

Mining useful alleles for climate change adaptation

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labs

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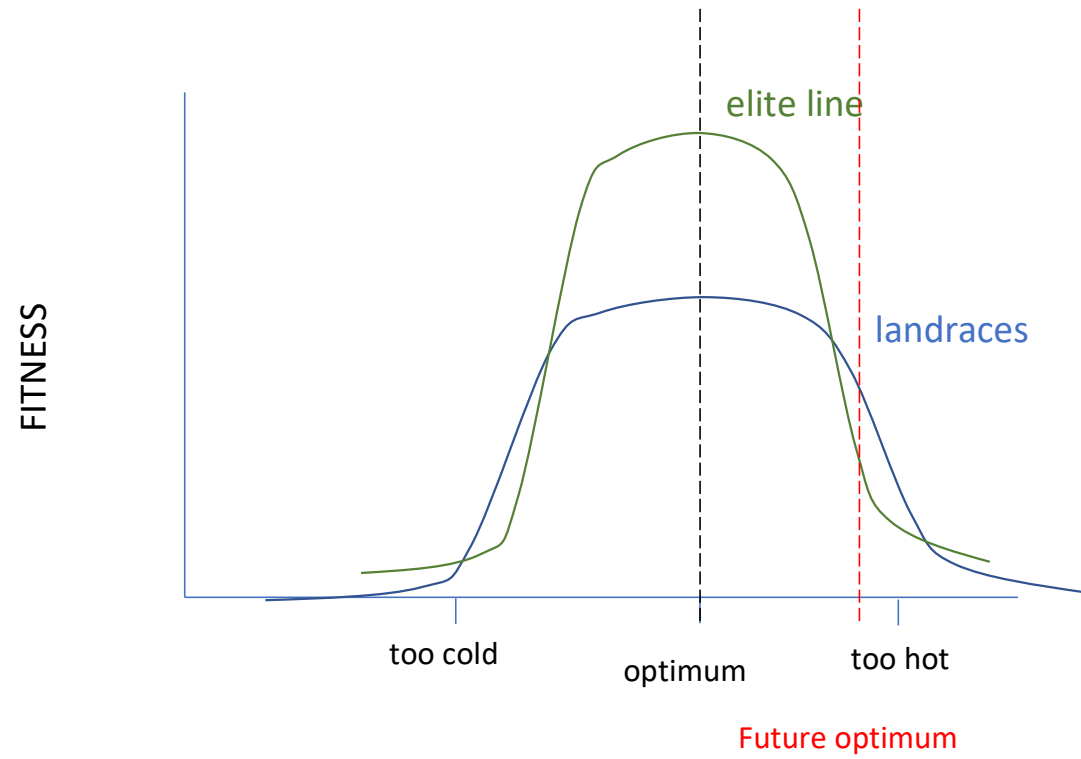
Introduction

- The goal:

To find out what would be the most effective way to use GEA in developing breeding lines?

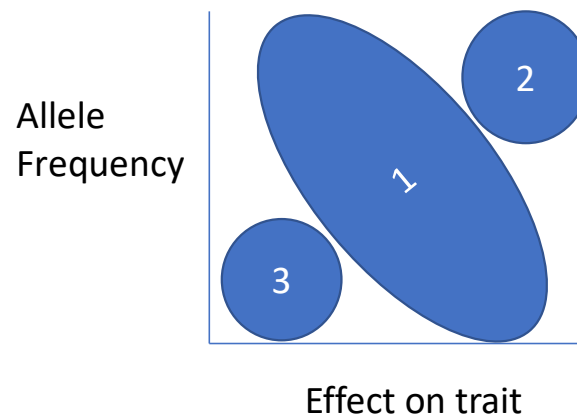
- We would like to take into consideration:
 - Genetic architecture of the trait
 - Breeding strategies

Future environmental optimum



Genetic architecture of the trait

Different breeding strategies success is expected to depend on the genetic architecture.
If we look at a space of allele frequencies and their effect on the trait:



- 1 - large effect alleles are rare, small effect allele are common
- 2 - large effect, common alleles
- 3 - small effect, rare alleles

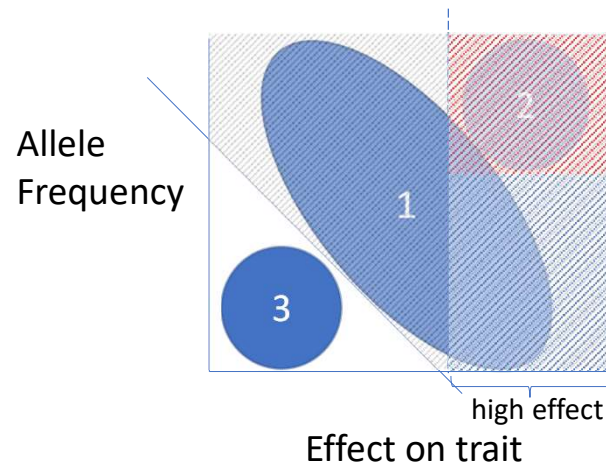
Which breeding strategies are most likely to work under a certain genetic architecture?

We will combine simulations of the above genetic architecture scenarios together with different breeding strategies, to find out what would work better.

The approaches that will be tested:

1. Genotype and environmental association (GEA) & Marker Selection
 - Use GEA to select **candidate markers** and introgress these into elite lines
2. Prediction & QTL mapping
 - Use Genomic Prediction to select **candidate lines** that may have good QTL
 - Make **landrace x elite** mapping populations and identify QTL to introgress into elites
3. Prediction & Recurrent Selection
 - Use Genomic Prediction to select **candidate lines**
 - Make crosses among the lines and elites to create a synthetic population
 - Advance this synthetic population with Recurrent Selection in target environment

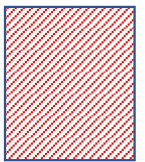
Genetic architecture of the trait



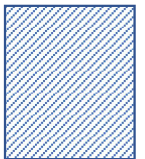
Expected performance of each approach:

GEA

Will work best when the effect is high and the alleles are common



Prediction + QTL mapping will work when the effect is high

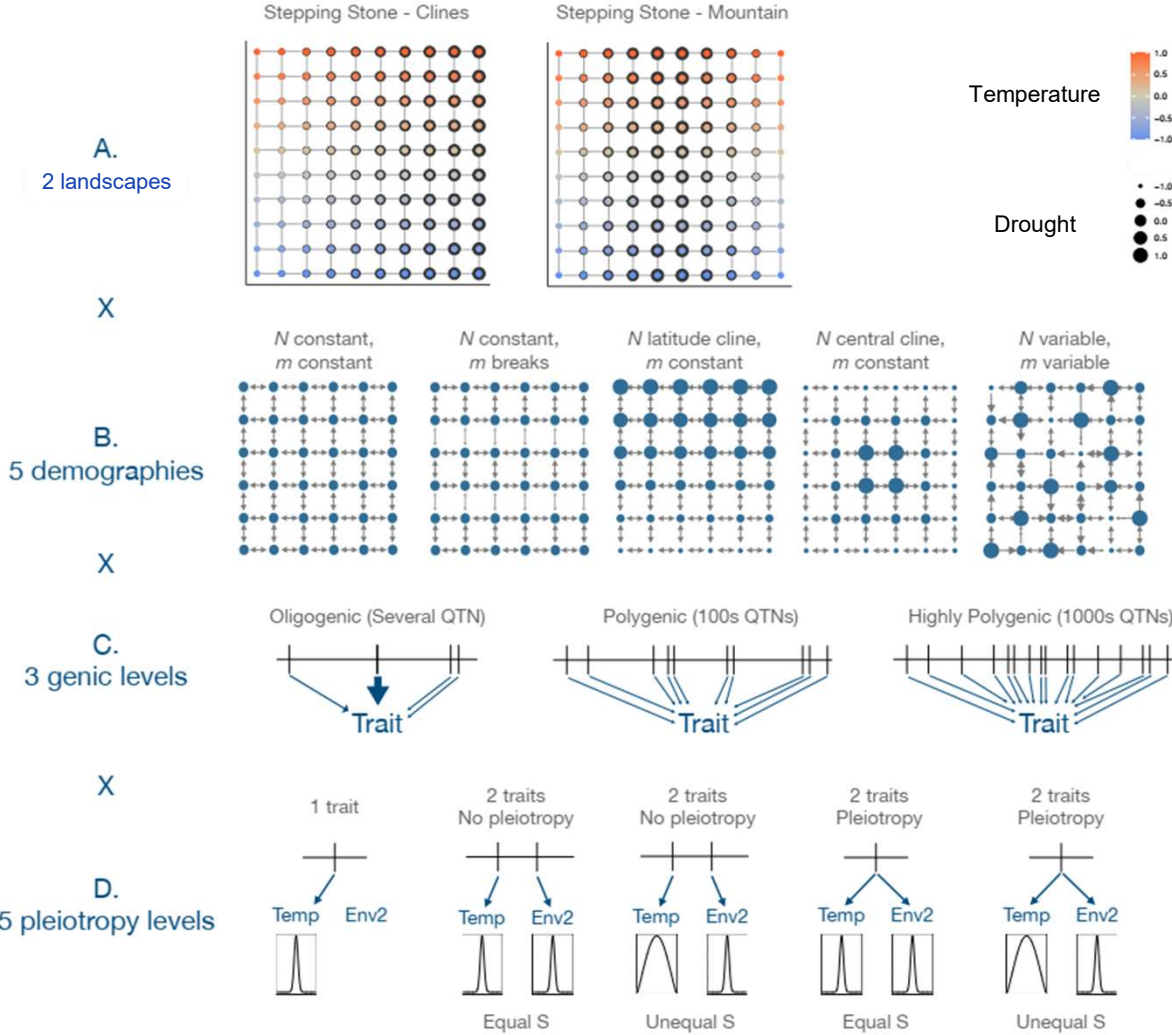


Prediction + genetic selection will work when the effect is not too small



Data:

Simulated demography and environmental data to identify factors for predicting which breeding strategy is most likely to work for a specific crop



Adapted from Lotterhos 2022

- GEA and Marker Selection

1. GEA methods like LFMM / linear model / mixed models will be used for selecting 50 best markers
2. Each L1 line will be crossed to the breeding line B1
3. Phenotype + Genotype
4. Significance test to test if the marker is useful
5. Introgress useful markers into B1 by backcrossing

Breeding simulations:

L1 X Inbred B1
(Selected by GEA marker)

F1



F2

Phenotype (yield) + Genotype; Significance test

Advantages:

Genotype only at the target marker

Problems:

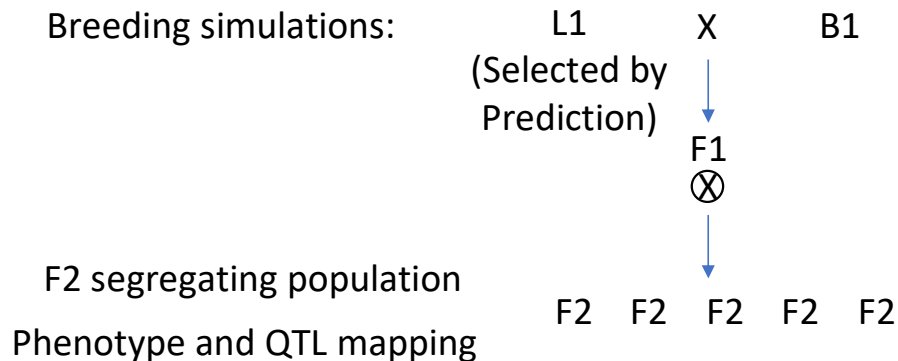
Might not catch rare alleles;

Could be that an advantage in heat environment

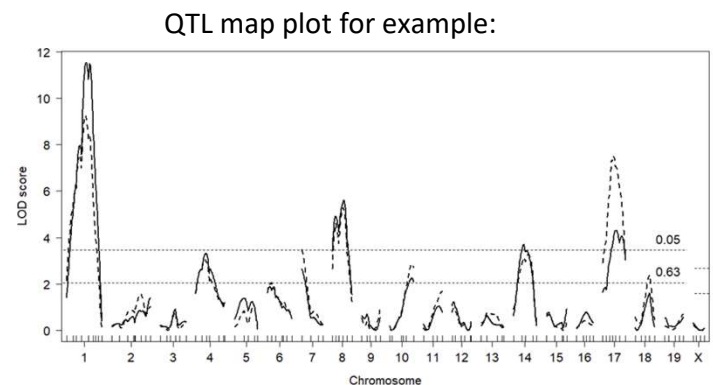
does not lead to advantage in yield (in a different genetic background)

- Prediction and F2 QTL mapping

1. Prediction methods will be used for selecting lines L1
2. QTL mapping will be done to F2 individuals to identify potential markers
3. Introgress beneficial QTL into B1 by backcrossing, genotyping at markers for each QTL



Advantages:
Here we test in 'real' environment;
Rare, large effect alleles can cause a line to be high ranked
No need to identify the beneficial alleles at the beginning

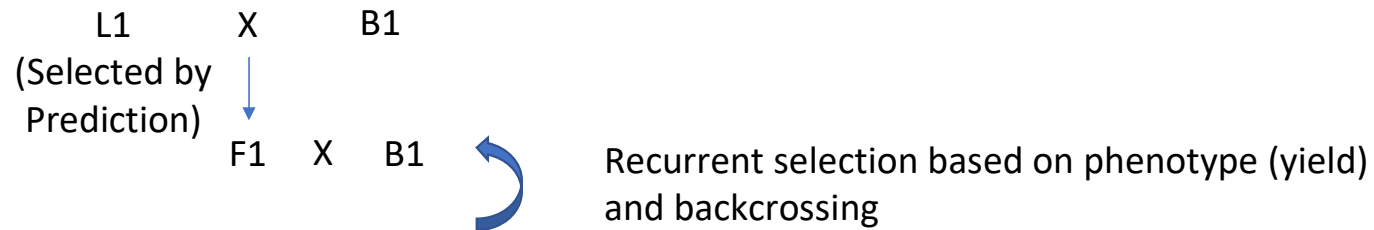


- Prediction & Recurrent Selection

1. Prediction methods will be used for rating lines

2. Highly rated lines L1 will be crossed to breeding line B1; Recurrent selection, based on phenotype.

Breeding simulations:



Advantages:

No need to identify the beneficial alleles at the beginning;

We could catch polygenic adaptation since we do not choose based on a single allele;

Lines can be selected based on rare alleles, but progress is possible even if all alleles have small effect;

We test in 'real' environment

Questions to the breeding specialists:

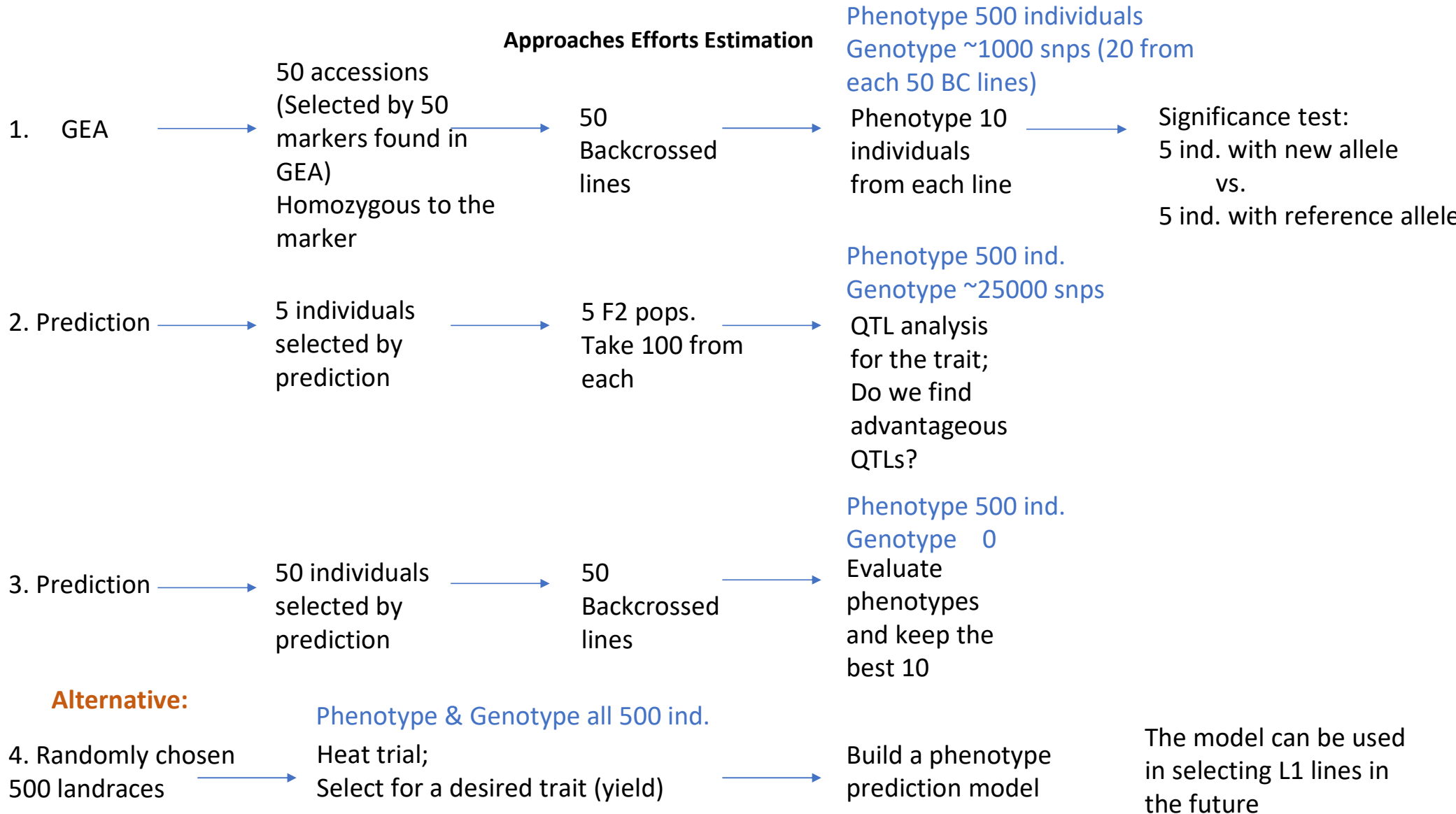
Are there **other breeding approaches** for incorporating beneficial landrace alleles that you are applying, and we should add to the evaluation?

Are there other simulations to consider? Demography / maps ?

How should we evaluate cost?

- How many **individuals** will be grown?
- How much **genotyping** (#loci * #individuals) and phenotyping will be done?

Approaches Efforts Estimation



Questions, suggestions, remarks, etc. are welcome!

Thank you!