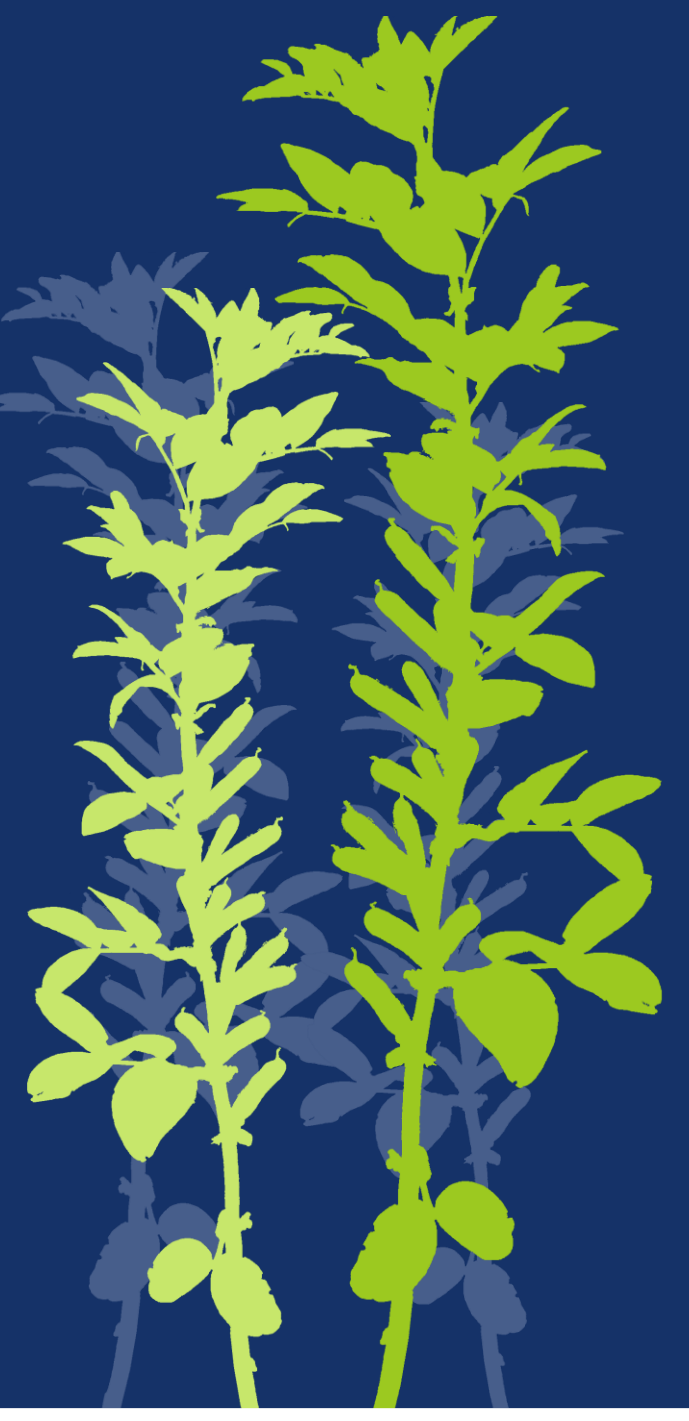


GWAS in winter faba bean (*Vicia faba* L.) for grain yield and further agronomic traits using data from 189 inbred lines and their progeny across 16 years: Début

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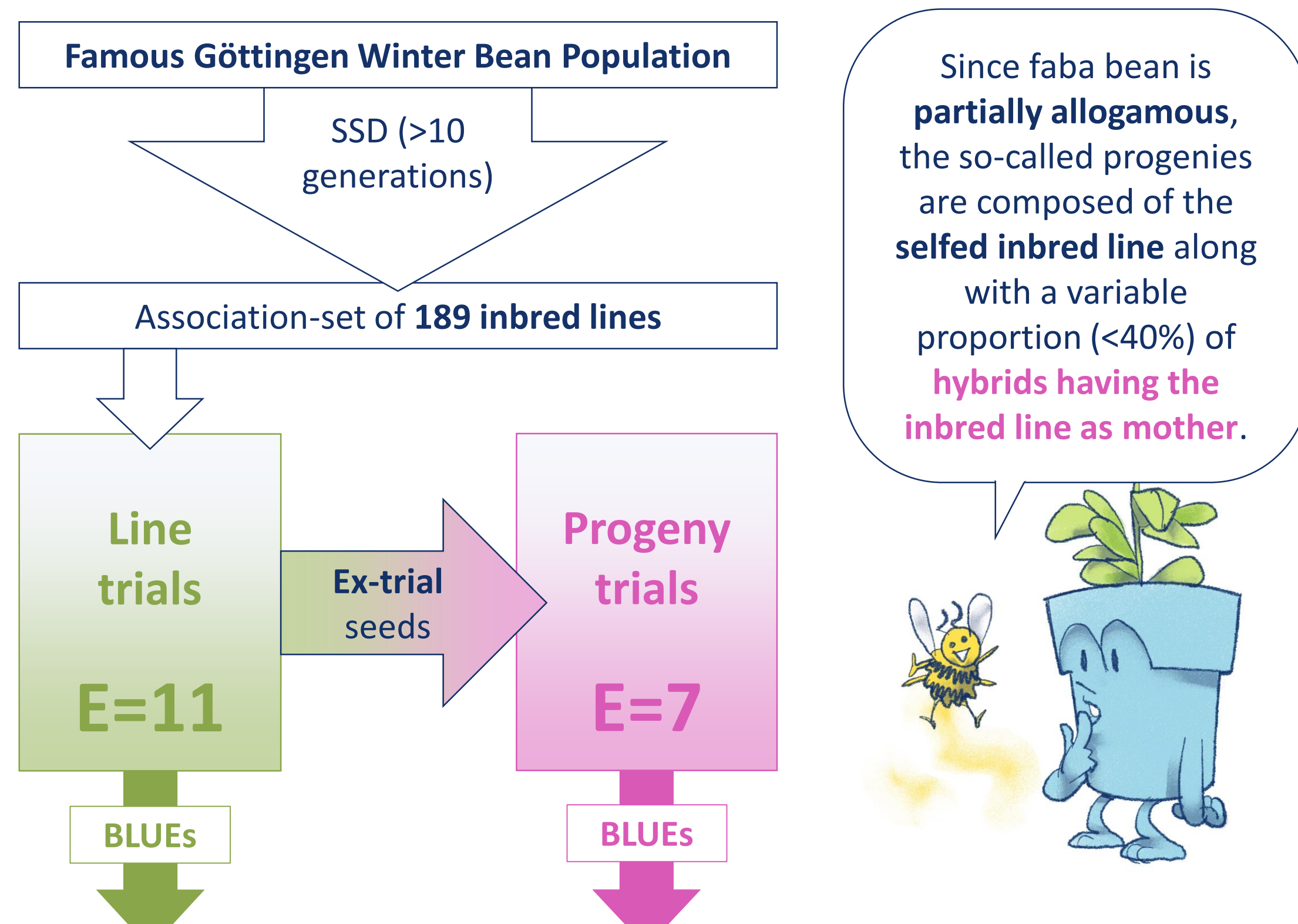


Faba bean...

a grain legume standing out for its high protein content, symbiotic performance and climatic adaptation.

In Germany, its acreage is still relatively low, partly because of yield instability and high seed cost.

Nicht gut genug

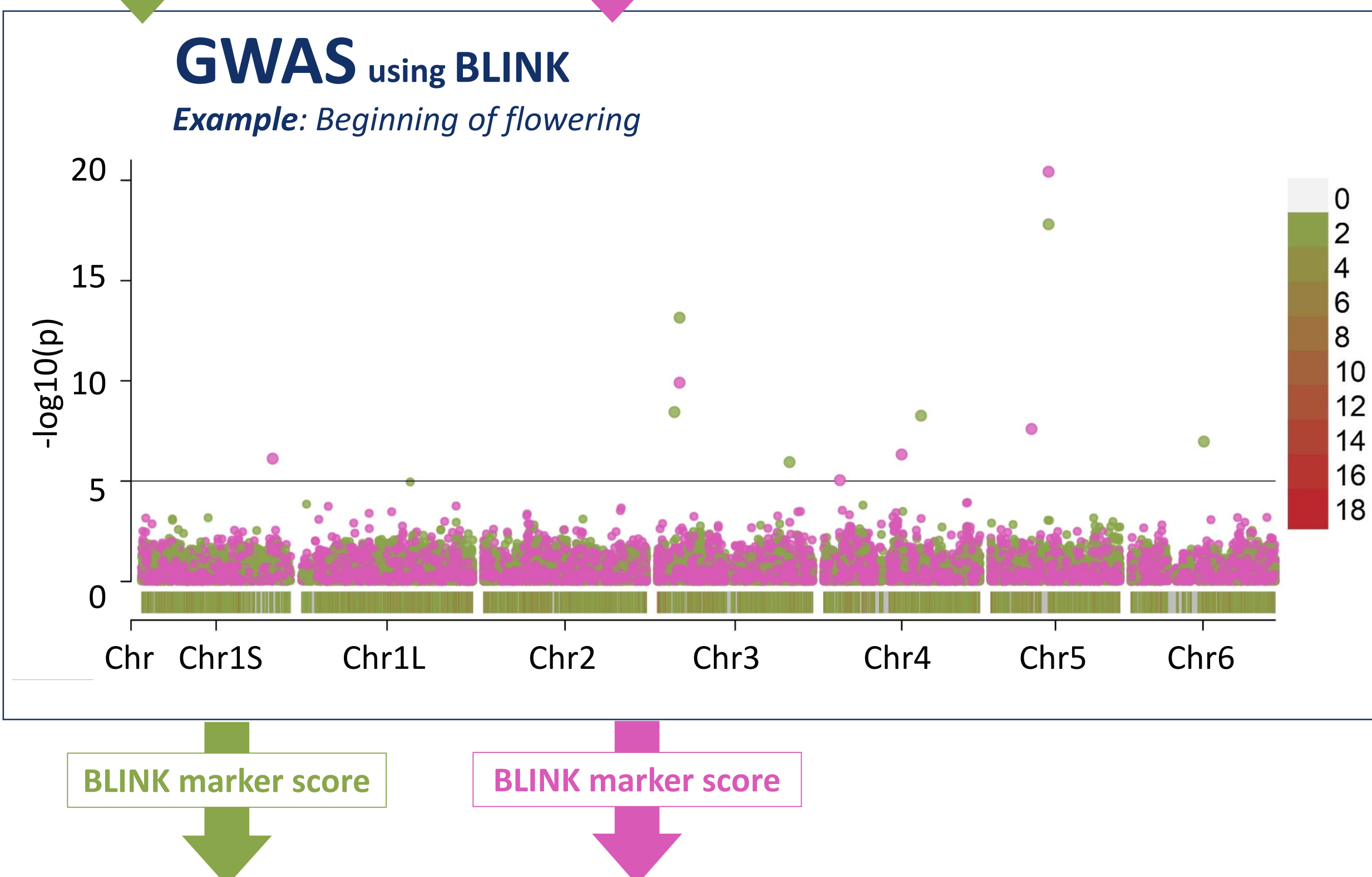


Historical field data (phenotypic data from E=11 and E=7)

Trait	Abbr.	Correlation between traits						Correlation		
		Ph	Flbeg	Lg	Ma	TGW	YLD	Heritability	between lines and progenies	
Plant height	Ph	1	0.15	0.28	-0.30	0.21	0.36	0.90	0.68	0.46
Beginning of flowering	Flbeg	0.32	1	0.09	-0.16	-0.28	0.07	0.94	0.89	0.84
Lodging	Lg	0.19	0.01	1	0.07	-0.11	-0.18	0.83	0.76	0.70
Maturity	Ma	-0.30	-0.32	0.03	1	-0.20	-0.06	0.84	0.62	0.21
Thousand grain weight	TGW	0.30	-0.10	0.06	-0.11	1	0.10	0.87	0.90	0.84
Yield	YLD	0.58	0.23	-0.10	-0.13	0.23	1	0.76	0.71	0.45

Winter faba bean especially, although it has several advantages over spring beans, is little cultivated because of the high risk of winter kill caused by harsh winter conditions.

To develop better winter faba bean varieties through breeding, we performed a genome-wide association study (GWAS) for grain yield and further agronomic traits in winter faba bean



Trait	Marker-trait associations	Common MTAs (line & progeny)
Plant height	9	0
Beginning of flowering	7	6
Lodging	3	3
Maturity	0	0
Thousand grain weight	7	4
Yield	0	4

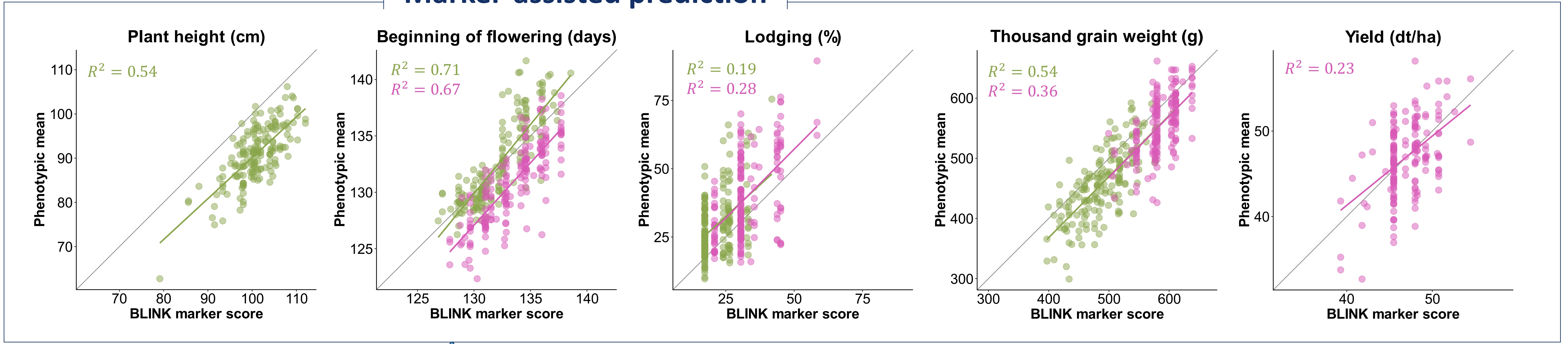
SNP-Filtering was done based on SNP missingness, individual heterozygosity and SNP minor allele count. A total of 17227 SNPs were used.

Imputation of missing data was performed using LD-kNNi algorithm.

The 3 first PCs of the PCA were used to account for population structure.

The false discovery rate threshold was set to 5%.

Marker-assisted prediction



In the end, among the six traits presented here, we found several QTLs for each trait, except Maturity. Some of them were found using phenotypic data from both the lines and their progeny.

We obtained large phenotypic variance explained for some marker-trait associations, especially for flowering time and also yield!

For these traits, faba bean breeders can see a huge potential in using the detected markers for marker-assisted selection.

Select this one!

Furthermore, data of the lines and their progeny will be used as training population in the scope of the Abo-Direkt project to develop genomic prediction in winter faba bean...

...with the aim of identifying breeding-relevant genotypes within the Göttingen Winter Bean Population, and globally support the breeders in optimizing the selection of winter faba bean for several traits.

References

[1] Pupkes AM (2023) First GWAS in winter faba beans for grain yield and further agronomic traits in 189 inbred lines and ex-trial offspring utilizing data from 18 field trials across 16 years, MSc thesis, DNPW, Georg-August Univ. Goettingen.

[2] O'Sullivan DM, Angra D, Harvie T et al. (2019) A genetic toolbox for *Vicia faba* improvement. In: International conference on legume genetics and genomics, May 13–17, 2019. Dijon, France.

