



John Innes Centre

Unlocking Nature's Diversity

Mapping nutritional quality traits in pea and faba bean using genome-wide association studies (GWAS)

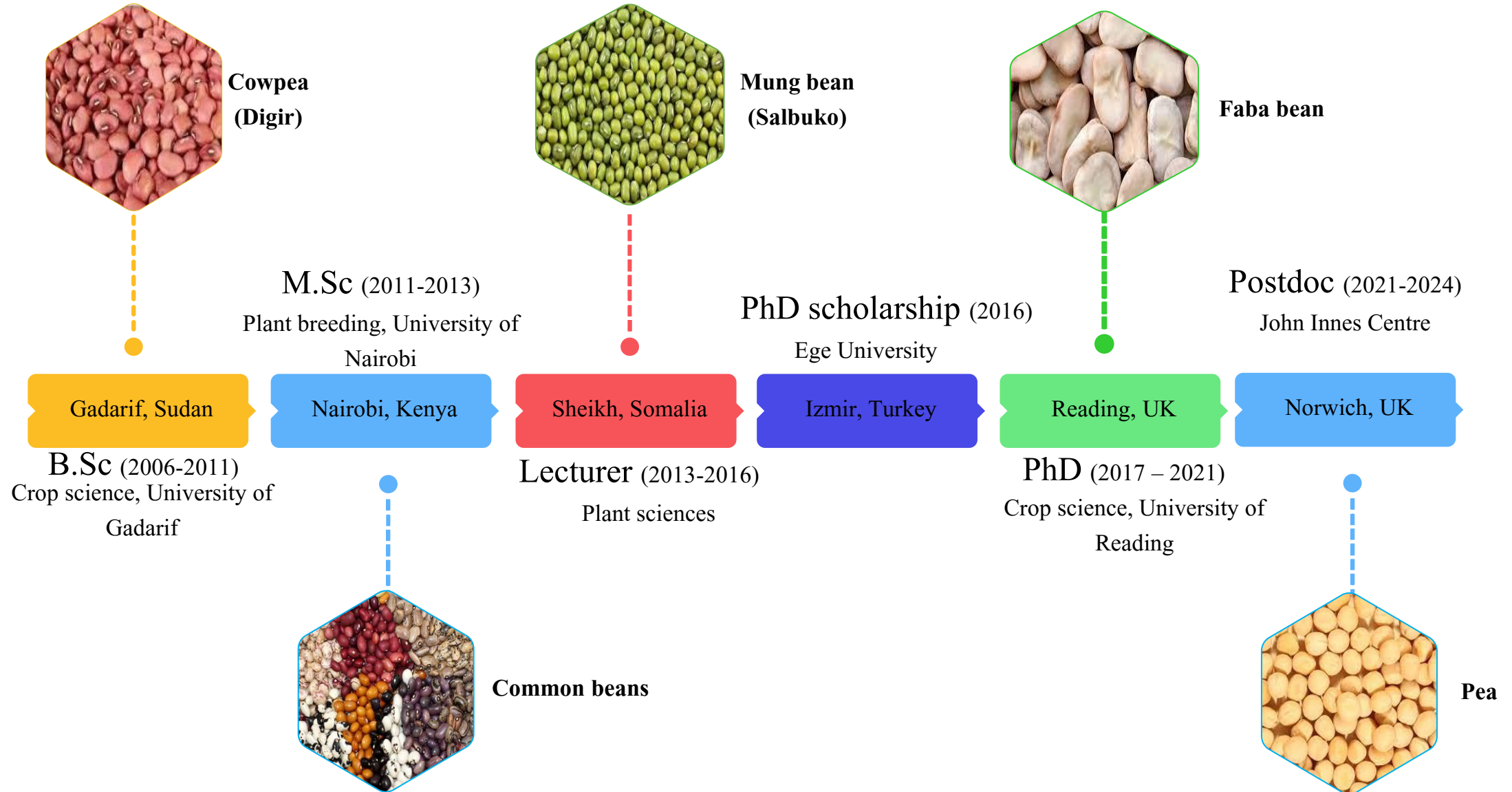


Ahmed Warsame
Postdoctoral Researcher,
John Innes Centre, UK



Kirkhouse Trust Annual Meeting 2023 , Livingstone, Zambia

My career to date has been all about pulses!



..also, the world is interested in pulses



On the pulse: why beans, peas and lentils are making a comeback

Legumes research gets flexitarian pulses racing with farming guidance

Plant more bean-like crops in Europe and consider 'healthy diet transition' to beat climate crisis, say scientists

PLANT-BASED PUSH: UK SALES OF MEAT-FREE FOODS SHOOT UP 40% BETWEEN 2014-19

FOOD SCIENCE

Give peas a chance

A series of in vitro, ex vivo and in vivo studies show that starch structure and plant tissue intactness control glucose release from pea-based foods. Modification of these characteristics through plant breeding and food processing may provide opportunities for enhanced food formulation, but challenges for labelling and communication.

Michael J. Gidley



Setting pulses racing: the Reading scientists perfecting broad bean bread



Legume gap



DemoNet ErbBo



Legume Futures



DevRAM



Legumes Translated

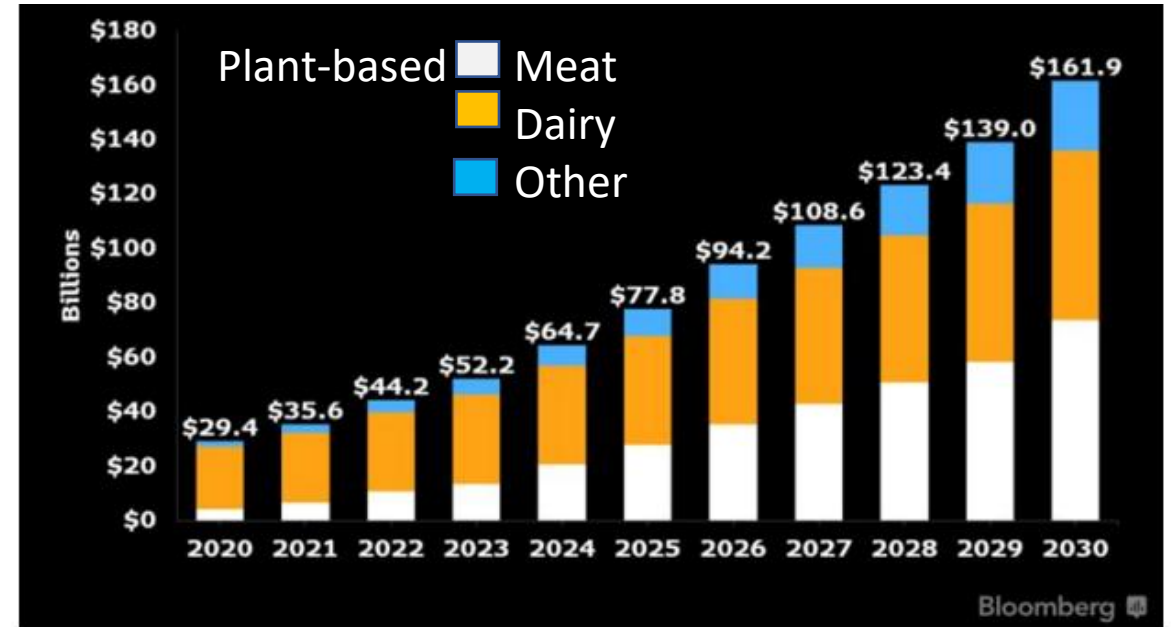


LegValue



Ecofeed

Bloomberg data: Total Global Plant-based Retail Market Size





Current postdoc project:

Discovering genetic variation for important quality traits and mapping the underlying genes.

- Grain protein content
- Protein composition
- Starch composition (amylose/RS)
- Minerals (Fe, Zn, Mg, P, Ca)
- Phytate
- Raffinose family oligosaccharides
 - ✓ Raffinose
 - ✓ Stachyose
 - ✓ Verbascose
 - ✓ Others



Department
for Environment
Food & Rural Affairs

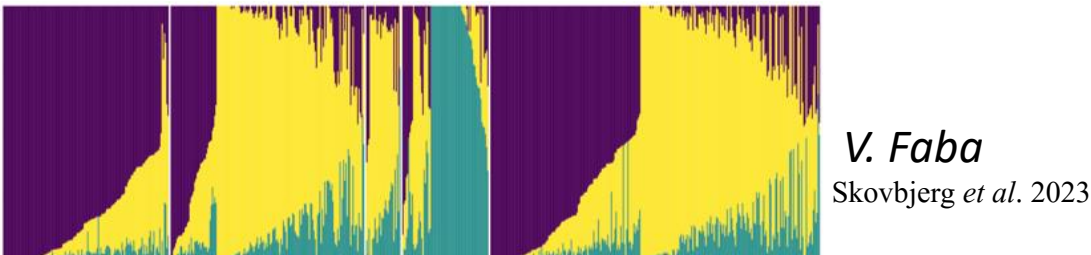
Tools for trait mapping in pea and faba

A reference genome for pea provides insight into legume genome evolution

Kreplak, et al. (2019) Nature Genet.

The giant diploid faba genome unlocks variation in a global protein crop

Jayakodi, ..., Warsame, et al. (2023) Nature (**in print**)



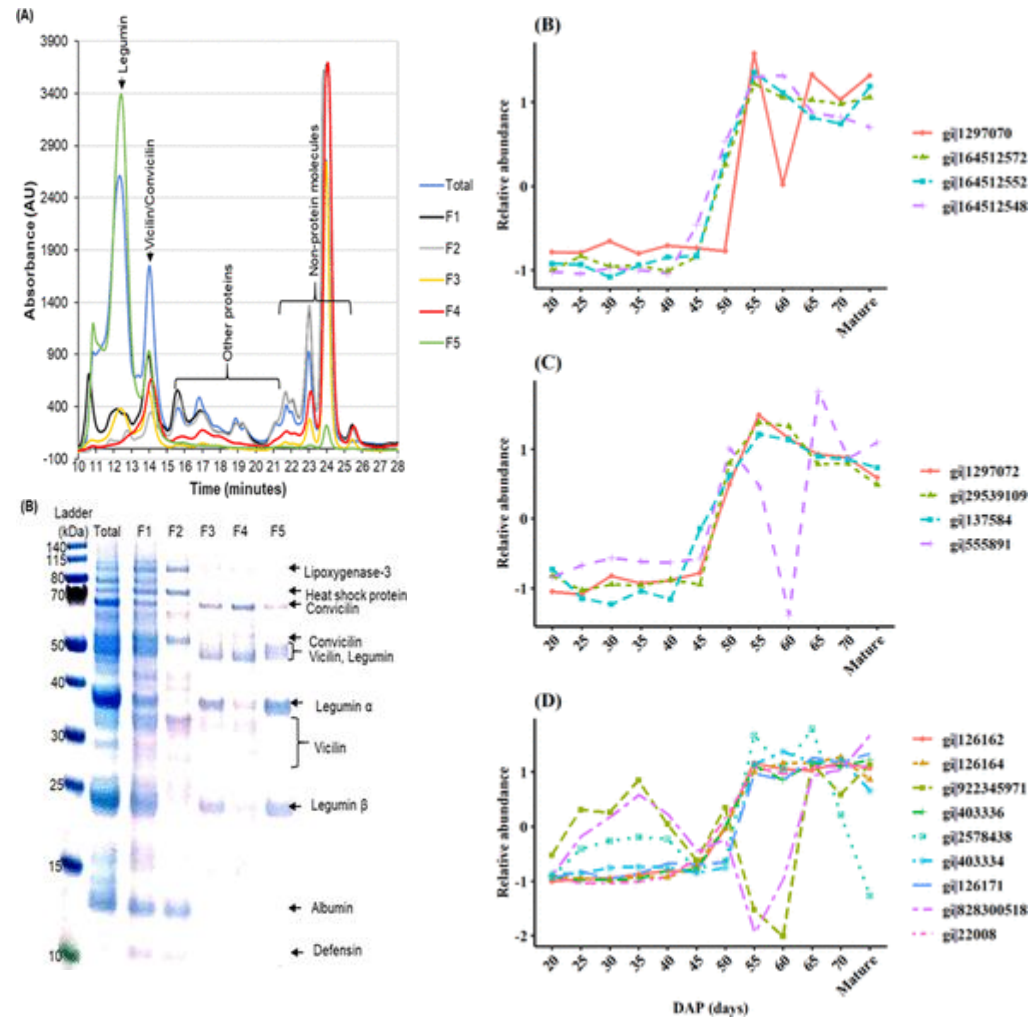
Genetic analysis of global faba bean germplasm maps agronomic traits and identifies strong selection signatures for geographical origin

Skovbjerg, ..., Warsame, et al. (2023). Theor. App. Gen. (**in print**)

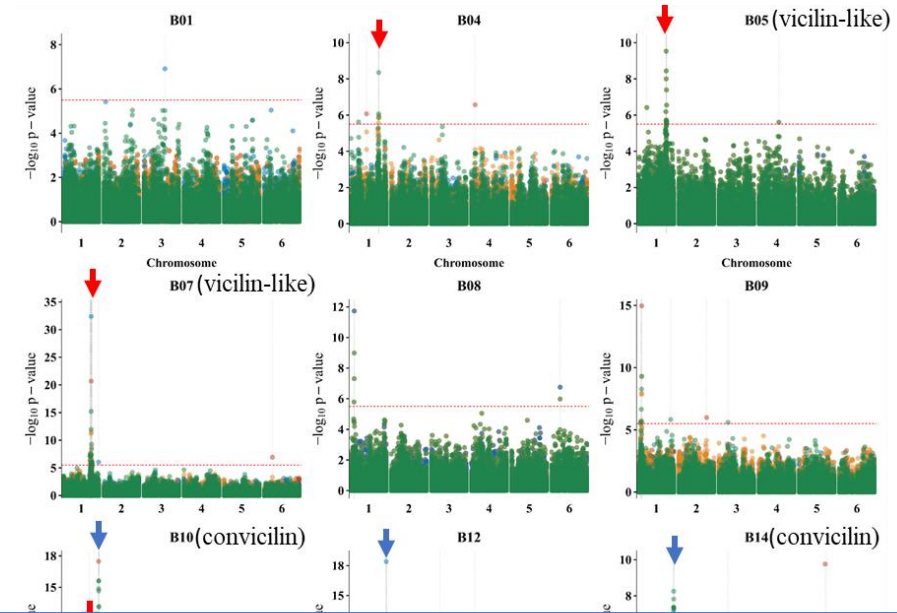
- Reference genomes.
- Diversity panels:
 - Pea: 224 accessions
 - Faba: 167 multi-parent lines
- High-density SNP markers (Pea=90K, faba bean=60K).
- High-throughput assays
 - Protein analysis
 - Minerals
 - Phytate
 - Sugars
 - starch

GWAS analysis of protein composition in faba bean

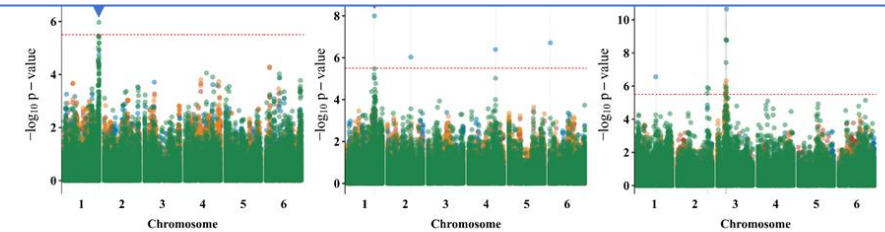
Characterization of faba bean seed proteins



GWAS analysis of seed protein bands

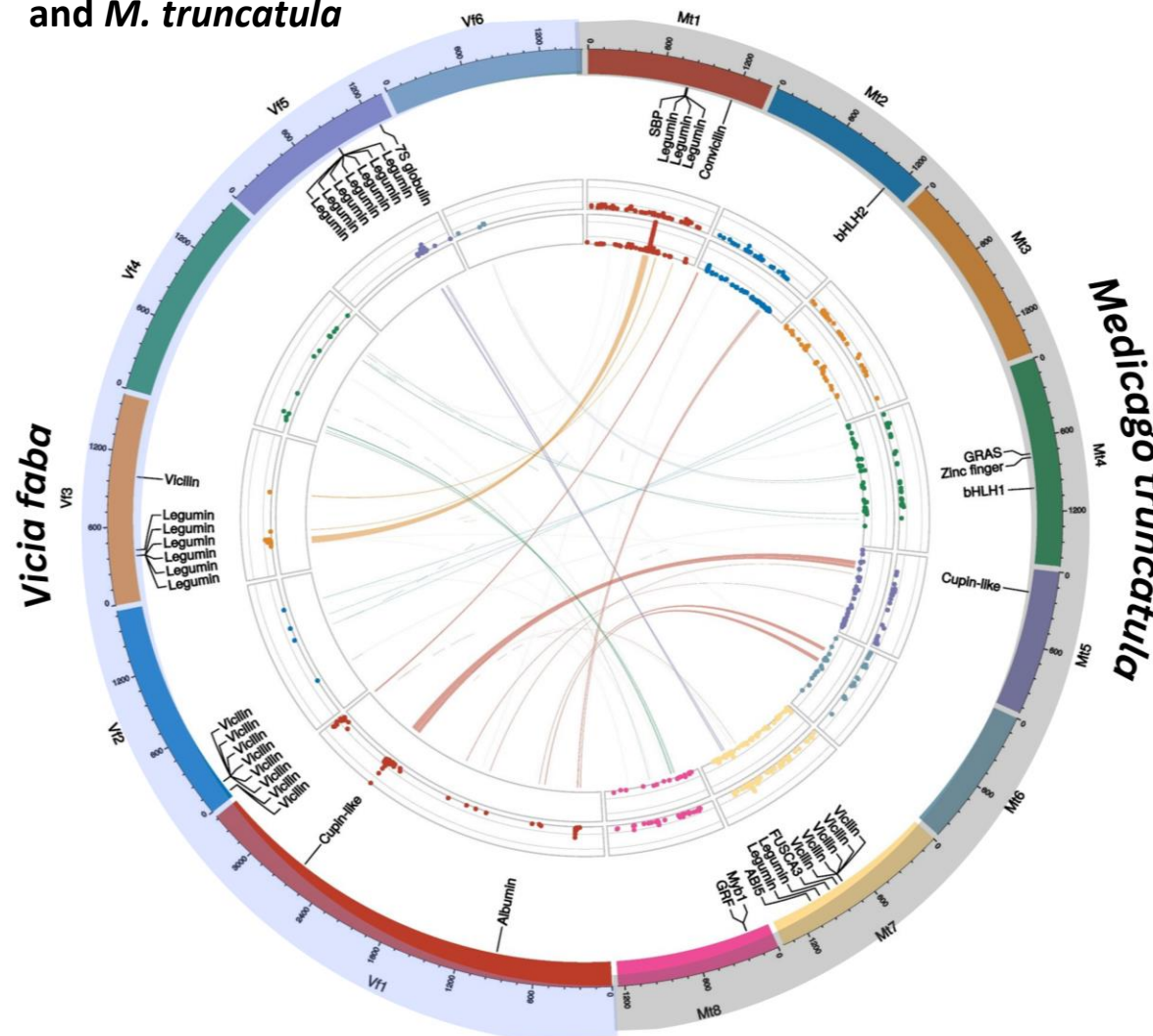


❖ Many highly significant associations, including two regions on Chr1 associated with several proteins.



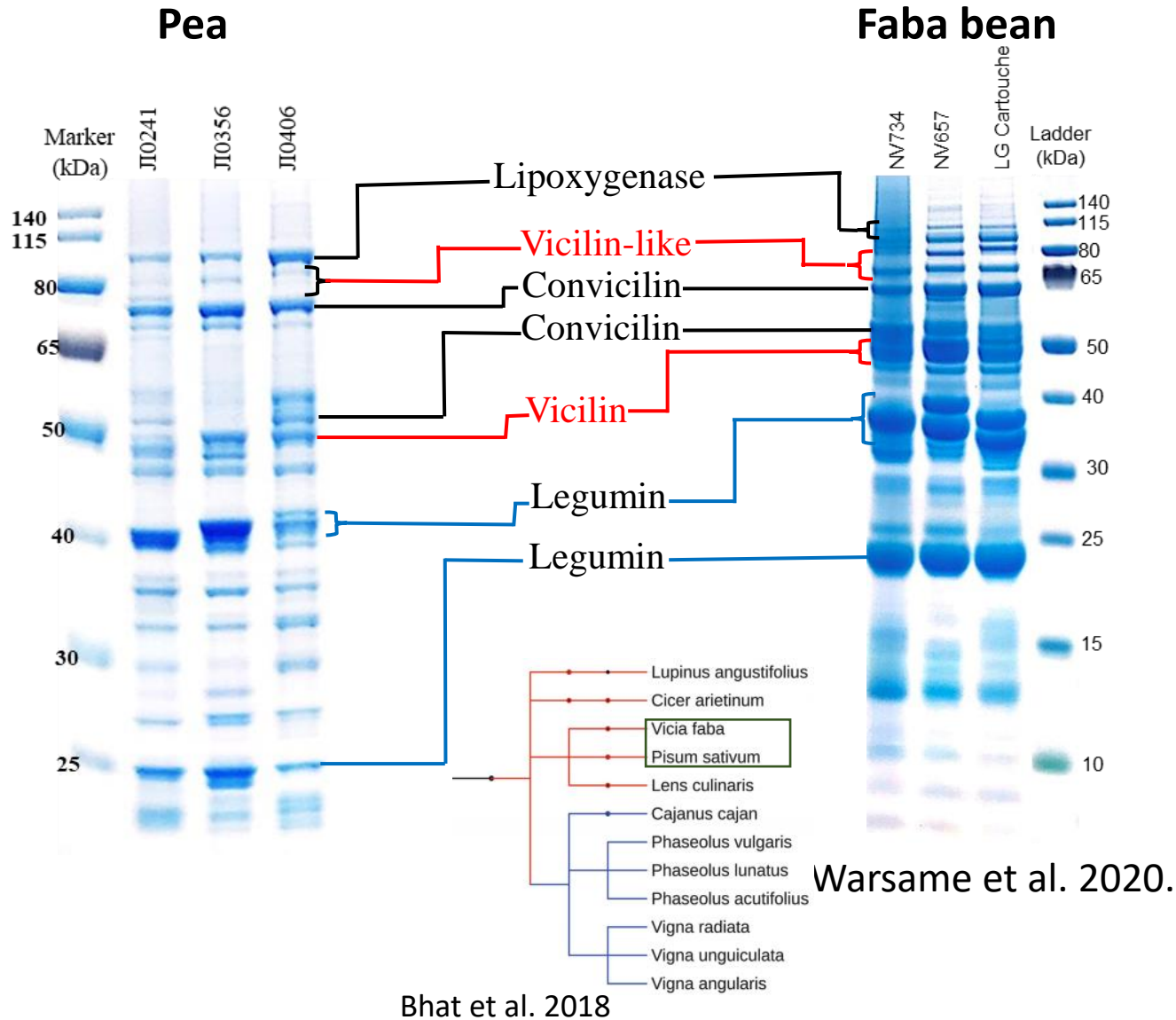
GWAS analysis of protein composition in faba bean

Overlap between GWAS signals for protein composition in *V. faba* and *M. truncatula*

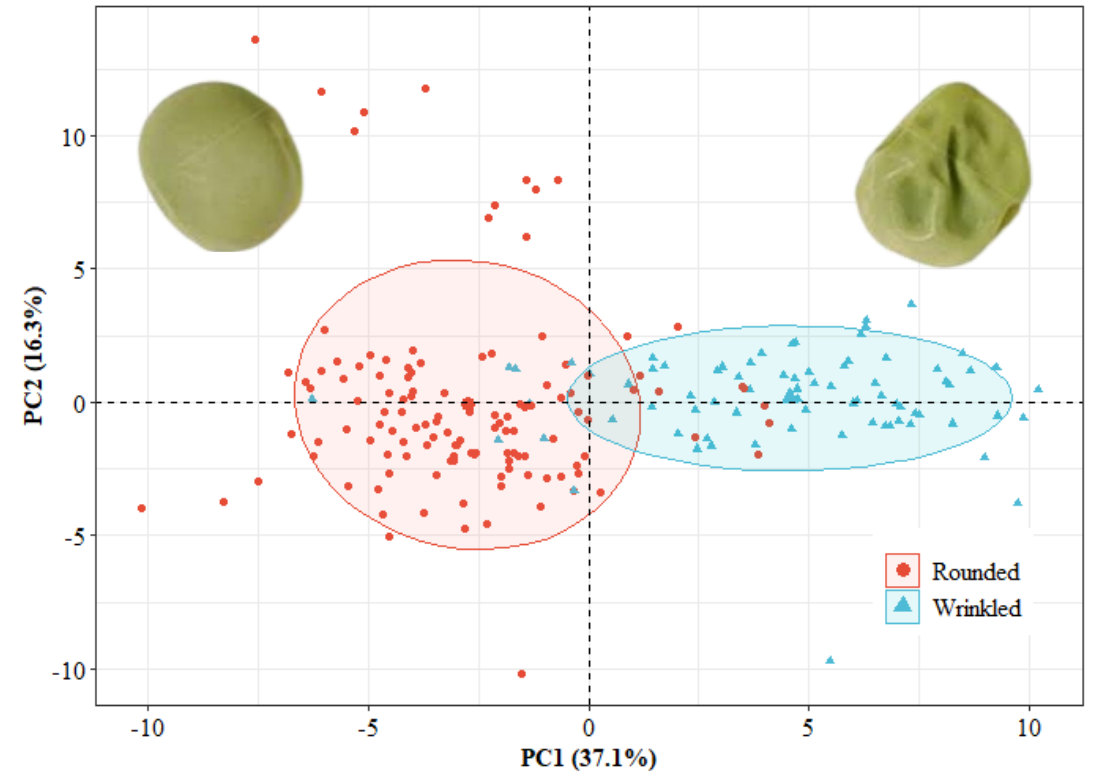


- ❖ Several seed protein genes are clustered and many of the GWAS signals identified in faba bean and Medicago overlap in syntenic regions.
- ❖ Some of the GWAS signals are near structural or regulatory genes which facilitates further characterization of the candidate genes.

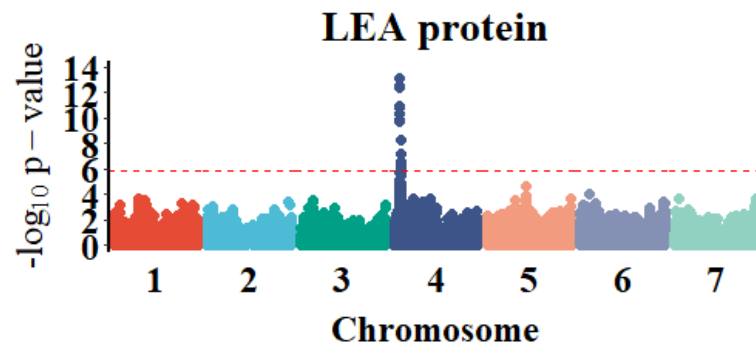
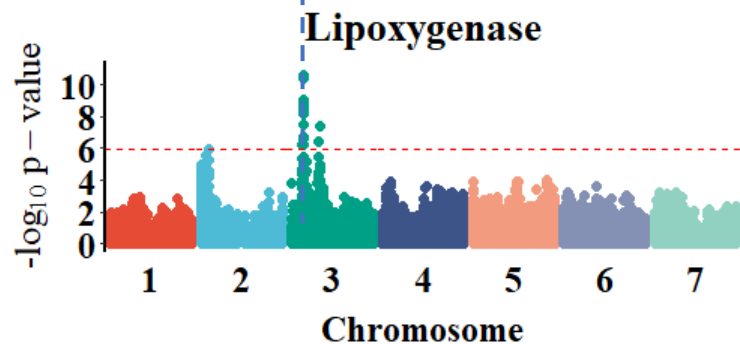
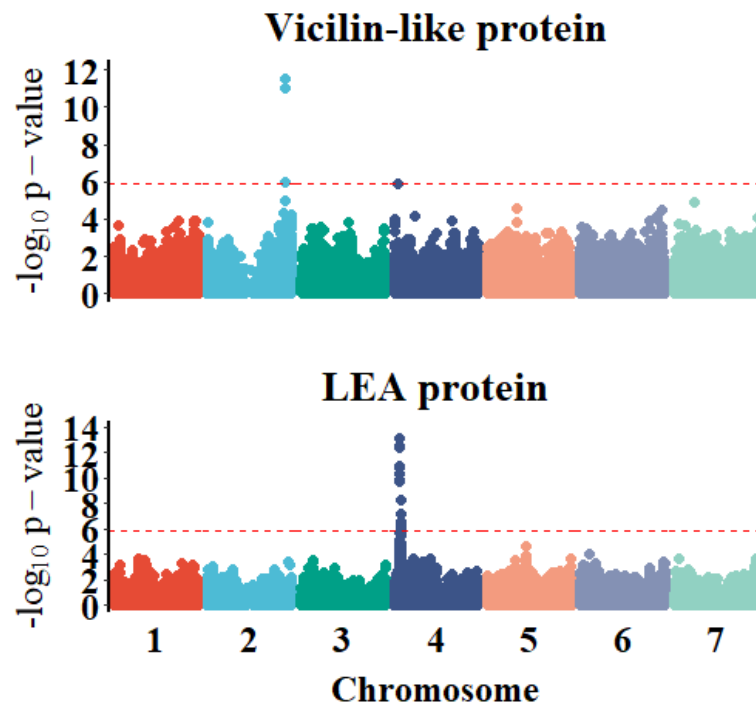
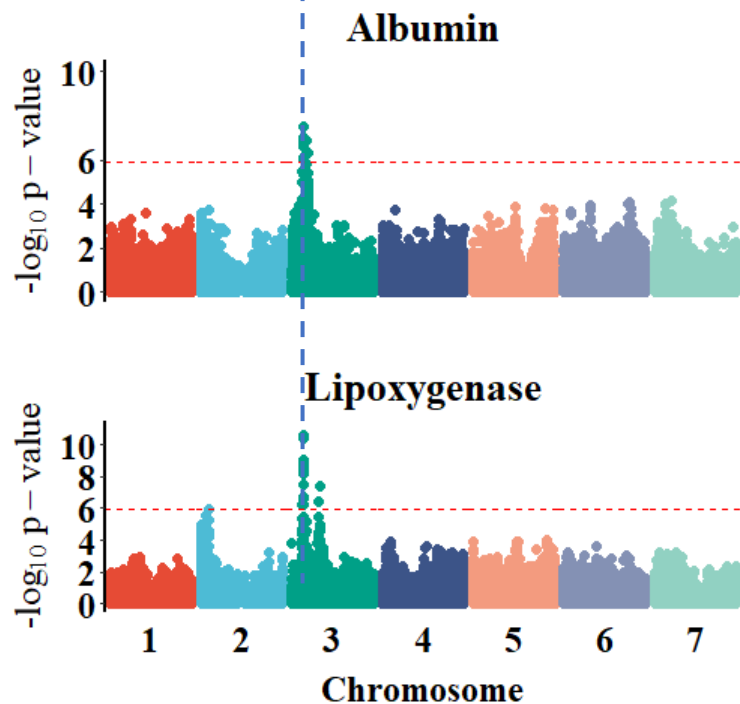
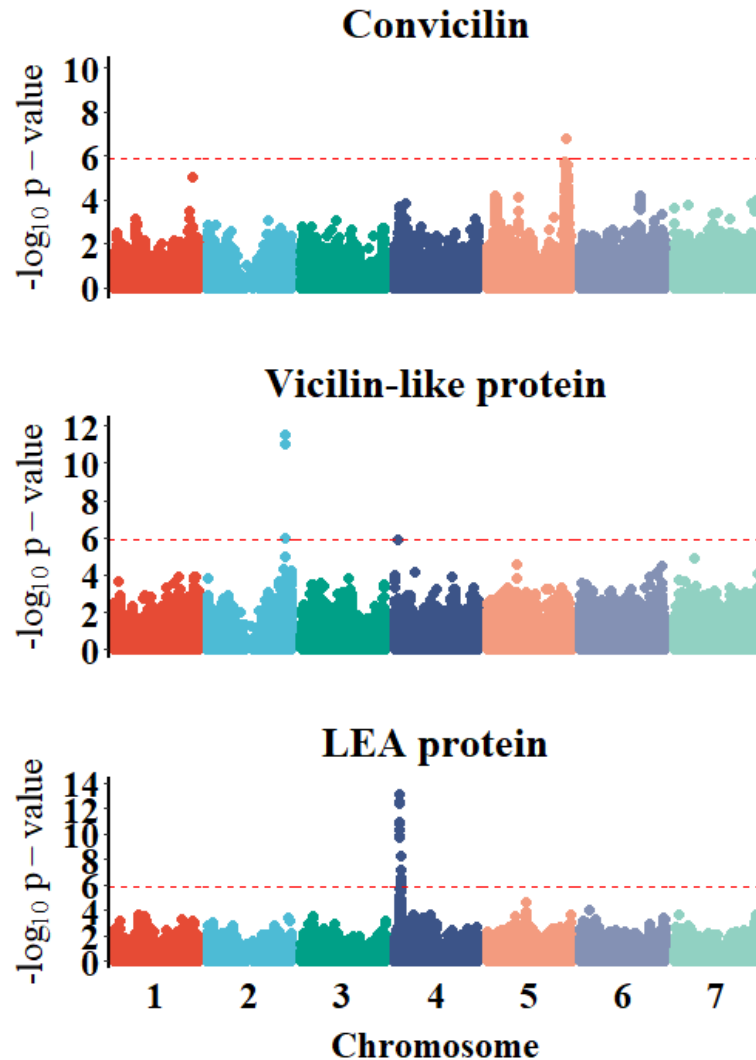
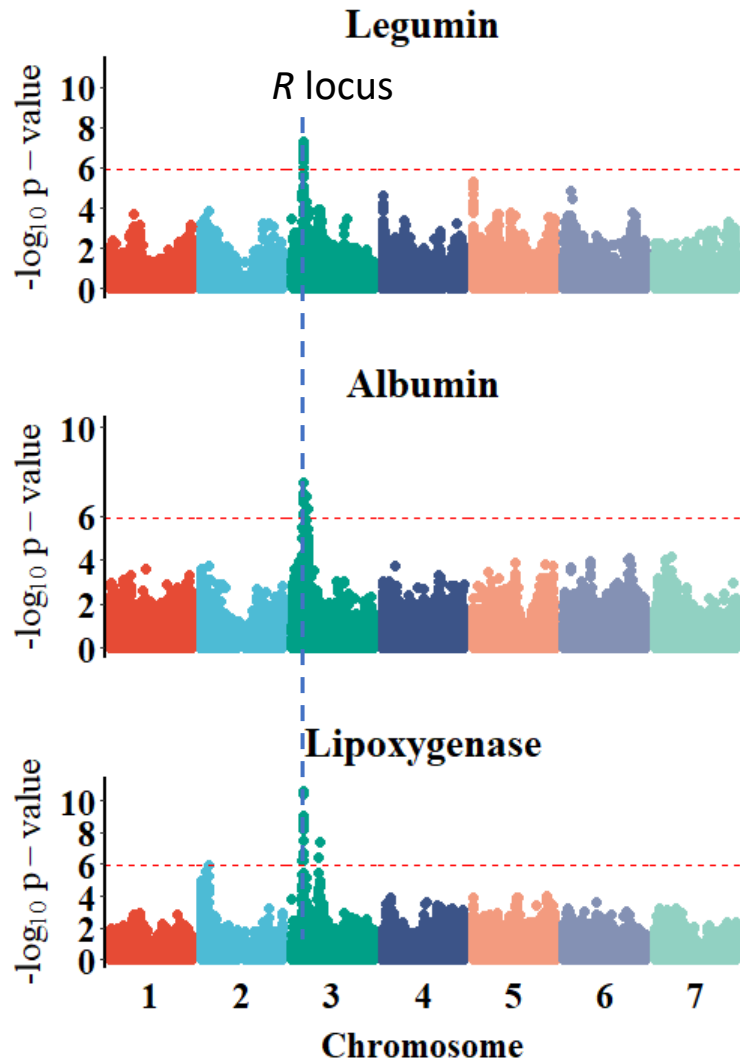
Pea protein composition



❖ Pea protein composition is significantly correlated with round/wrinkled phenotype (*R* locus)

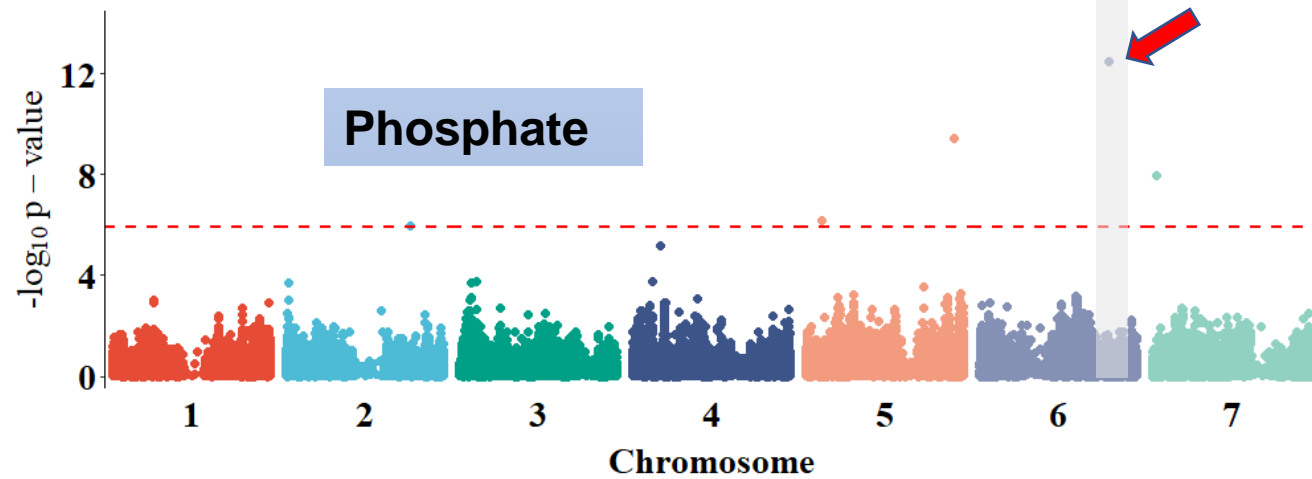
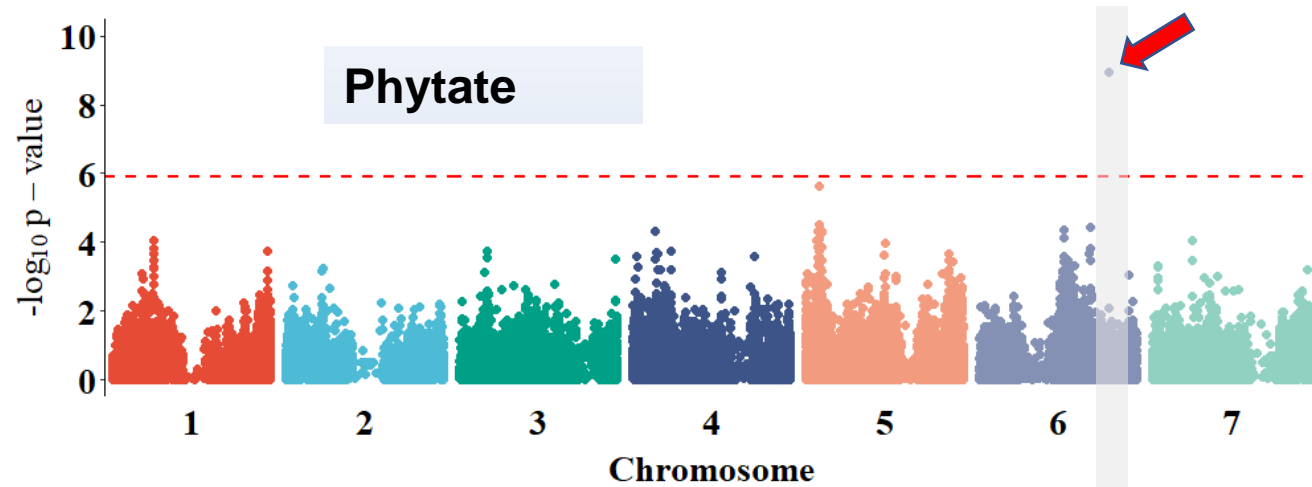
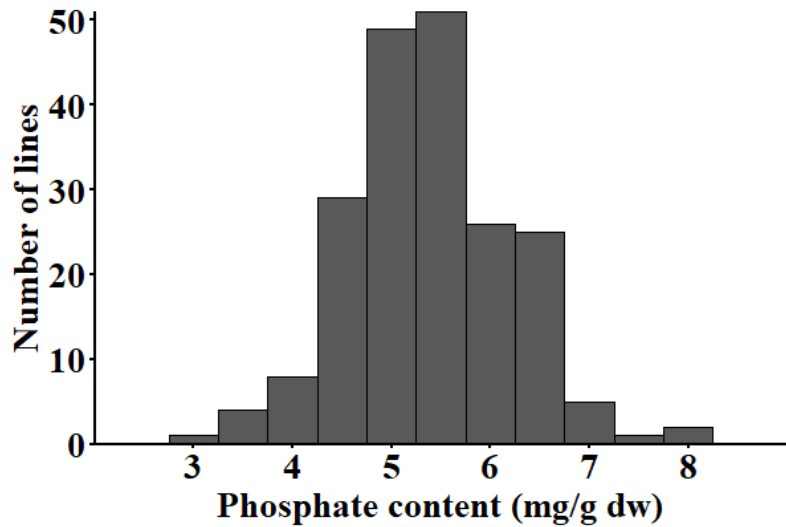
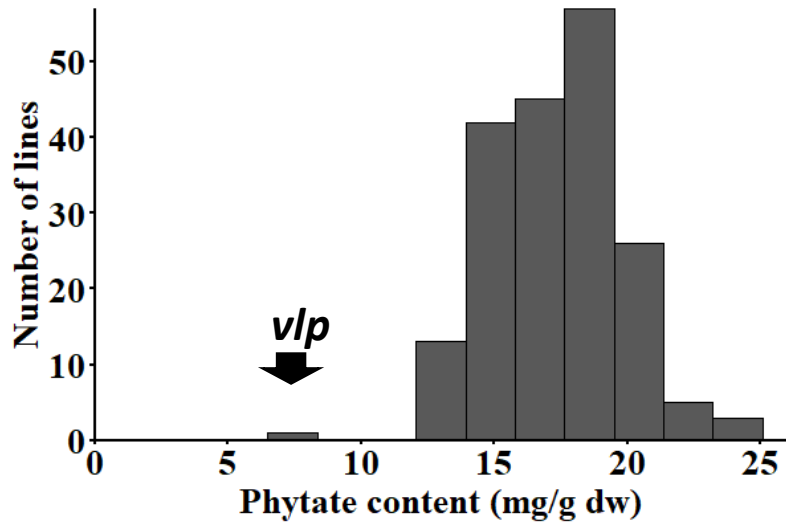


GWAS analysis of pea protein composition



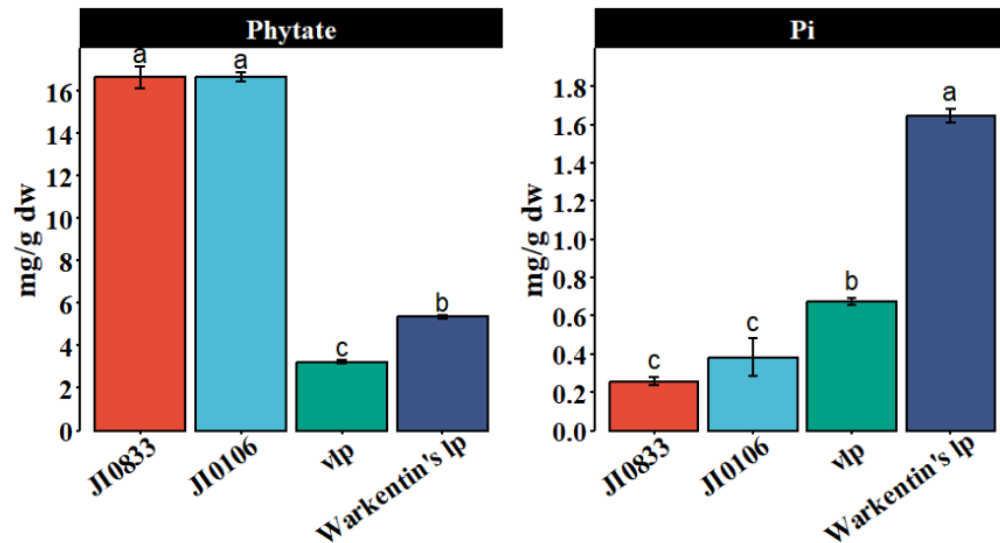
- ❖ Abundance of major seed proteins in pea is controlled by mutation in *R* locus (*STARCH BRANCHING ENZYME1* = *SBE1* gene).
- ❖ Identification of loci independent of *R* locus will require targeted screening of the two seed types.

Mapping phytate content in pea



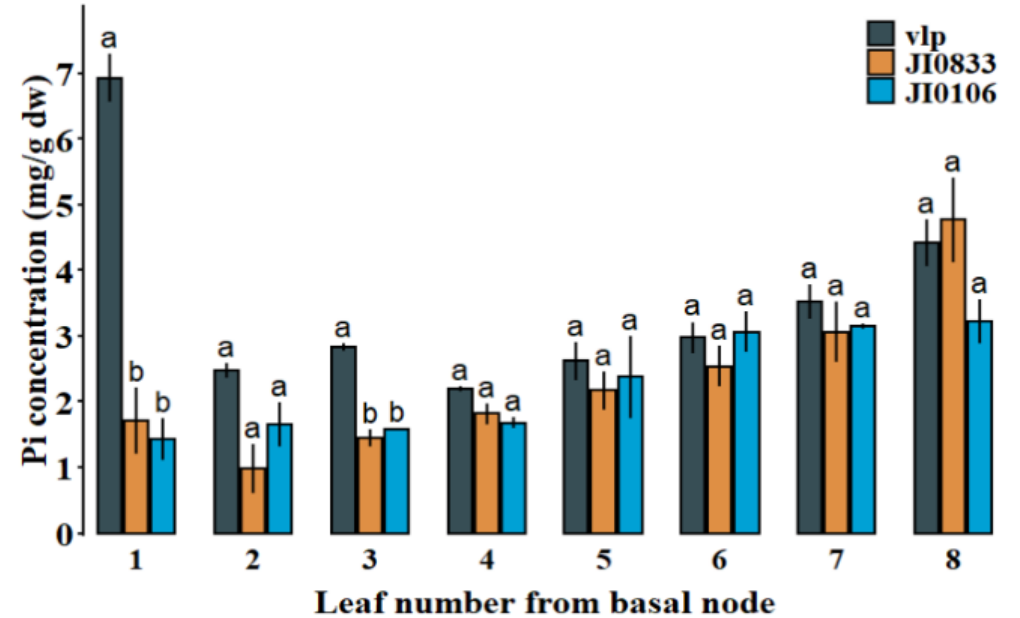
Characterization of the *vlp* pea

vlp pea seeds have low phytate and low Pi



- ❖ *vlp* is not primarily due to a block in Pi-to-phytate biosynthesis

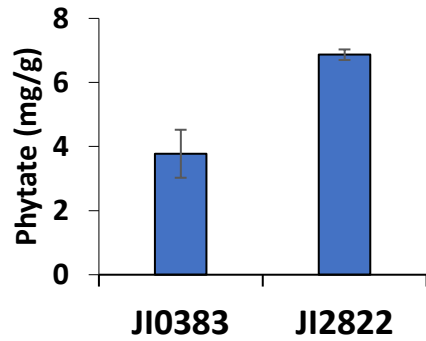
vlp has higher Pi in lower leaves



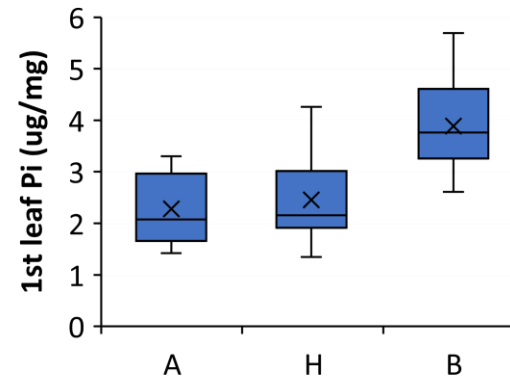
- ❖ *vlp* may have defect in Pi recycling and/or transport to the seeds?

Mapping the *v/p* locus in the F2 population

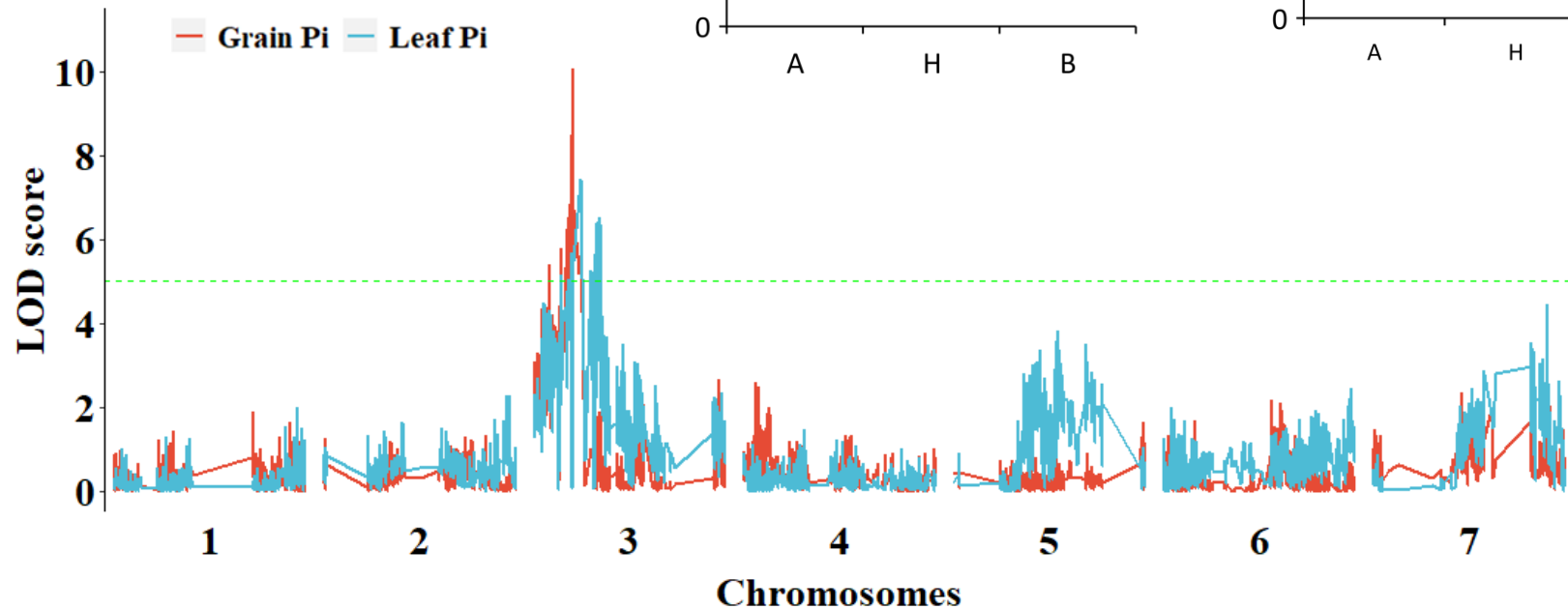
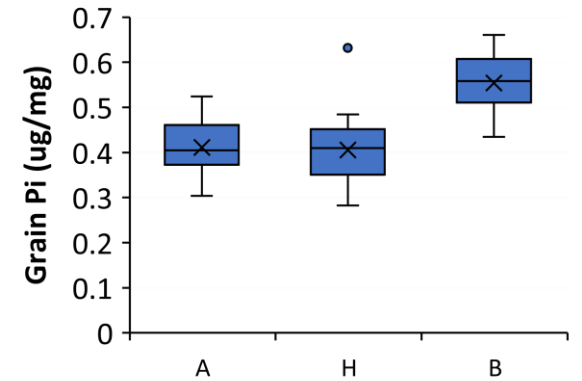
Mapping population: 70 F2 lines from
JI0383 X JI2822



Leaf Pi Top SNP: AX-183893237



Grain Pi Top SNP: AX-183873232





Summary

- There is considerable variation among available pea and faba bean germplasm for many important quality traits.
- GWAS is a powerful tool to discover the genetics of desirable quality traits.
- We must work with the industry to refine our research priorities and develop suitable assays to screen for desired quality traits in an industrial setting.

Acknowledgments

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Department
for Environment
Food & Rural Affairs

