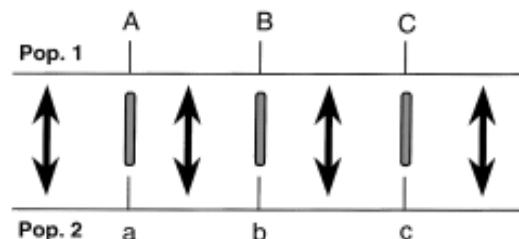
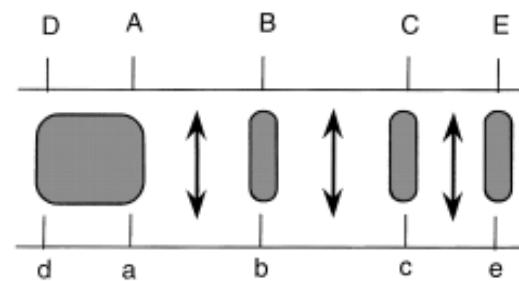


Week 10

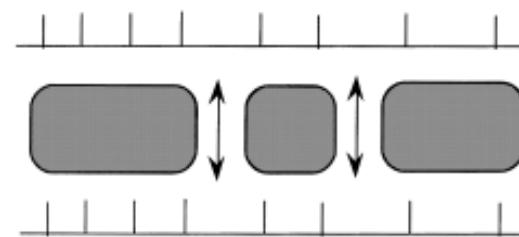
Genomic divergence during speciation



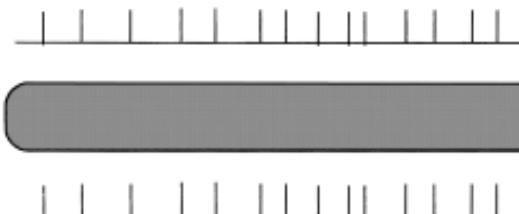
Stage I –
Populations/races with
differential adaptation;
RI not apparent.
3 divergent loci shown
here.



Stage II –
Transition between race and
species with some degree of RI;
populations may fuse or diverge.



Stage III –
Divergent populations beyond
the point of fusion but still share
a portion of their genomes via
gene flow; good species.



Stage IV –
Species with complete RI.

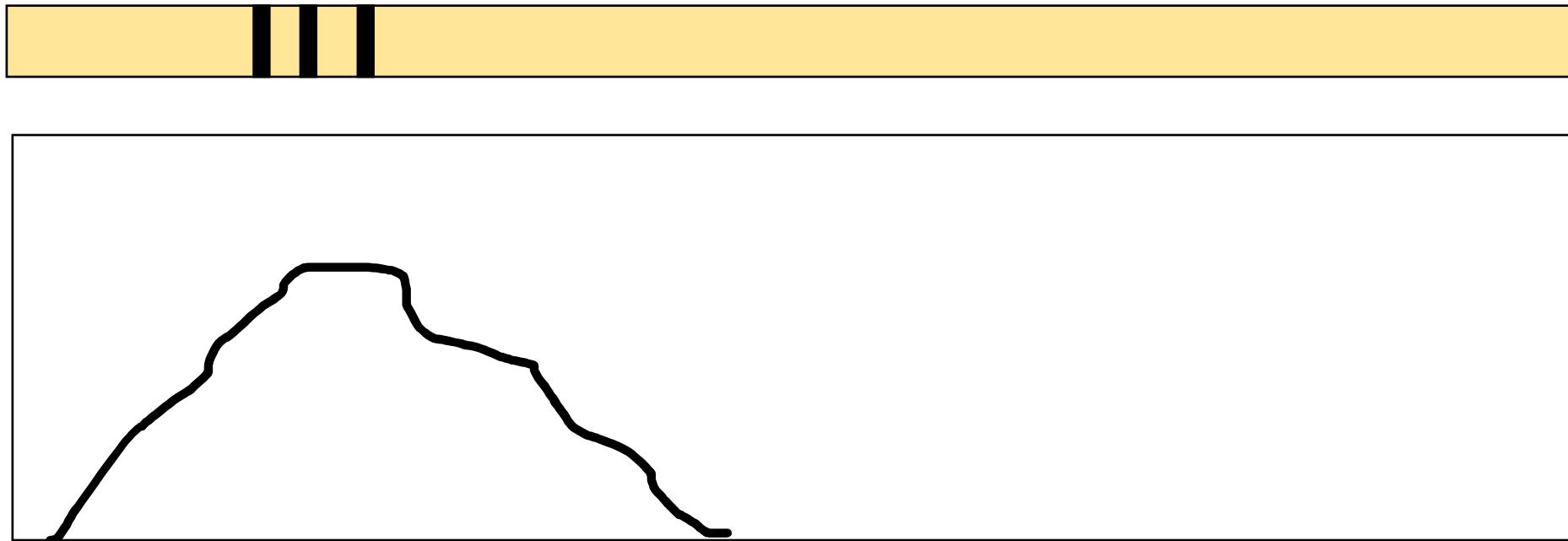
Phase 1: Adaptive divergence at a subset of the genome

Gene underlying adaptation



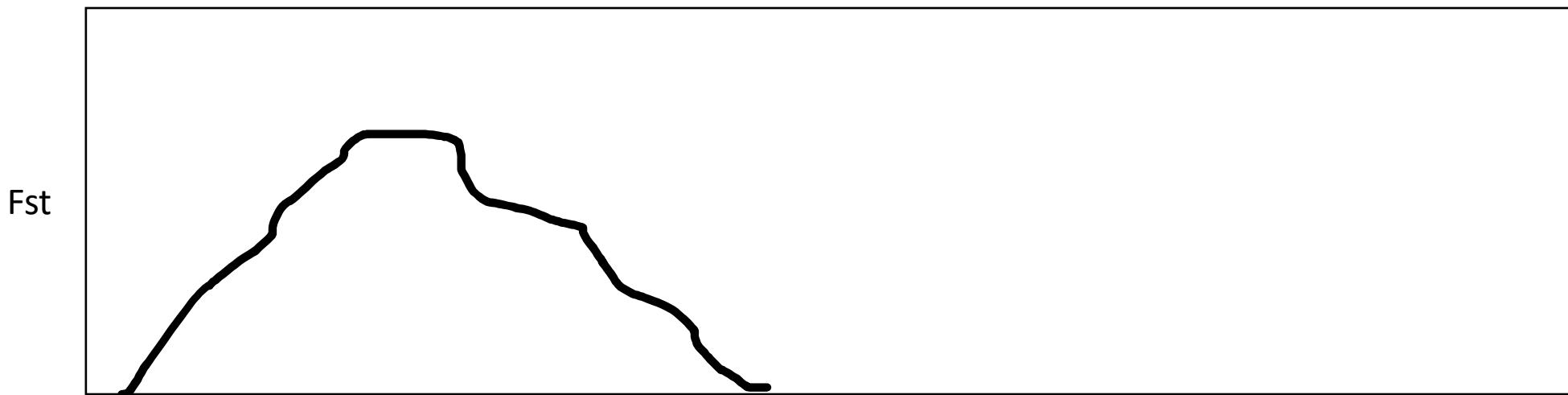
Phase 2: Divergence hitchhiking

Gene underlying adaptation

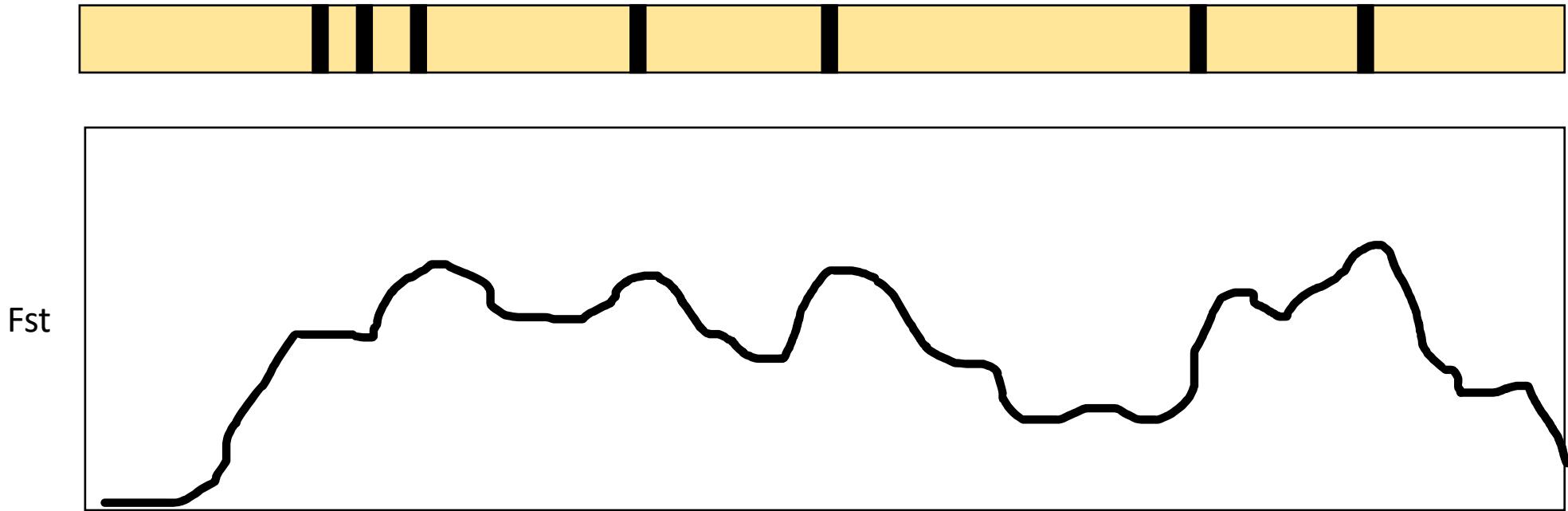


Phase 2: Divergence hitchhiking → inversions

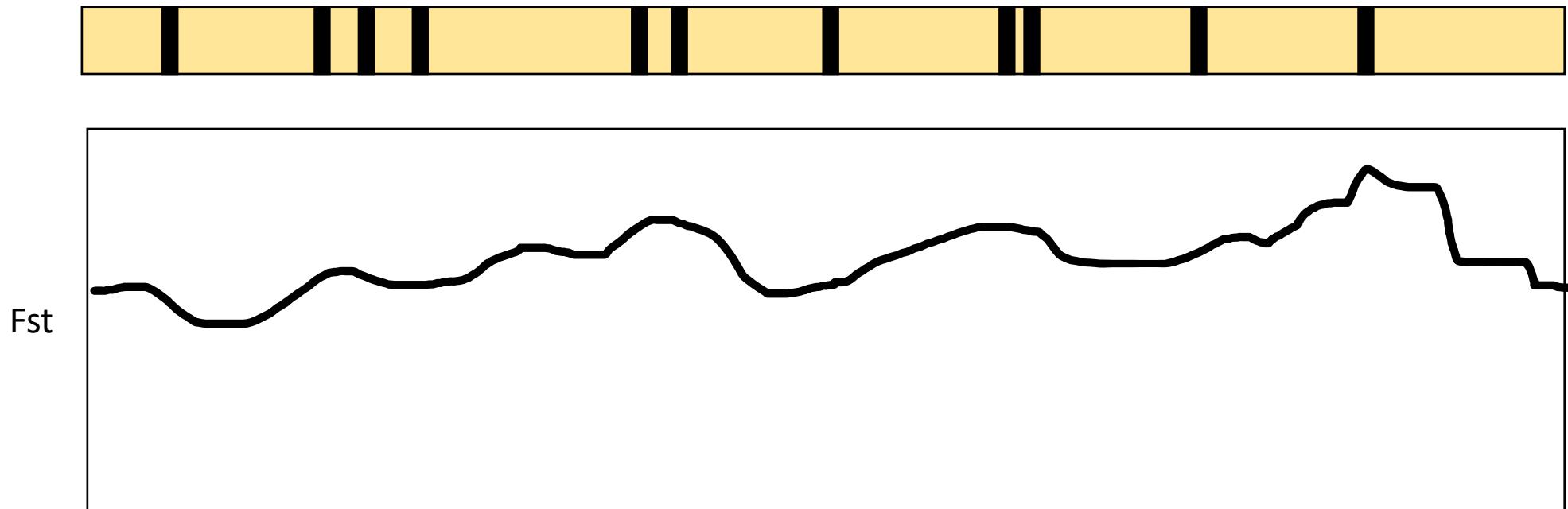
Inversions link multiple adaptive alleles



Phase 3: Genome hitchhiking

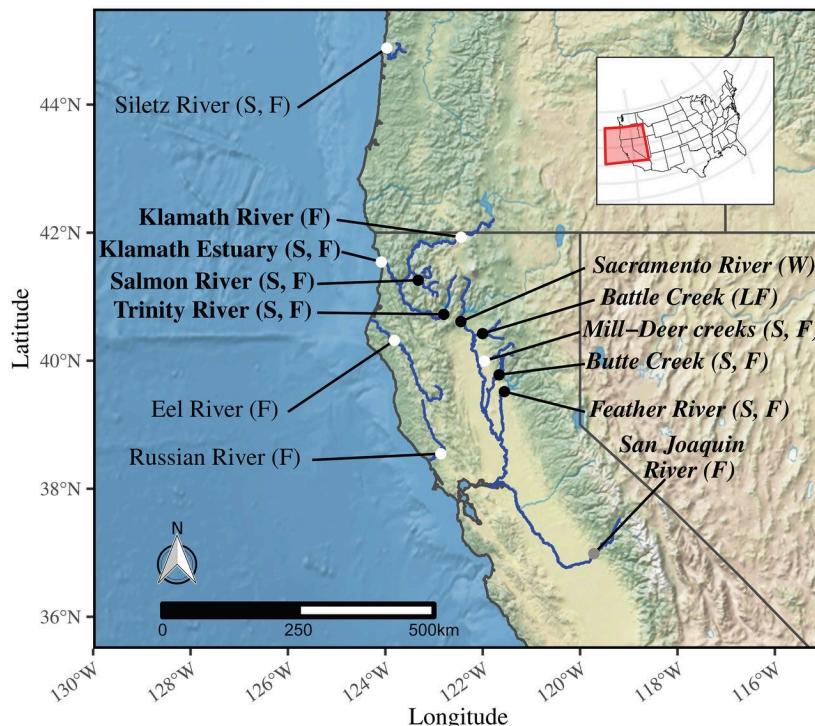


Phase 4: Speciation and genome-wide divergence

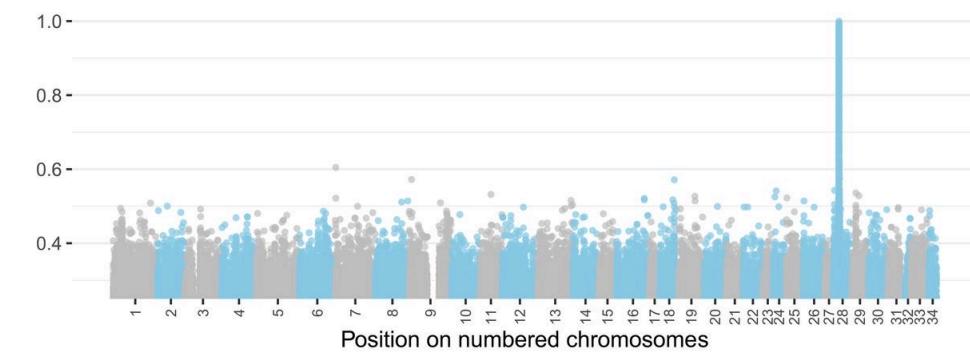


Phase 1:

Gene underlying adaptation



Difference in allele frequency between early and late run

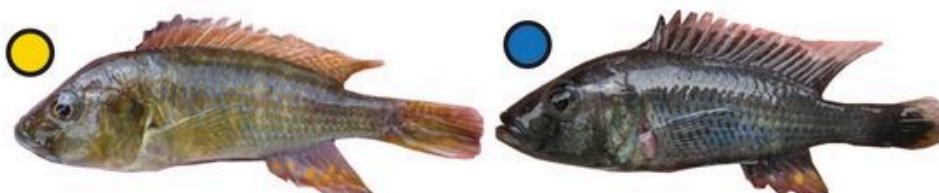


Phase 1:

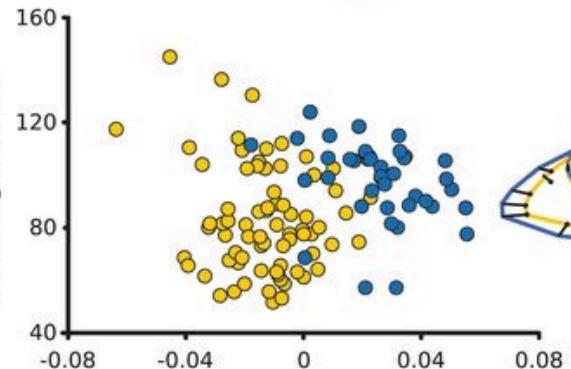
Gene underlying adaptation



B

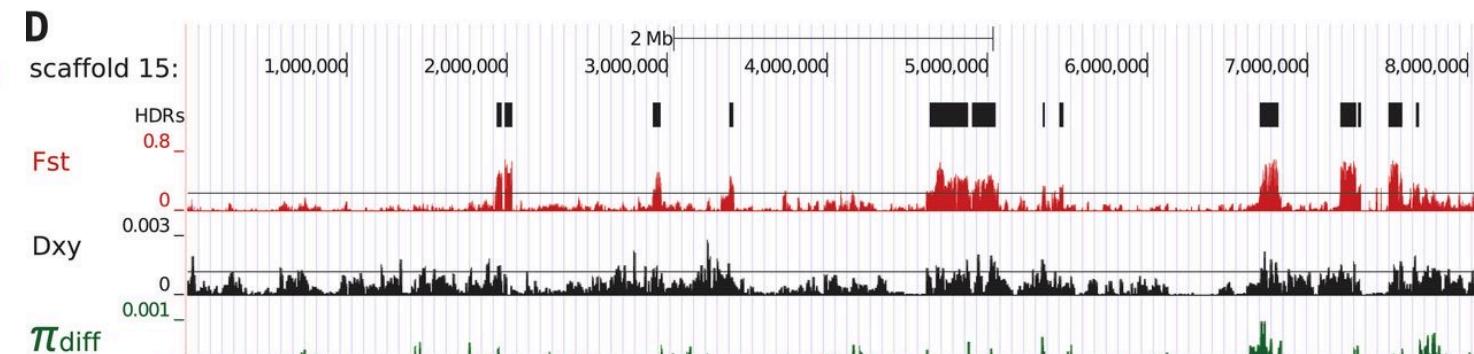


C Total length (mm)



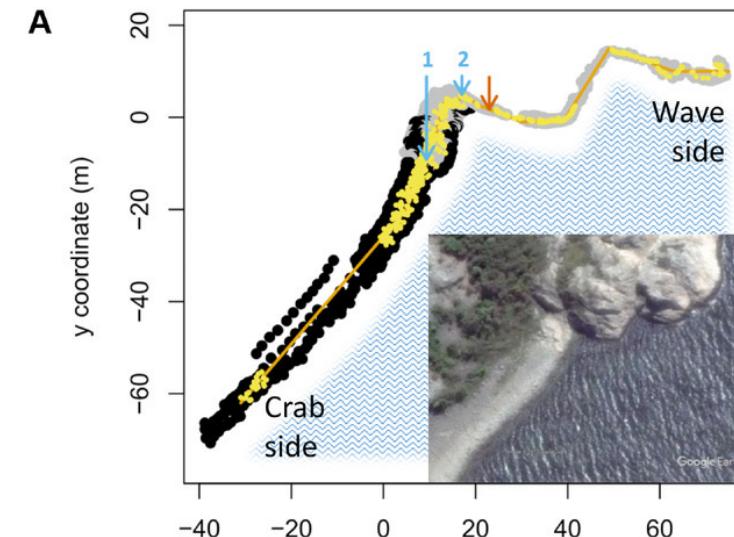
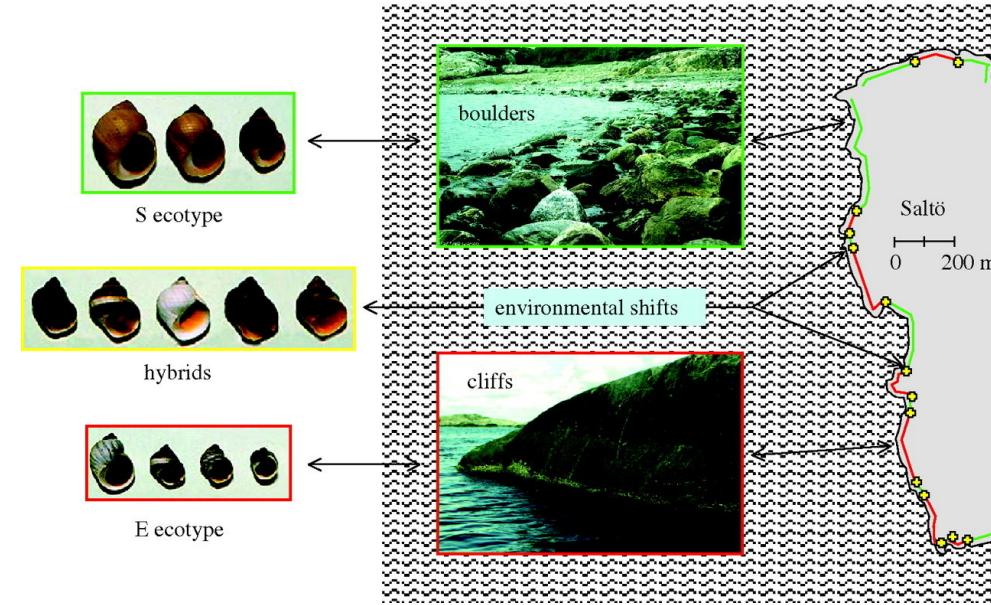
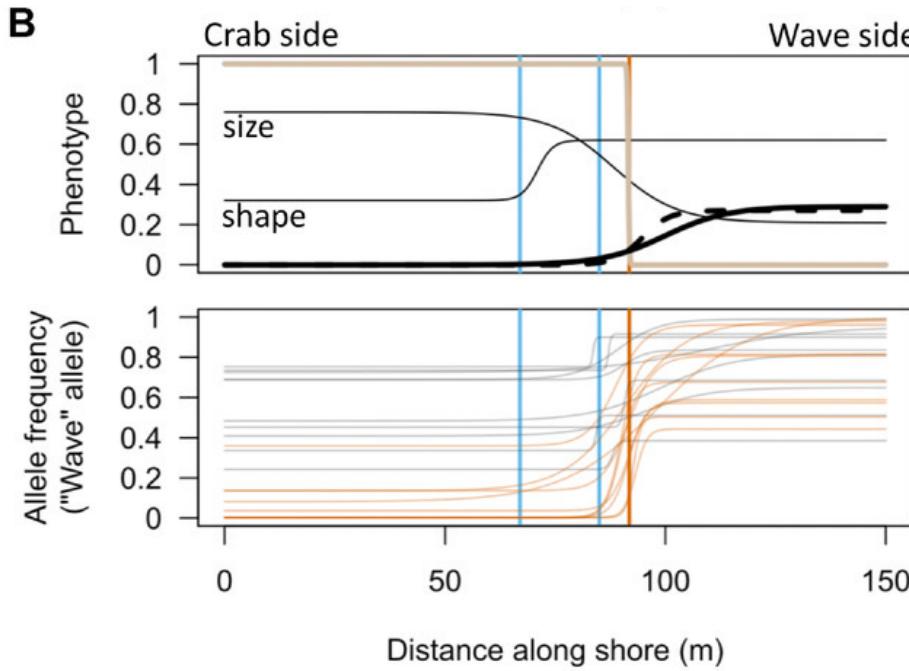
Principal component axis 1 (29.7% of shape variation)

D



Hybridization as natural experiments

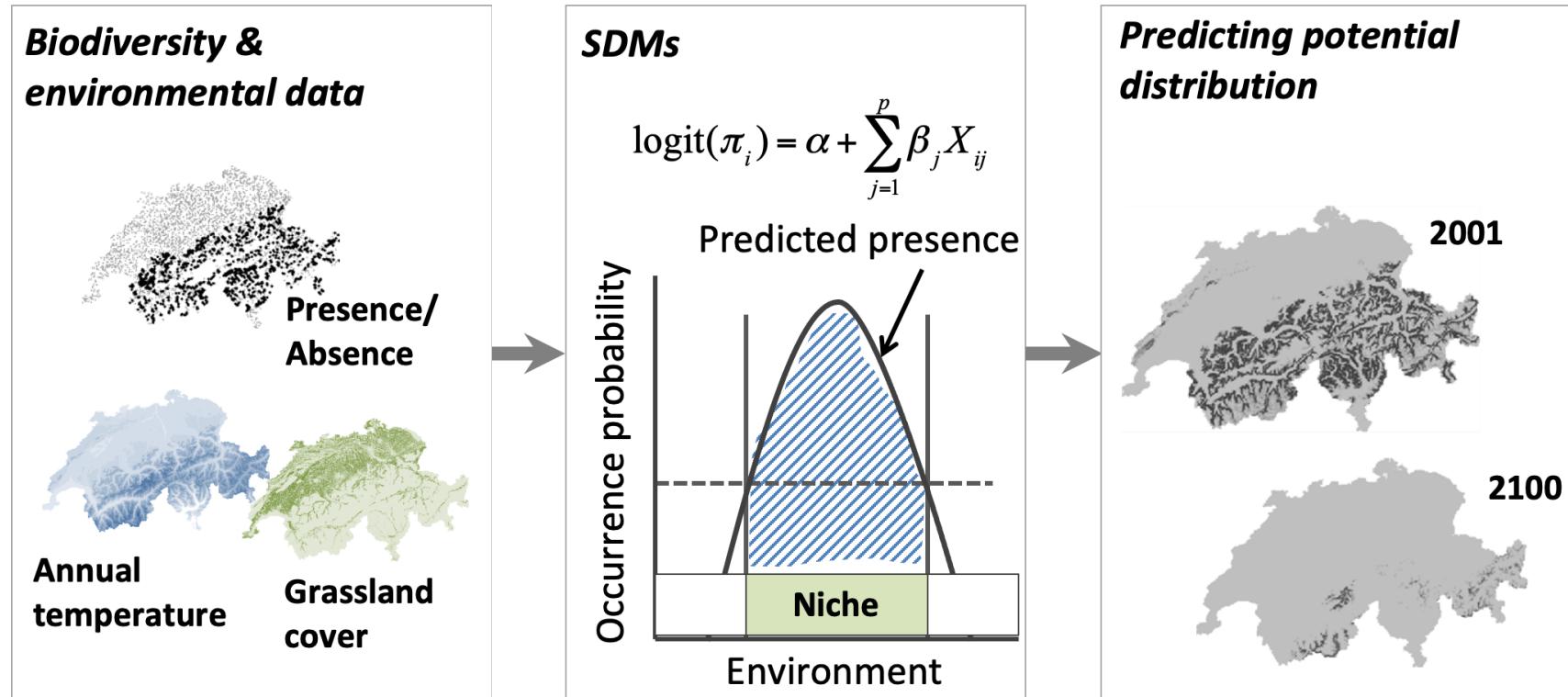
- *Littorina saxatilis*



Now for some applied stuff...

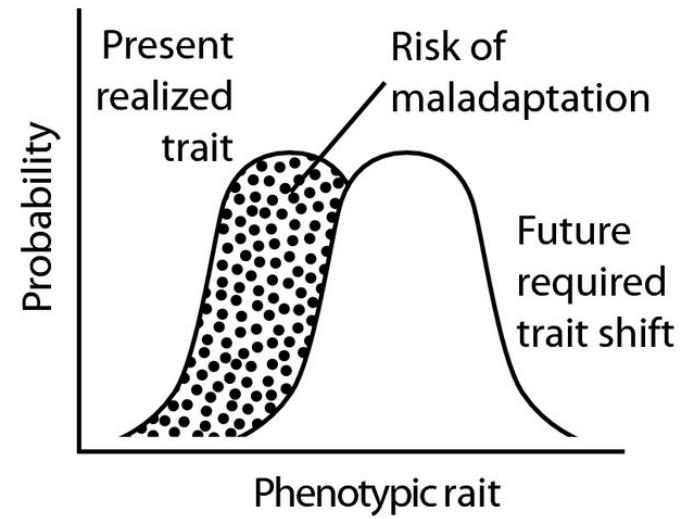
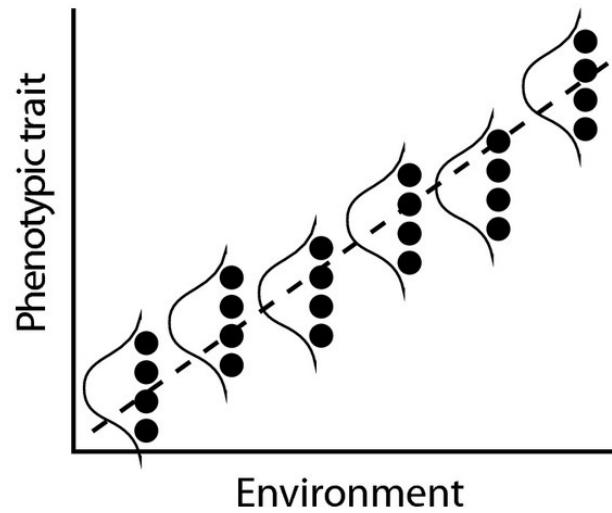
How do we predict which populations will be at risk to environmental change?

- Ecological niche modeling/species distribution modeling
 - suitable niche of a species is modeled occurrence records and climatic data then



How do we predict which populations will be at risk to environmental change?

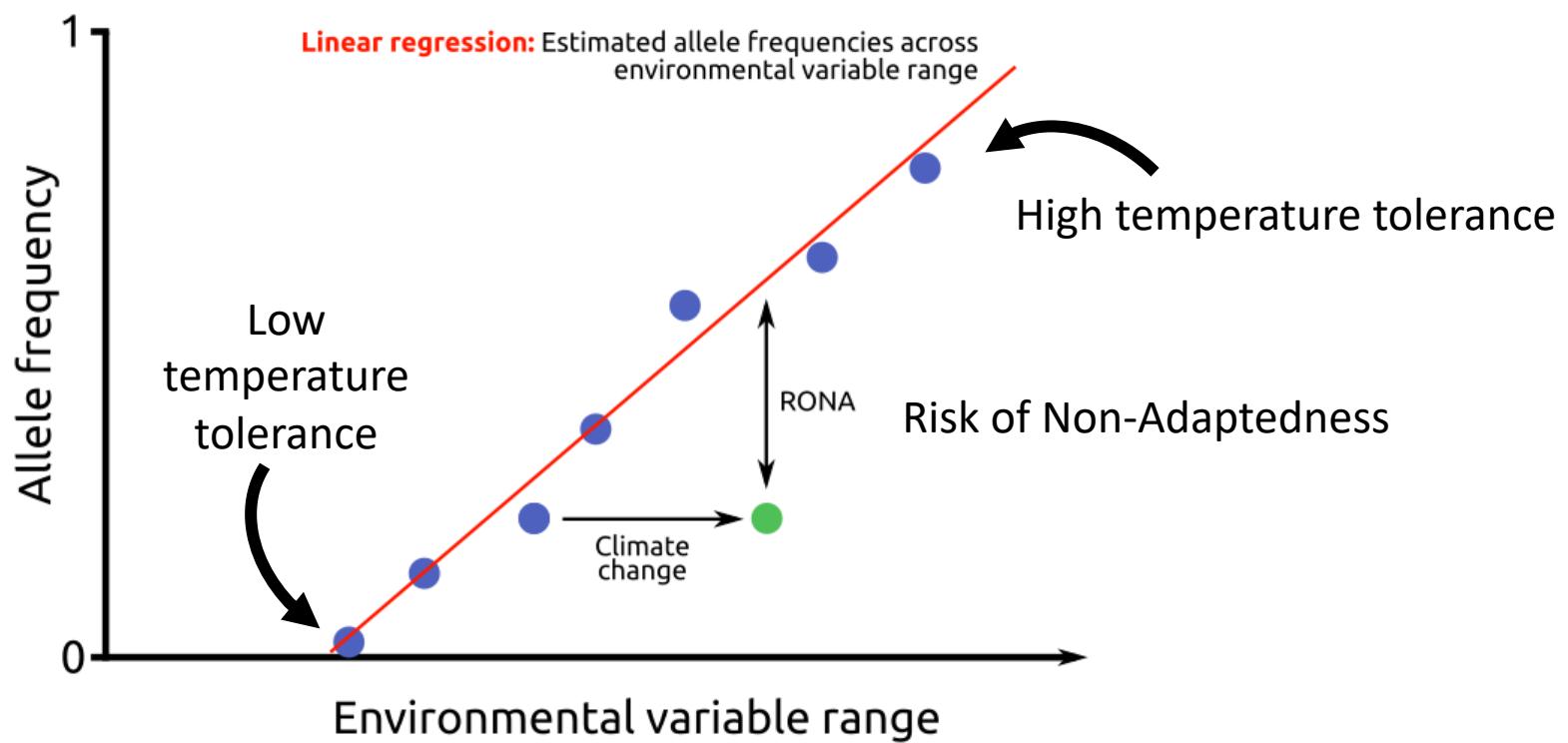
- Common gardens



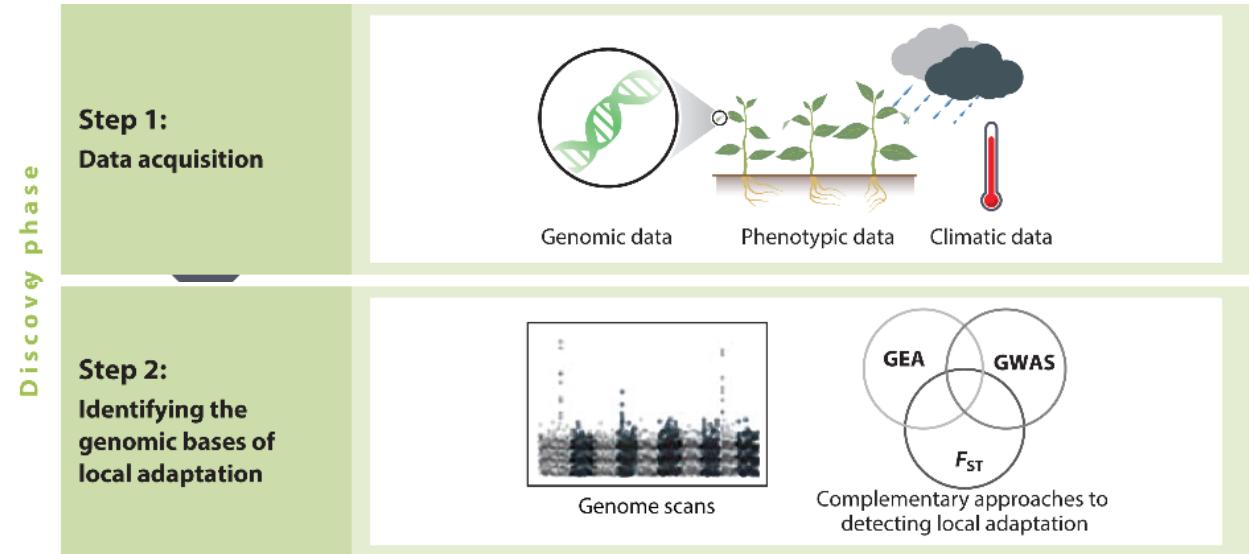
Genomic vulnerability/offset

- The distance between the current and required genomic composition in a set of putatively adaptive loci under a future/changed environment.
(Rellstab et al., 2021)
- Given current patterns of genetic variation, where might there be a mismatch in the future?

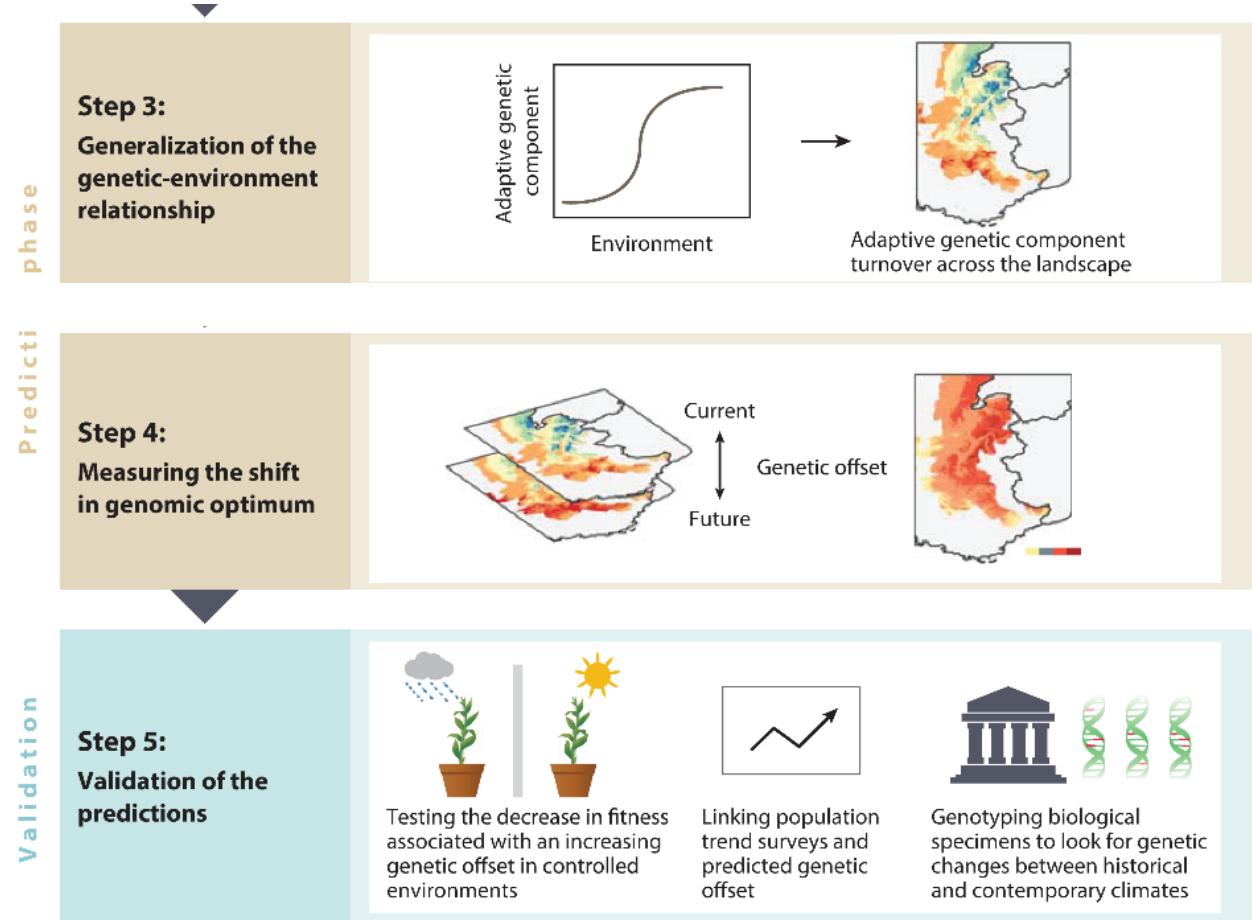
Identify the loci
that are associated
with tolerance to
an environmental
condition

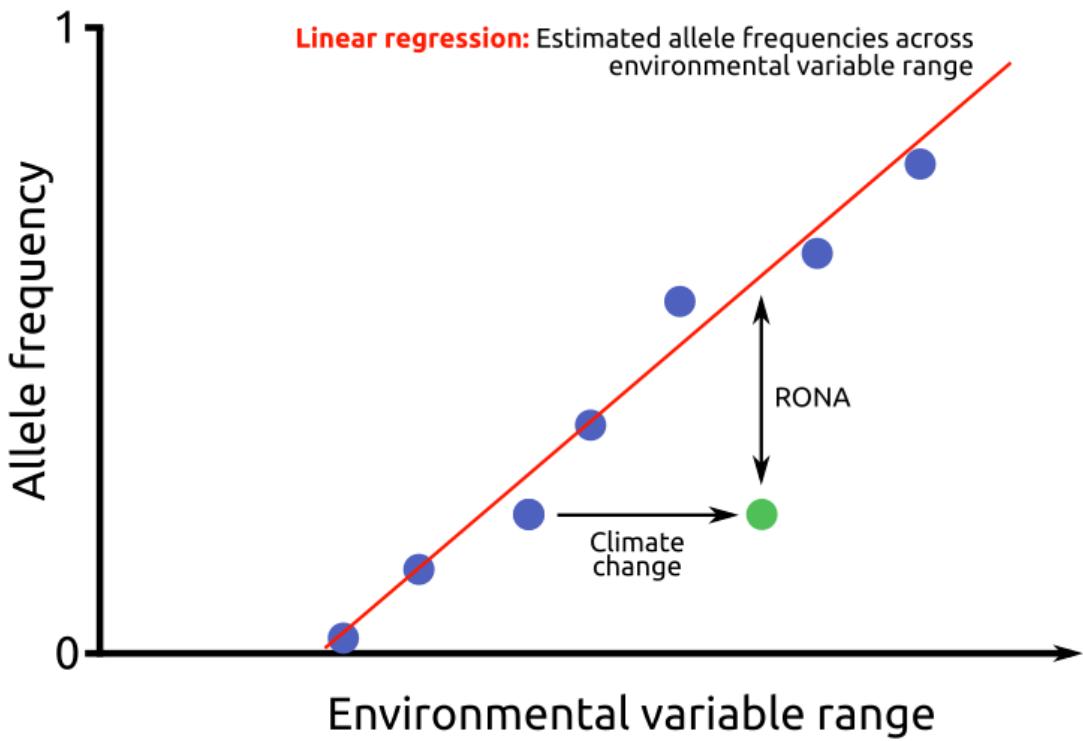


Genomic vulnerability/offset



Genomic vulnerability/offset





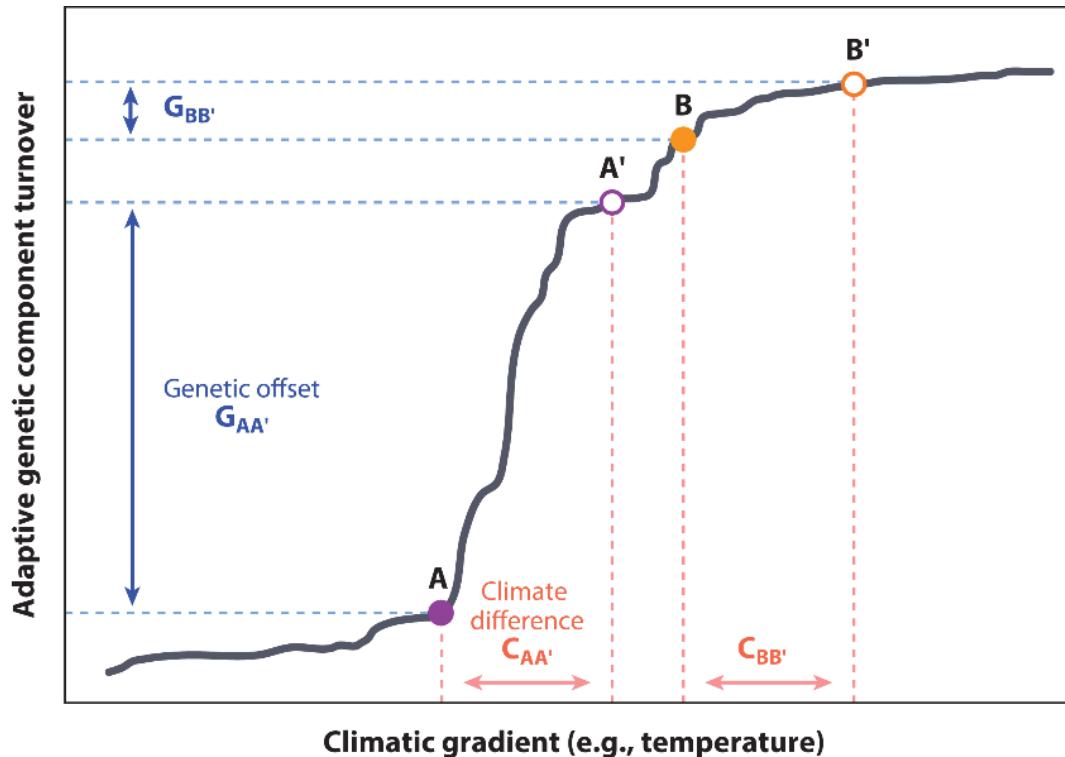
Assumptions:

1. Populations are locally adapted
2. Alleles have same effect in different genetic backgrounds
3. Linear effect on phenotype
 - Machine learning methods don't make this assumption

Direct estimate of allele frequencies in future environment

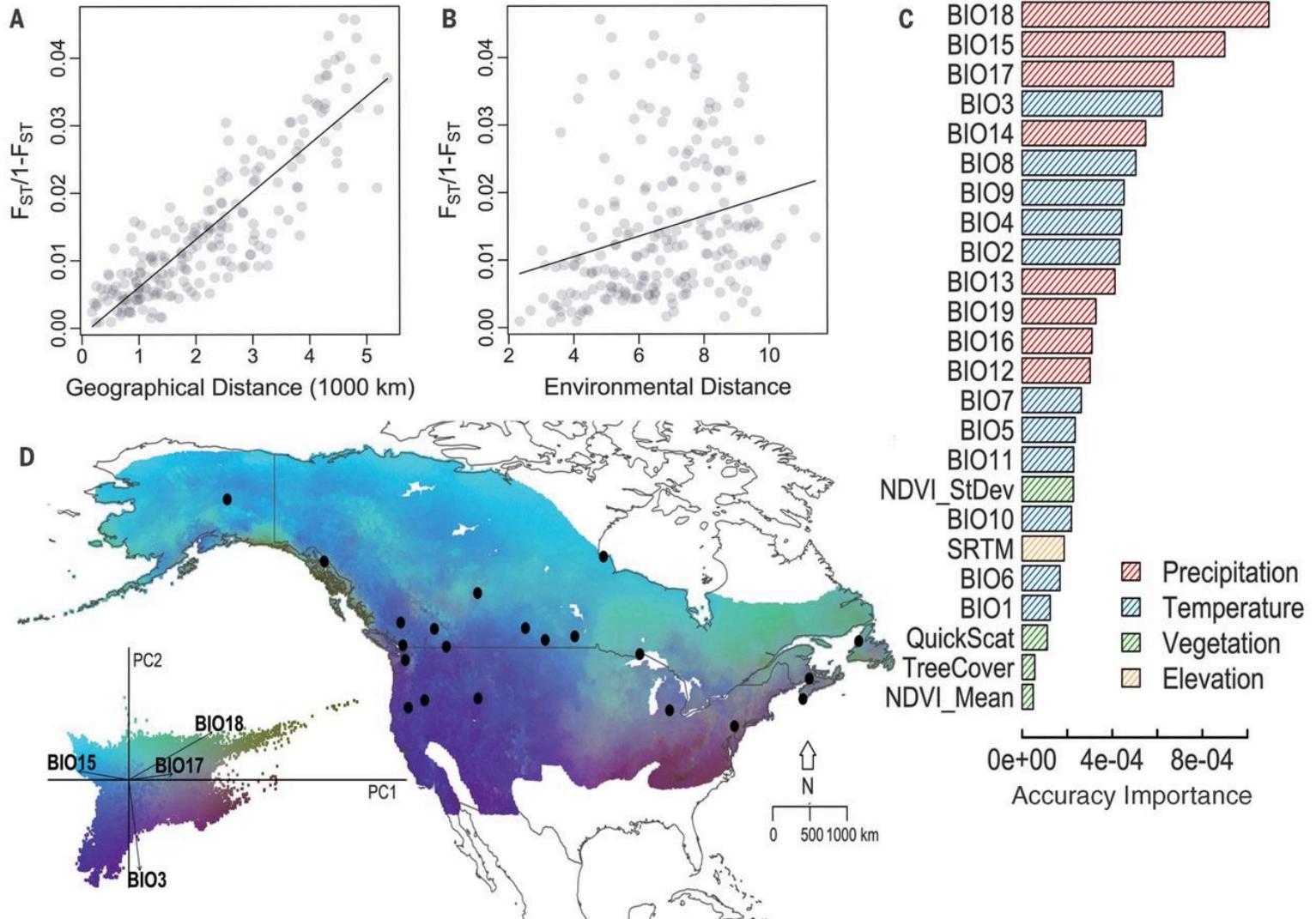
Genomic vulnerability/offset

- Machine learning → gradient forests

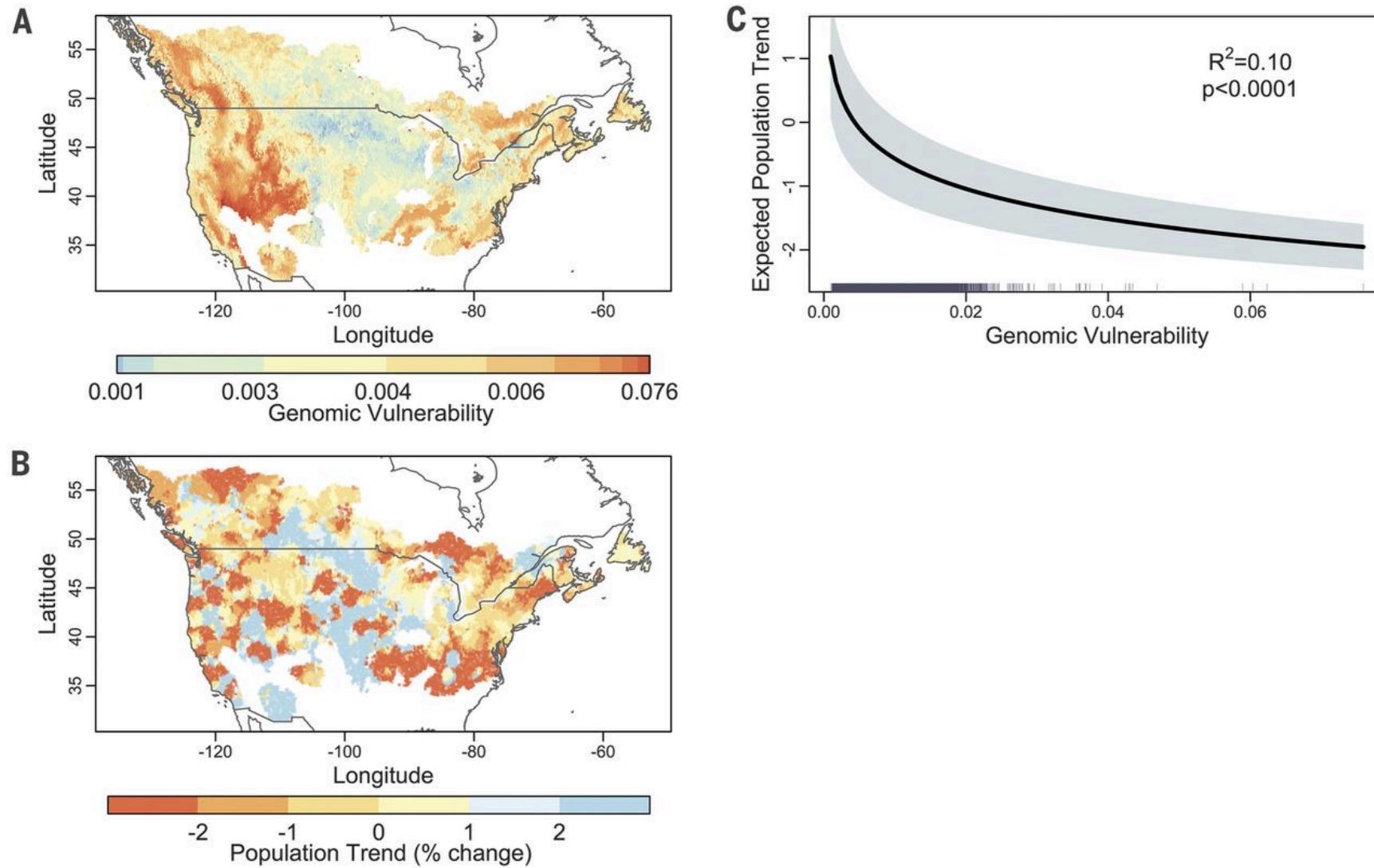


- how genomic patterns vary along multiple environmental gradients
- identify the primary environmental drivers associated with genomic variation
- quantify the strength of relationships between genomic patterns and each environmental gradient.

Warbler genotype-environment association

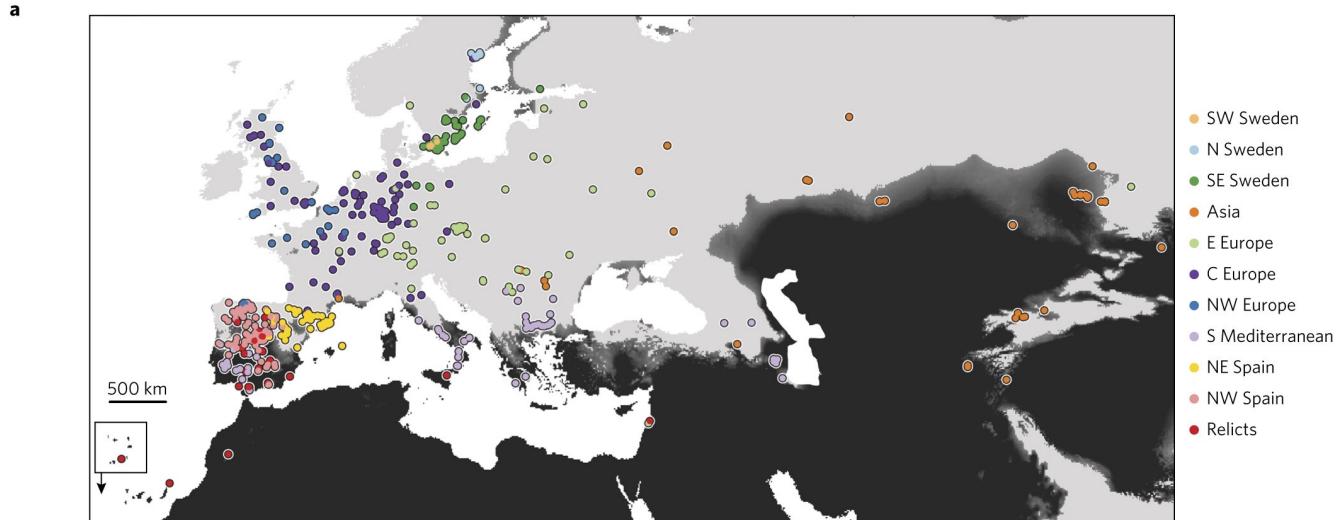


Genomic vulnerability correlates with population decline



Predicting evolutionary potential

211 populations in drought experiment

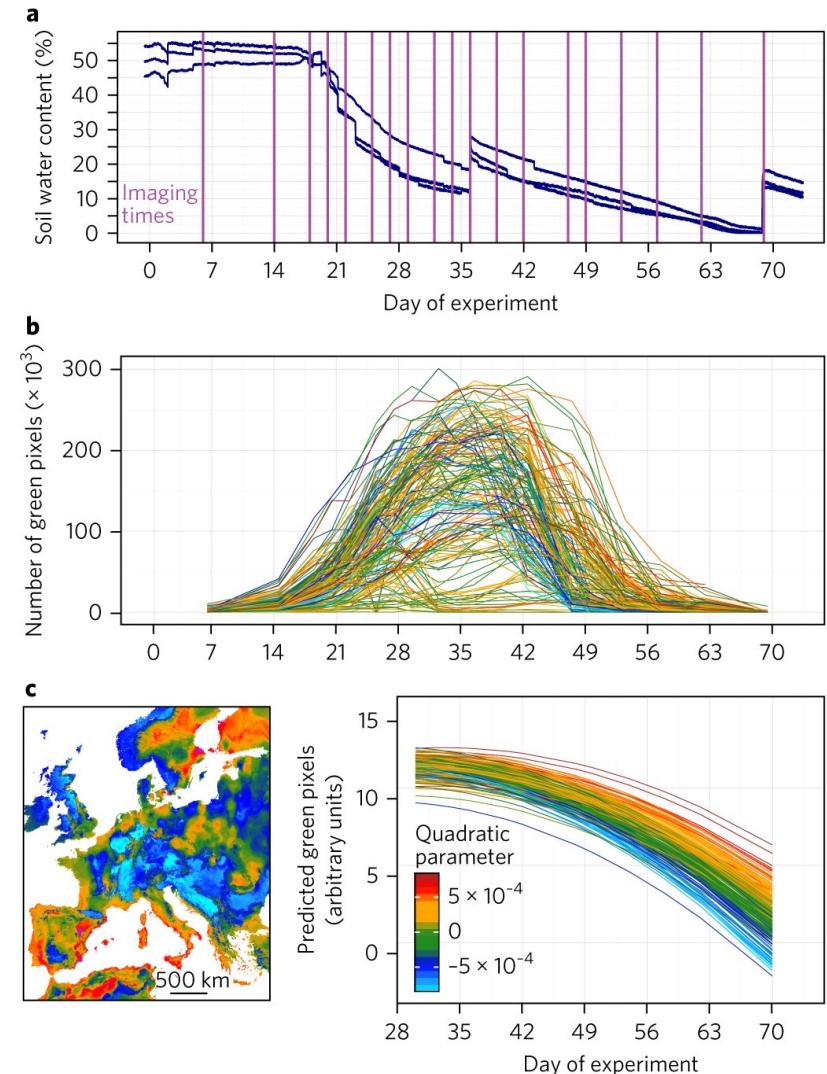


Quantify drought tolerance

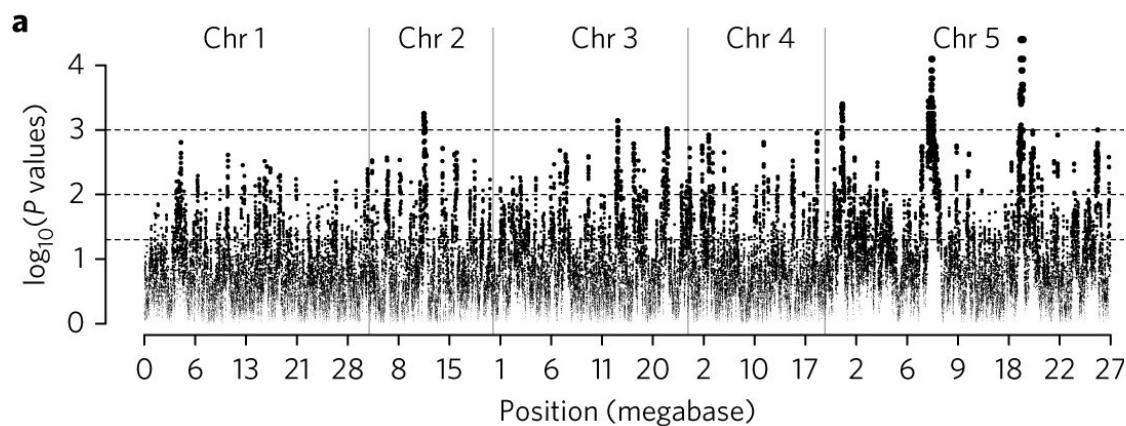
Map tolerance onto range

Genomic basis and evolutionary potential for extreme drought adaptation in *Arabidopsis thaliana*

Moises Exposito-Alonso, François Vasseur, Wei Ding, George Wang, Hernán A. Burbano & Detlef Weigel



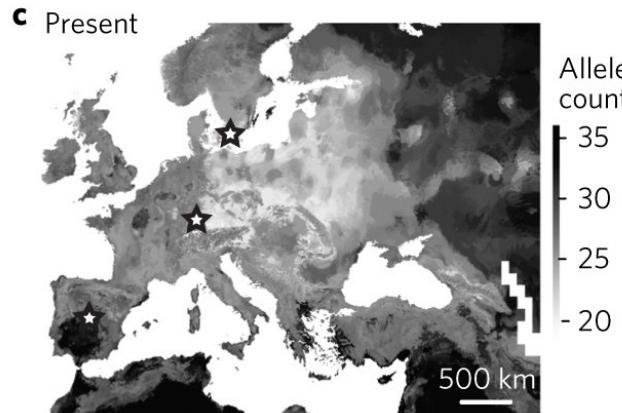
Link drought tolerance to genotype



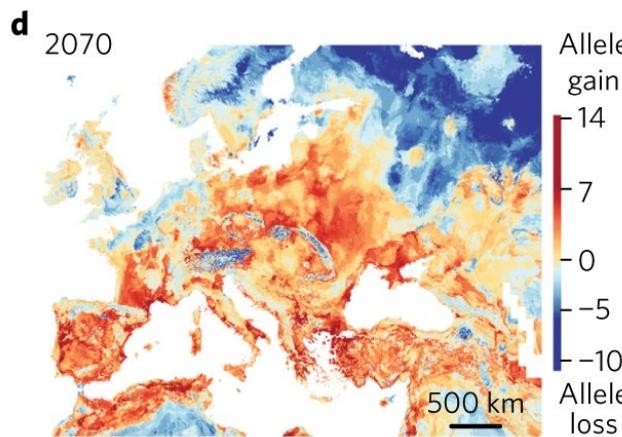
Is adaptation possible?

What is the necessary strength of selection?

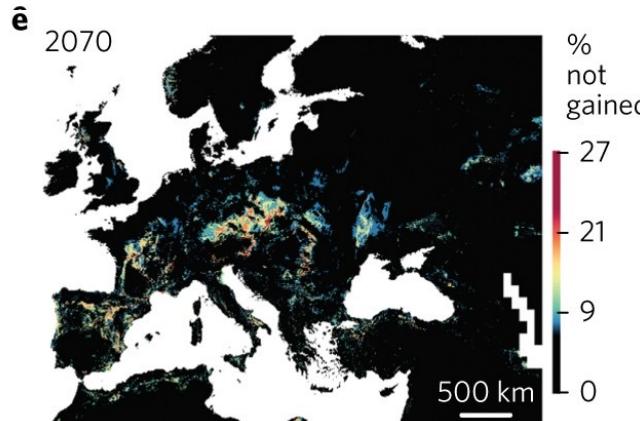
What role does migration play?



Current distribution of adaptive alleles



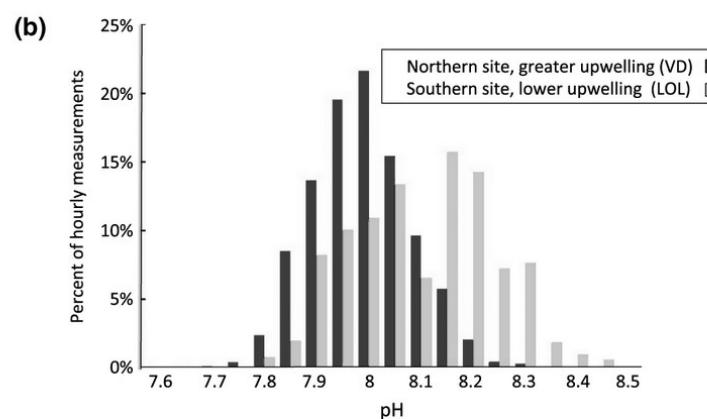
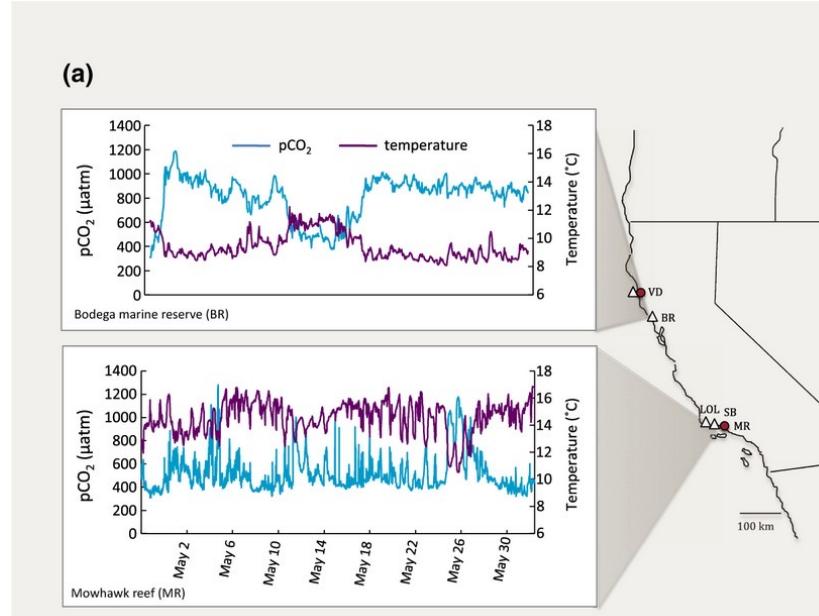
Necessary change in adaptive alleles in future conditions



Populations in the north and the south most likely to adapt → have more drought tolerant alleles

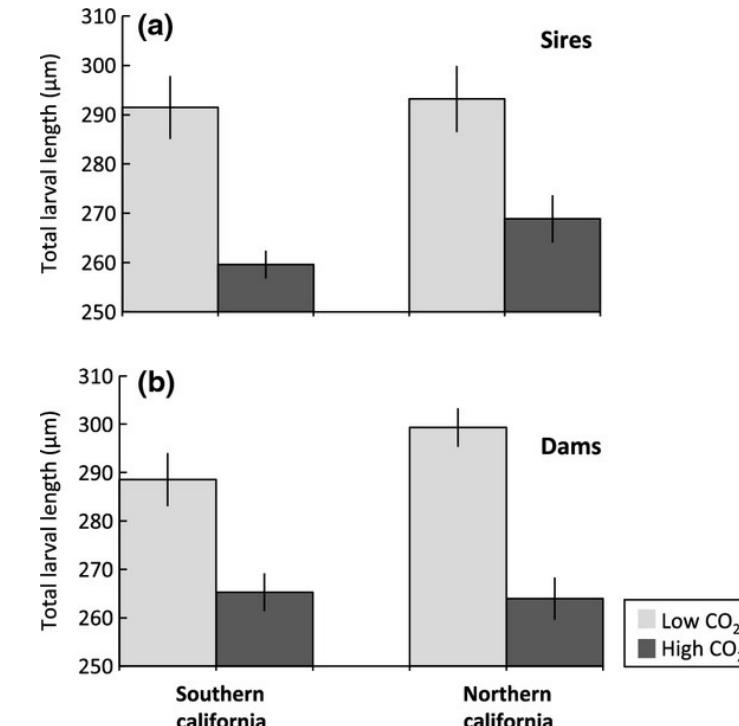
Adaptive potential?

- Quantitative genetics



Natural variation and the capacity to adapt to ocean acidification in the keystone sea urchin *Strongylocentrotus purpuratus*

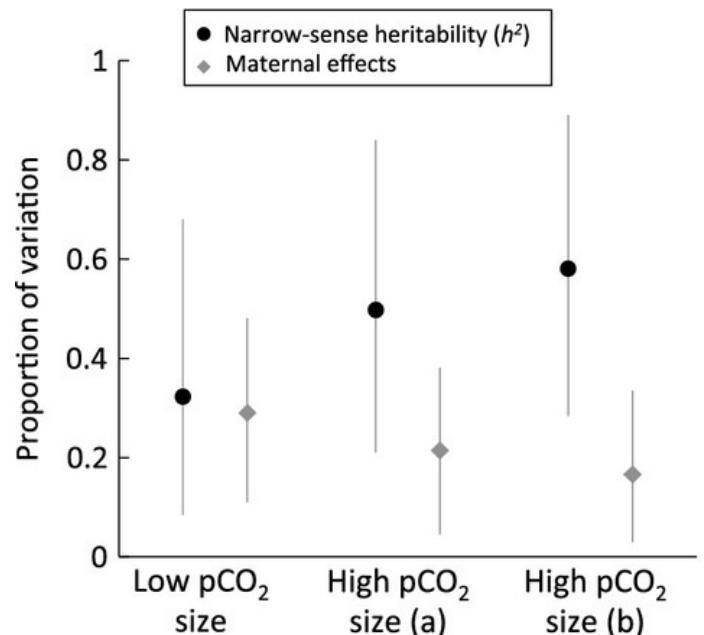
Morgan W. Kelly, Jacqueline L. Padilla-Gamiño, Gretchen E. Hofmann



Adaptive potential?

- Quantitative genetics

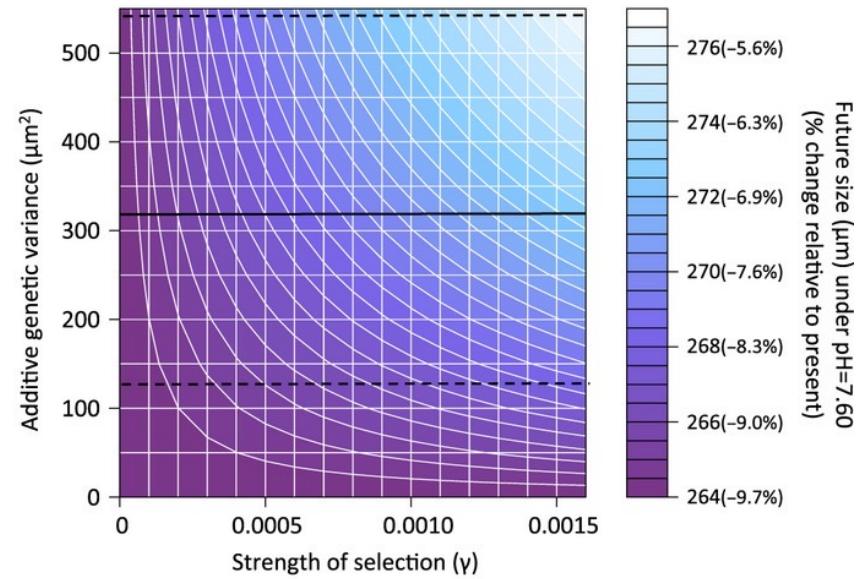
- Cross populations with different pH regimes
- Estimate heritability
- Model potential evolution under CO₂ change



(a)

$$\Delta z_t = 2.8 - \gamma \sigma_A^2 (\bar{z}_t - \theta)$$

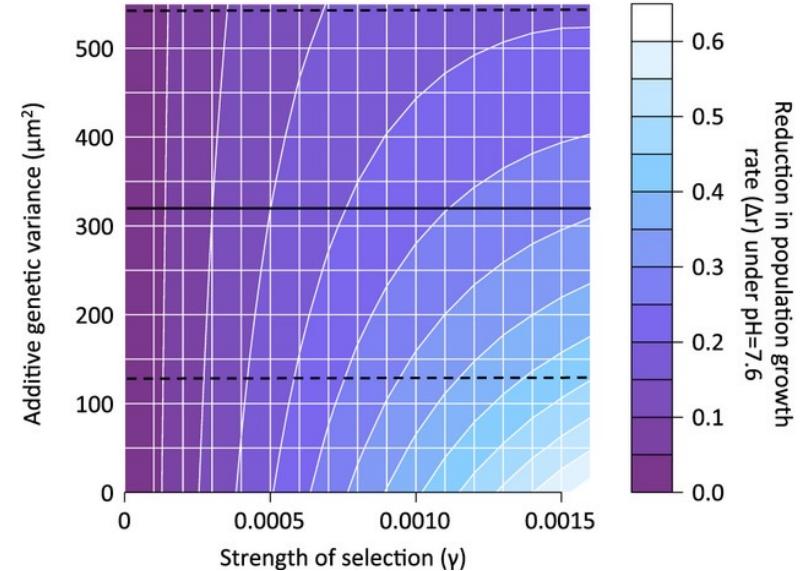
Δz_t = change in size at time t
 γ = strength of selection
 σ_A^2 = additive genetic variance for size
 \bar{z}_t = mean size at time t
 θ = optimum size



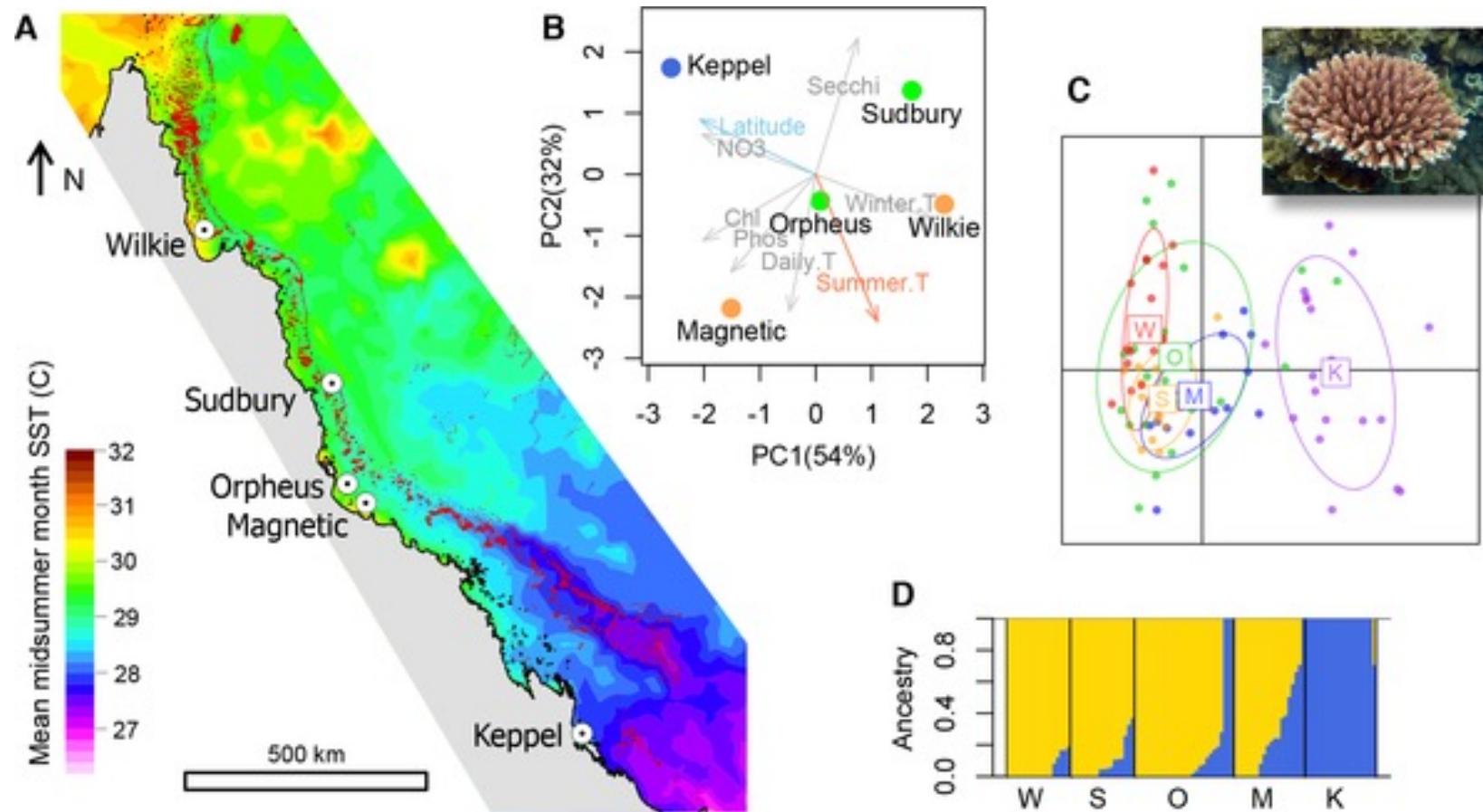
(b)

$$\Delta r_t = (\gamma/2)(\bar{z}_t - \theta)^2$$

Δr_t = reduction in population growth rate at time t
 γ = strength of selection
 \bar{z}_t = mean size at time t
 θ = optimum size

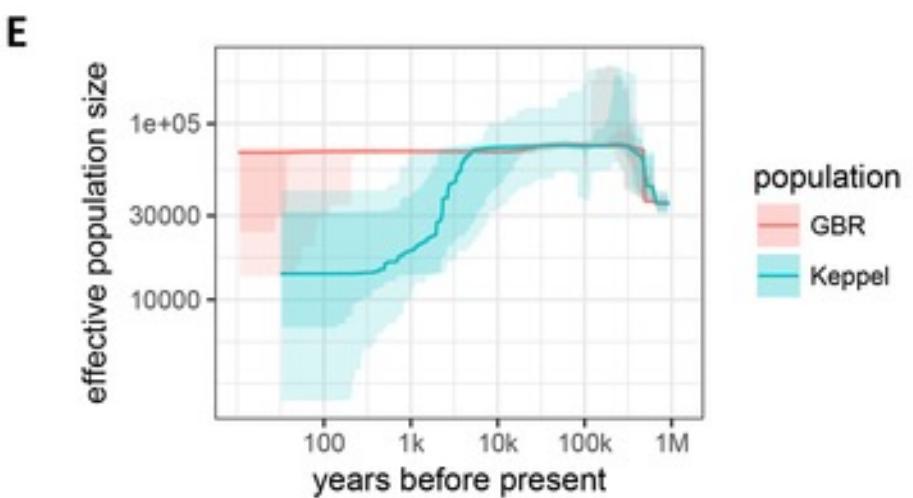
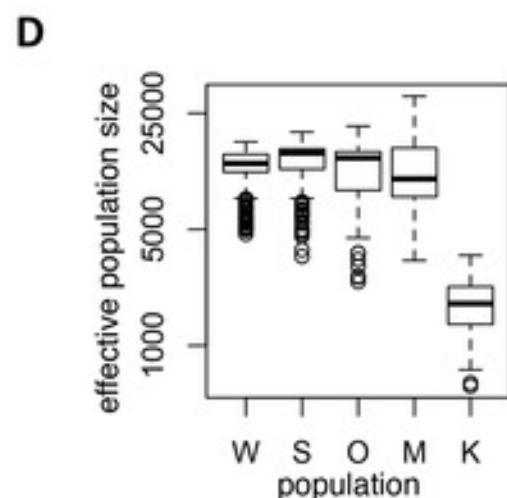
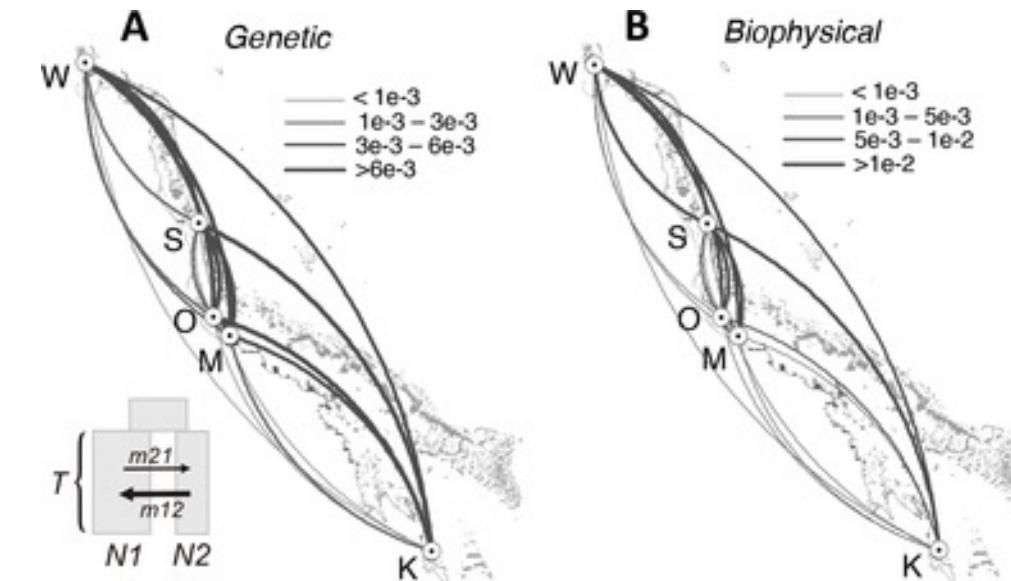


Modeling adaptive potential

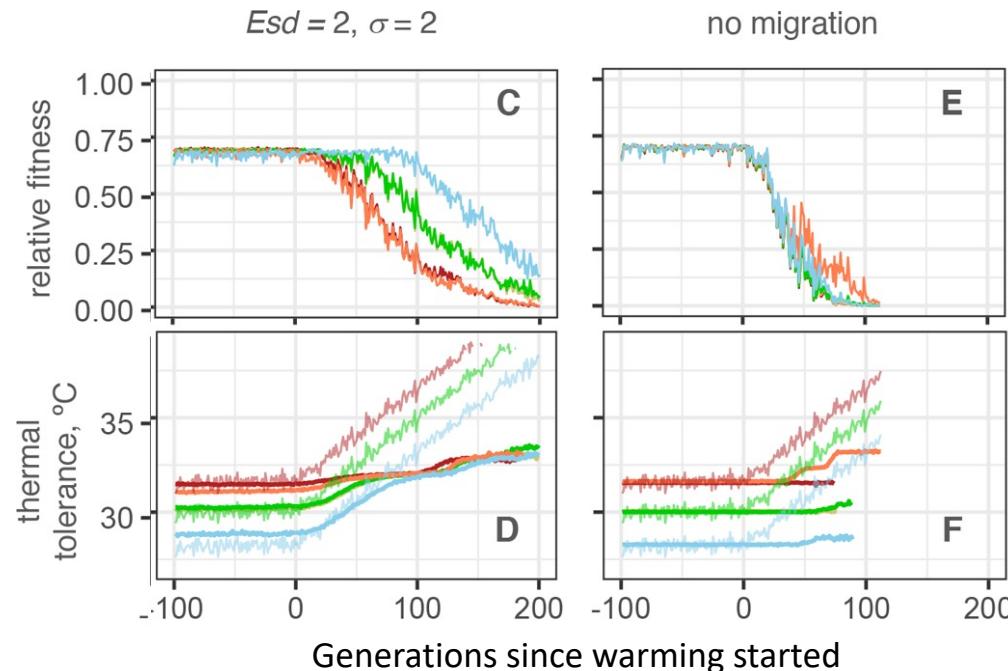


Potential and limits for rapid genetic adaptation to warming
in a Great Barrier Reef coral

- Estimate population parameters



How does migration influence adaptive potential?



Effect of genetic architecture and population size?

