

# Genome-Wide Association Studies of Mineral Content in Pea

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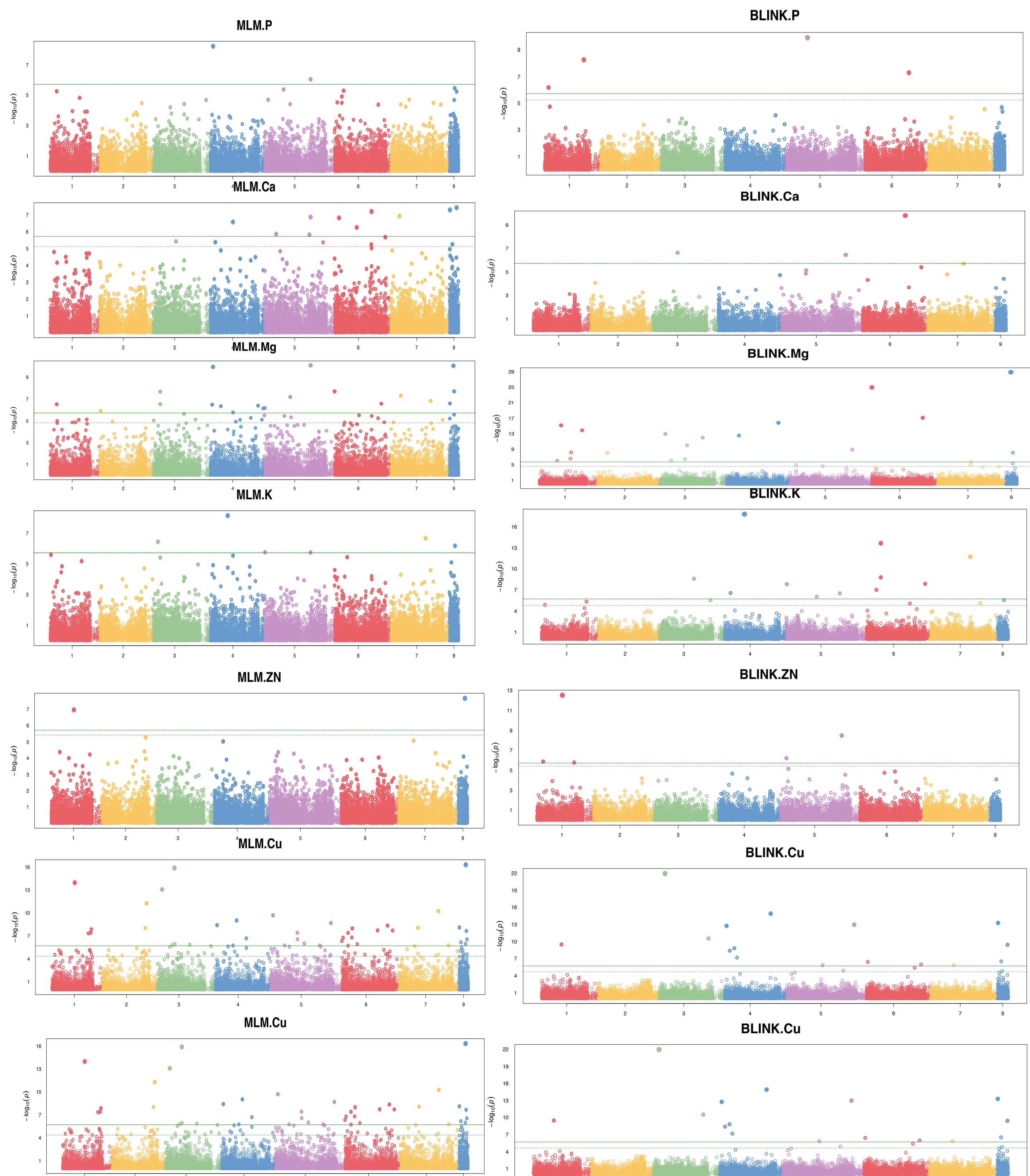
## INTRODUCTION

Pea (*Pisum sativum*) is a nutrient-rich crop that provides essential minerals like phosphorus, calcium, magnesium, and iron, supporting human health. Improving its mineral content through genetics can boost its nutritional value and help combat micronutrient deficiencies. This study aimed to investigate the genetic basis of mineral accumulation in pea seeds using a genome-wide association study (GWAS). The analysis was conducted on 324 diverse, previously genotyped *Pisum* accessions, including *P. sativum*, *P. fulvum*, *P. abyssinicum*, and several *P. sativum* subspecies.

Seed mineral content was measured using Inductively Coupled Plasma (ICP-OES) Spectroscopy

Table 1. Variance components, heritability and descriptive statistic by phenotypic data set and its trait.

Mineral	Average (mg/100g)	Standard Error (SE):	Range	Skewness	Coefficient of Variation (CV%)	Heritability (H <sup>2</sup> )	Accuracy
Phosphorus (P)	356.77	3.22	501.68	0.60	26.25	0.47	0.68
Calcium (Ca)	106.60	1.62	372.51	0.93	44.41	0.71	0.84
Magnesium (Mg)	140.40	0.88	188.49	0.52	18.33	0.63	0.79
Potassium (K)	1112.68	6.67	1277.19	0.75	17.47	0.59	0.77
Zinc (Zn)	3.47	0.04	8.54	1.80	35.94	0.79	0.89
Iron (Fe)	4.40	0.05	15.91	1.21	35.41	0.64	0.80
Copper (Cu)	0.82	0.01	2.96	3.38	35.89	0.54	0.73
Manganese (Mn)	1.01	0.00	1.63	0.69	24.28	0.48	0.69



Overall, given the high heritability, moderate to high CV percentage, and variation in the degree of skewness, it is confirmed that the studied minerals are genetically traceable and suitable for downstream linkage mapping

- ❖ Among the eight minerals examined, 151 DArTseq markers showed significant association with at least one mineral in either or both models.
- ❖ A total of **50 candidate genes** were identified across all seven chromosomes:

**Chr 1:** 6 genes  
**Chr 2:** 4 genes  
**Chr 3:** 7 genes  
**Chr 4:** 9 genes  
**Chr 5:** 11 genes  
**Chr 6:** 9 genes  
**Chr 7:** 4 genes

- ❖ These candidate genes are likely involved in processes related to **mineral accumulation**, including primary and secondary metabolism, **cell wall modification**, **ion transport**, **DNA transcription regulation**, and **stress responses**.

GWAS was performed with both **MLM** and **BLINK** models using GAPIT 3.0. Candidate genes were identified using the pea ZW6 reference genome browser

## CONCLUSIONS

- ✓ The identified genomic regions provide valuable insights into the genetic control of nutrient accumulation and serve as potential targets for breeding programs aimed at improving the nutritional quality of pea seeds.