

# Genetic diversity of soybean accessions from early maturity groups

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## Introduction

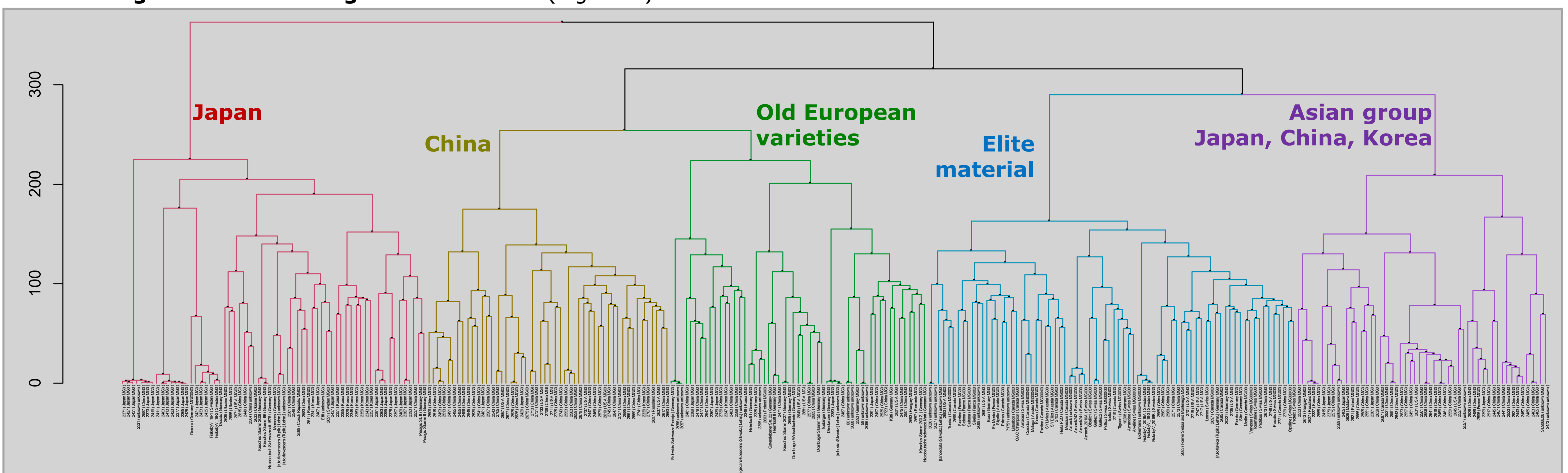
Soybean (*Glycine max* (L.) Merr.) is extensively used as high-protein feed ingredient in livestock and poultry production. The **increasing demand in Germany and Europe for GMO-free soybean products** against the backdrop of the increasing cultivation of genetically modified seeds speak for the expansion of national breeding activities. **Securing the domestic protein supply**, in particular in the organic production of livestock and poultry feed, presupposes the availability of climate-adapted, high and constant yielding soybean varieties with high protein content.

Due to the climatic conditions in Germany, suitable breeding material for the national soybean cultivation can be only developed from the **very early to early maturity gene pool** (MG0000 to MG00). For our activities, unselected and less characterized soybean lines from gene banks of the United States, Canada and Germany as well as approved elite varieties from France, Canada and Switzerland are available as base material. Besides the phenotypic selection, **genetic diversity** of this material was i.) analysed **genome wide** by using high-throughput genotyping (Figure 1) and ii.) examined in **candidate genes for breeding-relevant traits** (Figure 2).

## Genome-wide genetic diversity

A set of 80 varieties and 214 gene bank accessions is genotyped with the Illumina Soy6kSNPChip containing 5.403 SNPs that are evenly distributed across the 20 chromosomes of the soybean genome. More than 1.4 Mio data points are generated and used to determine the genome-wide genetic diversity. A cluster analysis based on 4.869 SNPs with MAF>5% and missing values<5% revealed a classification **mainly according to origin** separating Japanese, Chinese and European accessions (Figure 1). The current **elite varieties** cluster in a distinct branch and thus are **genetically very close** in comparison to the studied gene bank material. Our findings are in agreement with diversity studies of Hahn and Würschum (2014) and Bandillo et al. (2015). No clustering according to maturity groups is observed indicating the need for a national classification of worldwide soybean material.

Figure 1. Cluster analysis of 294 soybean lines genotyped with the Soy6kSNPChip (N=4.869 SNPs) using a clustering algorithm implemented in R (RStudio Team (2015)). The colors of branches indicate the five different clusters.



## Genetic diversity in candidate genes

Missing or low sensitivity to photoperiod is necessary for short-day crops, such as soybean, to adapt to high latitudes. Photoperiod insensitivity in soybean is controlled by two genetic systems and involves three important genes: *E1*, *E3* and *E4* (Xu et al. 2013). We were assessing the genotypes of four maturity genes (*E1-E4*) in our gene bank material to elucidate the molecular diversity of these genes and identified early flowering and ripening accessions under climate conditions in Southern German.

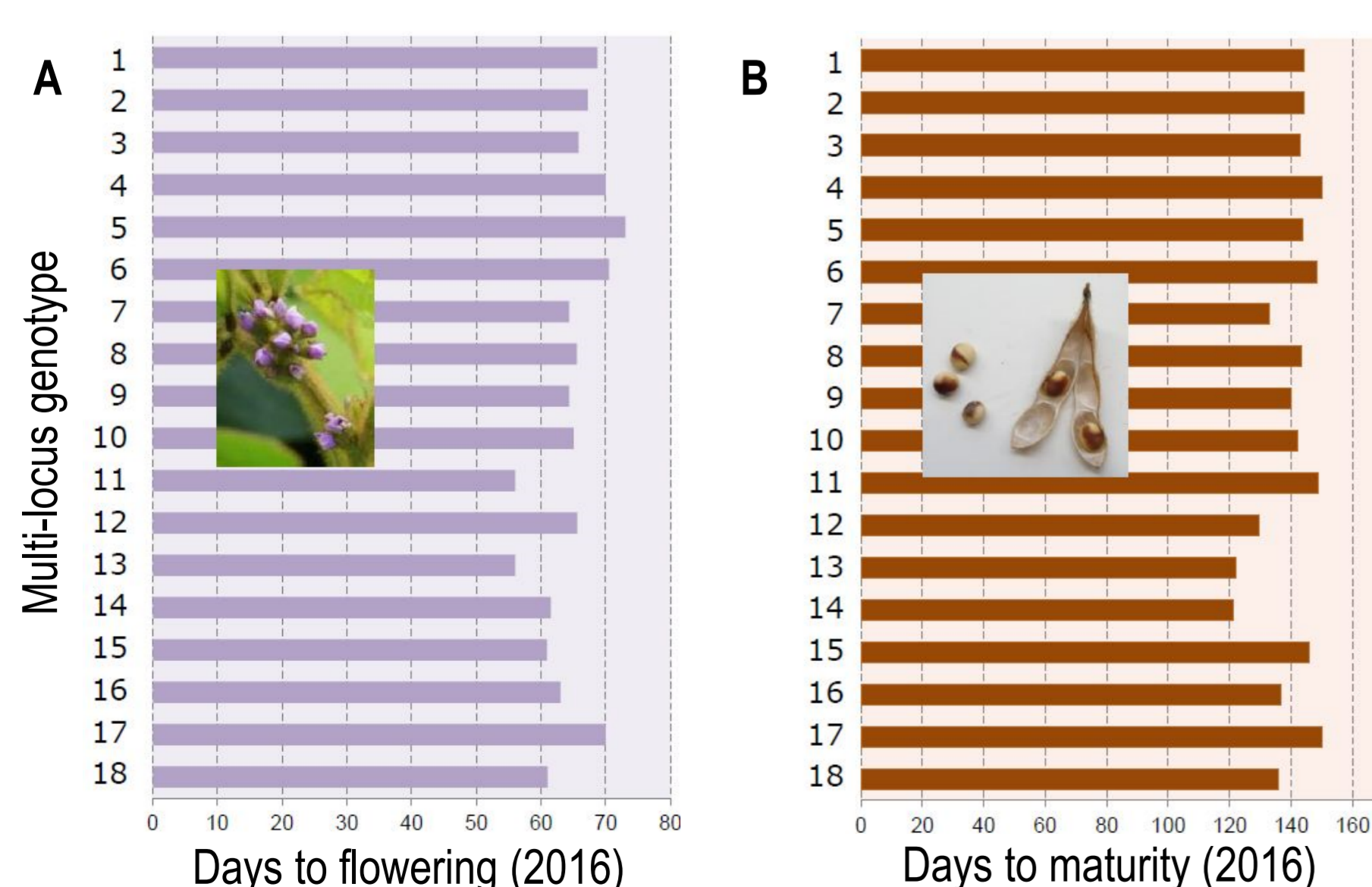


Figure 2. Multi-locus genotypes of the three flowering and maturity genes *E1*, *E3* and *E4* related to phenotypic data for flowering (A) and maturity (B) in 2016 at Oberhummel (48° N, 11° O).

## Outlook

In a next step, the narrow genetic base of the elite material will be extended by crossing selected high-protein and high yielding elite varieties with genetically divergent, early flowering and timely ripening gene bank accessions. Our goal is the establishment and integration of molecular markers in early breeding stages to select on early flowering, timely ripening, cold tolerance and high-protein content to secure profits for the farmer and good feed quality. With our investigations we will lay the foundation for a powerful soybean variety development by optimizing the breeding and selection methodology and using efficient molecular genetic procedures.

## References

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