QTL mapping for low-phosphorus tolerance in barley

Qinglan Wei

Master student

Supervisor: Meixue Zhou, Chenchen Zhao, Shubing Liu

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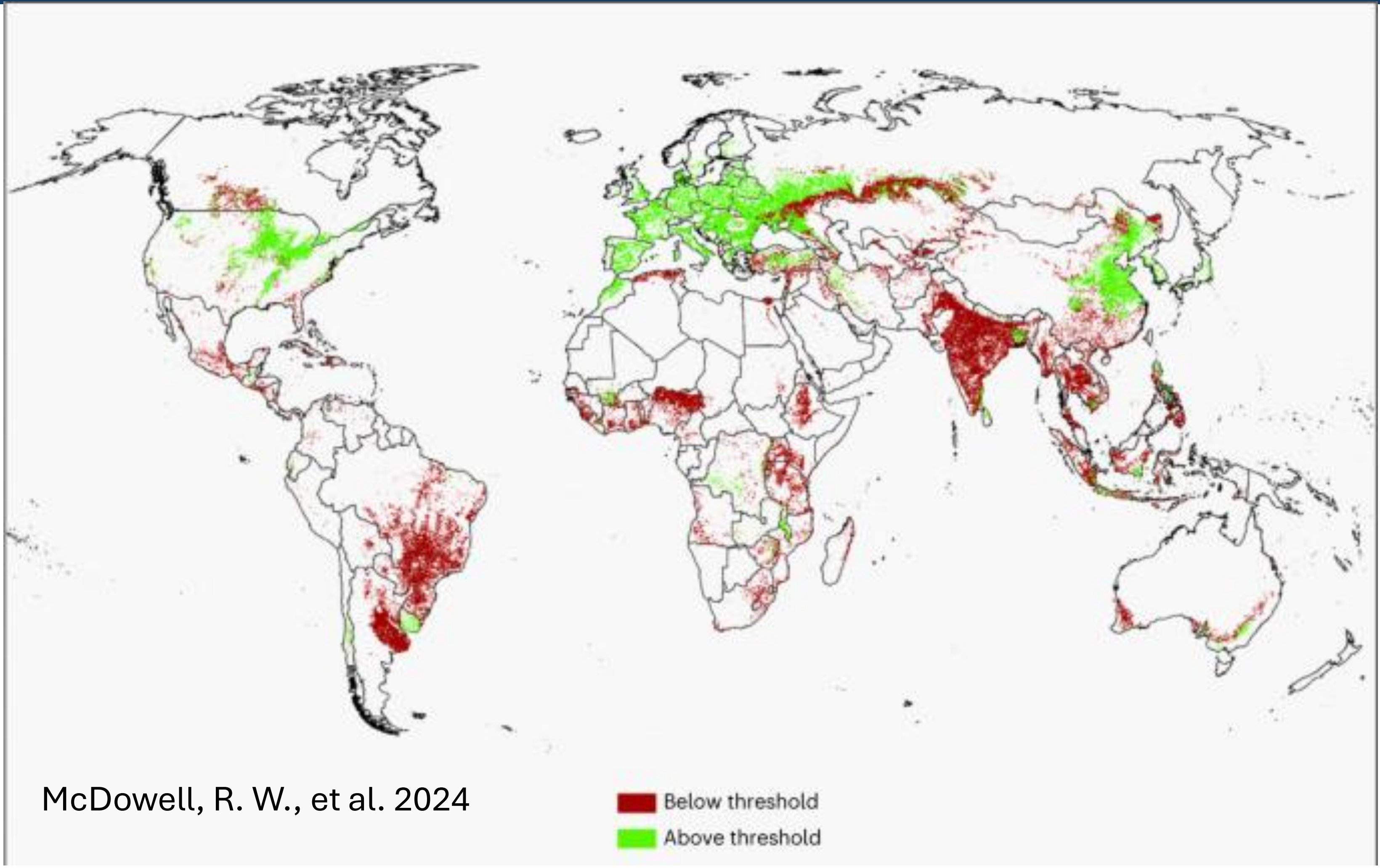
Background



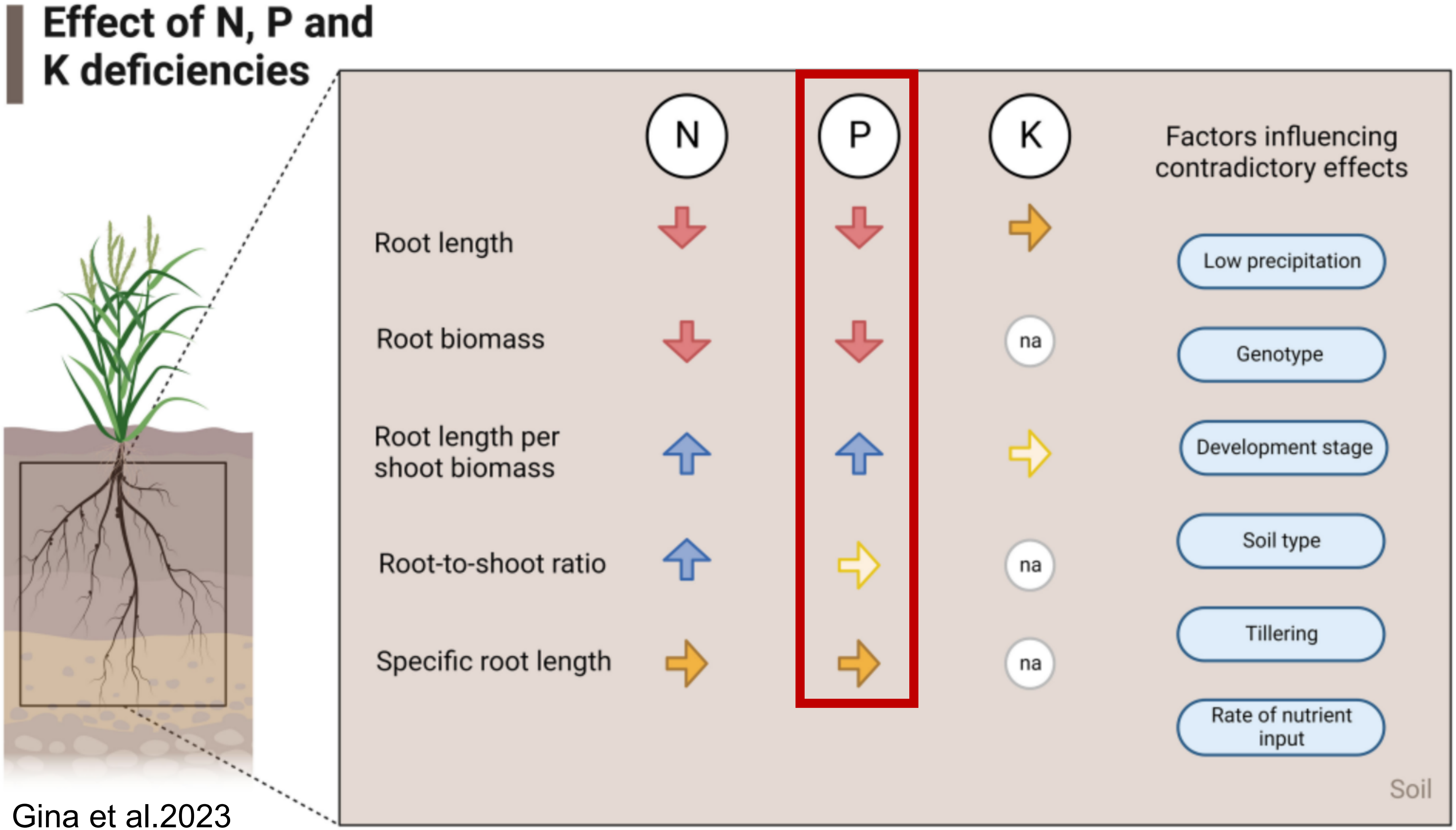
The global distribution of cropland growing major crops with soil phosphorus above or below the agronomic threshold of 15 mg kg^{-1}

Background

- Barley (*Hordeum vulgare* L.) is an important cereal crop that can grow under low-fertility conditions

- Genetic variation in phosphorus use efficiency makes barley a suitable crop for identifying QTLs related to low-phosphorus tolerance

Barley challenged by low phosphorus stress



Gina et al.2023

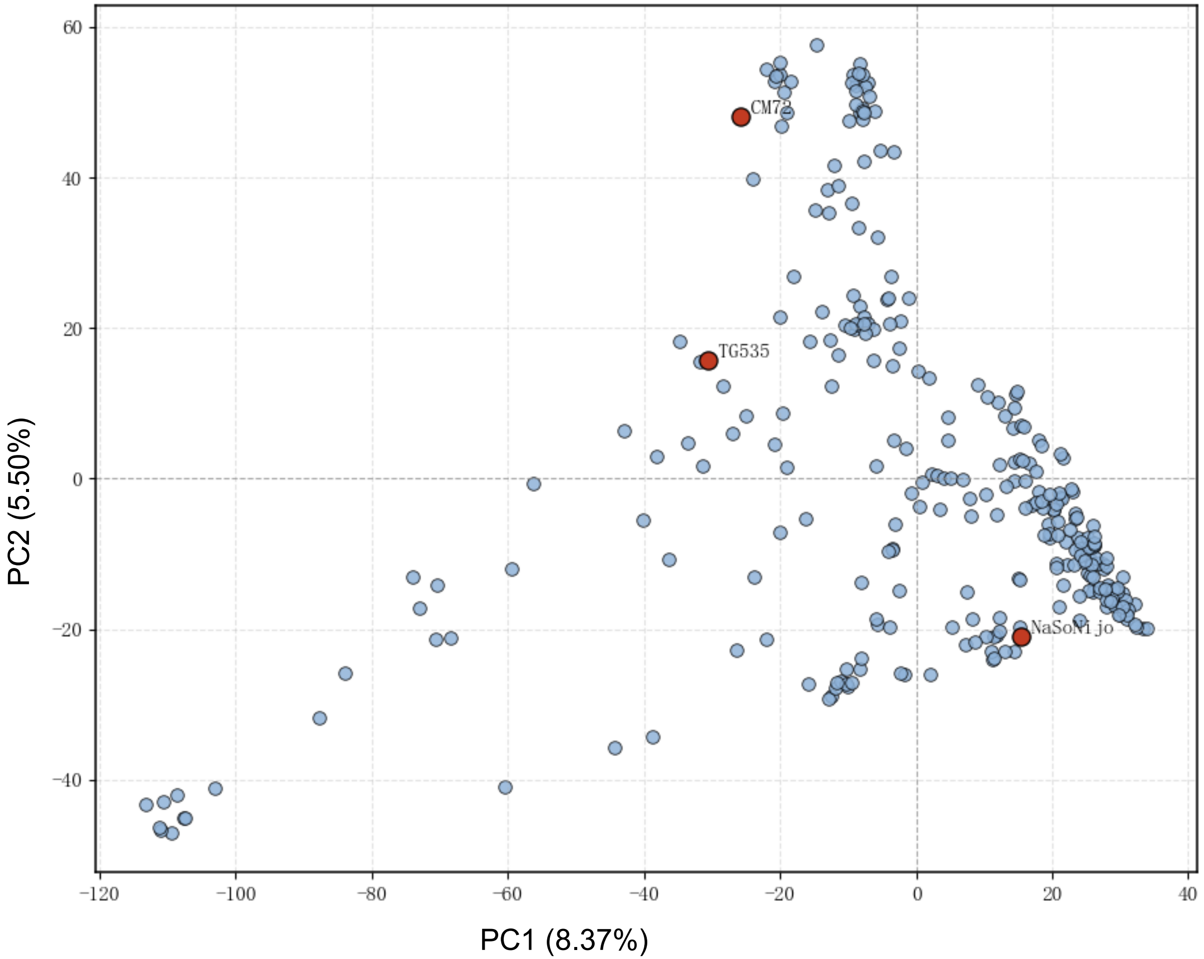
Objectives

- **To develop screening methods for low-phosphorus tolerance in barley**

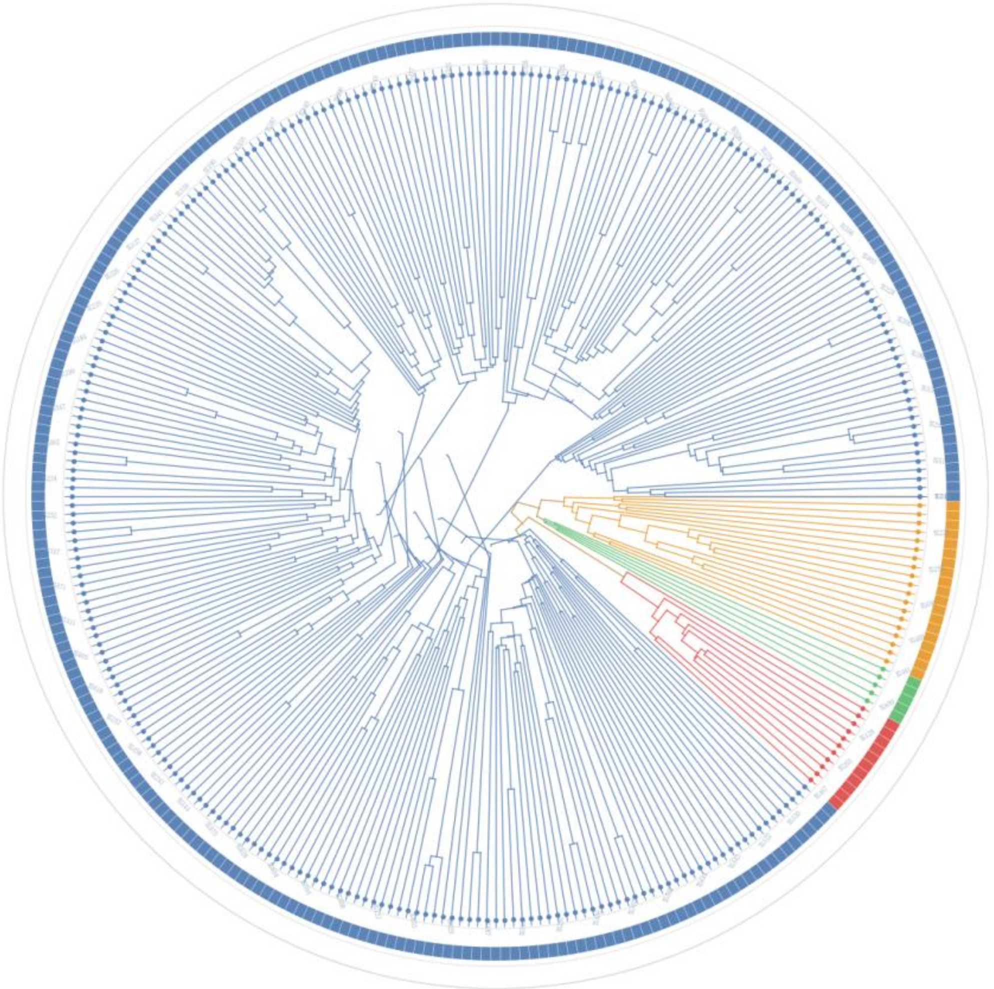
- **To identify QTLs associated with low-phosphorus tolerance**

Genetic relationship of the barley GWAS panel

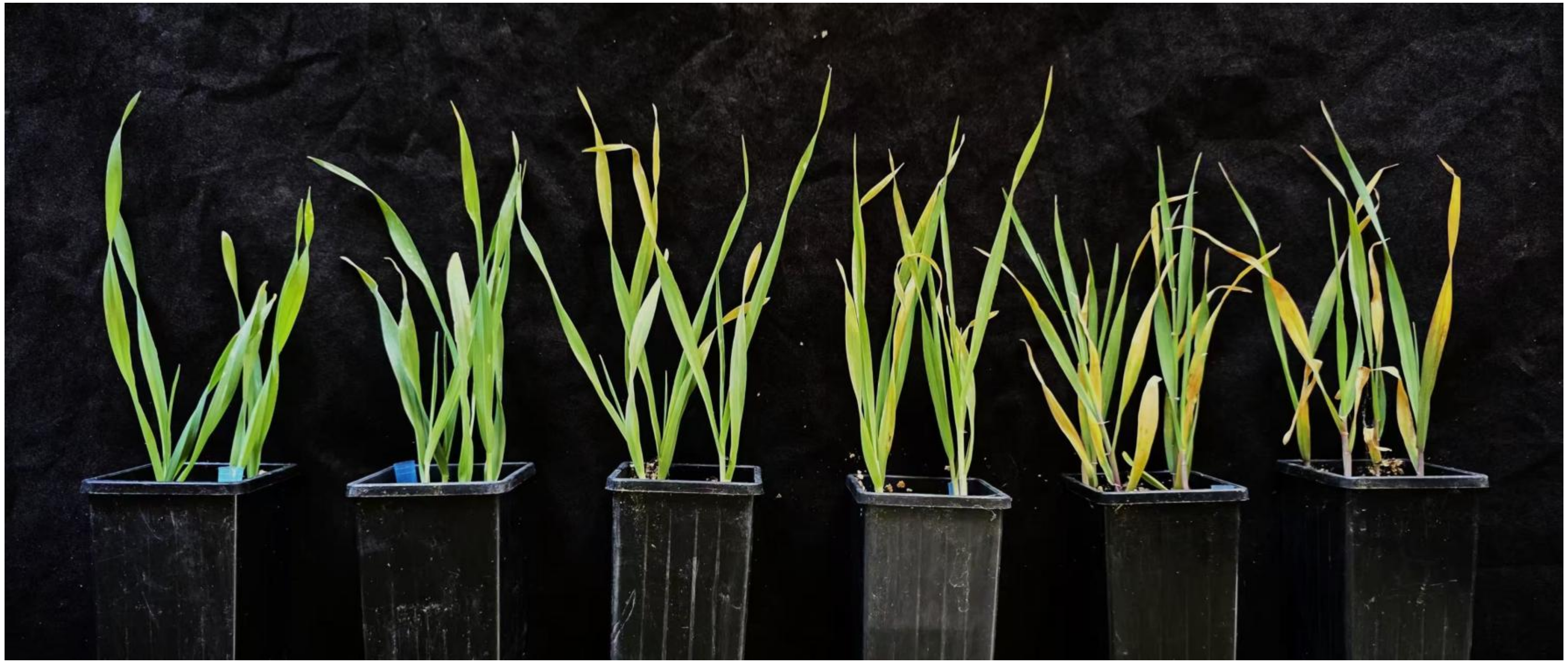
Principal Component Analysis (PCA) of the Natural Population



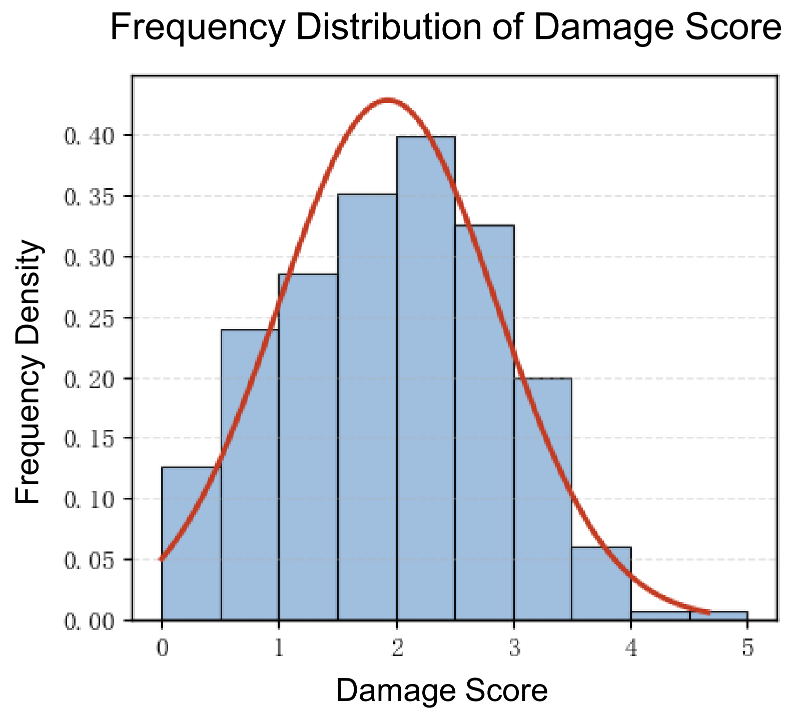
Phylogenetic tree of the barley natural population



Low-P tolerance grading in the natural population

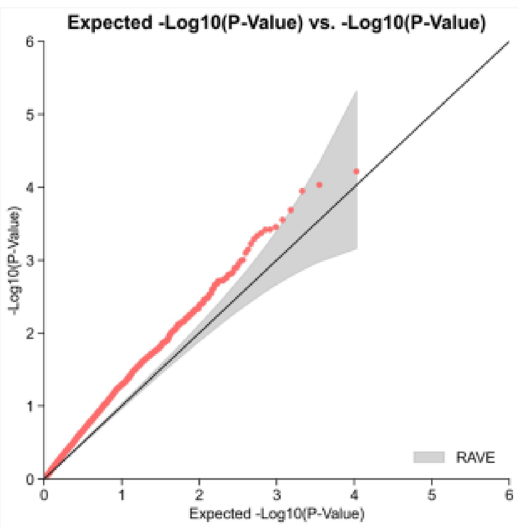


0 1 2 3 4 5

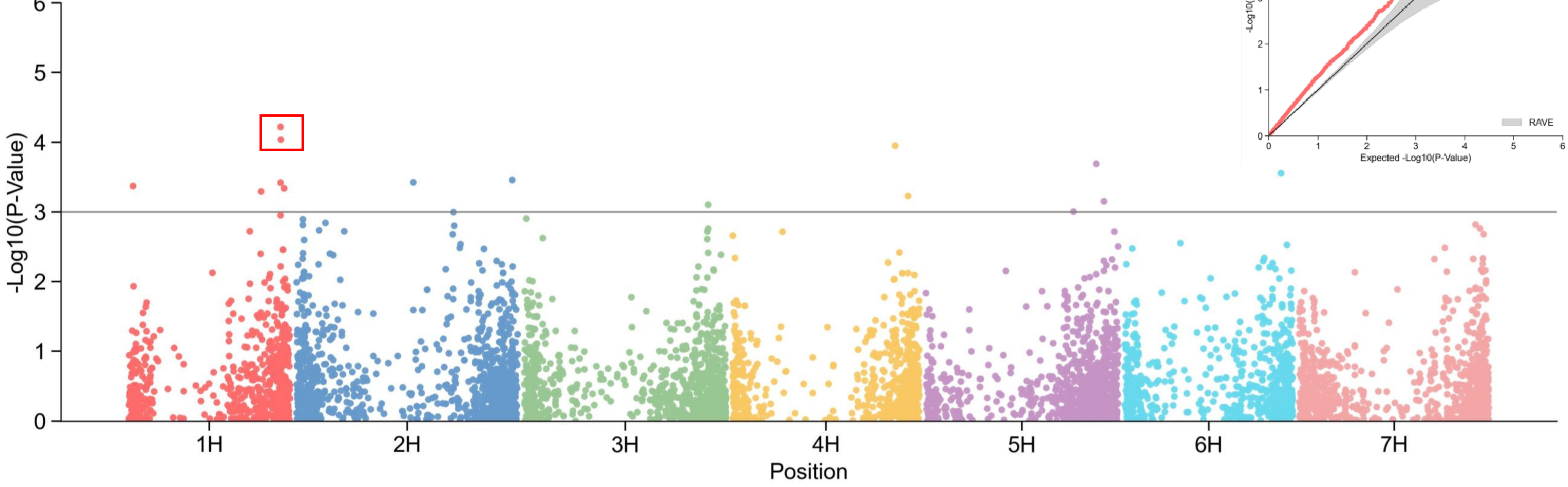


Low-P tolerance was evaluated using a 0–5 scoring scale based on leaf chlorosis and plant vigor.
Score 0 indicates highly tolerant plants with normal growth, while score 5 represents highly sensitive plants with severe chlorosis.

GWAS Manhattan plot



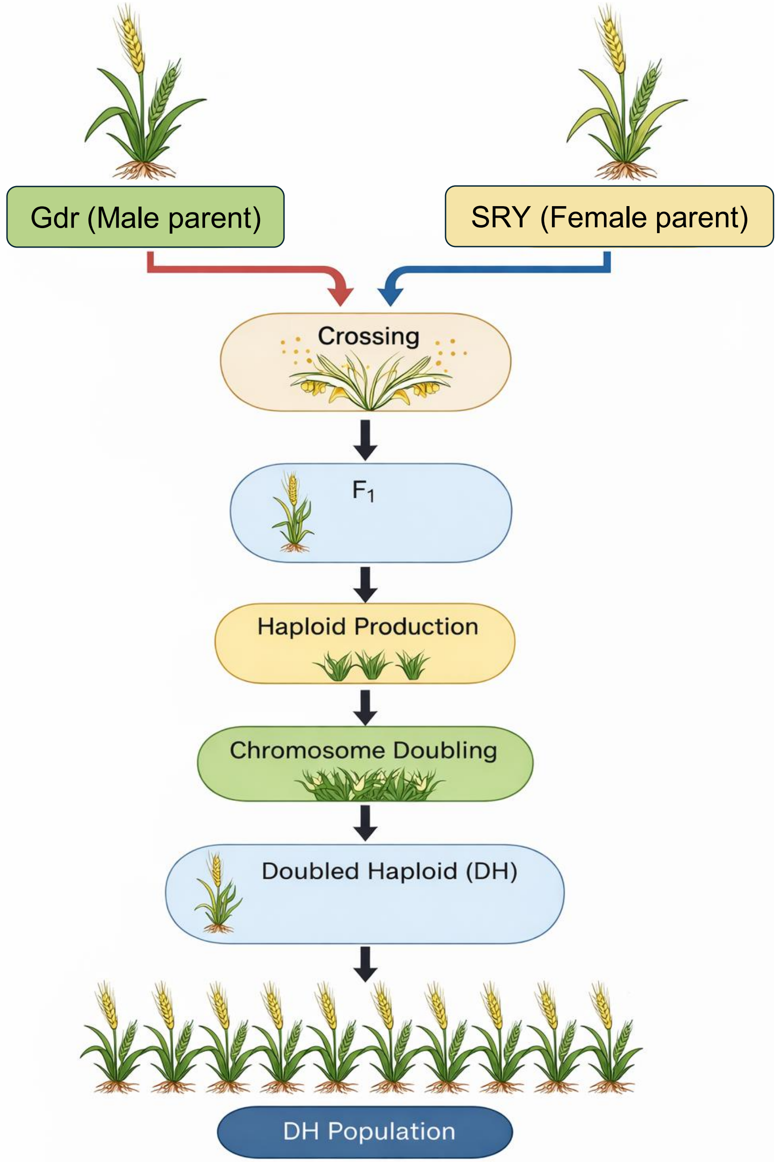
A significant SNP association was identified on chromosome 1H



Parental Performance and Development of the DH Population

Gdr SRY

Gdr SRY

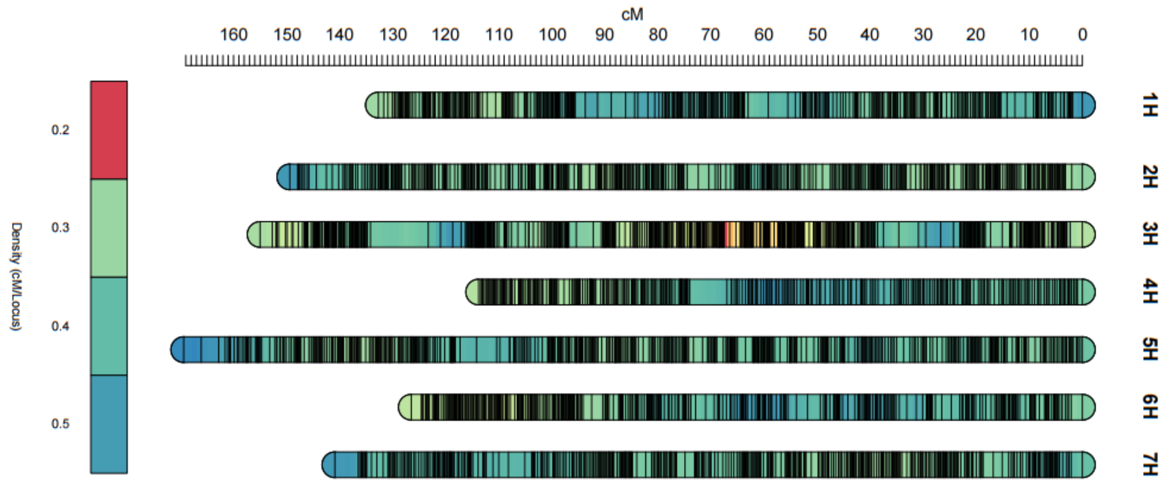


Phenotypic Analysis and Genetic Map of the Barley SGDH Population

Phenotypic statistics of traits under low-phosphorus stress

Trait	Plant Height (cm)	Tiller Number at 20 Days After Emergence	Damage Score	Tiller Number at 30 Days After Emergence	Shoot Dry Weight(g)	Total Dry Weight(g)	Root Dry Weight(g)
Mean	19.59	0.45	1.47	1.56	0.63	1.16	0.53
Max	27.89	1.50	3.50	2.42	1.01	1.73	0.94
Min	12.74	0.00	0.17	0.83	0.20	0.38	0.18
SD	3.42	0.31	0.81	0.33	0.16	0.27	0.14
CV(%)	17.46%	68.92%	54.78 %	21.01%	24.85%	23.22 %	25.60%

Genetic linkage map of the barley SGDH population



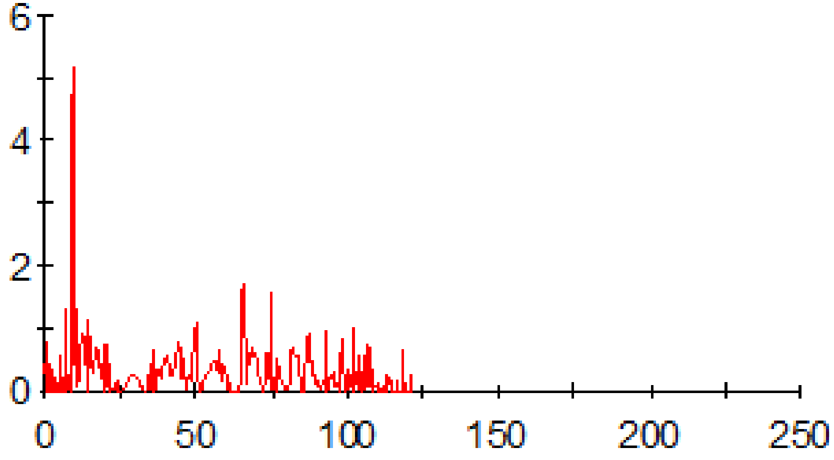
Substantial phenotypic variation was observed.Damage score showed the largest variation. The genetic map supports QTL mapping.

QTL for Damage Score under Different Sowing Conditions

A stable QTL controlling damage score was identified on chromosome 1H, with its effect varying under different sowing conditions.

PVE=14%

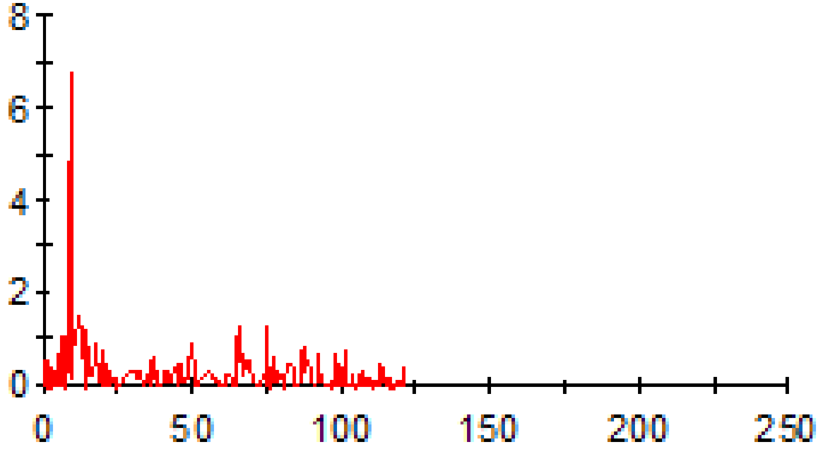
1H



Damage score QTL

PVE=22.6%

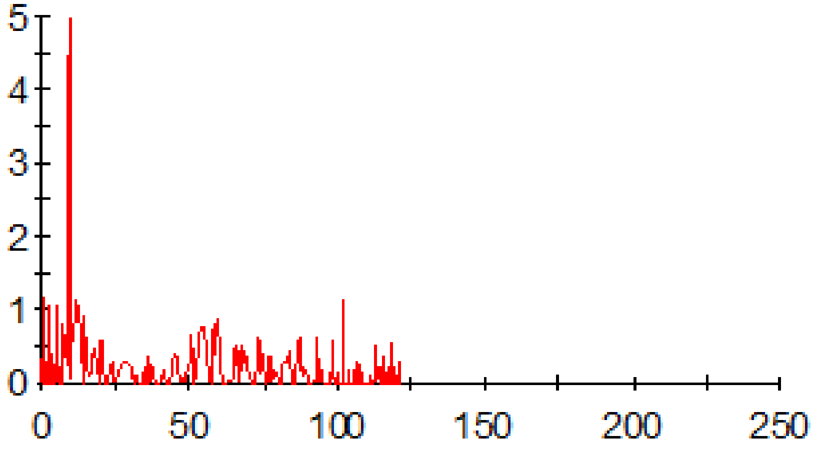
1H



Damage score QTL under spring sowing

PVE=19.3%

1H



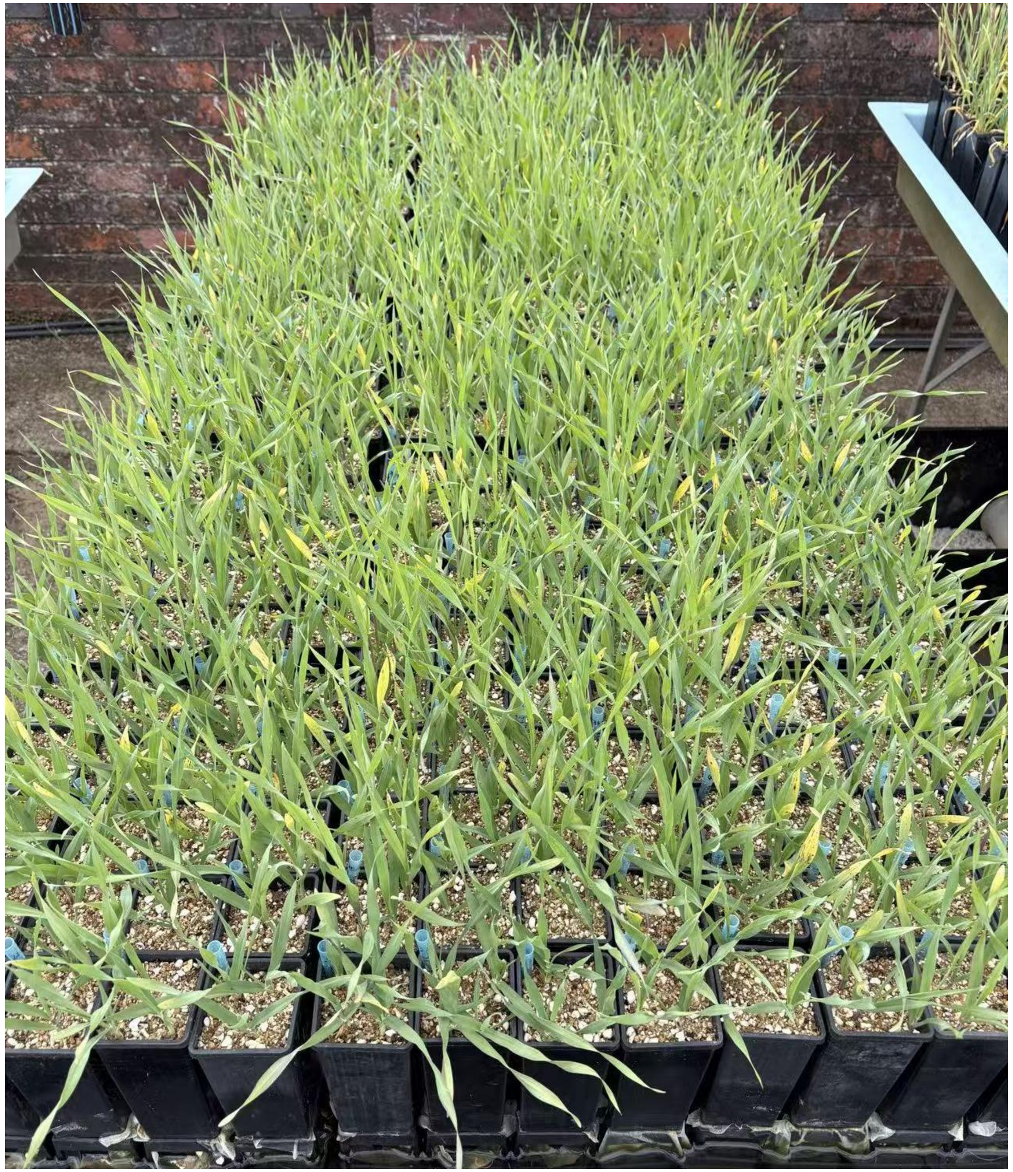
Damage score QTL under summer sowing

summary

1.A stable QTL for damage score identified on chromosome 1H

2.Environmental conditions influenced the QTL effect

3.Provides a basis for marker-assisted breeding



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Thank you