

From theory to practice: Uses and misuses of genotype-environment associations to inform restoration and conservation

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(he/him)



Landscape Stewardship Collective
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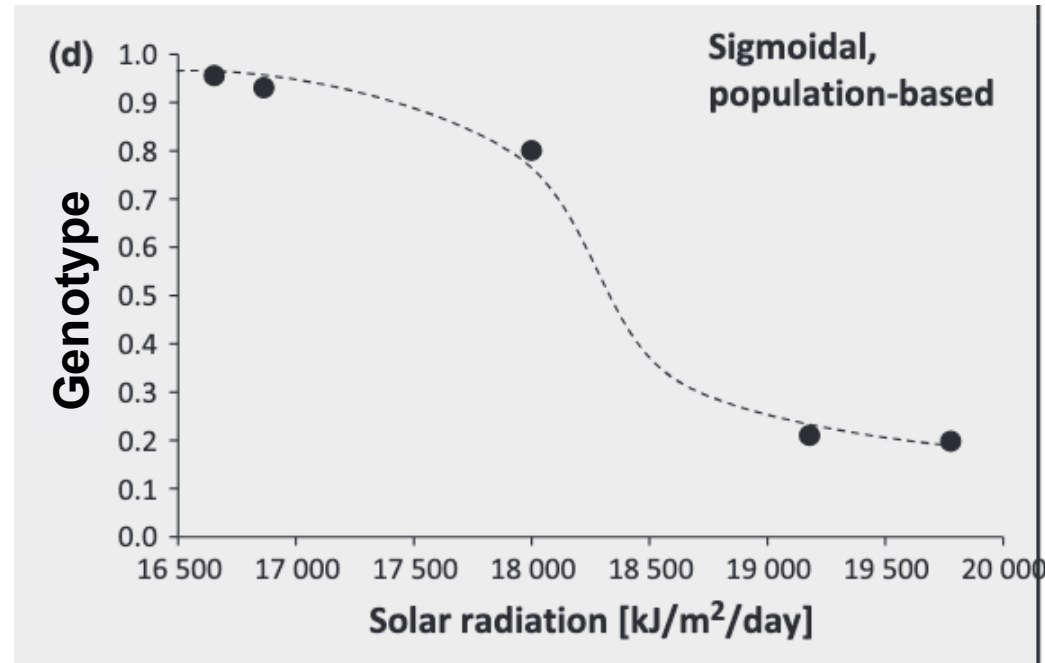
Genotype-environment associations (GEA)

Enables the ability to assess specific environmental variable's role in driving spatial genetic structure from sampling individuals in their natural habitat

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Simplest form:
GEAs are a correlation
between genotype and
environment



GEAs have two primary goals

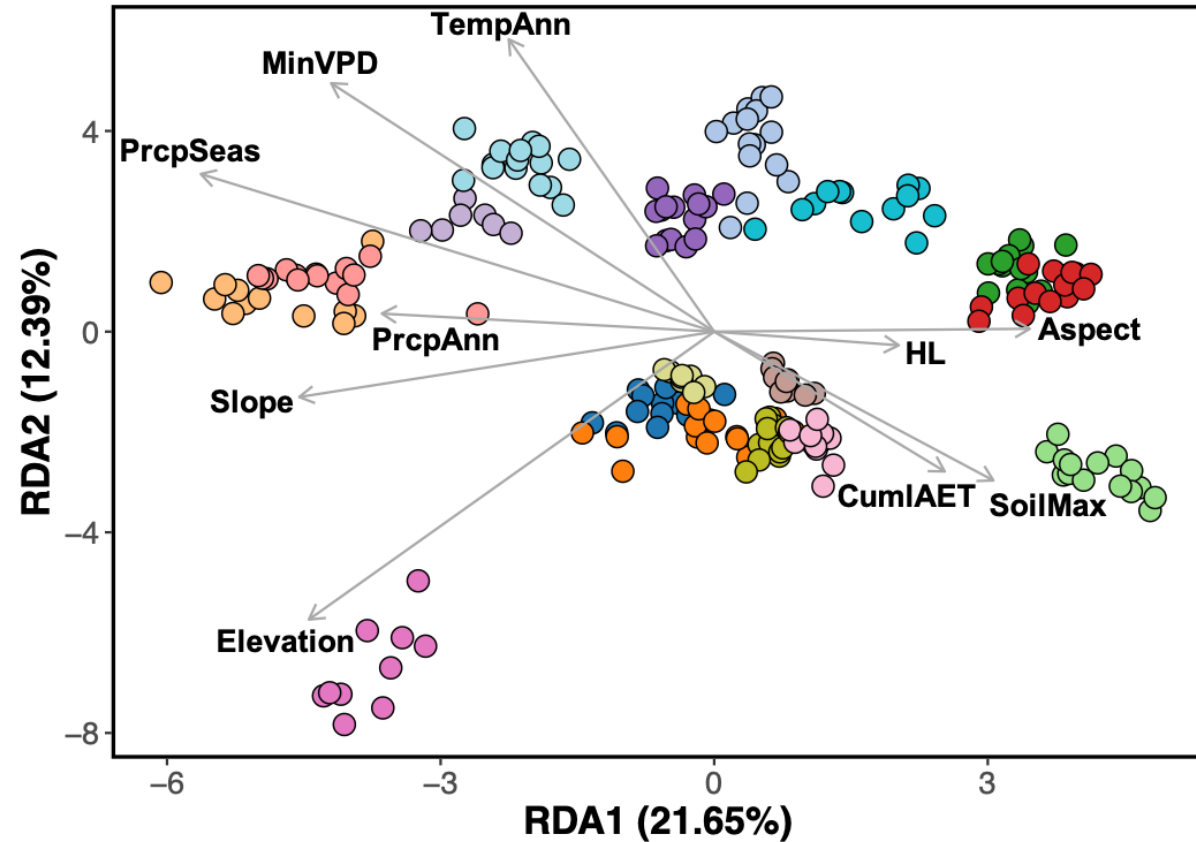
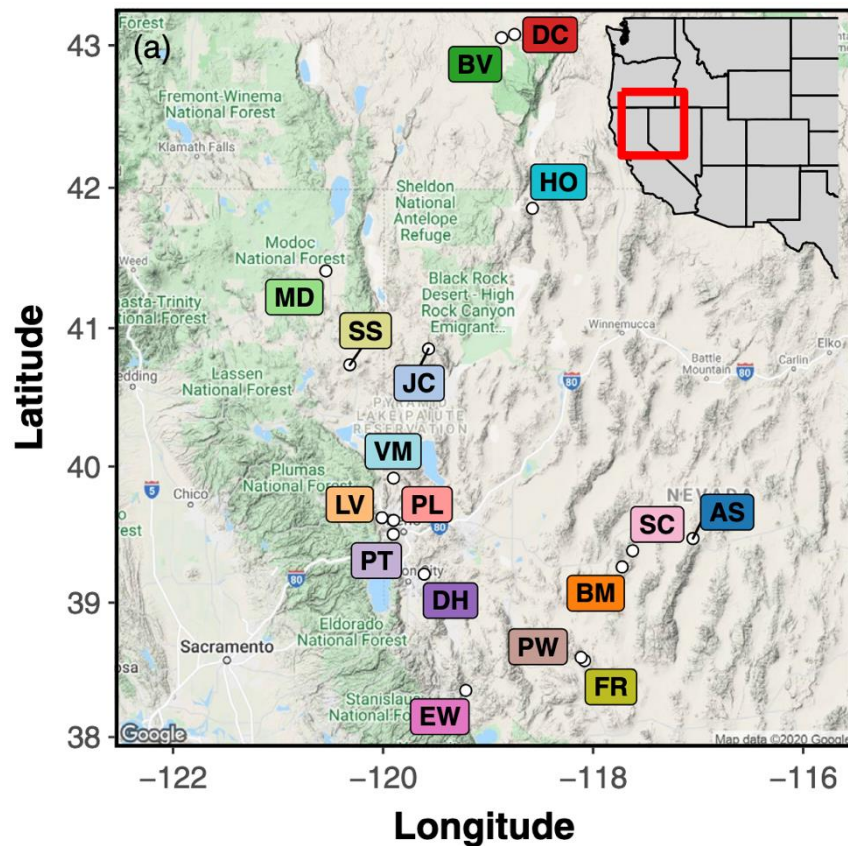
Environmental variables
driving genetic structure
among populations

Candidate adaptive loci
detection

GEA example: Redundancy analysis (RDA)

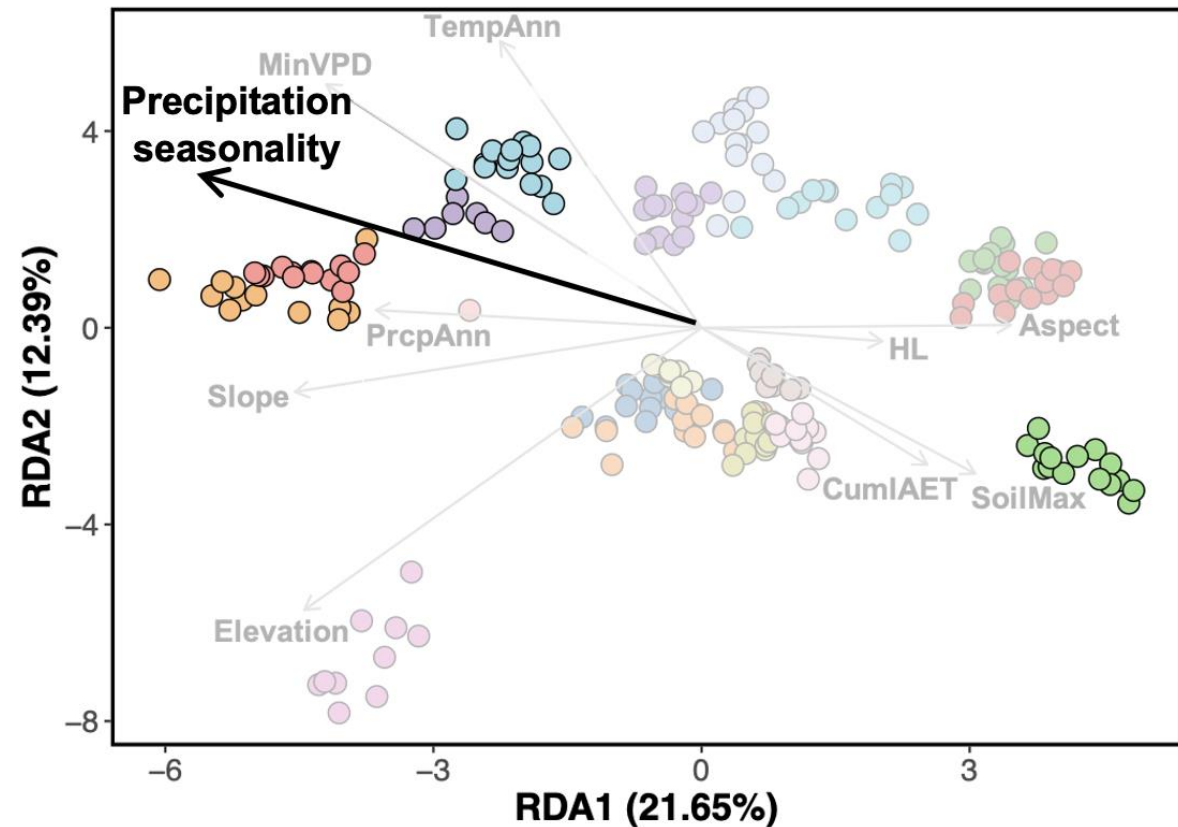
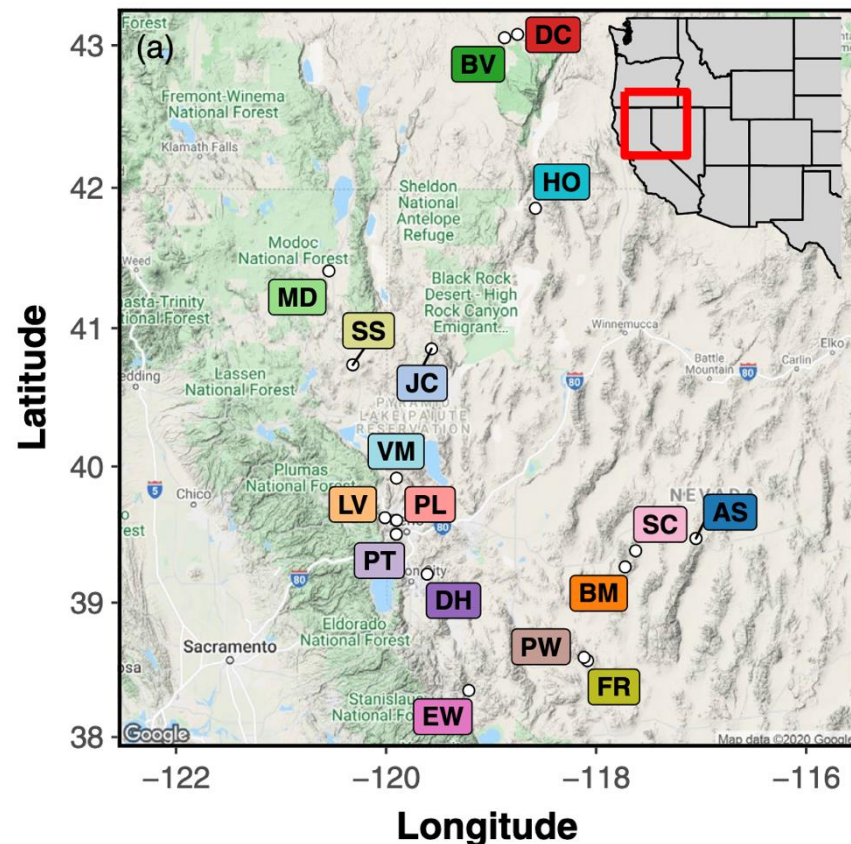
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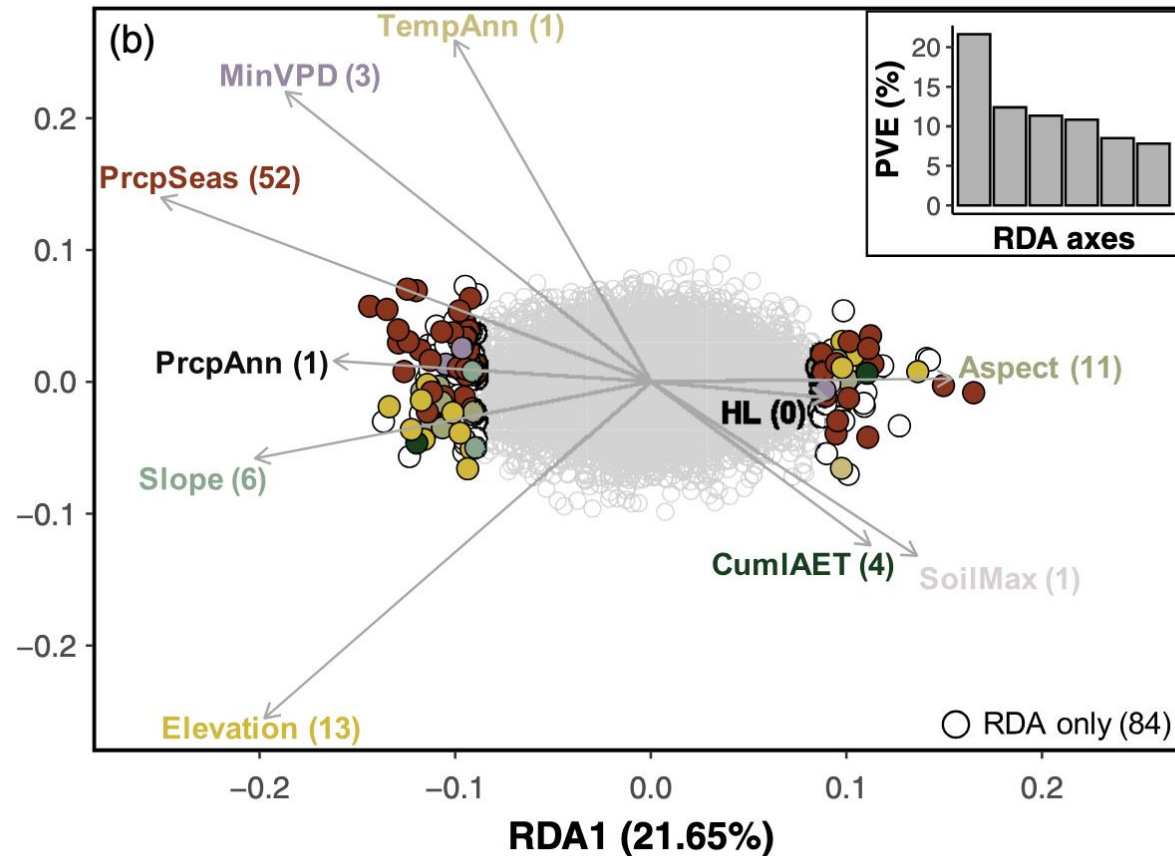
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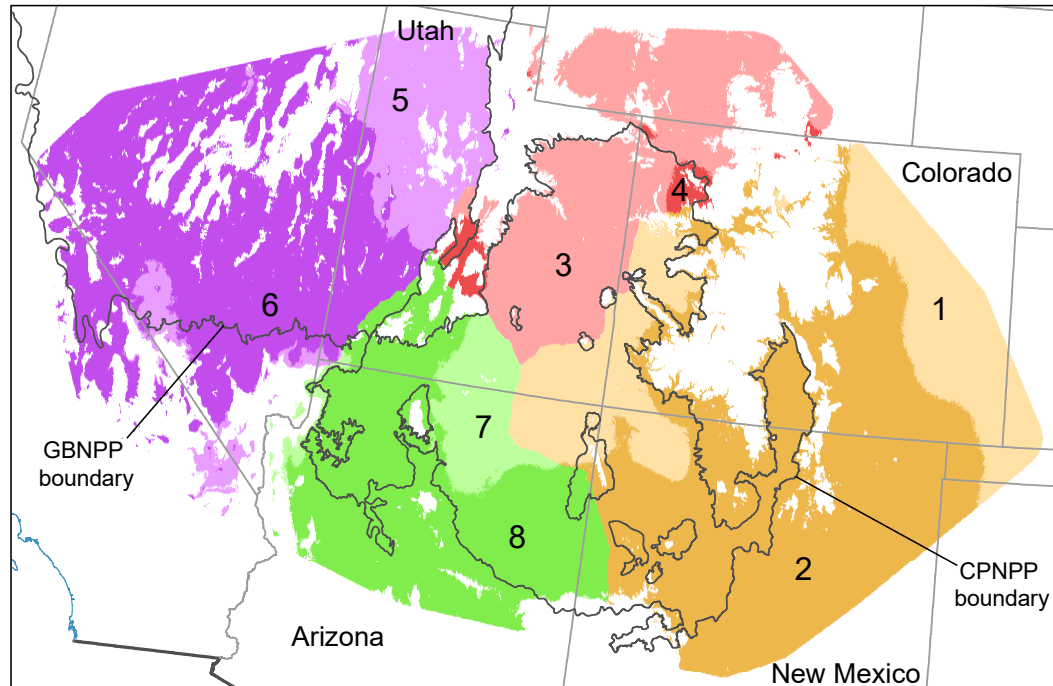
GEA management implementation example

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Genetic seed transfer zone

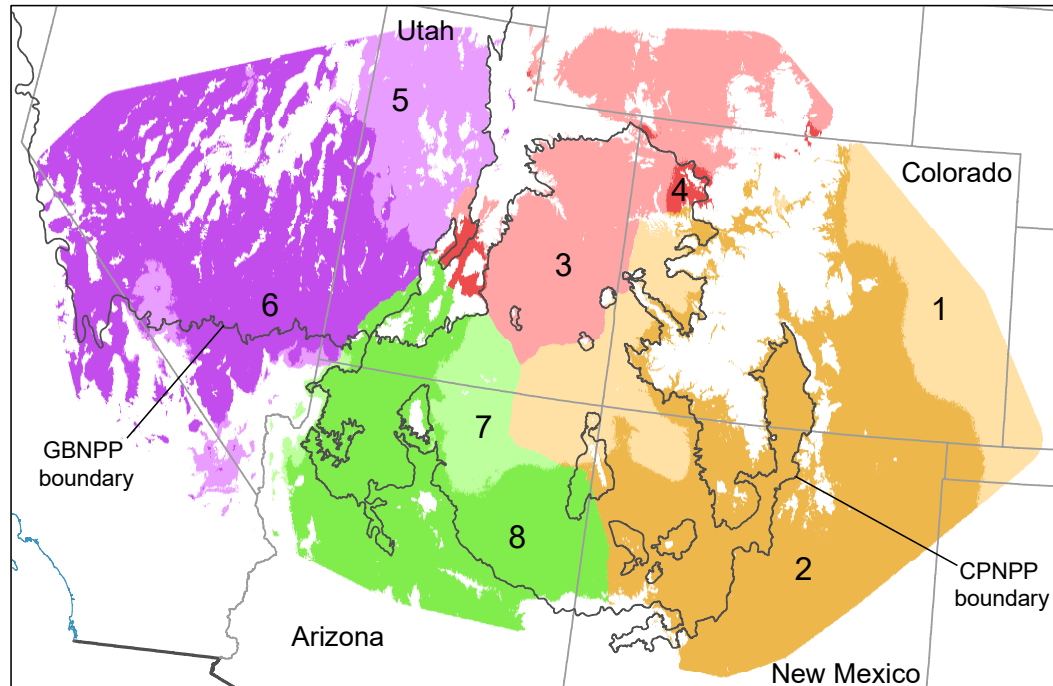


Massatti & Winkler 2022, *Methods in E&E*

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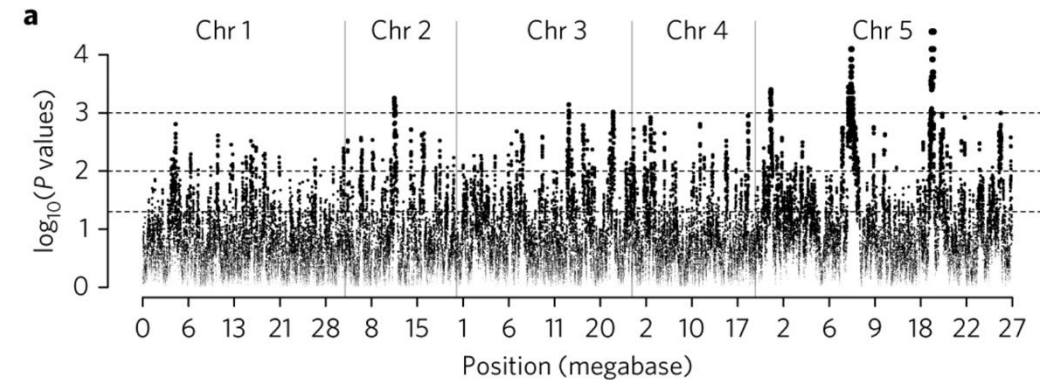
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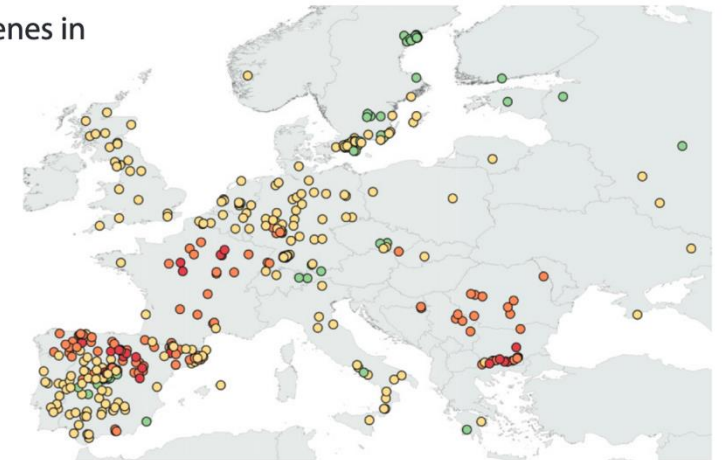
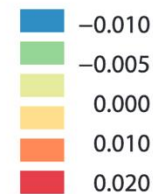
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C Drought-associated genes in
Arabidopsis thaliana

Change in selection intensity

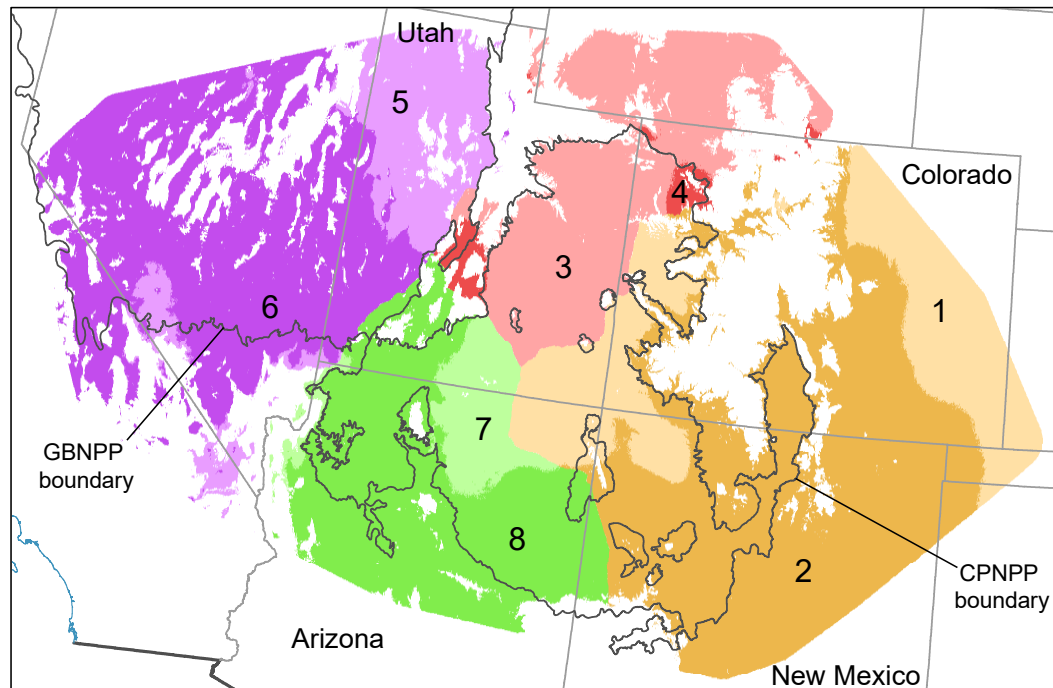


Capblancq *et al.*, 2020; Exposito-Alonso *et al.*, 2018

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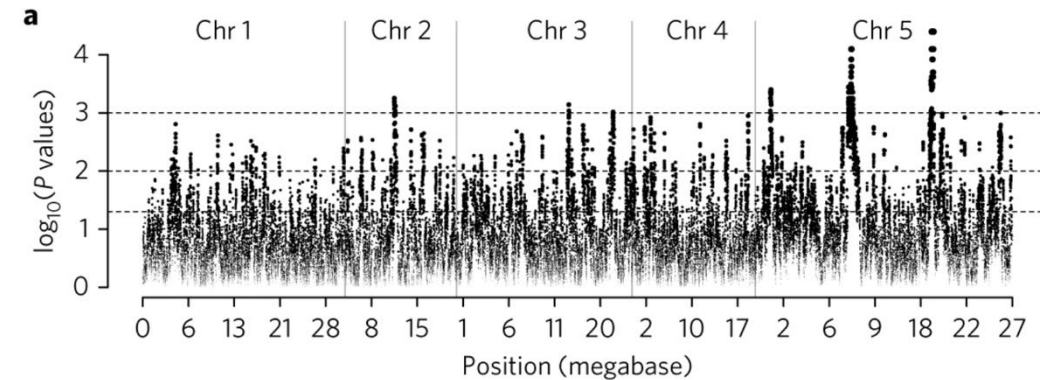
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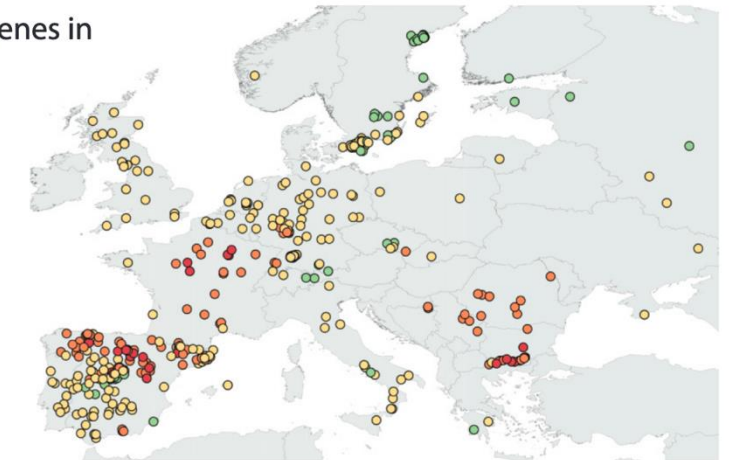
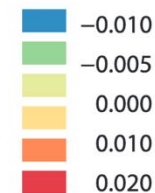
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Genotype-environment association (GEA) studies

The Promise

- Detect adaptive variation without common gardens
- Applicable to non-model species
- Large genomic datasets increasingly available

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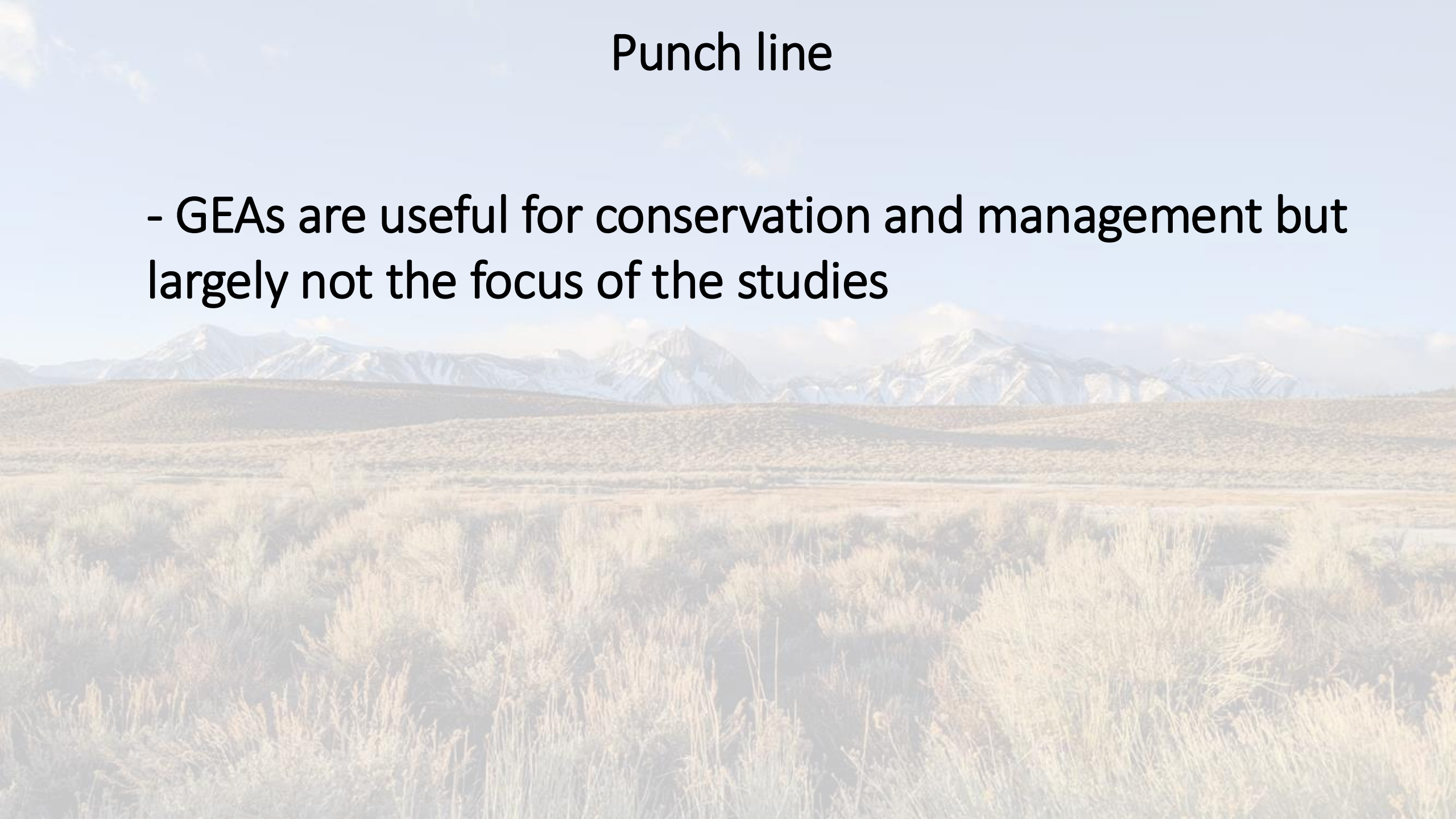
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The Problem

- Different GEA methods often produce different answers
- Management recommendations can depend heavily on analytical choices

Punch line

- GEAs are useful for conservation and management but largely not the focus of the studies



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- Many studies do not have adequate genomic resources for the methodologies they employ

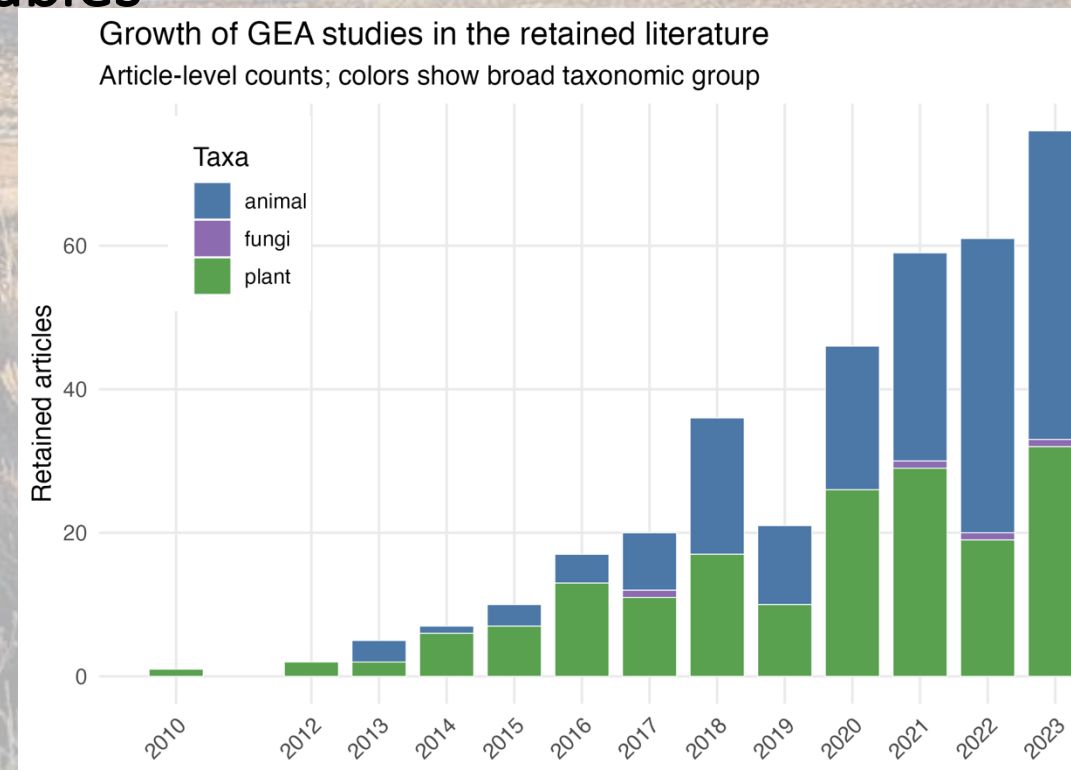
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- Many studies do not have adequate genomic resources for the methodologies they employ
- Using all the data available is better than using a subset of candidate adaptive loci

Literature review of GEA papers

- 1113 papers searched
- 367 passed filtering (2010 – 2023)
- Kept track of 41 methodological variables

- Types of analysis
- Genomic space
- Candidate loci detection
- Management forward



Punch line

- **GEAs are useful for conservation and management but largely not the focus of the studies**
- Many studies do not have adequate genomic resources for the methodologies they use
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GEAs focus more on discovery rather than decision-making management practice

367 total studies

334 (91%)

Conducted candidate
adaptive loci analysis

213 (58%)

Alluded to
management
implications

51
(14%)

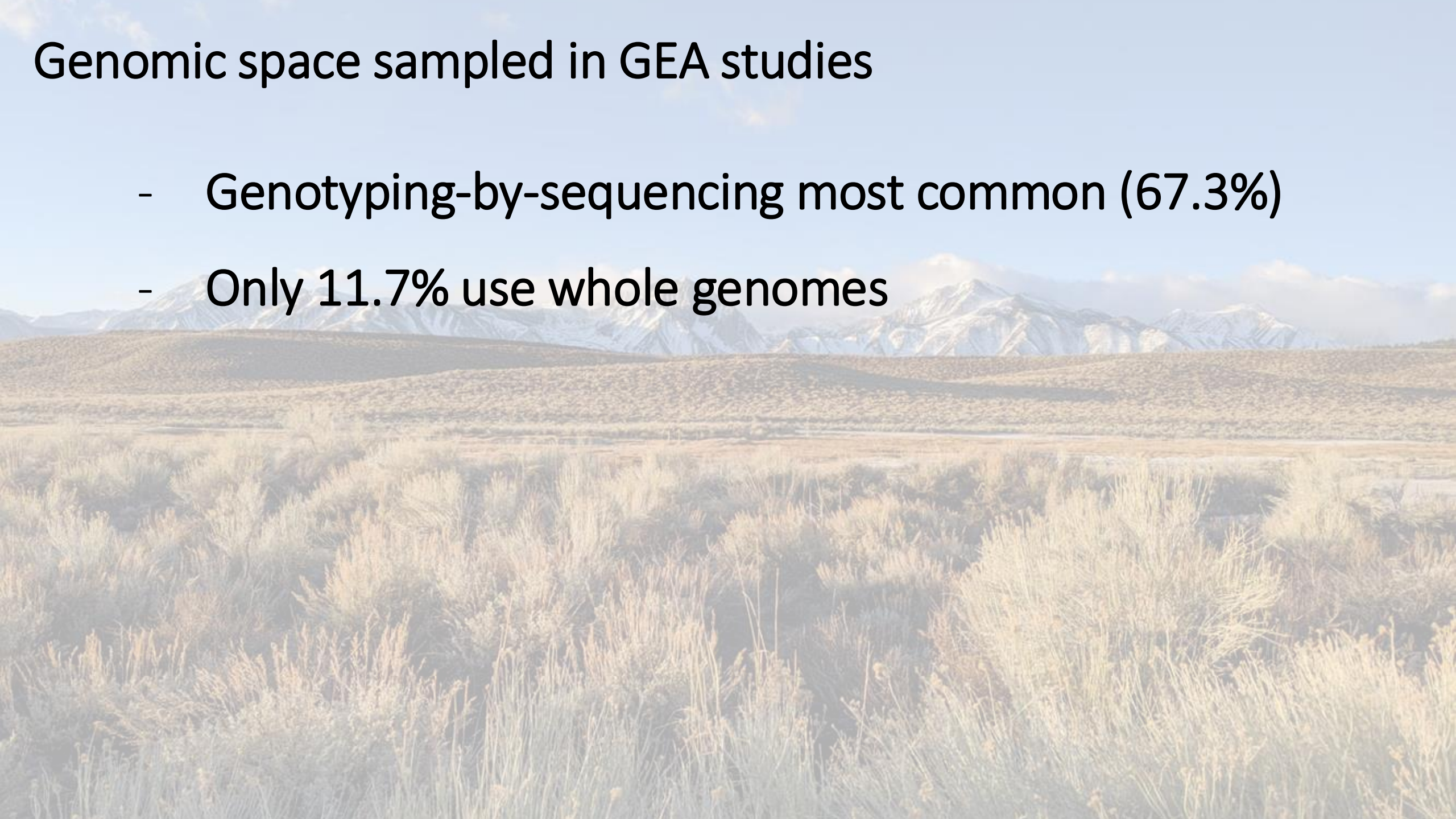
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Genomic space sampled in GEA studies

- Genotyping-by-sequencing most common (67.3%)
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Genomic space sampled in GEA studies

- Genotyping-by-sequencing most common (67.3%)
- Only 11.7% use whole genomes
- Median # of genetic loci: 10,040
 - 0.000641% of genome
- Median # of candidate adaptive loci: 145.5
 - 0.000011% of genome

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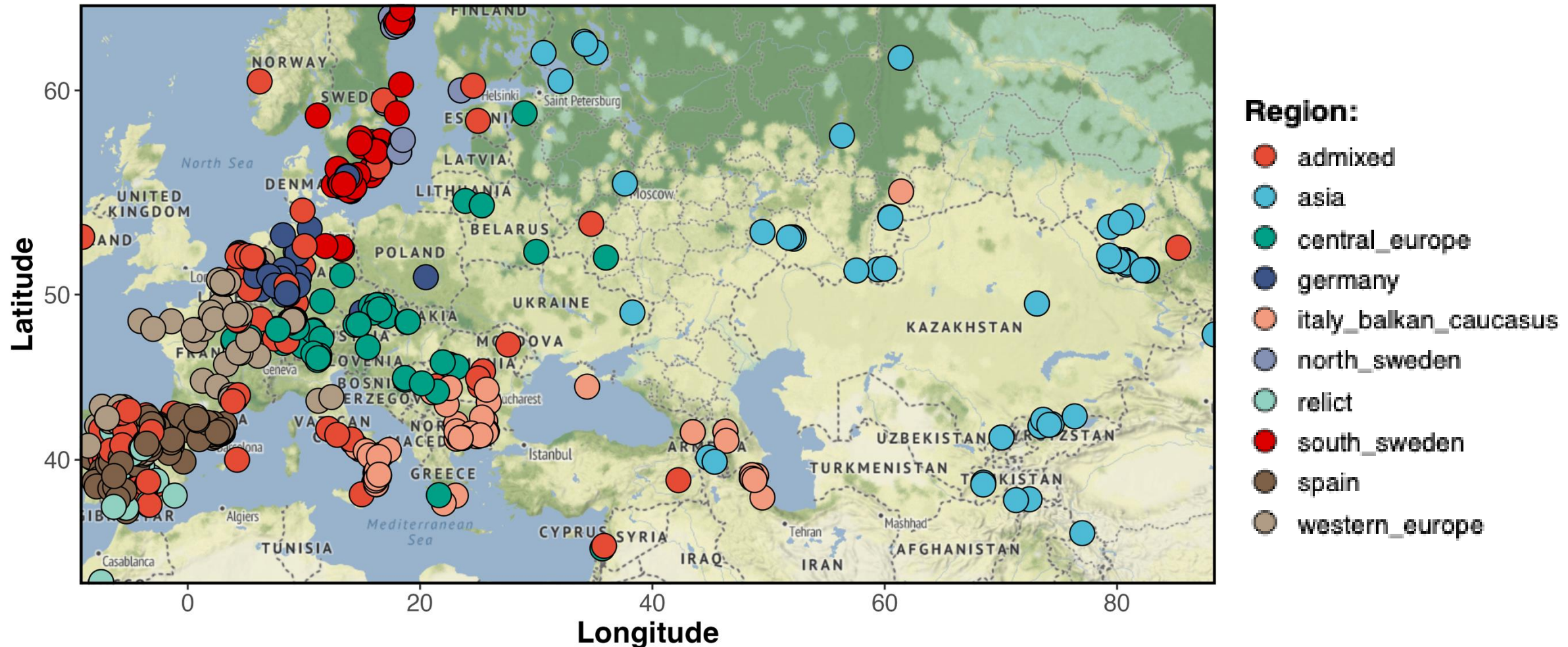
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Using all the genomic data available is better than using a subset of candidate adaptive loci

- Use WGS from *Arabidopsis* 1001 genome project
- Use RDA and back transformation of values to predict environmental variables as efficiency or accuracy metric
- Two questions:
 - How many loci needed to recapitulate genetic structure?
 - Do adaptive loci do better than random loci across genome to recapitulate genetic structure?

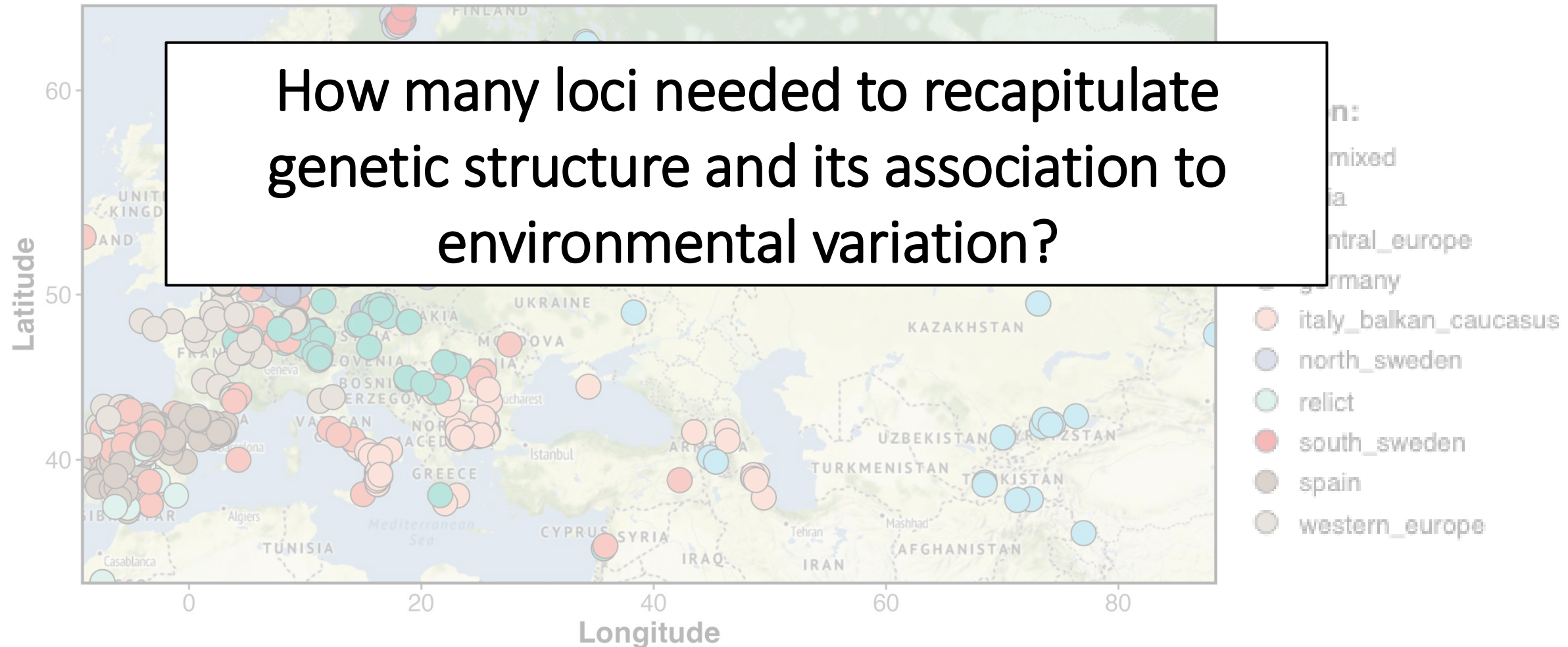
Arabidopsis 1001 genomes dataset used

2+ million genetic markers

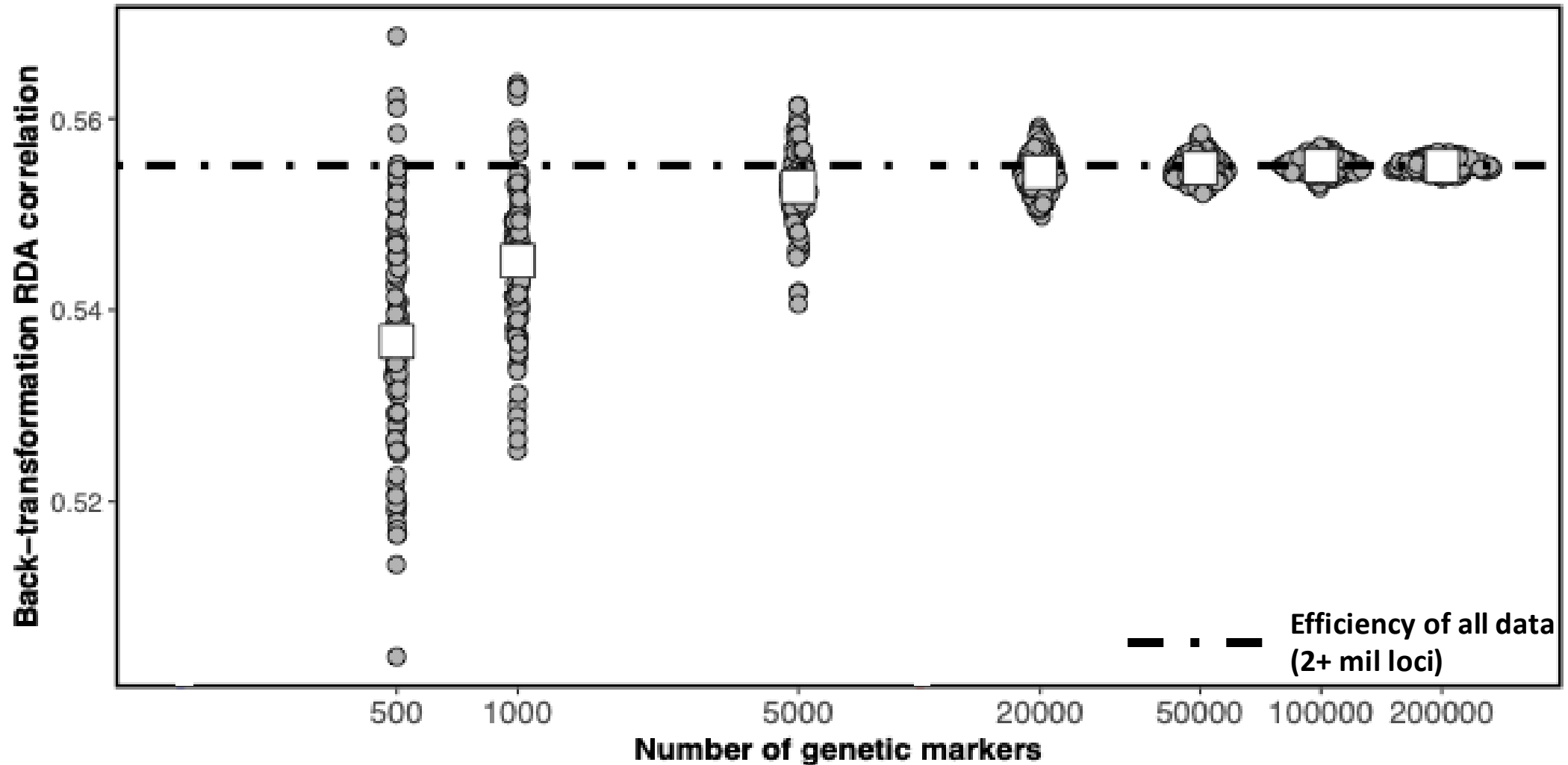


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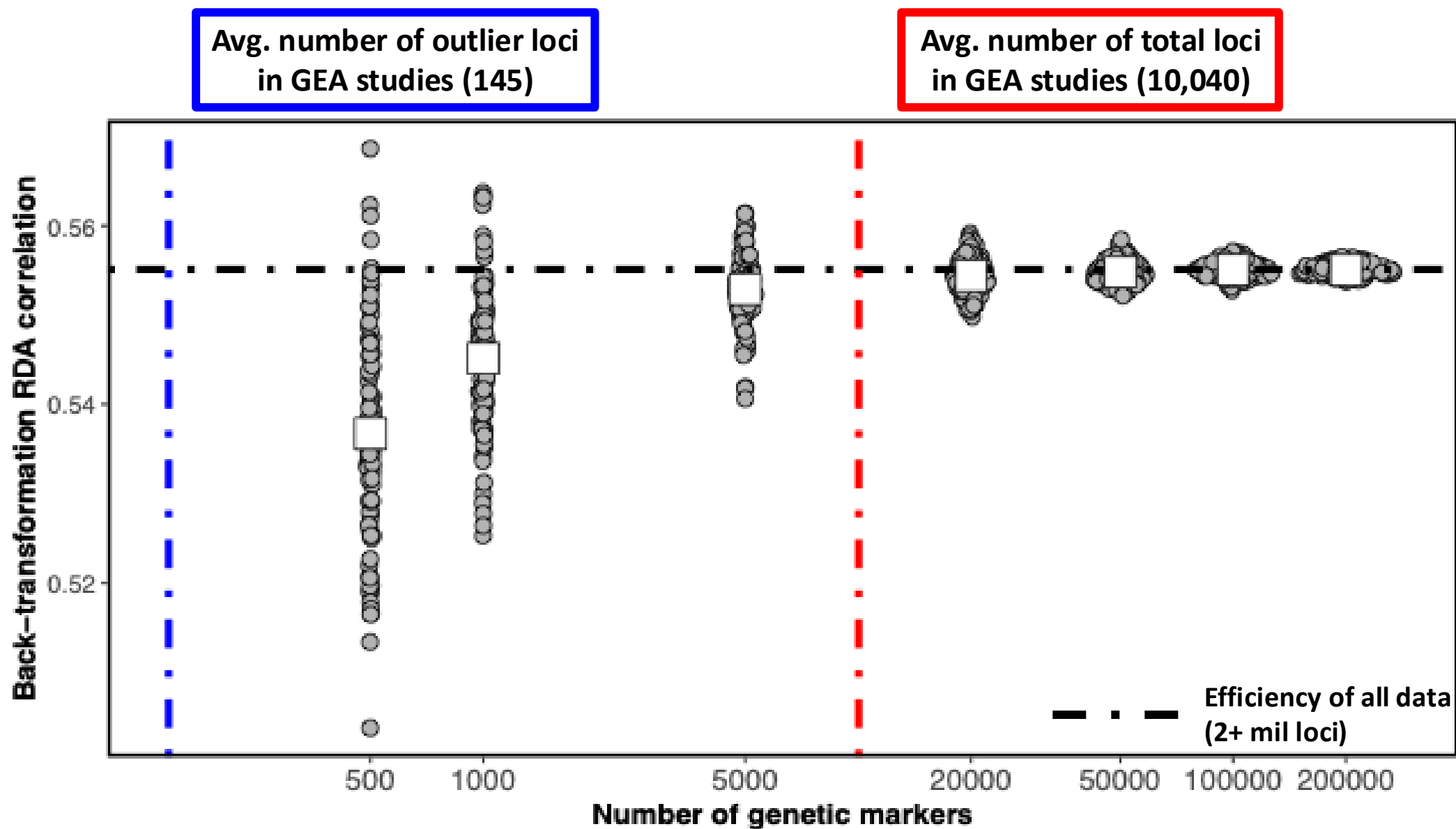
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RDA efficiency reduces drastically below 1000 loci

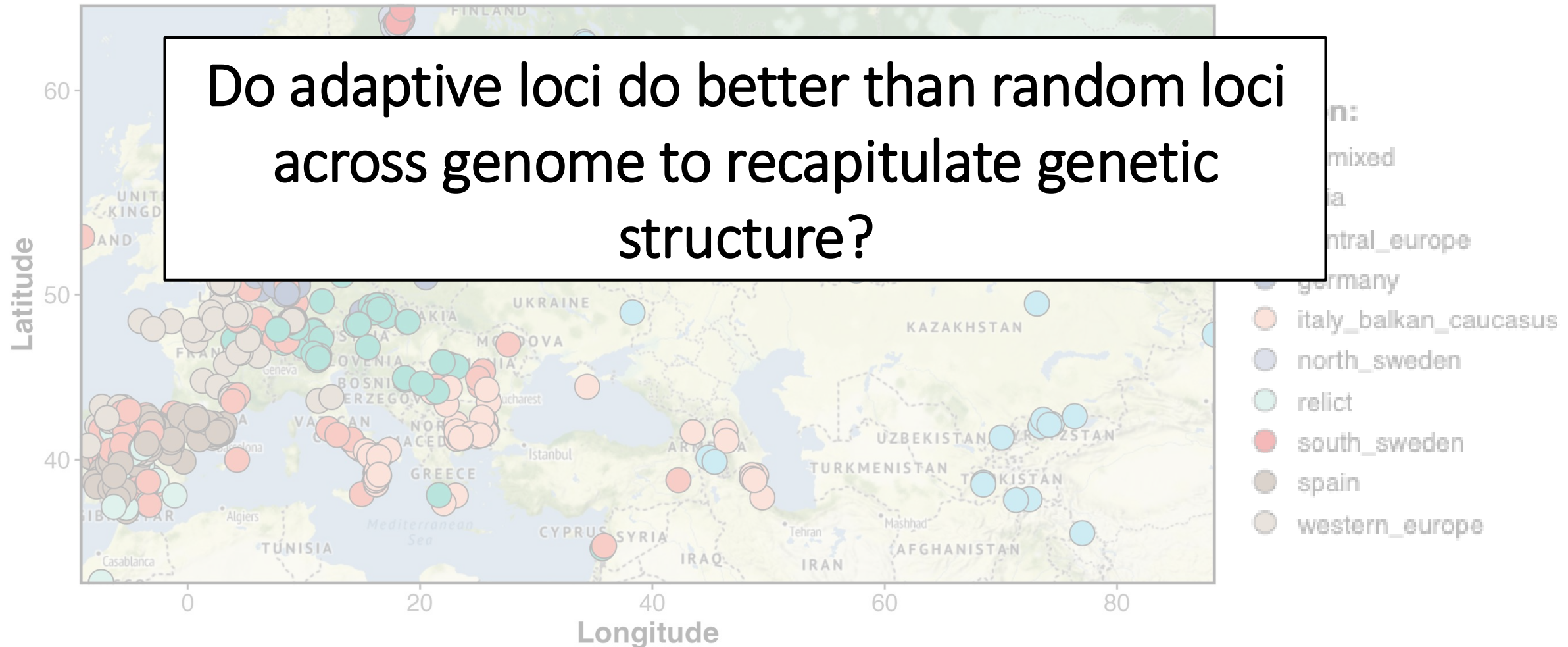


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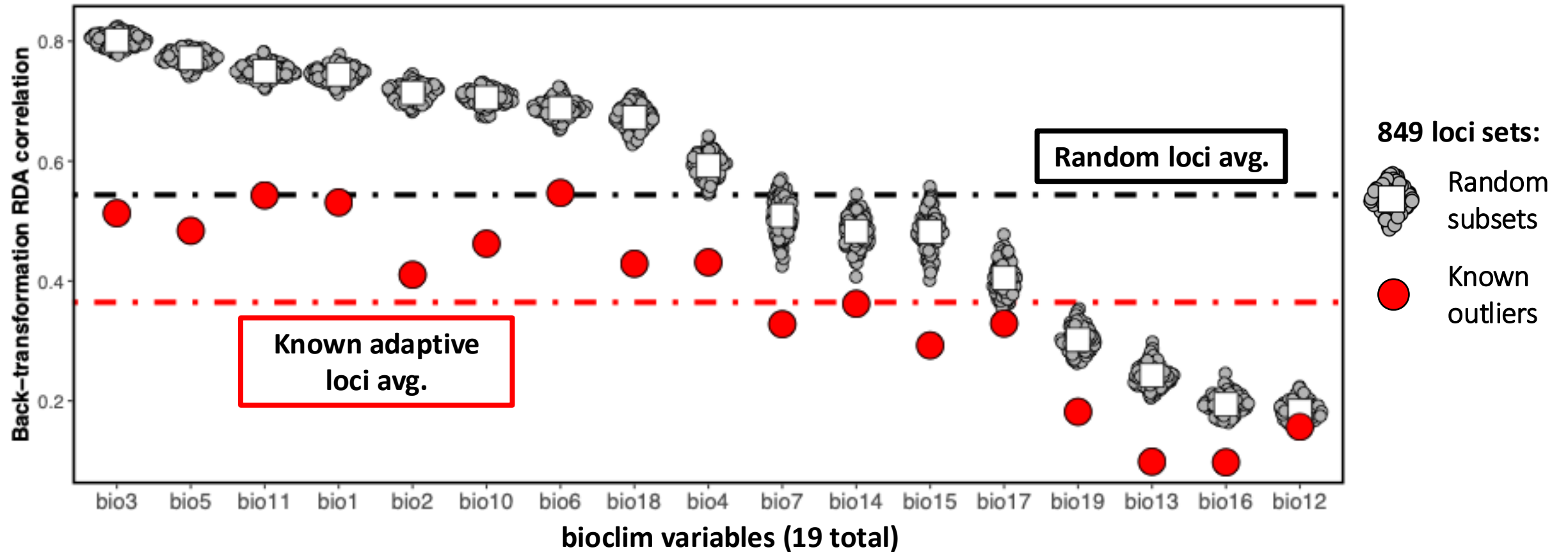


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Random sets of loci perform better than known adaptive loci from another GEA study (849 known)



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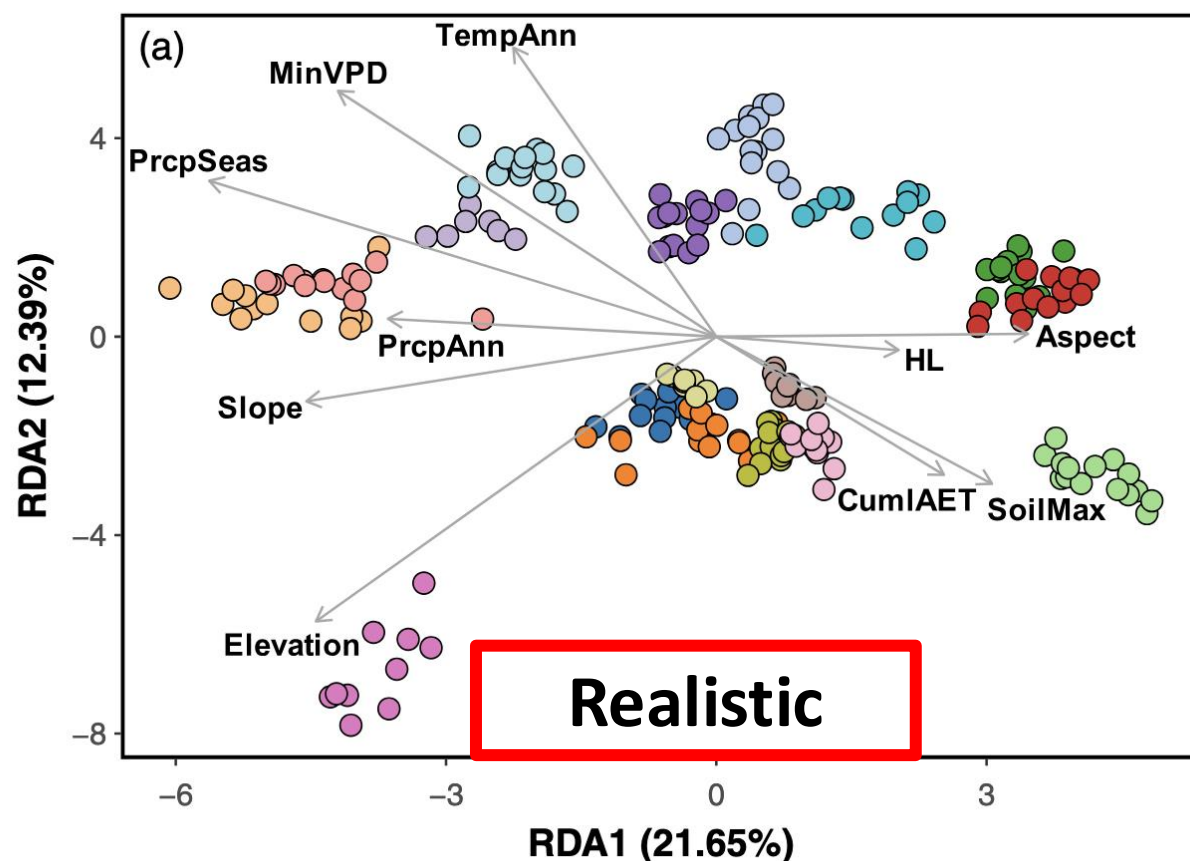
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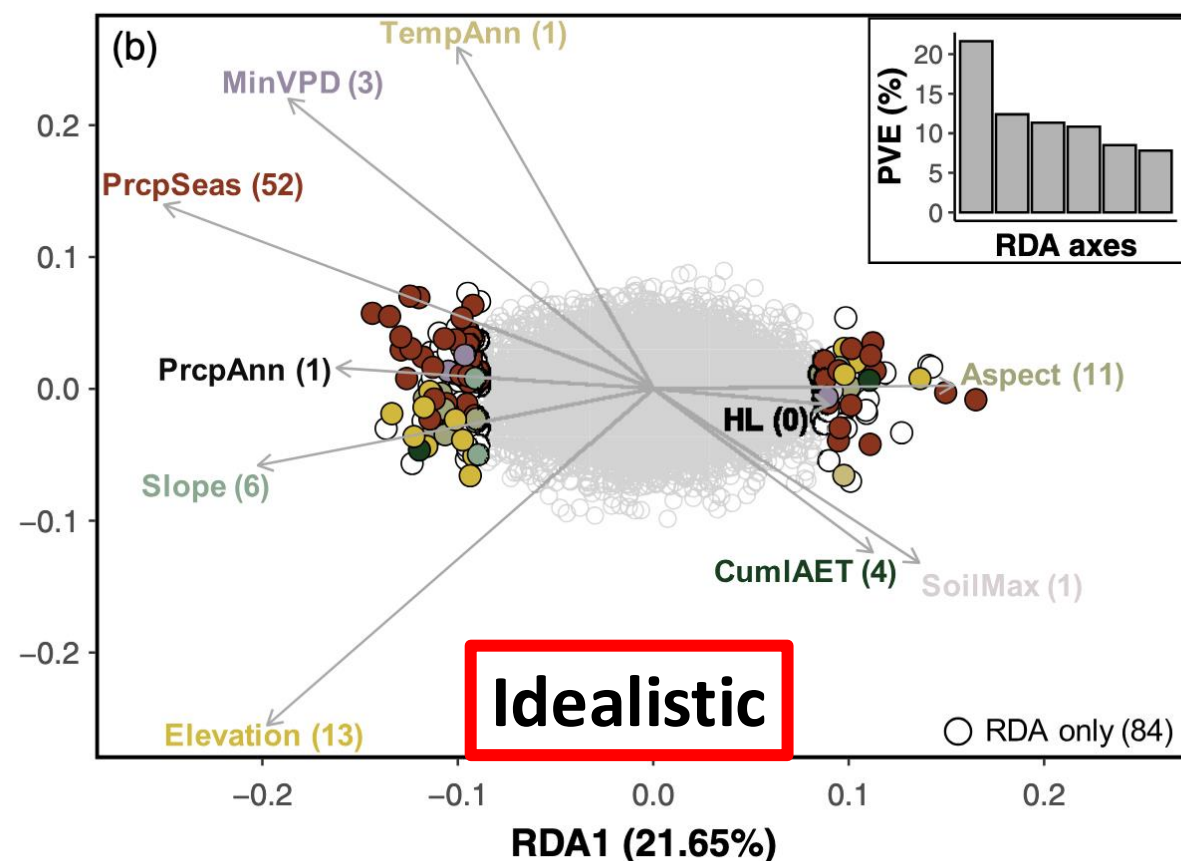
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Conclusions and recommendations

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