP 3, all divergences: clear mechanisms, unclear data



# Conclusions & future directions?

1. Divergence matters! Sometimes...
  - a. Adaptation more repeatable among more closely related lineages
2. More empirical research across wide scales
  - a. What are suitable selection pressures?
3. Better knowledge & timing of mechanisms

# THANK YOU FOR ATTENTION!

## And many thanks to:

**Katie Peichel (Bern)**

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**Graham Coop (Davis)**

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Veronika Konečná

Sivan Yair

Sian Bray

And many others!



**Evolutionary ecology (Bern)**



**Plant ecolgen (Prague)**



@MajdaHolcova

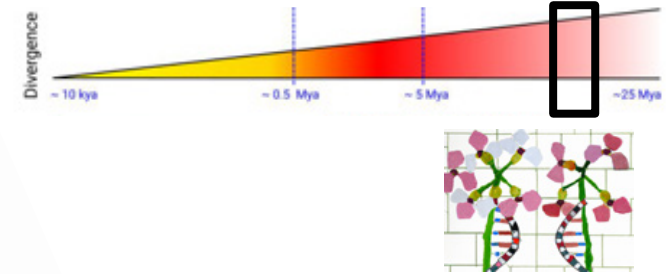


## 2. Deeper divergence levels

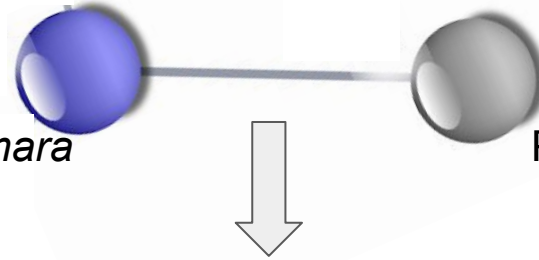
CS4: Bohutínská et al. 2021, MBE

CS5: Bohutínská et al. 2021, MBE

Different genes, interacting protein products?

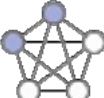


Protein A, selected in *C. amara*

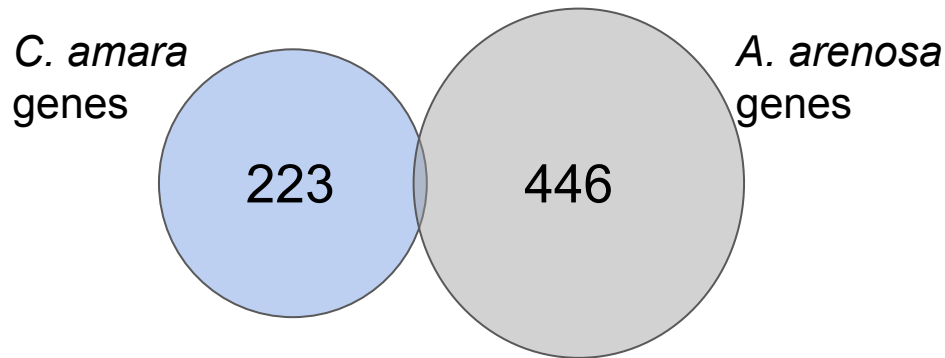


Protein B, selected in *A. arenosa*

joint contributions to similar function

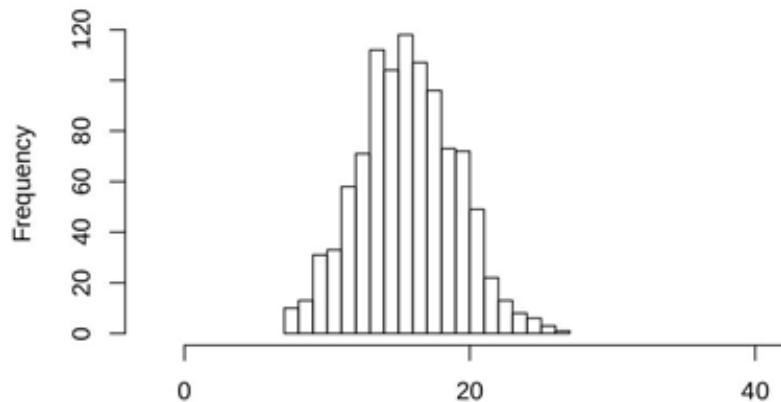
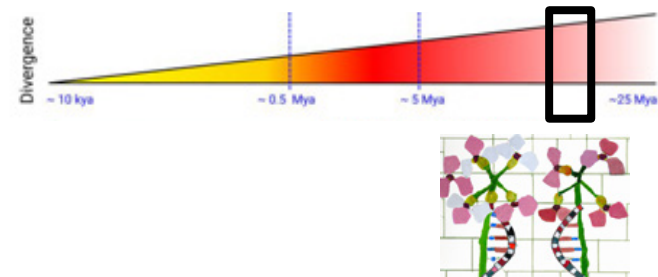
- Protein-protein interaction prediction:  **STRING**

## 2. Deeper divergence levels



CS4: Bohutínská et al. 2021, MBE

CS5: Bohutínská et al. 2021, MBE



Number of interactions when candidate lists sampled randomly



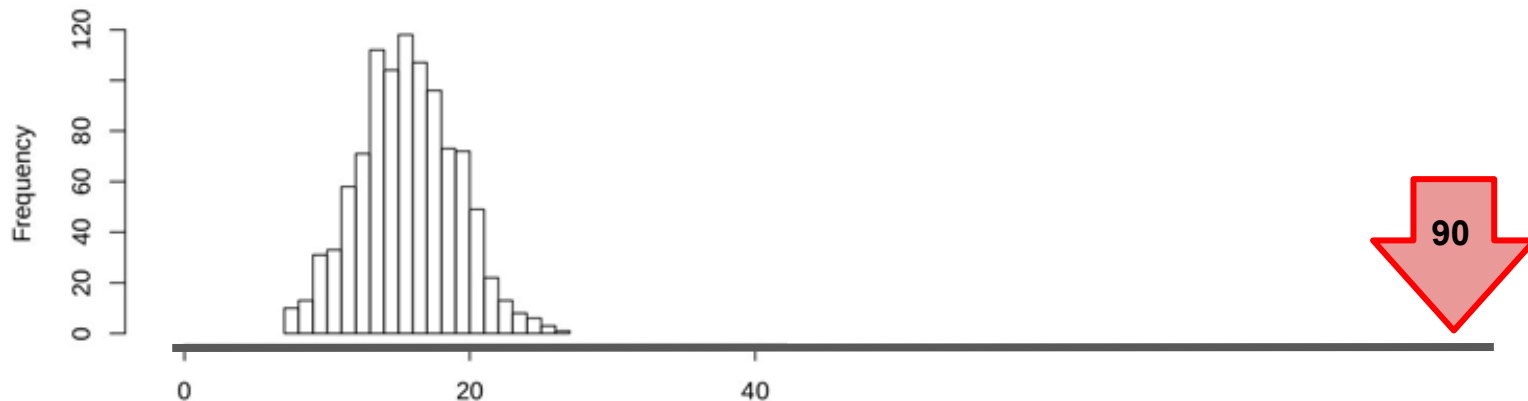
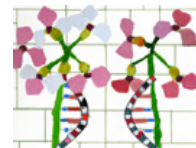
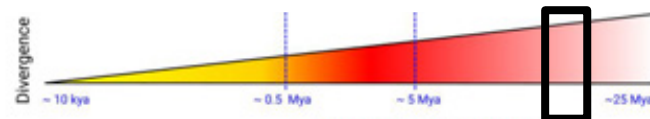
## 2. Deeper divergence levels

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CS5: Bohutínská et al. 2021, MBE

229 *C. amara* WGD adaptation candidates:

- 90 interact with WGD adaptation candidate in *A. arenosa*



Number of interactions when candidate lists sampled randomly

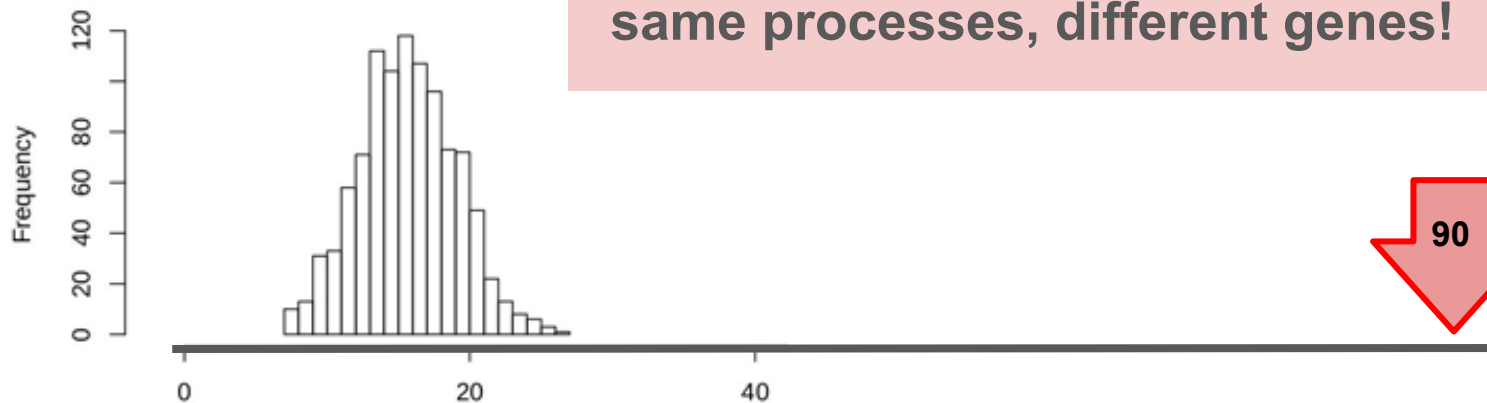
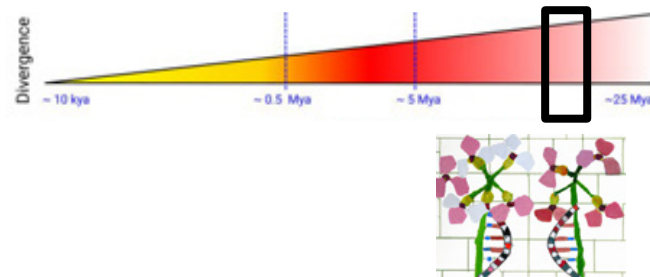
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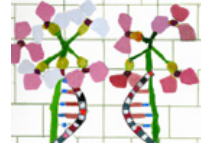
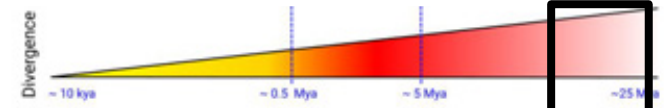
CS6: Bray et al., in prep.

### Adaptation to WGD

*Cochlearia* & *Cardamine amara* & *A. arenosa*

Deepest divergence covered - ~ 25 Mya

- **Limited** gene reuse
- **Function** reuse



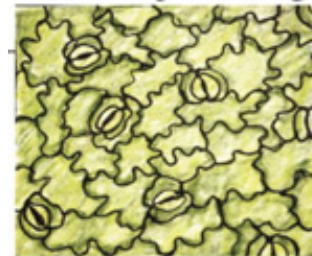
meiosis



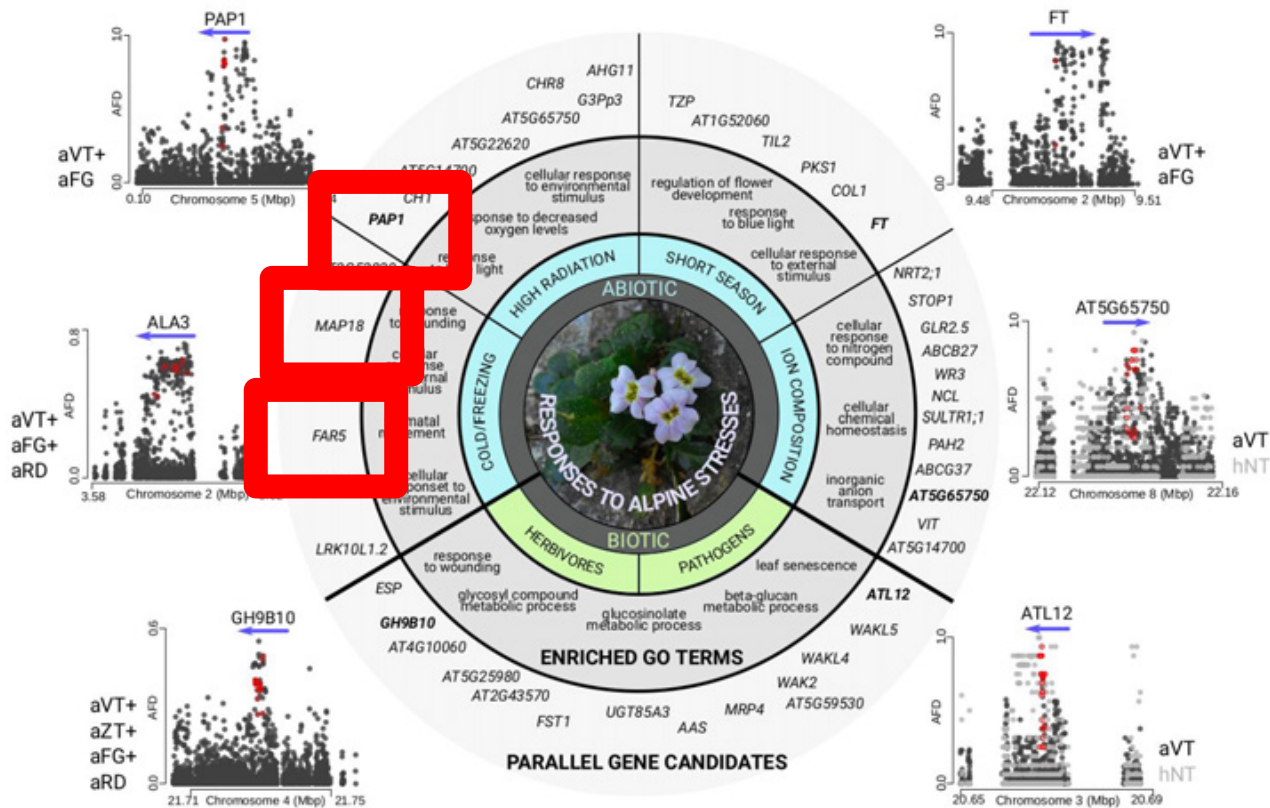
pollen tubes



stomatal patterning

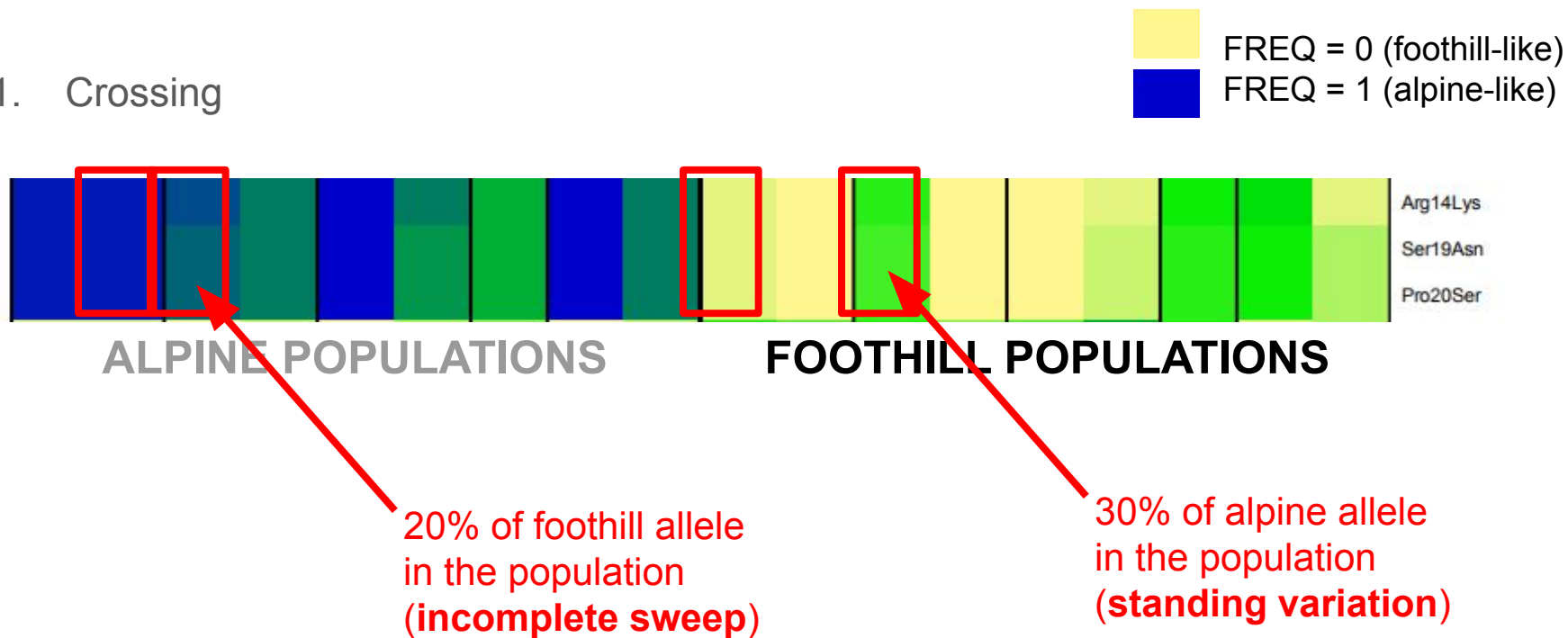


## 2. The phenotypic and fitness effect of convergent alpine genes



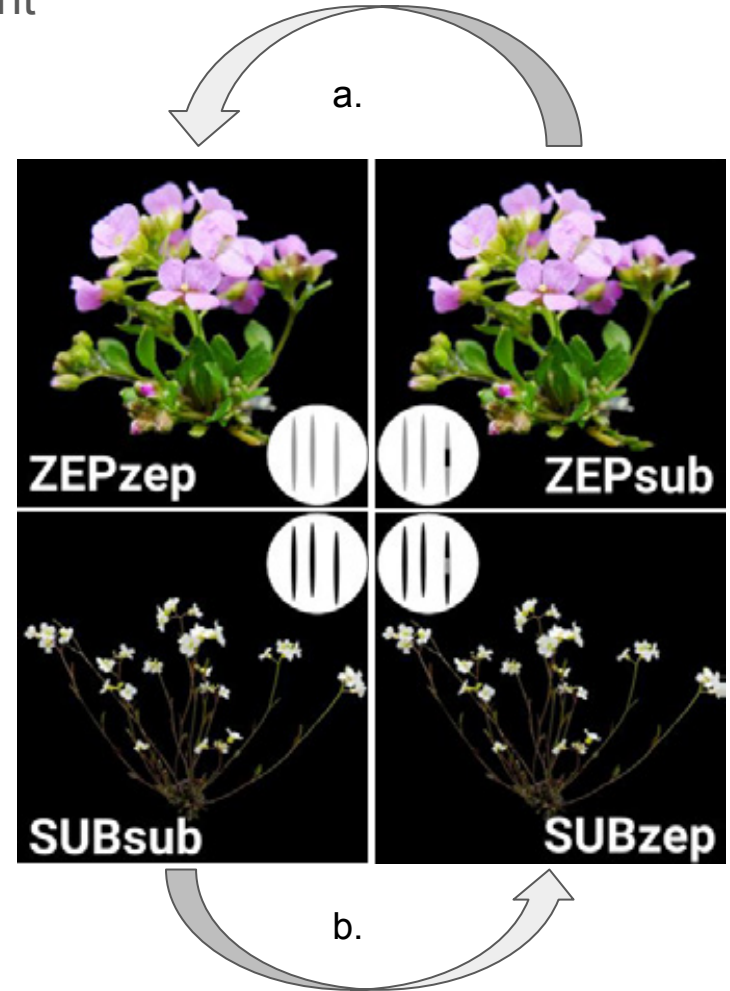
## 2. The phenotypic and fitness effect of convergent alpine genes

### 1. Crossing



## 2. The phenotypic and fitness effect of convergent alpine genes

1. Crossing -> contrasting allele and genome background
2. Transplant + common garden experiment
  - a. The fitness gain under alpine conditions
  - b. Fitness loss under foothill conditions - negative side-effects?





## 2. The phenotypic and fitness effect of convergent alpine genes

1. Crossing -> background

2. Transplant  
a. The fitness  
b. Fitness negative

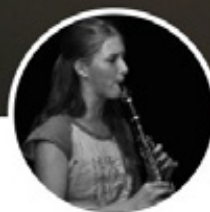
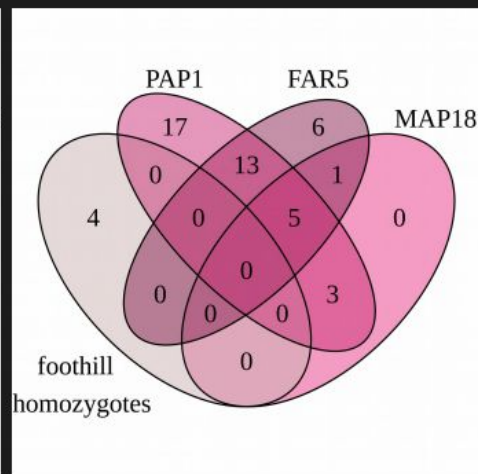
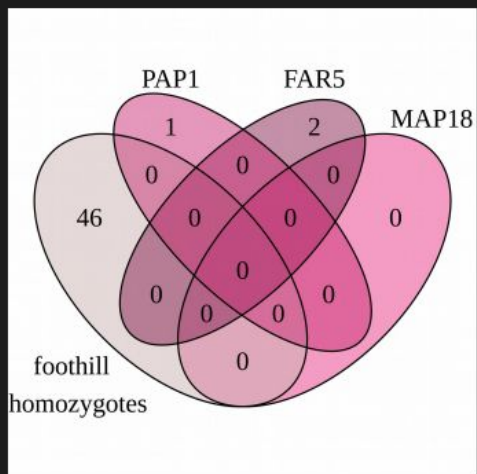
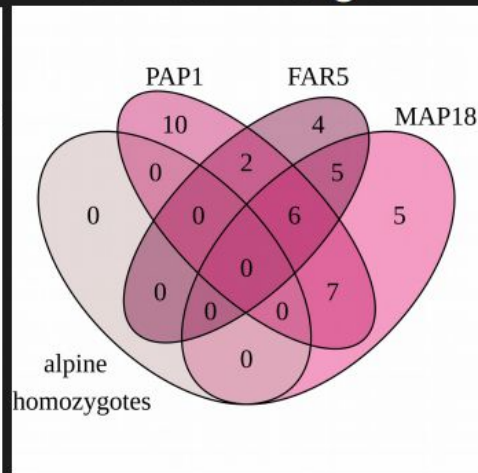
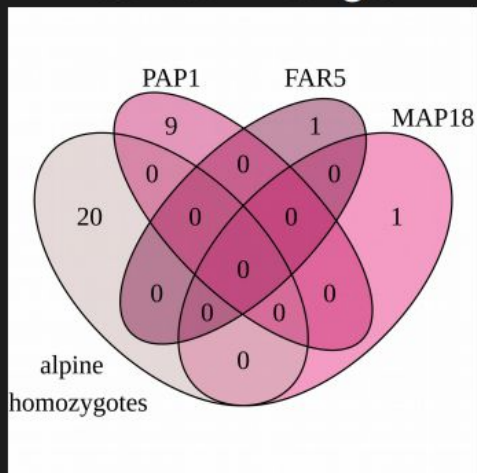


b.

# Proportion of heterozygotes

mountain range 1

mountain range 2



**Alžběta Poštulková**

@BetyPostulkova Follows you

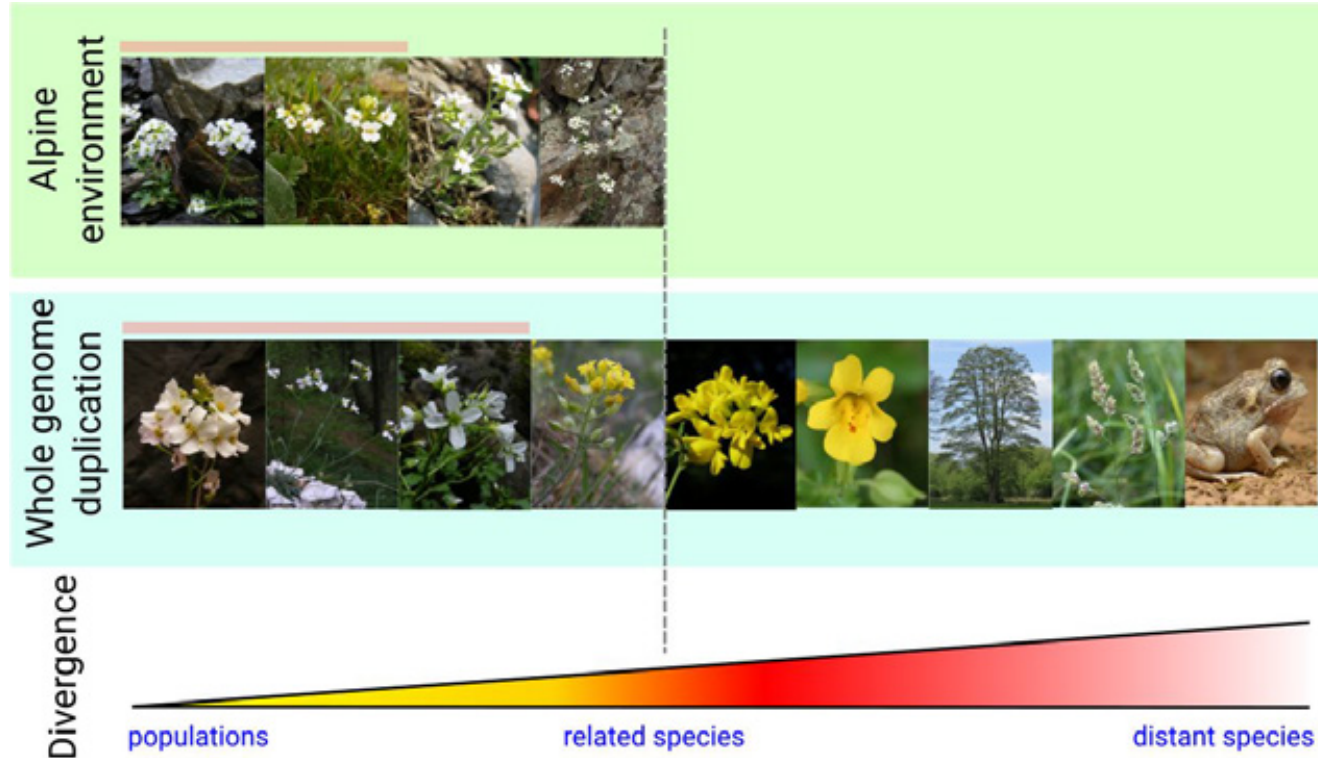
alpine populations

foothill populations



# Further research directions?

The effect of constraints? Pop-gen analyses & experimental validation



# Follow up - what determines the probability of gene reuse?

- **Testing for effect of:**

- **Availability of shared variation** (DMC)
- **Pleiotropy** ( ~ network connectivity, Josephs, 2017, regulatory/coding variation)
- **Selective constraints** ( ~ nonsyn/syn diversity, conservation of protein sequence across plant genomes)
- **Mutational target size** ( ~ gene length, pocet intronu/exonu - velky vyznam v regulaci napr. Alternativnim splicingem - cim vic, tim vetsi variabilita v alternativnim splicingu - uplatitelne v evoluci?)
- **Protein co-evolution** ( ~ correlation in allele frequencies, selection sweep ages)
- **Position in the pathway - zacatek/uplne konce/misto, kde se rozbiha vice downstream drah**
- **Compensatory mutations** (???)

