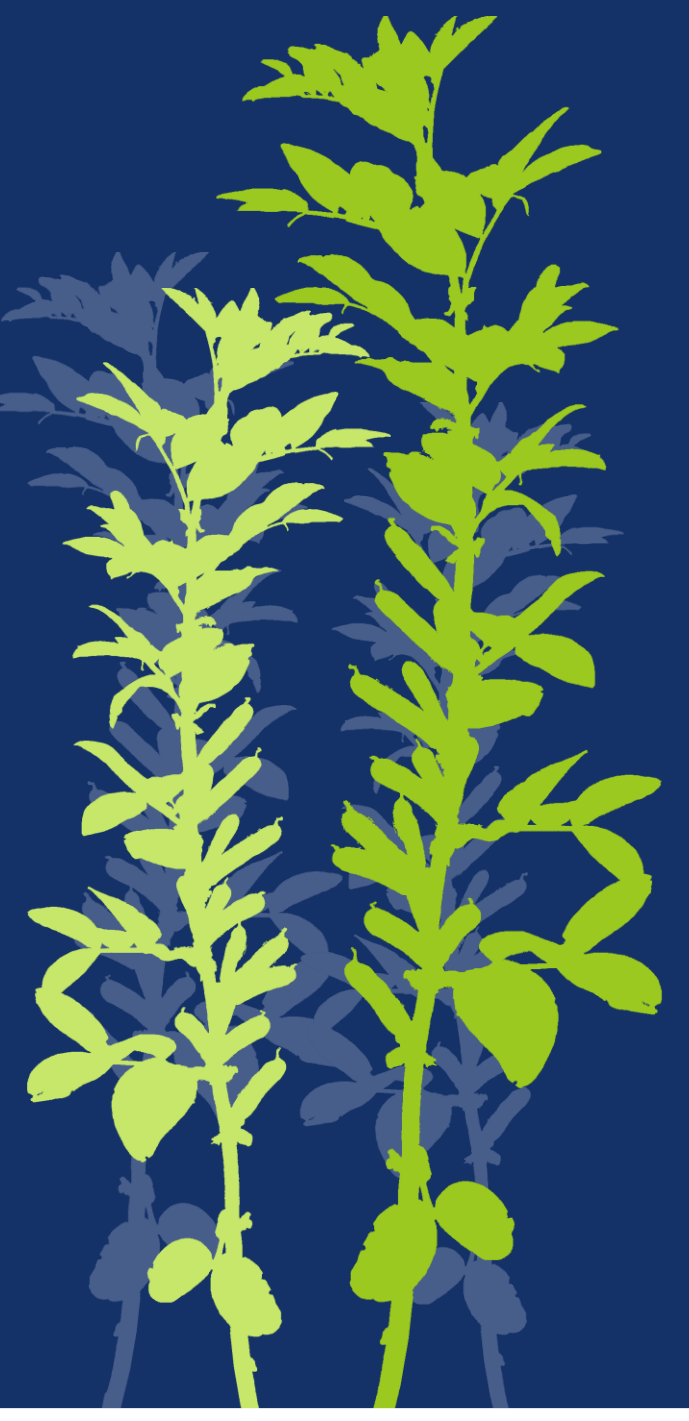


# Identification of a priori available inbred individuals in faba bean (*Vicia faba* L.) populations and prediction of their genetic value for breeding

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**Faba bean...**  
a grain legume standing out for its...

high seed **protein** content,...

Here are my nodules!  
EH EH  
high **symbiotic** performance...

and high **genetic** diversity.

But the farmers are reluctant to grow it because of...  
MMAH HA... This is not enough yield...  
its **yield instability**.

A solution?  
Yes, **breeding!**

For breeding, **inbred lines** are needed. But faba bean is a **partially allogamous** crop, cross-fertilized by pollinators.

Faba bean plants must undergo a series of **selfings** and must always be grown in **isolation cage** to avoid access of pollinators.

Moreover, to ensure an efficient seed set, the plants must be **"tripped"** to stimulate self-fertilization.

inbred individuals are a priori **already available** in faba bean populations!

This study aims to develop a cost-efficient method to **identify inbred individuals** in faba bean populations and **predict their breeding value** from SNP data.

There is **no DH technique** available. So, production of inbred lines is **laborious** and takes several years.

The population we use is the famous **Göttingen Winter Bean Population (GWBP)**.

To identify inbreds among all individuals, we defined a set of 50 KASP SNP markers to estimate their **inbreeding coefficient (F)**.

1. Their **distribution** along faba bean **genome**.

2. Their **allele frequency**. The higher the minor allele frequency, the more accurate F.

3. No or few **missing values**.

There are several formulas to calculate F from SNP data.

Once the inbred individuals are identified, we will genotype them using the **"Vfaba\_v2" Axiom chip!**

A wonderful technology, which will allow us to get a huge amount of SNP data to perform genomic prediction!

We will use the available...  
phenotypic...  
and genotypic data...  
of a set of inbred lines earlier derived from GWBP to **calibrate our genomic prediction model**.

On the other hand, we will propagate the newly detected inbred individuals from GWBP to phenotype them in a **multi-location trial**.

Additionally, we will also develop a non-destructive method to extract DNA from faba bean **"chipped" seeds**.

In the end, breeders will be able for any faba bean population, to extract DNA from seeds, identify inbred individuals and predict their genetic performance,...

facilitating the use of inbred lines in both line and population breeding.

References

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