



Legume  
Generation

**Boosting innovation in breeding  
for the next generation of legume crops for Europe**

Progressing the  
breeding of  
soybean





**Boosting innovation in breeding for the next generation of legume crops for Europe**

## **Progressing the breeding of soybean**

Johann Vollmann  
BOKU University, Vienna, Austria

Volker Hahn  
University of Hohenheim, Germany

Donal Murphy-Bokern  
Kroge-Ehrendorf, Germany

Mária Škrabišová  
Palacký University in Olomouc, Czech Republic

August 2025

### **Legume Generation Report 9**



Legume Generation (Boosting innovation in breeding for the next generation of legume crops for Europe) has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No.101081329. It also receives support from the governments of the United Kingdom, Switzerland and New Zealand.

## **Legume Generation**

Legume Generation (Boosting innovation in breeding for the next generation of legume crops for Europe) is an innovation action funded by the European Union through Horizon Europe under grant agreement 101081329. It also receives support from the governments of the United Kingdom, Switzerland and New Zealand. The Legume Generation consortium comprises 33 partners in 15 countries.

## **Disclaimer**

The information presented here has been thoroughly researched and is believed to be accurate and correct. However, the authors cannot be held legally responsible for any errors. There are no warranties, expressed or implied, made with respect to the information provided. The authors will not be liable for any direct, indirect, special, incidental or consequential damages arising out of the use or inability to use the content of this publication.

Views and opinions expressed are those of the author(s) only and do not necessarily reflect those of the European Union or the European Commission. Neither the European Union nor the granting authority can be held responsible for them.

## **Copyright**

© All rights reserved. Reproduction and dissemination of material presented here for research, educational or other non-commercial purposes are authorised without any prior written permission from the copyright holders provided the source is fully acknowledged. Reproduction of material for sale or other commercial purposes is prohibited.

## **Citation**

Please cite this report as follows:

Vollmann, J., Hahn, V., Murphy-Bokern, D. and Škrabišová, M., 2026. Progressing the breeding of soybean. Legume Generation Report 9. Available from [www.legumegeneration.eu](http://www.legumegeneration.eu) and [www.legumehub.eu](http://www.legumehub.eu). DOI: <https://doi.org/10.5281/zenodo.18919804>

## **Acknowledgement of data contributions**

Martin Pachner, Benedikt Piller, Charlotte Nothelfer (BOKU University), Claude-Alain Bétrix (Agroscope), Małgorzata Niewińska, Agnieszka Katańska-Kaczmarek (DANKO), Amandine Gras (RAGT Seeds), Anelia Iantcheva (ABI), Klaus Oldach, Ahmad Fardin Malikzai (KWS), Ivana Kaňovská (UP Olomouc), Maximilian Lanz (SZ Gleisdorf), Roman Ferrant (Lidea Seeds), Jasmin Karer (Donau Soja).

## List of partners in Legume Generation

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK, Germany)  
Donal Murphy-Bokern (DMB, Germany)  
University of Natural Resources and Life Sciences (BOKU, Austria)  
Julius Kuhn-Institute, Federal Research Centre for Cultivated Plants (JKI, Germany)  
Universita Politecnica Delle Marche (UNIVPM, Italy)  
Donau Soja (DS, Austria, Serbia, Ukraine)  
Radboud University (SRU, Netherlands)  
KWS Lochow GmbH (KWS, Germany)  
International Hellenic University (IHU, Greece)  
Saatzucht Gleisdorf GmbH (SZG, Austria)  
University of Hohenheim (UHOH, Germany)  
Bavarian State Research Center for Agriculture (LfL, Germany)  
Danko Hodowla Roslin. (DANKO, Poland)  
Aarhus University (AU, Denmark)  
RAGT Seeds (RAGT, France)  
Lidea Seeds, (Lidea, France)  
Keyserlingk Institut (Keyserlingk, Germany)  
Palacký University Olomouc (UP, Czech Republic)  
Serida - Regional Service for Agrofood Research and Development (SERIDA, Spain)  
University of Basilicata (UNIBAS, Italy)  
ESKUSA GmbH (ESKUSA, Germany)  
Institute of Plant Genetics, Polish Academy of Sciences (IPG, Poland)  
Euroseeds (EURS, Belgium)  
Agrobioinstitute (ABI, Bulgaria)  
John Innes Centre (JIC, United Kingdom)  
Germinal Holdings Ltd (GER, United Kingdom)  
Aberystwyth University (ABER, United Kingdom)  
Earlham Institute (EI, United Kingdom)  
United States Department of Agriculture (USDA, United States of America)  
WBF Agroscope (AGS, Switzerland)  
AgResearch (AGR, New Zealand)  
Van Waveren Seeds GmbH (vanW, Germany)  
Oxford University (OU, UK)

# Contents

- Summary ..... 6
- Introduction ..... 6
- The Legume Generation Soybean Innovation Community ..... 7
- Our soybean improvement plan ..... 8
  - Implementation of the soybean improvement plan ..... 8
- Genotype sets and experiments ..... 9
- Results of yield and adaptation experiments .....10
  - Yield performance .....12
  - Maturity and other traits .....14
- Results from food-grade soybean experiments .....21
  - Seed protein content .....22
  - Amino acid composition .....24
- Development of a novel, trait-informed marker panel for soybean genotyping .....27
- Results from digital phenotyping .....29
- Conclusions and outlook .....33
- Annex .....35
  - References to annex Table 1 .....36

## Summary

Soybean is the key legume crop in European agriculture for food and feed protein production. In the Legume Generation project (Horizon Europe), the European Soybean Innovation Community with its major breeding programmes have joined forces to boost soybean breeding. As there is a growing need for improved varieties, the project supports the innovation community in its breeding and innovation efforts for better adaptation to European growing conditions, competitive yield performance, and improved end-use quality for food production. The innovation community has set up an improvement plan for adaptation of new breeding materials to the main soybean production regions of Europe covering the relevant soybean maturity groups ranging from 000 or earlier to 0 and I. In the 2024 season, field trials with new varieties and advanced breeding lines were carried out in locations in France, Germany, Switzerland, Austria, Poland, Bulgaria and Romania. Average yields of 3 to 4 t/ha in experimental plots were achieved in locations with sufficient water supply, whereas yields were much lower under drought. Time to maturity was highly variable, and the correlation between yield and time to maturity was different between environments and maturity groups indicating a differential adaptation potential. Seed protein content was ranging between 380 and 460 g/kg and was highest in food-grade breeding materials. Seed analysis also confirmed the high lysine concentration in soybean protein, whereas variation in the overall amino acid pattern was low among all genotypes analysed. Major innovation is also delivered to soybean breeding through novel genotyping and digital phenotyping approaches. For genotyping, a new marker panel with over 5,000 markers and including 355 trait-specific markers has been compiled. Based on resequencing data, the marker panel better represents European germplasm and diversity patterns than previous panels, and it will now be utilised to analyse the different breeding materials of the project. Canopy development and physiological processes were monitored using digital phenotyping. Hyperspectral reflectance measurement was utilised to characterise all breeding materials in a large number of different traits describing dynamic processes such as biomass formation, nitrogen accumulation, and canopy water levels indicating drought sensibility or tolerance. Significant differences between genotypes in water indices or in nitrogen-related indices have been found which were also related to seed yield or other agronomic traits. The digital phenotyping results suggest that there are new options to characterise genotypes. These might support selection in the future. Thus, collaborative phenotyping by the soybean innovation community members with agronomic results across multiple environments, seed quality properties, results from stress tests, digital phenotyping parameters, and diagnostic as well as trait specific marker data will all contribute to an in-depth characterisation of breeding materials supporting the selection of superior soybean lines.

## Introduction

Soybean is playing an increasingly important role in European agriculture as a source of protein for food and feed uses. According to the recent OECD-FAO Agricultural Outlook 2025-2034<sup>1</sup>, the EU-27 soybean production will increase by 23% by 2034 compared to the 2022-2024 average, while the domestic soybean growing area is projected to increase by 16% by 2034. Such expansion will depend on adapted and competitive cultivars suitable

---

<sup>1</sup> OECD/FAO, 2025. OECD-FAO Agricultural Outlook 2025-2034. OECD Publishing, Paris/FAO, Rome. <https://doi.org/10.1787/601276cd-en>.

for commercial production under European conditions. However, compared to the breeding of cereals, soybean breeding has a rather short history in Europe with mainly smaller and regional breeding programmes in place. Moreover, soybean is a strictly self-pollinated crop of pure-line varieties with which farmers frequently make use of farmer-saved seed. This reduces the revenue for breeders and consequently results in low investment in breeding programmes.

The Horizon Europe innovation action project Legume Generation aims to support intensified breeding efforts in soybean. This is accomplished by a collaborative evaluation of breeding materials utilising different approaches within our Soybean Innovation Community. Breeding materials such as latest cultivars and advanced breeding lines are tested at different partner locations for yield, adaptation and end-use seed quality. In addition, digital phenotyping and stress tests are utilised to gain insight into variation of physiological characteristics associated with stress tolerance and resource capture. In genotyping, a unique marker panel based on Flex-seq technology has been established for characterising the breeding material. This panel contains both diagnostic and trait-specific markers and has been specifically adapted to the genetic diversity characteristics of European germplasm. Beside analysing the specific Legume Generation genotypes, the marker set is also open for use by the innovation community members and other stakeholders for additional breeding materials.

Here we present preliminary Legume Generation project results achieved in the first 24 months of the project (up to August 2025). In summary, the data indicate considerable phenotypic variation in agronomic characters, phenology and seed traits between genotypes and soybean maturity groups as well as between locations across Europe.

## **The Legume Generation Soybean Innovation Community**

The existing informal European Soybean Innovation Community was based on the earlier network ESIN (European Soybean Improvement Network) established in 2018. It supported the Haberlandt project (soybean variety exchange and analysis between China and Europe). In that project, Chinese and European elite cultivars were reciprocally exchanged and investigated for reciprocally increasing genetic diversity of early maturity germplasm<sup>2</sup> and improving the potential for regional adaptation<sup>3</sup> both in Chinese and European soybean production regions.

Through Legume Generation, the European Soybean Innovation Community was renewed and strengthened. Apart from the established plant breeding representatives engaging with soybean for decades already, new partners such as KWS Lochow, Radboud University, Euroseeds, Palacký University Olomouc, IPK Gatersleben and AgroBioInstitute Sofia have been integrated, and links have also been established to innovation communities of the other legume crops and to the BELIS project. The Soybean Innovation Community had in-person meetings (Gatersleben / Germany 2023, Tulln / Austria 2024) for discussing the

---

<sup>2</sup> Yao, X., Xu, J.-Y., Liu, Z.-X., Pachner, M., Molin, E.M., Rittler, L., Hahn, V., Leiser, W., Gu, Y.-Z., Lu, Y.-Q., Qiu, L.-J., Vollmann, J., 2023. Genetic diversity in early maturity Chinese and European elite soybeans: A comparative analysis. *Euphytica* 219, 17. <https://doi.org/10.1007/s10681-022-03147-0>

<sup>3</sup> V Yao, X., Pachner, M., Rittler, L., Hahn, V., Leiser, W., Riedel, C., Rezi, R., Béatrix, C.-A., Nawracała, J., Temchenko, I., Đorđević, V., Qiu, L.-J., Vollmann, J., 2024. Genetic adaptation of phenological stages in Chinese and European elite soybeans (*Glycine max* [L.] Merr.) across latitudes in central Europe. *Plant Breeding* 143, 695–705. <https://doi.org/10.1111/pbr.13197>

most essential project related matters and making strategic decisions on project implementation. In addition, video meetings, seed exchange, harvest-sample exchange for NIRS analysis and sharing of experimental data are being practised whenever needed. With support from the European soybean platform partner Donau Soja and the seed industry partner Euroseeds, essential information about soybean production, market developments, the seed business and other topics of relevance is regularly shared between interested partners. Information workshops for the innovation community on topics such as genome editing technologies and licencing CRISPR/Cas9 to plant breeding companies have been carried out.

## **Our soybean improvement plan**

The plan<sup>4</sup> for boosting the breeding of soybean in Europe is based on a collaborative research approach within our Soybean Innovation Community. This innovation community is representing major European breeding and research programmes and stakeholders along the soybean value chain including the food and feed industry and their related research as well. Together, private and public members of the innovation community are engaging in more than 10 breeding and pre-breeding programmes across all soybean growing regions of Europe.

As soybean is the most grown and used grain legume crop in Europe, the strategy within the soybean improvement plan is a joint research approach for better adaptation of soybean to diverse European growing environments and market needs. Facing the effects of global climate change in southeast and central European regions in recent years, improved tolerance to drought and high temperature are urgently needed characteristics for yield stability and overall competitiveness of soybean. Thus, detection of genetic differences in drought- and heat-related characteristics is relevant for selecting more stress tolerant breeding lines and future crossing parents. Another specific approach to adaptation is the photoperiodic and thermal adaptation process of soybean varieties to higher latitudes which is widely requested by the farming community in central and northern regions. This process is specifically supported through genotyping of the Legume Generation breeding materials for *E*-genes and photothermal response, and through field testing at experimental sites of different latitude. An additional long-term strategy arises from the increased need for food-grade soybean cultivars which requires selection for various product-quality features depending on specific processing needs (seed protein content, sucrose, taste components, seed size). This is in line with the overall European protein strategy as well as with growing consumer demands for sustainable and plant protein-based food products.

## **Implementation of the soybean improvement plan**

Our soybean improvement plan is realised in two different ways to support the innovation community, i.e., experiments supporting yield and adaptation, and development of food-grade quality features.

---

<sup>4</sup> Vollmann, J., Hahn, V., Murphy-Bokern, D., and Škrabišová, M., 2024. The plan for boosting the breeding of soybean. Legume Generation Report 1. Available from [www.legumegeneration.eu](http://www.legumegeneration.eu) and [www.legumehub.eu](http://www.legumehub.eu).

### *Yield and adaptation*

Soybean production is well-established in central Europe, including northern Italy. However, long day length suppresses flowering in soybean in more northern growing regions which causes delays in maturity and reduces grain yield. Therefore, adaptation to long-day conditions and progressing to maturity under relatively cool conditions (compared with the southern environments) is a key to adaptation. In addition, temperature and water stress as well as various biotic sources of stress (diseases, pests) are increasingly challenging European soybean production. At the same time, however, progress in soybean yield performance is essential to maintain the economic competitiveness of soybean in crop rotations.

### *Food-grade quality features*

Due to its high seed protein content of over 40%, soybean plays a major role in the transformation of the agri-food system towards an increase of plant-based protein used in human nutrition. However, dedicated efforts in breeding for food-grade traits such as high protein content or increased seed size are not attractive for commercial breeders at present due to negative correlations with grain yield and a lack of market mechanisms to reward specific harvest product qualities. Therefore, our collaborative approach within our innovation community supports the development of food-grade breeding materials with screening for specialty traits which are not available in conventional breeding materials at present but might be needed in future.

An important addition to the experimental pathways outlined above is the development of a new marker panel for soybean genotyping (see below) which is supporting in-depth characterisation of all European breeding materials provided by the project partners. Importantly, the marker panel will be open for use beyond the members of the innovation community participating in Legume Generation and also beyond the formal end of the project time through the commercial genotyping partner.

## **Genotype sets and experiments**

Based on unique market insights of the soybean innovation community members, we have assembled four sets of genotypes in line with the soybean improvement plan.<sup>5</sup> They are structured either by growing regions and connected requirements for time to maturity or by anticipated seed quality needs. These genotypes are representing the latest commercial varieties or advanced candidates which are also serving as parental genotypes for future hybridisation programmes. Thus, their in-depth characterisation both phenotypically and genetically is of high relevance. The sets are as follows:

Yield-1: MG 000 and earlier: 60 genotypes

Yield-2: MG 00: 45 genotypes

Yield-3: MG 0 and I: 30 genotypes

Food: 70 genotypes across all maturity groups

The full list of genotypes has been published in the soybean improvement plan.

---

<sup>5</sup> Vollmann, J., Hahn, V., Murphy-Bokern, D. and Škrabišová, M., 2024. The plan for boosting the breeding of soybean. Legume Generation Report 1. Available from [www.legumegeneration.eu](http://www.legumegeneration.eu) and [www.legumehub.eu](http://www.legumehub.eu)

Regular field experiments have been and are being conducted in partner locations in France, Switzerland, Germany, Austria, Poland, Romania and Bulgaria (see Figure 1 and description of preliminary results below for details; a field trial at a site in western Ukraine could not be realised). In addition, novel digital phenotyping approaches and physiological characterisation of genotypes are pursued in field screenings. Moreover, screenings of genotypes for high temperature stress tolerance under defined growth chamber conditions are in progress.



Figure 1. Partner locations for Legume Generation soybean field experiments

## Results of yield and adaptation experiments

Preliminary results from individual yield trials at different partner locations are presented here. As trial data are only available for the year 2024 at the present reporting stage, full evaluations remain subject to the time period after completing experiments in the 2025 season only. Nevertheless, significant differences have been found in agronomic and phenological characters between genotypes, maturity groups, and individual locations. Differences in time to maturity between genotypes within experiments are evident from Figures 2 and 3 for locations in Poland and Austria.



*Figure 2. Differences in time to maturity between plots of the Yield-1 experiment in mid-September 2024 at Kościan, Poland (Photo: Małgorzata Niewińska, DANKO)*



*Figure 3. Individual soybean genotype (cv. ES Comandor / LIDEA) with exceptionally early maturity in experimental group Yield-1 at Tulln/Austria in late August 2024 (Photo: BOKU University)*

Trials were harvested in a timely way at most experimental sites. Thus, appropriate yield data and samples for harvest quality analysis could be collected from individual experiments (Figure 4).



Figure 4. Experimental plot harvest for determination of grain yield in early October 2024 at Tulln, Austria (Photo: BOKU University)

## Yield performance

Variation in grain yield was considerable both between locations and genotypes within experiments (Figure 5 for Yield-1, Figure 6 for Yield-2). While average yield performance was higher in Yield-2 than in Yield-1 experiments, Yield-1 yields were higher than Yield-2 yields in the strongly water-limited location of Pavlikeny (Bulgaria). In general, plot yields were rather high in most environments which obviously is an over-estimation of the practically achievable grain yield due to small plot sizes and good management practices. High yields of Yield-1 genotypes at the northern locations of Kościan (Poland) and Wohlde (Germany) also indicate a considerable potential of adaptation for these regions under favourable seasonal conditions. Similarly, a high variation in grain yield was observed for late maturity Yield-3 experiments indicating large environmental effects in southern locations as well (Figure 7).

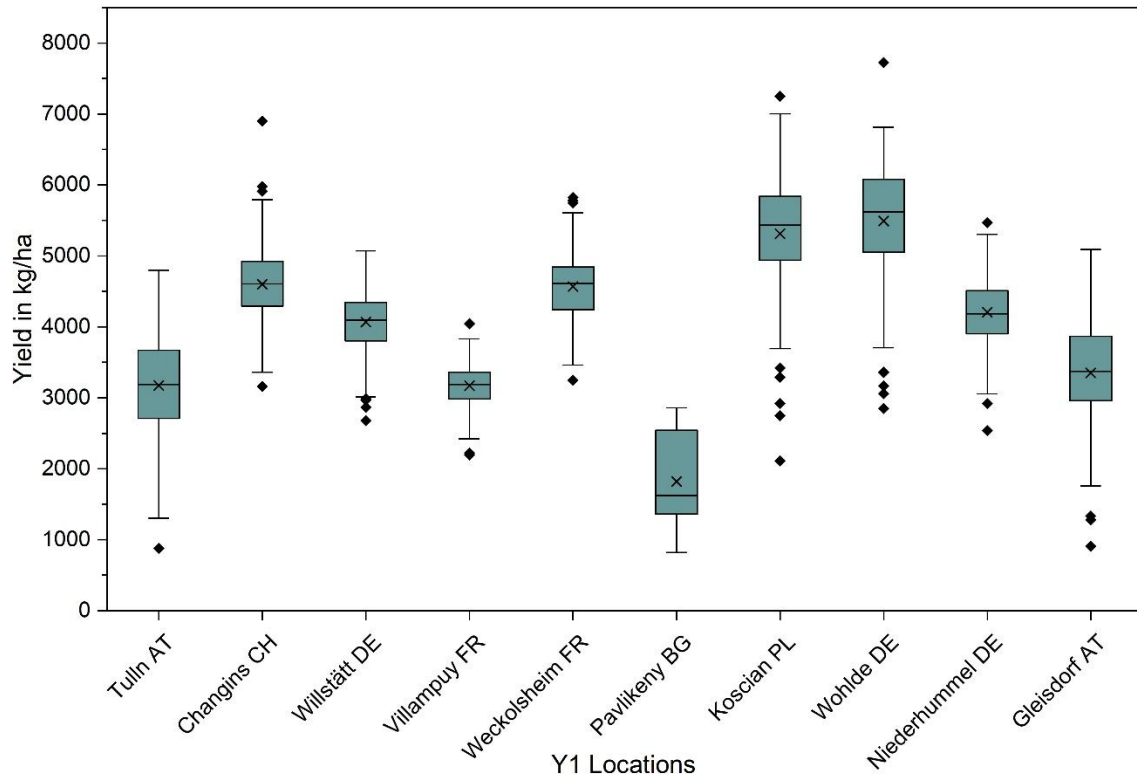


Figure 5. Variation in soybean grain yield across different partner locations in the experiment Yield-1 (very early maturity)

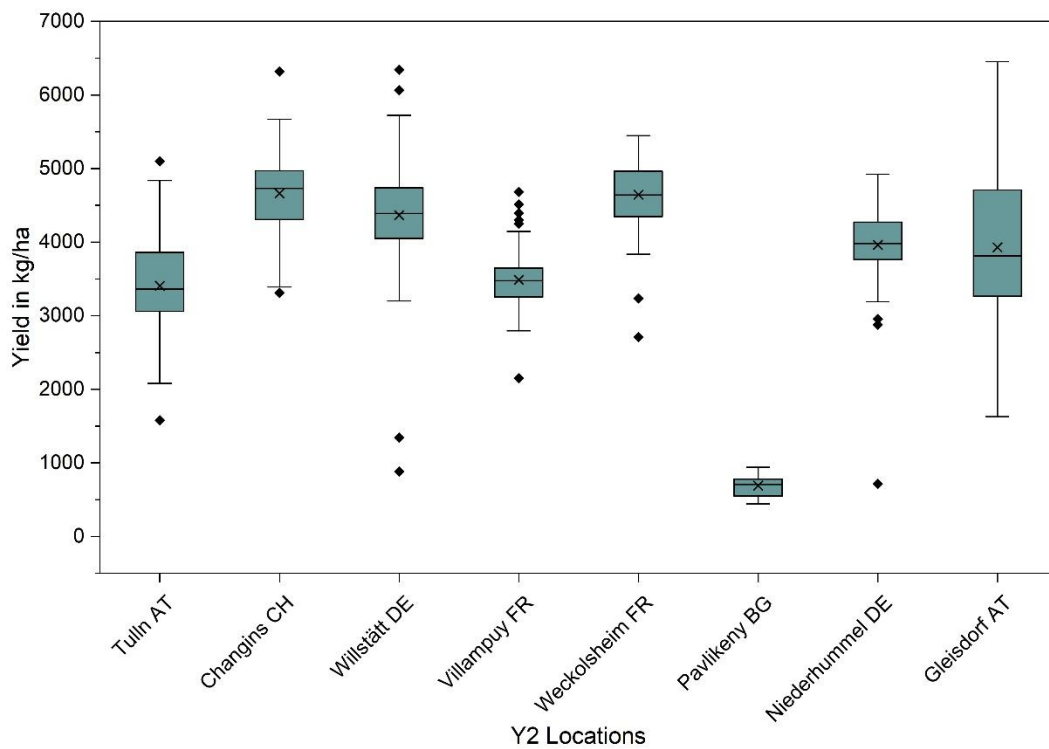


Figure 6. Variation in soybean grain yield across different partner locations in the experiment Yield-2 (mid-early maturity)

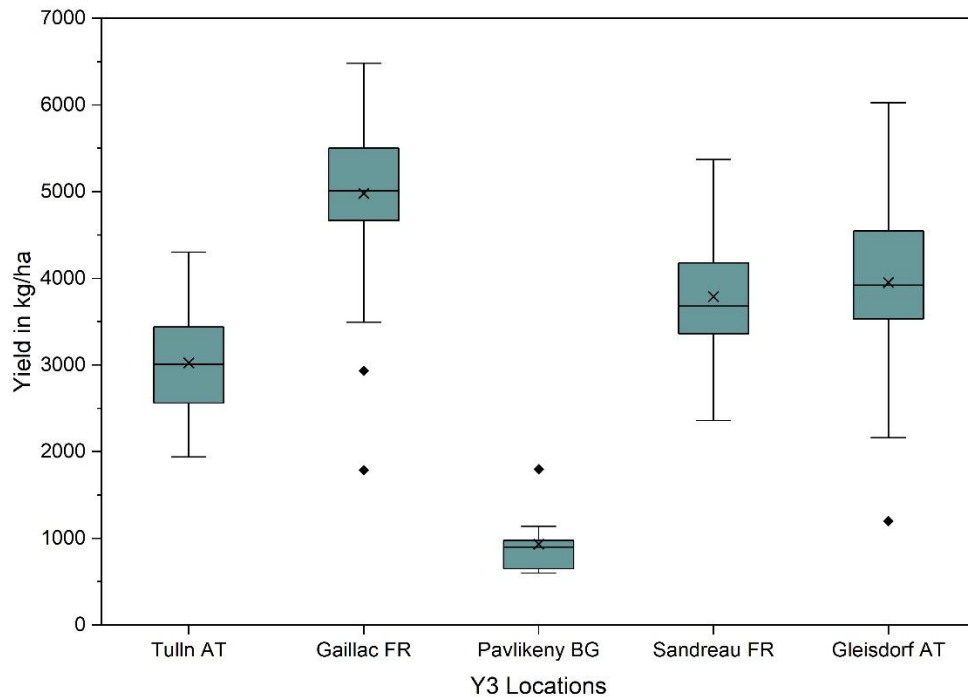


Figure 7. Variation in soybean grain yield across different partner locations in the experiment Yield-3 (later maturity)

### Maturity and other traits

In most locations, flowering time was rather similar between Yield-1 and Yield-2 genotypes, while flowering in Yield-3 genotypes was clearly later. For time to maturity, which is an important requirement of regional adaptation, differences were very clear between experimental groups (Figure 8). Variations in time to maturity within groups and overlap between experimental maturity groups are evident in Figure 8 as well. They probably are not due to mis-classification of maturity but due to site-specific genotype x photoperiod interactions. For genotypes of the Food set, the range in time to maturity is very wide, because food-grade genotypes across all maturity groups have been collected for that particular set.

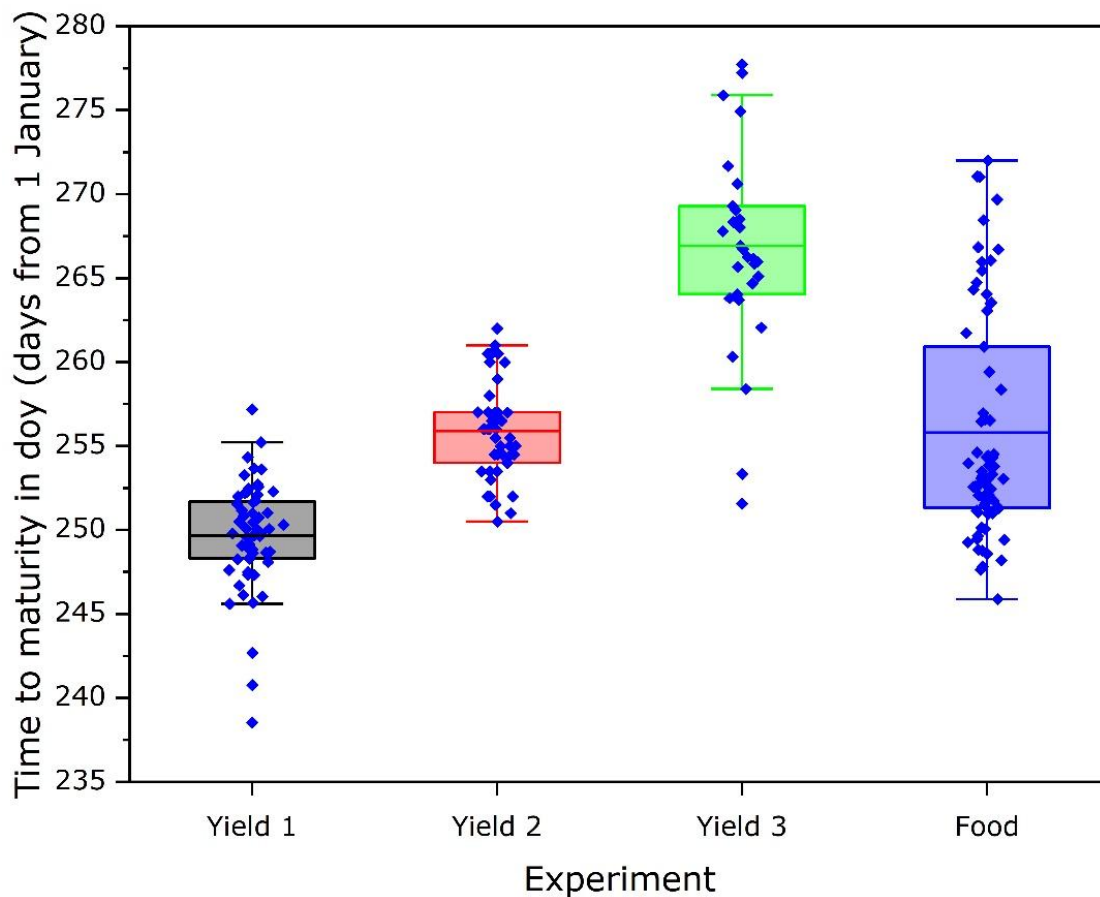


Figure 8. Variation in time to maturity (expressed in calendar days from 1 January) in different yield trials as well as in the Food group at the Tulln/Austria location in 2024

While time to maturity is the key characteristic indicating adaptation to a given geographical location, optimum time to maturity is also indicated by highest yields achievable at the respective location. For the Tulln (Austria) 2024 environment, phenotypic time to maturity and grain yield were significantly positively correlated for the early set Yield-1 (Figure 9a), not significant for the mid-early set Yield-2 (Figure 9b), and significantly negative for the late maturity set Yield-3 (Figure 9c). As yields were highest for set Y2, that set (i.e., genotypes of soybean maturity group 00) indicates optimum adaptation to that specific environment.

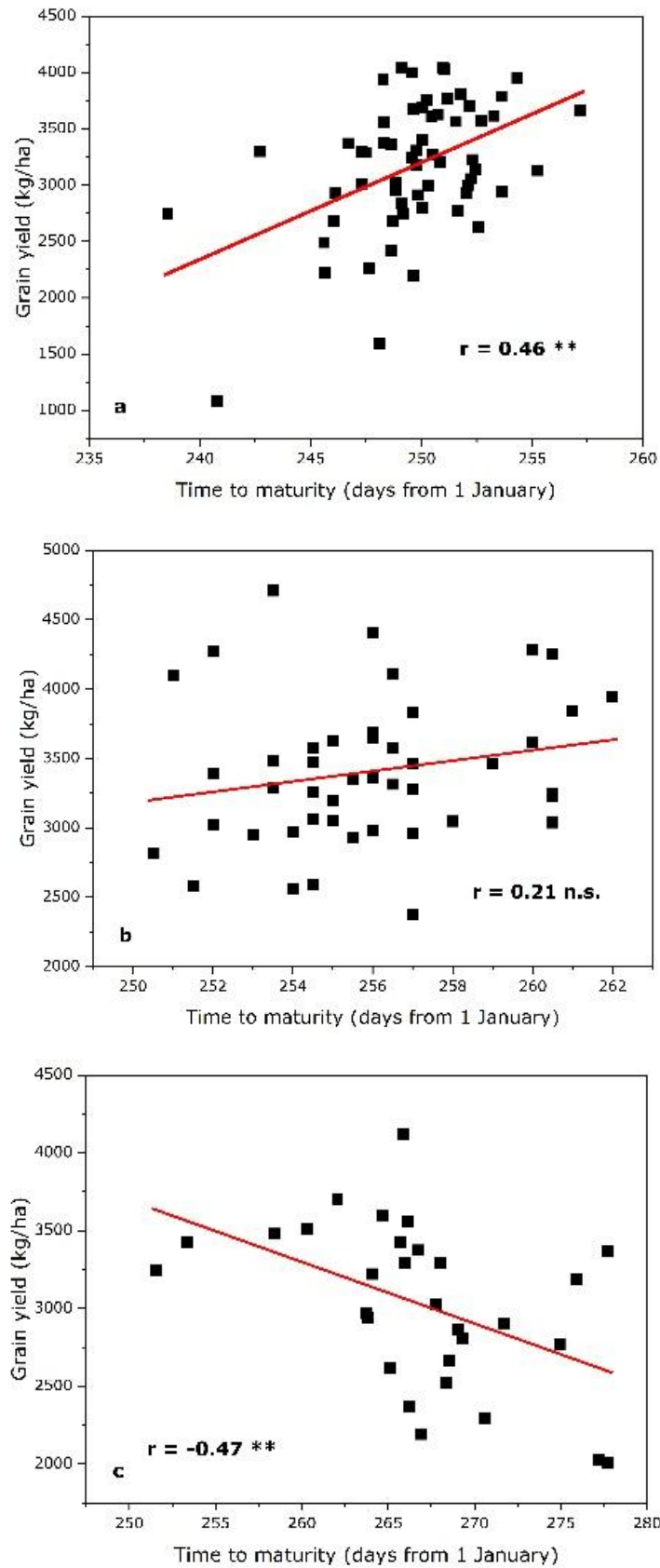


Figure 9. Relationship between time to maturity and grain yield for yield experiments Y1 (a), Y2 (b), and Y3 (c) at Tulln/Austria in 2024

In other locations of central and northern Europe, grain yield was also positively correlated to time to maturity in the early maturity set Yield-1, whereas no significant correlation was found for the set Yield-2 confirming the results from above. As an example, Yield-1 correlations between time to maturity and grain yield are illustrated in Figure 10 for Changins (Switzerland), Kościan (Poland) and Weckolsheim (France) indicating that under a very short growing period a relatively longer time to maturity has a positive effect on yield due to a prolonged stages of resource capture and biomass accumulation. According to preliminary visual scorings (to be confirmed by genotyping later), most of the Yield-2 genotypes are exhibiting the *Dt2* semi-determinate stem termination whereas Yield-1 genotypes are indeterminate. This might contribute to the missing correlation between time to maturity and yield in Yield-2 genotypes; from the perspective of adaptation to particular locations and utilisation of growing conditions, Yield-1 genotypes appear to be more adaptive to environmental conditions whereas Yield-2 genotypes are less flexible in terminating their flowering and pod set due to stronger genetic control and with less environmental influence.

Other agronomic characters such as early development, canopy cover, plant height, lodging, leaflet size, leaflet shape, or seed shattering have been recorded at individual locations. For all characters, significant differences between genotypes have been found which will be further evaluated across environments after completion of the 2025 season.

For better understanding the variation in traits related to drought tolerance, additional phenotyping of the Yield-2 set was carried out during the 2024 vegetation period at Tulln (Austria). This included counts of stomata density on lower leaf surfaces, recording of hyperspectral reflectance during the flowering and early seed filling stages, and evaluation of water indices calculated from hyperspectral measurements.

Counts of stomatal density were based on microscopic images (Figure 11) of lower leaf epidermis samples. Both sampling and counting are rather laborious and would not allow for handling large numbers of genotypes in high-throughput screenings.

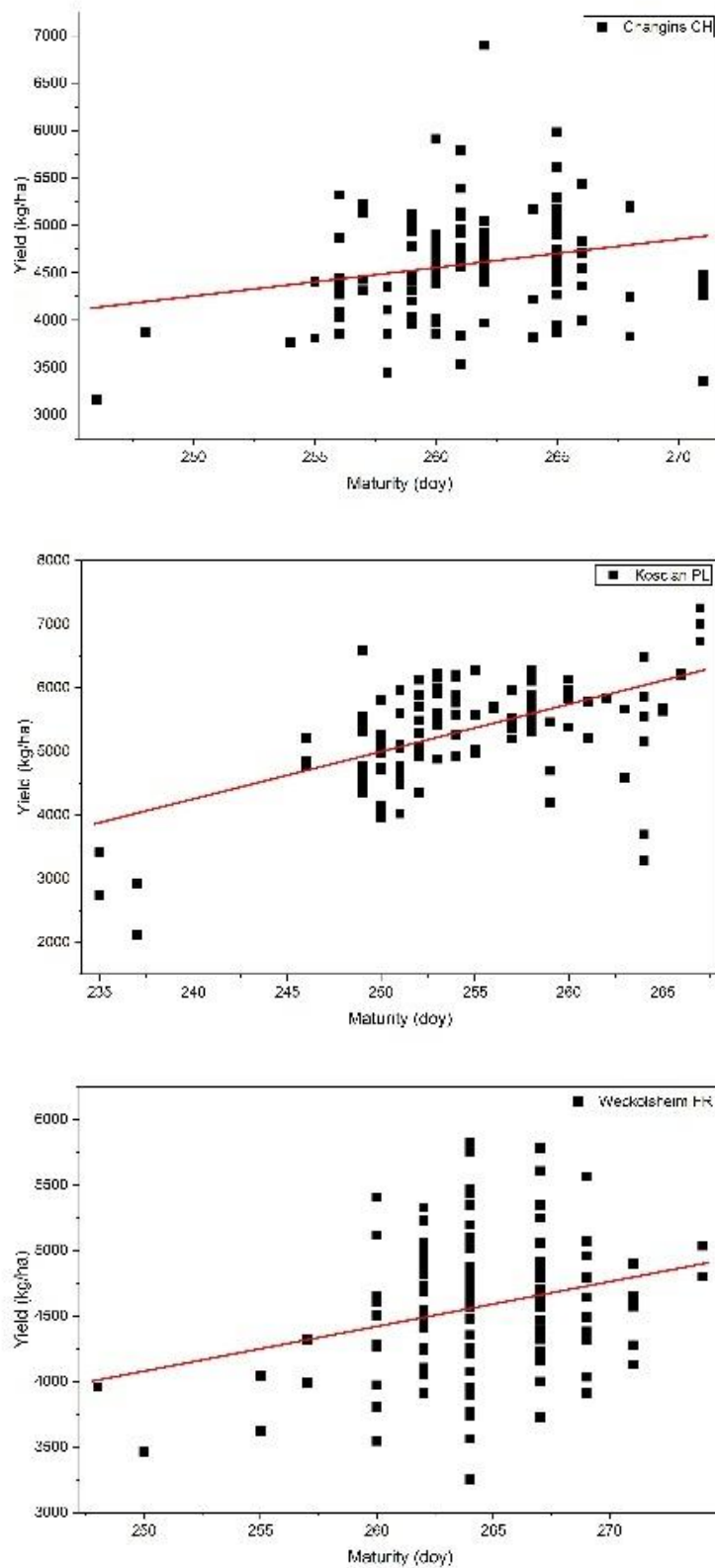
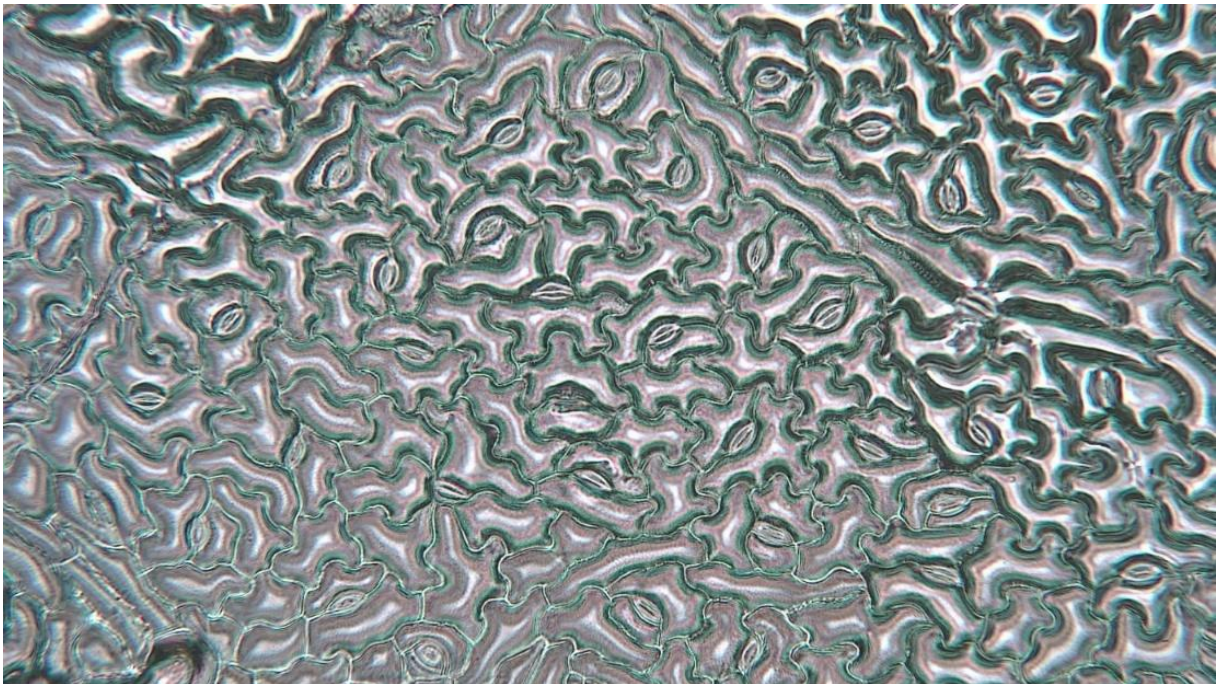


Figure 10. Relationship between time to maturity (Days after 1 January) and grain yield for experiment Yield-1 at Changins (Switzerland), Kościan (Poland) and Weckolsheim (France) in 2024

Other agronomic characters such as early development, canopy cover, plant



*Figure 11. Sample image of a lower soybean leaf epidermis section with stomata (Photo: Martin Pachner, BOKU University)*

Based on established sampling protocols, 15 pictures per plot were collected representing one replication of a particular genotype. After analysis of stomatal density across the whole Yield-2 experiment with 2 replications, significant differences between genotypes were determined, as presented in Figure 12. Despite a rather large LSD5 due to experimental error and significant differences in stomatal density between lattice blocks and replications, this is the first determination of differences in stomatal density between modern European early maturity soybean cultivars. However, clear relations between leaf stomatal density and other traits could not be established so far.

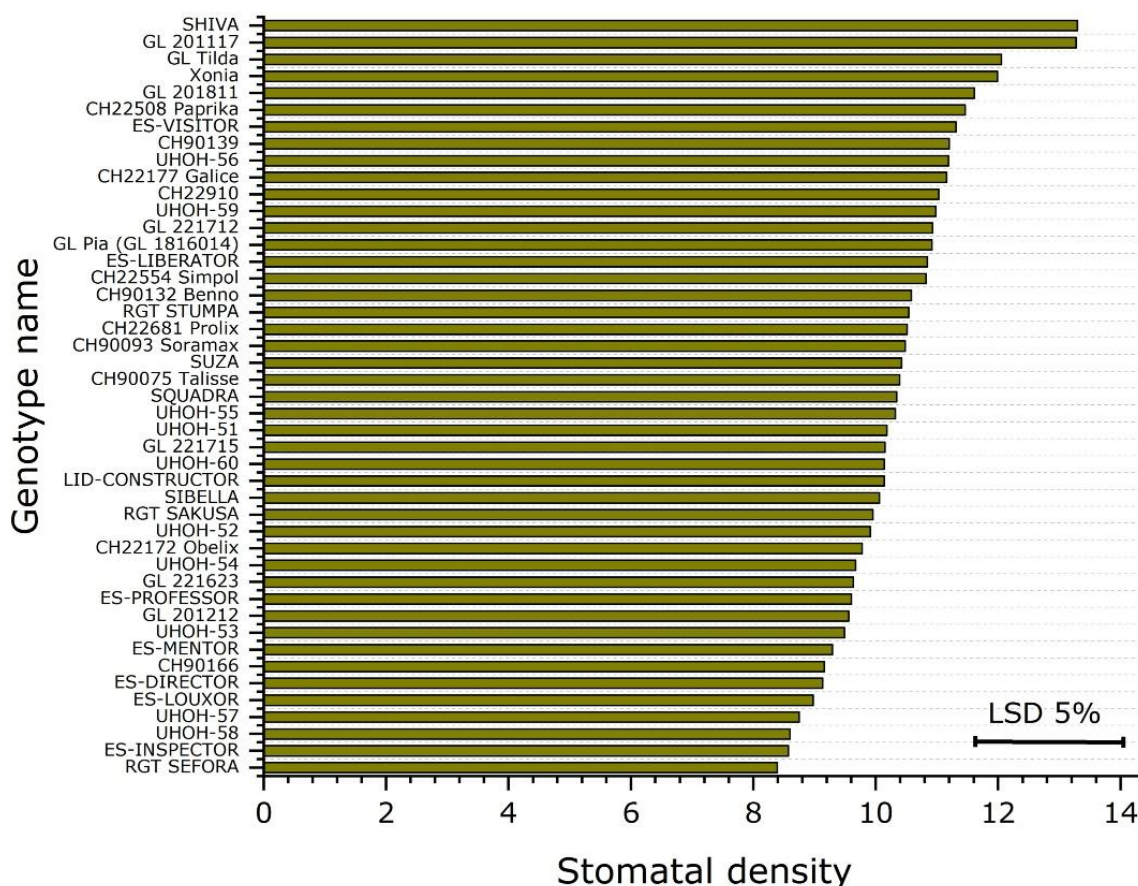


Figure 12. Stomatal density (stomata per 0.04 mm<sup>2</sup>) on lower leaf epidermis of 45 genotypes of the Yield-2 set

After harvest, seed quality traits such as 1000-seed weight, seed protein and oil content were determined. Genetic differences were present in all seed traits within the different sets of genotypes. An in-depth evaluation of seed traits including protein yield per unit area will be carried out after the 2025 season.

In some locations (e.g., Tulln / Austria, Willstätt / Germany), harvested seed appeared shrivelled or cracked and some seed was covered with a white mold which indicates the occurrence of the *Diaporthe* / *Phomopsis* seed decay complex. This can reduce the value of soybean seed due to a decrease in seed germination rate and subsequently a lower field emergence. In selected samples, the disease was clearly visualised on sterile growth media (Figure 13). As indicated by shrivel scores, Yield-1 seeds were most strongly affected, whereas the Yield-2 and Yield-3 sets had a lower disease incidence, and genotype difference where highly significant within each of the three sets.



Figure 13. *Diaporthe* / *Phomopsis* infection complex of soybean seeds after harvest visualised on a sterile growth medium with typical yellowish droplets of exudate formed by the mycelium colony (Photo: BOKU University, Nicole Laure)

## Results from food-grade soybean experiments

Soybean is a source of protein both for human nutrition and in livestock feeding. Thus, seed protein content and amino acid composition are relevant for processing and nutritional value. In the Food set, genotypes differing in seed quality characteristics were assembled for a comparative screening of seed quality. Depending on utilisation, seed size (1000-seed weight), oil and sucrose content, lipoxygenase-free and allergen-reduced traits as well as seed coat characteristics (hilum colour, seed coat colour) might be of interest as well.

## Seed protein content

Seed protein content in the Food set had a wide variation both between genotypes and experimental locations. Over all locations analysed, the location average was over 410 g/kg (dry matter basis) protein, and a seed protein content of over 460 g/kg was reached by individual genotypes (Figure 14).

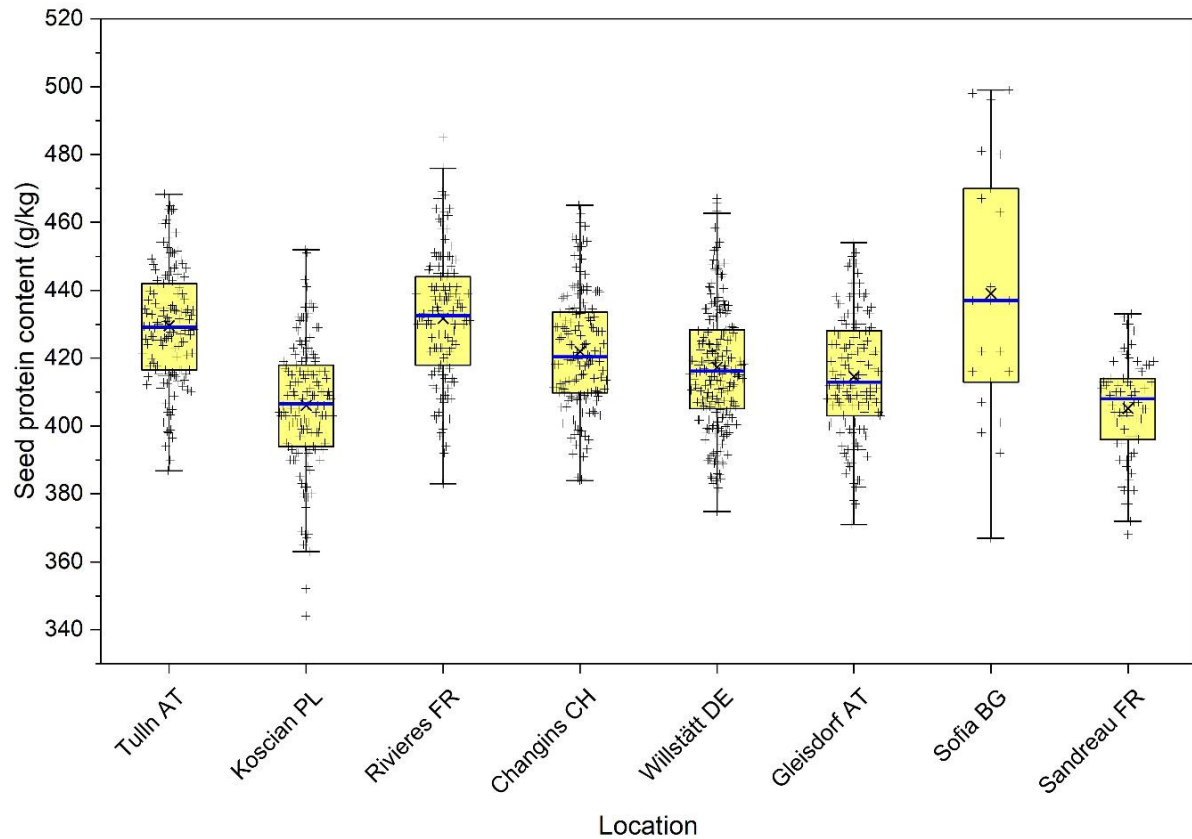


Figure 14. Variation in soybean seed protein content in samples from the Food set harvested across different partner locations in 2024

Phenotypic diversity was also high in seed sucrose content, which is negatively correlated to seed protein content (Figure 15 for the Tulln/Austria experiment). Beside seed protein content, which determines much of the nutritional and processing value of soybean, sucrose content is associated with the taste of products and therefore is also of interest for consumer acceptance.

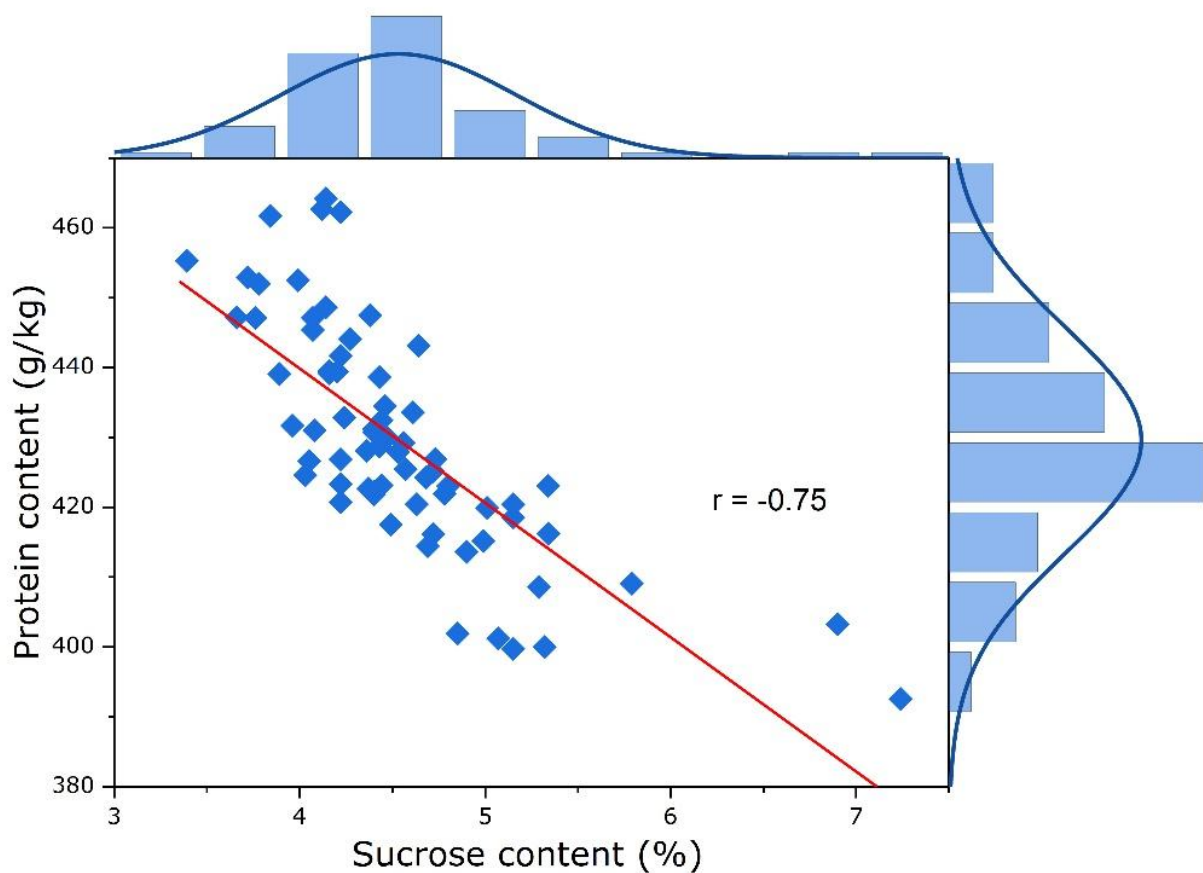


Figure 15. Distributions and correlation between seed sucrose and seed protein content in the Food set ( $n=70$ , Tulln/Austria, 2024 experiment)

Similarly, while seed size (*i.e.* 1000-seed weight) is around 200 g in conventional soybeans on average, a much wider range (100 – 350 g) was found in the Food set (Figure 16 for illustration).



*Figure 16. Seed samples of food-grade soybean cultivars with very small (left) or very large (right) seed size (Photo: BOKU University)*

A wide variation in seed quality traits is relevant for meeting different requirements of soybean processors particularly in the food industry.

### **Amino acid composition**

Amino acid composition of plant proteins is an important determinant of both their nutritional value and functional properties. Apart from abundant amino acids such as arginine, aspartic and glutamic acid, soybean protein is comparatively high in the most essential amino acid lysine which is the base of its outstanding nutritional value (Figure 17). Similar to other legume proteins, methionine and cysteine are present at lower concentrations in soybean protein.

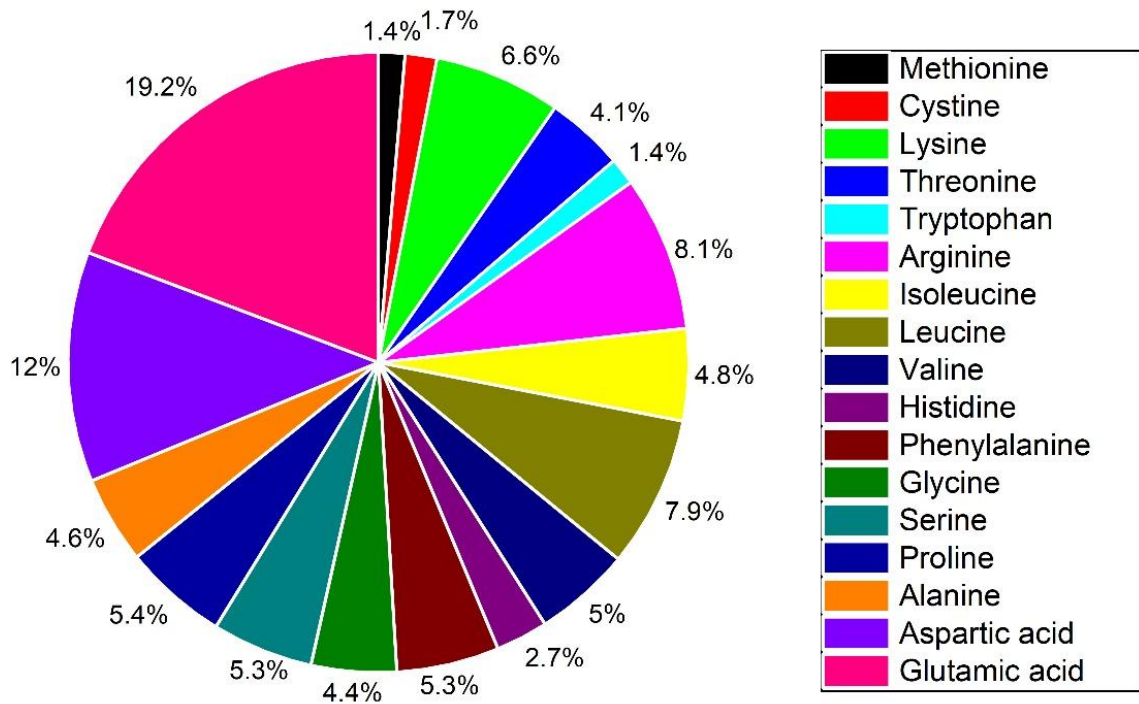


Figure 17. Amino acid composition of soybean protein: Concentration (%) of individual amino acids in the seed protein (average over 70 Food genotypes from Tulln (Austria) and Willstät (Germany) experiments in 2024 based on NIRS analyses)

Variation between genotypes in amino acid concentration is rather low due to their genetically fixed sequence and ratio in different proteins (Figure 18). Nevertheless, significant genetic differences between genotypes in the Food-set have been found for all individual amino acids. Due to genetically fixed amino acid ratios, amino acid concentrations are correlated with each other which is mainly reflecting differences in total seed protein content between genotypes (Figure 19).

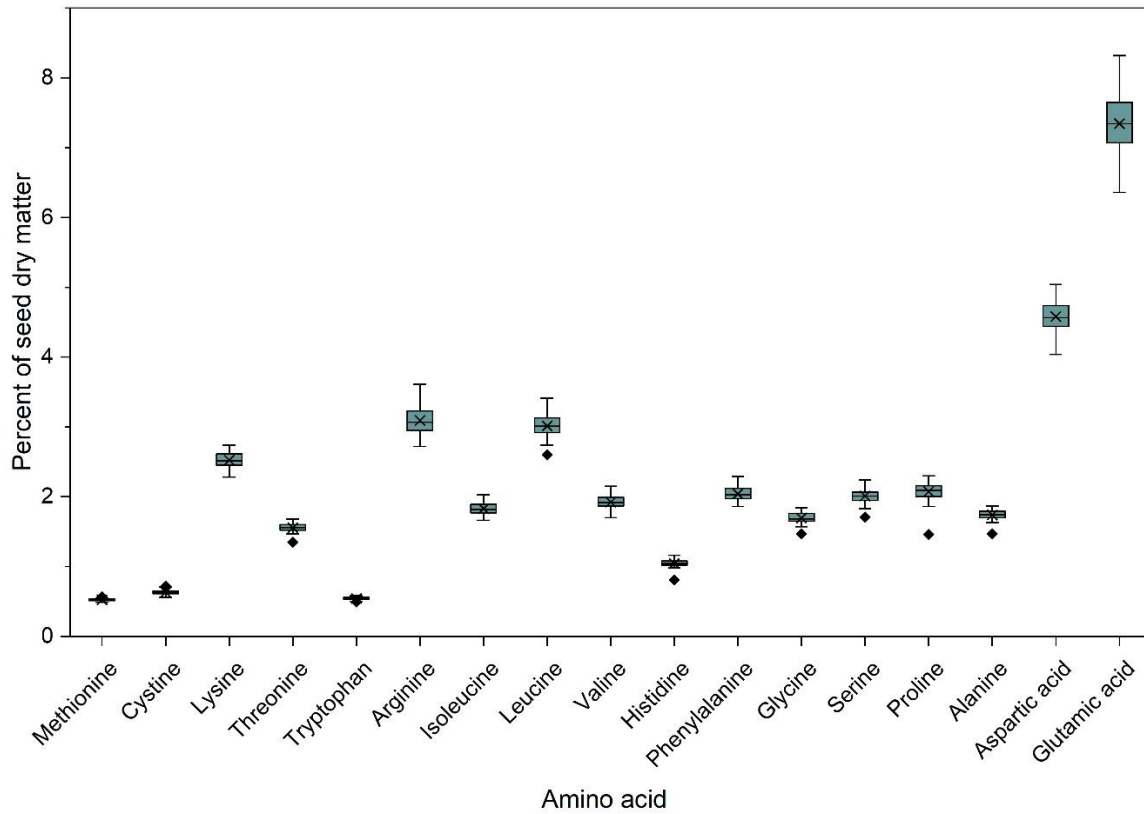


Figure 18. Variation in amino acids of soybean in 70 Food genotypes from Tulln (Austria) and Willstätt (Germany) experiments in 2024

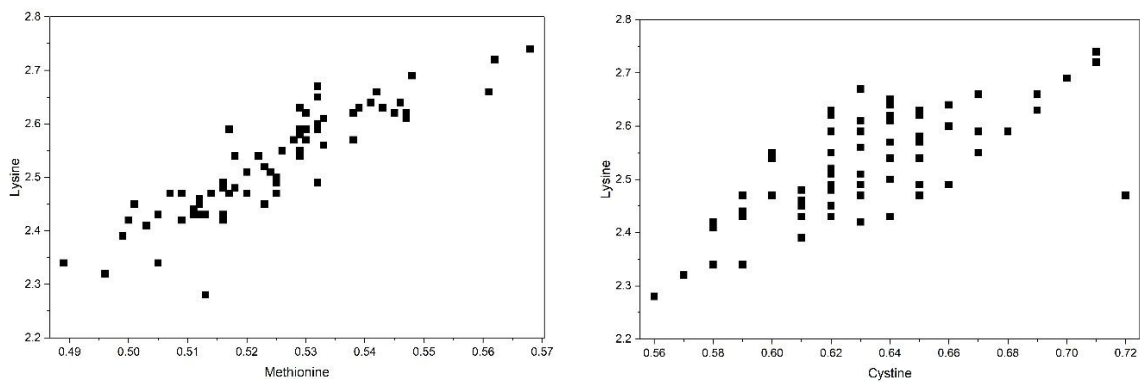


Figure 19. Scatter plots between concentrations (in % per seed dry matter) of methionine (left) or cysteine (right) and lysine in 70 Food genotypes from experiments in 2024

## Development of a novel, trait-informed marker panel for soybean genotyping

To support high-resolution genotyping in soybean breeding, we have developed a new marker panel tailored to the specific needs of European soybean varieties (maturity groups MG 0000–I), with the goal of improving trait selection precision and ensuring future compatibility with emerging causal gene discoveries. This effort responds to both recent advances in soybean genomics and the limitations of existing commercial marker panels.

Originally, the Agriplex 1K Soybean Community Panel was proposed for genotyping. However, with increasing genomic resources and resequencing datasets becoming available, the need to modernise and expand the marker content became apparent. In particular, current commercial panels often fall short in three key aspects:

1. Limited representation of European-specific germplasm.
2. Poor interoperability between panels due to differing design criteria and reference genome versions.
3. Absence of markers tagging causative mutations (CMs) in causal genes critical for trait-informed breeding.

To address these limitations, we performed a comprehensive bioinformatics analysis of resequenced soybean accessions originating from publicly available data sets that have been aggregated in the soybean diversity panel currently counting over 4,000 accessions. Using Soybean Allele Catalog Tool (Chan et al., 2023<sup>6</sup>), we explored variation in protein coding regions of known causal genes underlying important traits and evaluated presence/absence and frequencies of their non-/functional alleles. The Soybean Allele Catalog tool was also used to verify GWAS-derived candidate genes from recently published works and also, to predict additional existing alleles in known genes not characterised elsewhere.

In parallel to this CM-focused analysis, we evaluated all available marker panels from varying commercial providers or communities and conducted *in silico* genotyping of European germplasm to identify a robust and informative marker set optimised for diversity, trait prediction, and backward compatibility. To achieve this, we utilised the AccuCalc tool (Biová et al. 2024<sup>7</sup>) that allows for user-defined input genotype and phenotype files and calculates a measure of direct correspondence between a variant position and binarised phenotypic categories, the accuracy (Škrabišová et al., 2022<sup>8</sup>). This approach enabled identification of markers in perfect correspondence (close to 100% accuracy) with CMs of a complicated genetic nature (larger indels, etc.).

---

<sup>6</sup> Chan, Y.O., Dietz, N., Zeng, S., Wang, J., Flint-Garcia, S., Salazar-Vidal, M.N., Škrabišová, M., Bilyeu, K., Joshi, T., 2023. The Allele Catalog Tool: a web-based interactive tool for allele discovery and analysis. *BMC Genomics* 24, 107. <https://doi.org/10.1186/s12864-023-09161-3>

<sup>7</sup> Biová, J., Dietz, N., Chan, Y.O., Joshi, T., Bilyeu, K., Škrabišová, M., 2023. AccuCalc: A Python Package for Accuracy Calculation in GWAS. *Genes* 14, 123. <https://doi.org/10.3390/genes14010123>

<sup>8</sup> Škrabišová, M., Dietz, N., Zeng, S., Chan, Y.O., Wang, J., Liu, Y., Biová, J., Joshi, T., Bilyeu, K.D., 2022. A novel Synthetic phenotype association study approach reveals the landscape of association for genomic variants and phenotypes. *Journal of Advanced Research* 42, 117–133. <https://doi.org/10.1016/j.jare.2022.04.004>

## Marker panel composition

Our final marker panel consists of 5,039 markers, including 355 trait-specific markers, and was carefully structured into the following categories:

- Diagnostic markers – Selected for their ability to differentiate genotypes within the European soybean pool, especially within MG 0000–I maturity groups, while keeping original selectivity for germplasm from other geographical regions (Americas, Asia, etc.).
- Causative mutations (CMs) – Known functional polymorphisms controlling key agronomic and nutritional traits screened for yield and food-grade traits within this project and beyond (e.g., *E*-genes for flowering time and maturity; plant architecture and morphology; anti-/nutritional traits, special traits). All known alleles at each CM locus were included to allow multi-allelic resolution.
- CM proxies – For larger InDels or structural variants not easily captured by SNP genotyping, proxy SNPs were selected based on high linkage and predictive accuracy.
- Predicted CMs – Candidate variant positions from recent gene discovery pipelines (e.g., Allele Catalog, Multiple Allele Discovery Tool, GWAS-driven discoveries) were included in anticipation of ongoing trait dissection and validation efforts.
- Diagnostic, compatibility markers – Shared markers from legacy panels (e.g., SoySNP50K, LGC 5K, BARC 200K, 1K Agriplex) were retained to enable integration with historical datasets and promote interoperability across genotyping platforms. Majority of these markers are original, diagnostic markers previously identified (Bandillo et al., 2015<sup>9</sup>; Zhu et al., 2023<sup>10</sup>).
- Special request markers – Trait specific and/or diagnostic markers in use in breeding programs (drought, biotic/abiotic stress, chilling resistance/susceptibility etc.).

The panel is designed to be flexible, updatable, and future-proof, allowing seamless integration of ongoing genetic discoveries and enabling accurate trait tracking in breeding programmes.

## Genotyping technology: Flex-Seq™ by LGC Biosearch Technologies

Although we initially aimed in updating the Agriplex 1K Soybean Community Marker Panel to speed up the development, we requested various commercial genotyping providers to develop this improved and innovative marker panel for this project and beyond. We have established a partnership with LGC Biosearch Technologies to deliver this marker panel using their Flex-Seq™ platform. Flex-Seq is a multiplex PCR-based targeted amplicon

---

<sup>9</sup> Bandillo, N., Jarquin, D., Song, Q., Nelson, R., Cregan, P., Specht, J., Lorenz, A., 2015. A Population Structure and Genome-Wide Association Analysis on the USDA Soybean Germplasm Collection. *The Plant Genome* 8, plantgenome2015.04.0024. <https://doi.org/10.3835/plantgenome2015.04.0024>

<sup>10</sup> Zhu, X., Leiser, W.L., Hahn, V., Würschum, T., 2023. The genetic architecture of soybean photothermal adaptation to high latitudes. *Journal of Experimental Botany* 74, 2987–3002. <https://doi.org/10.1093/jxb/erad064>

sequencing method, optimised for mid- to high-throughput genotyping applications. Unlike random-fragmentation approaches such as genotyping-by-sequencing (GBS), Flex-Seq uses predefined primers to amplify specific genomic regions, ensuring reliable detection of known variants. Our panel of preselected markers was validated after several rounds of optimisation to ensure that the markers will capture the intended targets. Here, in this phase, some CM-based targets had to be replaced by newly designed associated markers.

Key advantages of Flex-seq technology include high multiplexing capacity; targeted precision where PCR-based enrichment minimises missing data and enables confident detection of SNPs and InDels, including those in complex genomic regions; panel flexibility; and cost-efficiency. This technology was chosen for its ability to accurately genotype all 5,039 markers in our custom panel, including the complex trait-specific and proxy markers that are critical for our strategy. By integrating this PCR-based targeted sequencing platform with a trait-rich, multi-allelic marker set, we provide a versatile genotyping solution that bridges legacy data, current breeding needs, and future discoveries. Another option would be resequencing at minimum 11x, which is still costly and time consuming (27 EUR vs. 300 USD per sample).

This design also serves as a template for building similar panels in other legumes, including common bean and pea.

## Results from digital phenotyping

Digital phenotyping tools based on various camera/imaging systems or spectroradiometers can be utilised for high-throughput phenotyping. Depending on the specific application, digital phenotyping proposes either higher precision than visual scoring or measurement of reflectance-based invisible traits such as physiological indices. At the Agroscope (Changins / Switzerland) partner location, soybean ground cover was measured using the Canopeo<sup>11</sup> (Oklahoma State University, USA) app. In measurements taken between July 1 and 22, the development of ground cover is clearly evident in Figure 20 for Yield-1 and Yield-2 sets of genotypes. For the Yield-2 trial, significant differences in ground cover between genotypes were detected at certain time-points.

---

<sup>11</sup> Patrignani, A., Ochsner, T.E., 2015. Canopeo: A powerful new tool for measuring fractional green canopy cover. *Agronomy Journal* 107, 2312-2320.

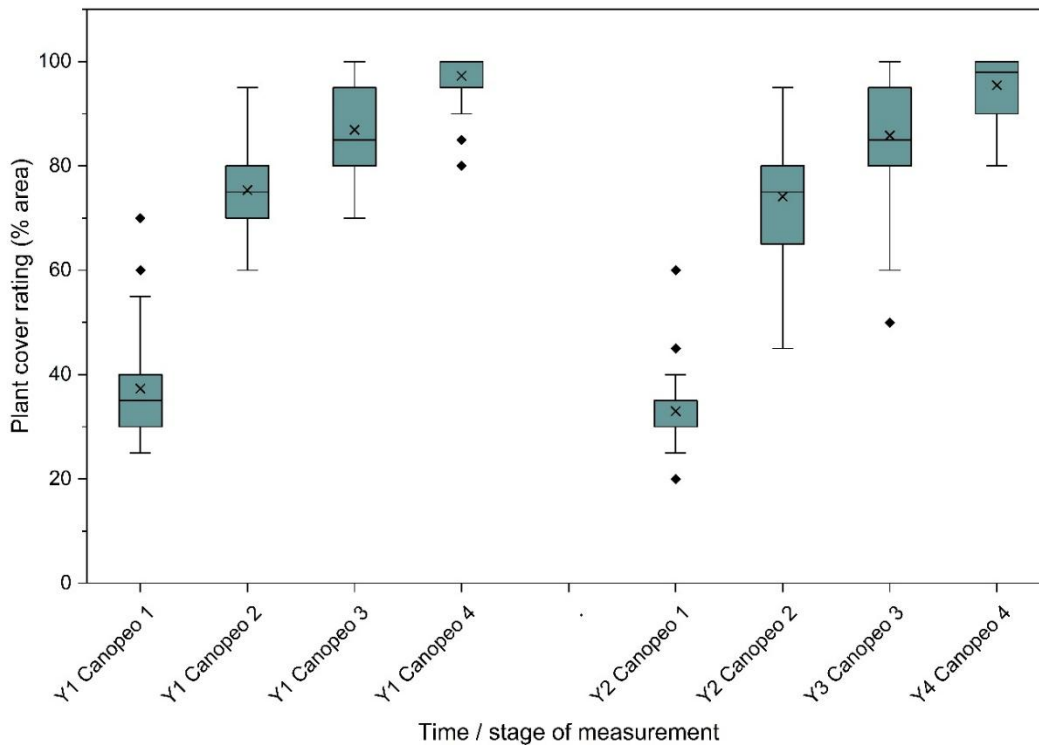


Figure 20. Development of ground cover (Canopeo) in Yield-1 and Yield-2 experiments at four time-points between July 1 and July 22, 2024 at Changins (Switzerland)

At the BOKU University (Tulln / Austria) location, hyperspectral reflectance<sup>12</sup> and canopy temperature were recorded at different time-points during flowering and early seed filling of the Yield-2 set of genotypes (Figure 21).



Figure 21. Hyperspectral reflectance (left) and thermographic imaging (right) of Yield-2 plots during early seed filling using hand-held devices for data collection (Photos: BOKU University)

<sup>12</sup> Vollmann, J., Rischbeck, P., Pachner, M., Đorđević, V., Manschadi, A.M., 2022. High-throughput screening of soybean di-nitrogen fixation and seed nitrogen content using spectral sensing. *Computers and Electronics in Agriculture* 199, 107169. <https://doi.org/10.1016/j.compag.2022.107169>

A total of 43 different vegetation indices were calculated from the hyperspectral reflectance data collected at each time-point (for description of indices see Appendix Table 1). Differences between Yield-2 genotypes were significant for most indices across all time-points of measurement. Phenotypic correlations are listed between selected indices taken at two time-points and agronomic and seed quality traits (Appendix Tables 2 and 3). Significant correlations between indices and grain yield or other end-of-season traits indicate the predictive potential of the indices calculated. Correlations between indices and traits were different between time-points of measurement. This indicates the need for several measurements throughout the vegetation period. Utilising data from time-point 2, 9 different water-related indices were utilised to describe genotype similarities in water status (Figure 22). This helps to characterise genotypes in water-related traits and possibly to explain differences in yield reduction under drought stress conditions. In contrast to hyperspectral reflectance measurements, canopy thermography appeared to be more volatile and influenced by various environmental conditions, and genotype differences could only be found in late afternoon measurements at certain time-points as compared to noon measurements.

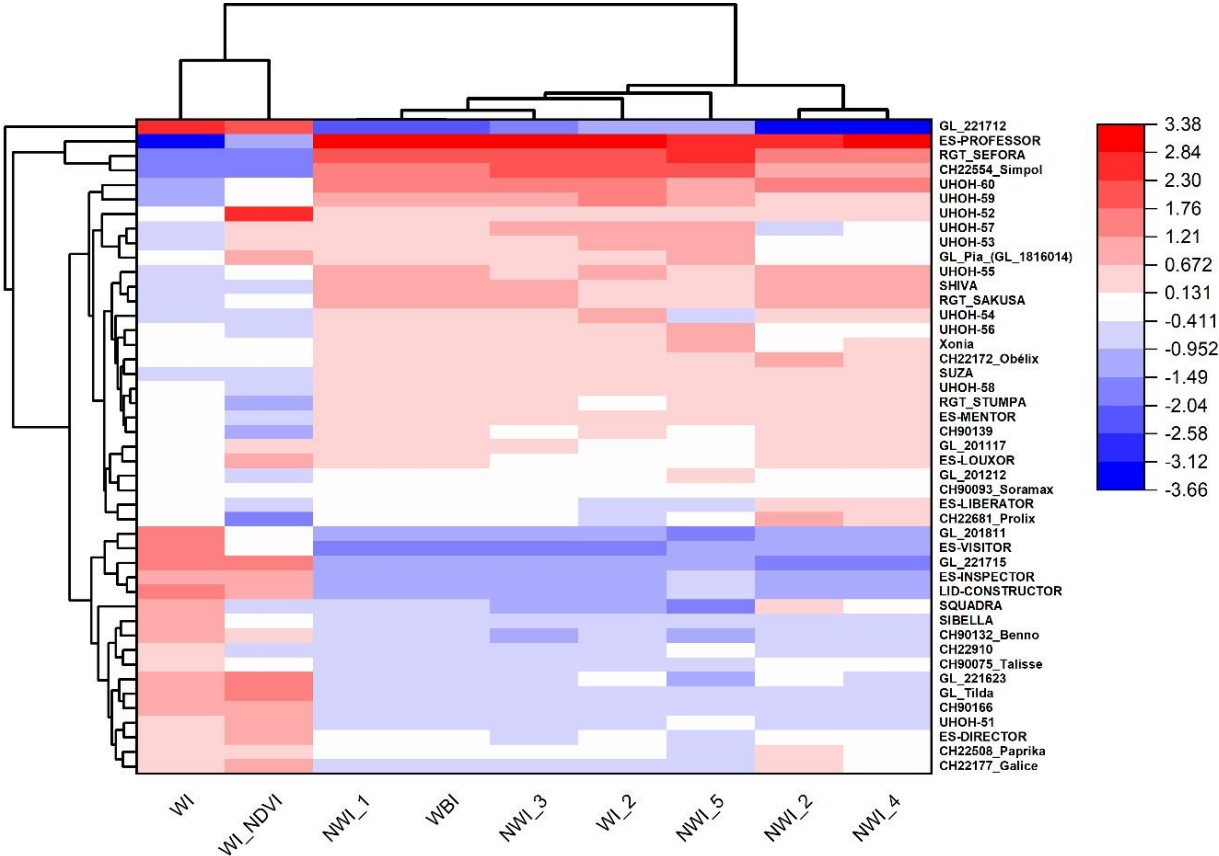


Figure 22. Heat-map illustrating similarities between genotypes of the soybean set Yield-2 in nine different water indices calculated from hyperspectral reflectance measurements at time-point 2 for the Tulln 2024 environment

Nodulation and di-nitrogen fixation are key traits of soybean and other legumes affecting grain yield and seed protein content as well. In organic farming, di-nitrogen fixation of legume crops is also important in crop rotations where legumes provide nitrogen input which is later available for follow-up cereals or other crops. As differences in nodulation

(see Figure 23) and di-nitrogen fixation are difficult to measure in plant breeding experiments under field conditions, hyperspectral reflectance indices can be utilised to estimate the amount of symbiotic nitrogen accumulation. Thus, nitrogen accumulation by soybean plants or canopies can be approximated, and significant correlations between nitrogen-related indices such as the red edge inflection point (REIP) and protein yield of the Yield-2 set of genotypes (Figure 24) can illustrate genetic variation in nitrogen accumulation traits which later translate into differences in yield and protein production per unit area.



*Figure 23. Phenotypic differences in root nodulation between roots of two soybean genotypes (Photo: BOKU University)*

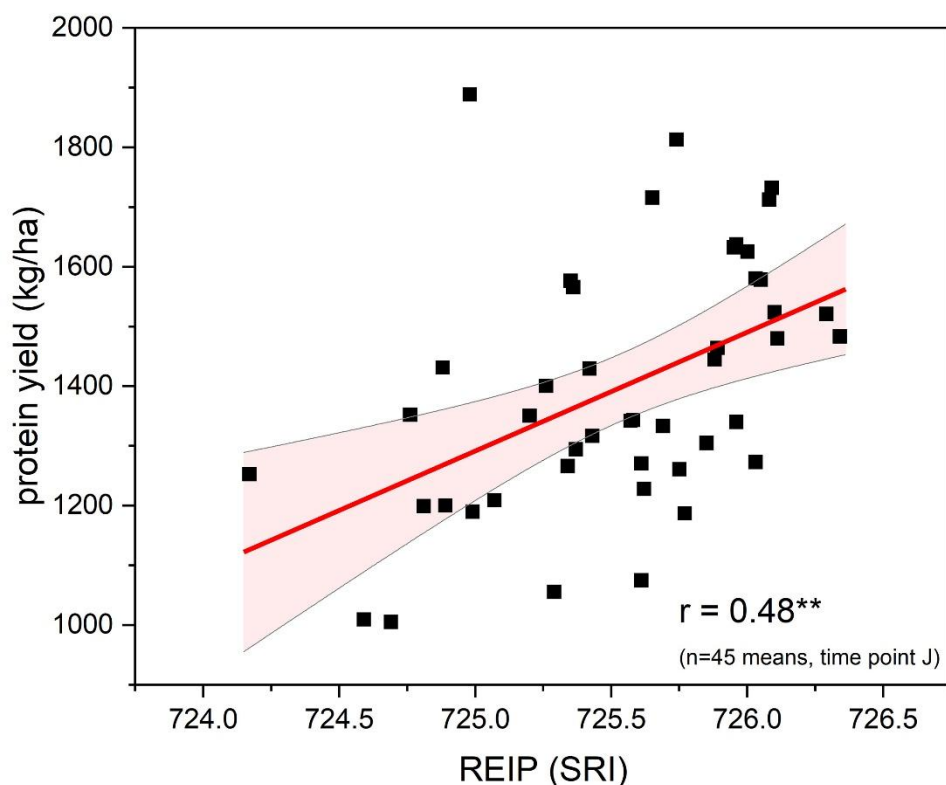


Figure 24. Correlation between the spectral index REIP (red edge inflection point) at early seed filling and soybean protein yield in the Yield-2 set of genotypes (Tulln/Austria, 2024)

## Conclusions and outlook

The preliminary results achieved from work up to August 2024 in Legume Generation to boost the breeding of soybean indicate that clear phenotypic variation is present in the elite soybean breeding materials evaluated. This applies to agronomic characters such as grain yield, phenology (time to flowering, time to maturity), and harvest product quality. As soybean is sensitive to latitude, temperature and other environmental conditions, such variation is needed as it bears the potential for adaptation to specific growing conditions. Adaptation is also necessary for optimised resource capture under specific conditions to be competitive with other crops, particularly in stressful environments affected by drought. Methods of digital phenotyping appear useful for characterising genotypes in physiological properties (spectral vegetation indices) which would also support better adaptation. Furthermore, genotyping with trait specific and diagnostic markers will produce unique insights into genetic diversity patterns within and between European breeding programmes. Genotyping will also help to select parental materials in crossing programmes, and will finally contribute to more efficient and precise selection of candidate varieties. The preliminary results also indicate a large variation in seed traits relevant for food-grade soybeans and for processing in different product lines. This includes a wide genetic and environmental variation in seed protein content, 1000-seed weight and other seed traits. The high concentration of essential amino acids such as lysine has also been confirmed, whereas overall variation in amino acid profiles appears to be rather low. Finally, further collaborative phenotyping and the joint analysis of genetic and phenotypic data will support the members of our Soybean Innovation Community in their future soybean

breeding programmes. In particular, the connection of the different information sources such as agronomic and phenology results across multiple environments, seed quality properties, results from stress tests, digital phenotyping parameters, and diagnostic as well as trait specific marker data will contribute to an in-depth characterisation of breeding materials which was not possible before.

## Annex

*Annex Table 1. Descriptive list of spectral reflectance indices (SRI) calculated with wavepoints utilised and reference to formulae and full description (From: Vollmann J. et al., 2022, Comput. Electron. Agric. 199:107169. doi: 10.1016/j.compag.2022.107169)*

<b>Index name</b>	<b>Description of index</b>	<b>Wavepoints used (nm)</b>	<b>Reference used</b>
<b>NDVI</b>	NDVI, normalised difference vegetation index (biomass, yield, leaf area)	670, 800	Jansen et al. 2014
<b>SIPI</b>	SIPI, structure insensitive pigment index (carotenoid / chlorophyll a ratio)	455, 680, 800	Jansen et al. 2014
<b>PSSRa</b>	PSSRa, pigment specific simple ratio (chlorophyll a)	680, 800	Jansen et al. 2014
<b>PSSRb</b>	PSSRb (chlorophyll b)	635, 800	Jansen et al. 2014
<b>CRI</b>	CRI 1, carotenoids reflectance index (carotenoid content)	510, 550	Jansen et al. 2014
<b>ARI</b>	ARI 1, anthocyanin reflectance index (anthocyanin content)	550, 700	Jansen et al. 2014
<b>PSSRc</b>	Pigment-specific simple ratio (carotenoid content)	470, 800	Mahlein et al. 2019
<b>NRI</b>	Nitrogen reflectance index	570, 670	Cao et al. 2015
<b>RVSI</b>	Red-edge vegetation stress index	712, 732, 752	Cao et al. 2015
<b>PSRI</b>	Plant senescence reflectance index	500, 680, 750	Cao et al. 2015
<b>CI</b>	CI read edge; Canopy chlorophyll and nitrogen content (red edge chlorophyll index)	710, 780	Chen et al. 2019
<b>PRI570</b>	Light use efficiency, drought indicator, PRI = phytochemical reflectance index; plant water status	531, 569	Rossini 2013
<b>DCNI</b>	Double-peak canopy nitrogen index	670, 700, 720	Duan et al. 2019
<b>GI</b>	Greenness index (chlorophyll)	554, 677	Duan et al. 2019
<b>GNDVI</b>	Green normalised difference vegetation index	550, 750	Duan et al. 2019
<b>VOG1</b>	Vogelmann index 1	720, 740	Inostroza et al. 2016
<b>VOG2</b>	Vogelmann index 2	715, 726, 734, 747	Inostroza et al. 2016
<b>VOG3</b>	Vogelmann index 3	710, 715, 734, 747	Inostroza et al. 2016
<b>R705</b>	Blue nitrogen index (leaf nitrogen content); $R705/(R717+R491)$	705, 717, 491	Tian et al. 2010, cited according to Feng et al. 2016
<b>R780/740</b>	Total N uptake	740, 780	Prey et al. 2020
<b>MSR705_445</b>	Modified simple ratio 705/445	705, 445	Prey et al. 2020
<b>REIP</b>	Red edge inflection point (nitrogen content)	670, 700, 740, 780	Prey et al. 2020
<b>WI</b>	WI, reflectance water index (water content)	900, 970	Prey et al. 2020
<b>NWI-1</b>	Norm. water index 1	900, 970	Prey et al. 2020
<b>NWI-2</b>	Norm. water index 2	850, 970	Prey et al. 2020
<b>NWI-3</b>	Norm. water index 3	920, 970	Prey et al. 2020
<b>NWI-4</b>	Norm. water index 4	880, 970	Prey et al. 2020
<b>NWI-5</b>	Norm. water index 5	930, 970	Prey et al. 2020
<b>WI_1</b>	Water index 1 (soybean)	915, 940	Christenson et al. 2016
<b>WI_2</b>	Water index 2 (soybean)	915, 990	Christenson et al. 2016
<b>WI_3</b>	Water index 3 (soybean)	940, 990	Christenson et al. 2016
<b>RNDVI_1</b>	red NDVI 1	680, 915	Christenson et al. 2016

<b>RNDVI_2</b>	red NDVI 2	680, 940	Christenson et al. 2016
<b>RNDVI_3</b>	red NDVI 3	680, 990	Christenson et al. 2016
<b>RENDVI_1</b>	red edge NDVI 1	715, 915	Christenson et al. 2016
<b>RENDVI_2</b>	red edge NDVI 2	715, 940	Christenson et al. 2016
<b>RENDVI_3</b>	red edge NDVI 3	715, 990	Christenson et al. 2016
<b>WI / NDVI</b>	WI : NDVI ratio	670, 800, 900, 970	Ihuoma 2019
<b>WBI</b>	Water band index (1/WI)	900, 970	Lausch et al. 2015
<b>MA1_N</b>	R5 NDVI normalised diff vegetation index 638_674	638, 674	Zhang et al. 2019
<b>MA1_R</b>	R5 RVI Ratio vegetation index 638_674 (optimized for soybean at R5)	638, 674	Zhang et al. 2019
<b>MB1_N</b>	R5 NDVI normalised diff vegetation index 634_678	634, 678	Zhang et al. 2019
<b>MB1_R</b>	R5 RVI Ratio vegetation index 634_678	634, 678	Zhang et al. 2019

### References to annex Table 1

Cao X., Luo Y., Zhou Y., Fan J., Xu X., West J.S., Duan X., Cheng D. 2015. Detection of powdery mildew in two winter wheat plant densities and prediction of grain yield using canopy hyperspectral reflectance. PLOS ONE. DOI: 10.1371/journal.pone.0121462.

Chen J., Li F., Wang R., Fan Y., Raza M.A., Liu Q., Wang Z., Cheng Y., Wu X., Yang F., Yang W. 2019. Estimation of nitrogen and carbon content from soybean leaf reflectance spectra using wavelet analysis under shade stress. Computers and Electronics in Agriculture 156, 482-489. DOI: 10.1016/j.compag.2018.12.003.

Christenson B.S., Schapaugh Jr. W.T., An N., Price K.P., Prasad V., Fritz A.K. 2016. Predicting soybean relative maturity and seed yield using canopy reflectance. Crop Sci. 56, 625-643. DOI: 10.2135/cropsci2015.04.0237.

Duan D.D., Zhao C.J., Li Z.H., Yang G.J., Zhao Y., Qiao X.J., Zhang Y.H., Zhang L.X., Yang W.D. 2019. Estimating total leaf nitrogen concentration in winter wheat by canopy hyperspectral data and nitrogen vertical distribution. J. Integr. Agricul. 18, 1562-1570. DOI: 10.1016/S2095-3119(19)62686-9.

Feng W., Zhang H.Y., Zhang Y.S., Qi S.L., Heng Y.R., Guo B.B., Ma D.Y., Guo T.C. 2016. Remote detection of canopy leaf nitrogen concentration in winter wheat by using water resistance vegetation indices from in-situ hyperspectral data. Field Crops Res. 198, 238-246. DOI: 10.1016/j.fcr.2016.08.023.

Ihuoma S.O., Madramootoo C.A. 2019. Sensitivity of spectral vegetation indices for monitoring water stress in tomato plants. Computers and Electronics in Agriculture 163. DOI: 10.1016/j.compag.2019.104860.

Inostroza L., Acuña H., Munoz P., Vásquez C., Ibáñez J., Tapia G., Pino M.T., Aguilera H. 2016. Using aerial images and canopy spectral reflectance for high-throughput phenotyping of white clover. Crop Sci. 56, 2629-2637. DOI: 10.2135/cropsci2016.03.0156.

Jansen M., Bergsträsser S., Schmittgen S., Müller-Linow M., Rascher U. 2014. Non-invasive spectral phenotyping methods can improve and accelerate cercospora disease scoring in sugar beet breeding. *Agriculture* 4, 147-158. DOI: 10.3390/agriculture4020147.

Lausch A., Salbach C., Schmidt A., Doktor D., Merbach I., Pause M. 2015. Deriving phenology of barley with imaging hyperspectral remote sensing. *Ecol. Model.* 295, 123-135. DOI: 10.1016/j.ecolmodel.2014.10.001.

Mahlein, A.K., Alisaac, E., Al Masri, A., Behmann, J., Dehne, H.W., Oerke, E.C. 2019. Comparison and combination of thermal, fluorescence, and hyperspectral imaging for monitoring Fusarium head blight of wheat on spikelet scale. *Sensors* 19, 2281. DOI: 10.3390/s19102281.

Prey L., Hu Y., Schmidhalter U. 2020. High-throughput field phenotyping traits of grain yield formation and nitrogen use efficiency: optimizing the selection of vegetation indices and growth stages. *Front. Plant Sci.* 10, 1672. DOI: 10.3389/fpls.2019.01672.

Rossini M., Fava F., Cogliati S., Meroni M., Marchesi A., Panigada C., Giardino C., Busetto L., Migliavacca M., Amaducci S., Colombo R. 2013. Assessing canopy PRI from airborne imagery to map water stress in maize. *ISPRS J. Photogr. Remote Sens.* 86, 168–177. DOI: 10.1016/j.isprsjprs.2013.10.002.

Zhang X., Zhao J., Yang G., Liu J., Cao J., Li C., Zhao X., Gai J. 2019. Establishment of plot-yield prediction models in soybean breeding programs using UAV-based hyperspectral remote sensing. *Remote Sens.* 11, 2752. DOI: 10.3390/rs11232752.

*Annex Table 2. Coefficients of correlation between selected spectral reflectance indices (determined on July 27) and agronomic or seed quality traits*

	ttf	ttm	SPAD	lsize	podse	plh	yield	tsw	prot	oil	sucr	proty	stom
NDVI	-0.057	-0.255	-0.031	0.092	0.472**	-0.511**	0.106	-0.076	-0.024	-0.067	-0.221	0.105	0.109
NRI	0.294	0.007	-0.257	0.393**	-0.008	-0.045	-0.147	0.112	-0.011	0.011	0.048	-0.161	0.134
CI	-0.336*	-0.279	0.120	-0.175	0.489**	-0.459**	0.278	-0.153	-0.039	-0.083	-0.214	0.283	0.106
REIP	-0.396**	-0.204	0.138	-0.309*	0.363*	-0.327*	0.357*	-0.299*	-0.071	-0.028	-0.193	0.359*	0.023
PSSRa	-0.125	-0.265	-0.006	0.036	0.460**	-0.496**	0.151	-0.088	-0.067	-0.083	-0.191	0.143	0.107
PSSRb	-0.120	-0.255	0.024	0.032	0.486**	-0.510**	0.170	-0.102	-0.048	-0.104	-0.229	0.167	0.094
MA1_R	-0.023	0.024	-0.052	0.012	-0.268	0.192	-0.202	0.072	-0.125	0.162	0.356*	-0.236	0.092
WI	-0.428**	-0.149	0.029	-0.410**	0.125	-0.038	0.346*	-0.082	-0.012	-0.071	0.125	0.353*	0.165
WI_1	0.109	-0.036	-0.050	0.069	0.124	-0.364*	-0.436**	0.069	-0.198	0.164	-0.027	-0.478**	-0.269
WI_2	0.371*	0.184	-0.044	0.407**	-0.241	0.237	-0.180	0.109	0.023	0.116	-0.104	-0.184	-0.158
WI_3	0.306*	0.186	-0.050	0.385**	-0.334*	0.440**	0.082	0.067	0.138	0.050	-0.150	0.103	-0.076
NWI_1	0.426**	0.152	-0.040	0.407**	-0.126	0.042	-0.339*	0.089	0.013	0.073	-0.128	-0.346*	-0.162
NWI_2	0.355*	0.012	-0.051	0.256	0.072	-0.275	-0.414**	-0.019	-0.087	0.105	-0.198	-0.438**	-0.249
NWI_3	0.447**	0.195	-0.049	0.454**	-0.163	0.109	-0.296*	0.098	0.043	0.047	-0.097	-0.295*	-0.132
NWI_4	0.385**	0.049	-0.065	0.323*	0.015	-0.191	-0.423**	0.048	-0.051	0.098	-0.163	-0.442**	-0.217
NWI_5	0.467**	0.189	-0.060	0.519**	-0.209	0.187	-0.232	0.147	0.112	-0.009	-0.095	-0.217	-0.103

ttf: time to flowering; ttm: time to maturity; SPAD: SPAD value; lsize: leaf size; podse: pod set score; plh: plant height; yield: grain yield; tsw: 1000-seed weight; prot: seed protein content; oil: oil content; sucr: sucrose content; proty: protein yield. For description of spectral reflectance indices see Appendix Table 1.

*Annex Table 3. Coefficients of correlation between selected spectral reflectance indices (determined on August 6) and agronomic or seed quality traits*

	ttf	ttm	SPAD	lsize	podse	plh	yield	tsw	prot	oil	sucr	proty	stom
NDVI	-0.042	-0.051	0.132	-0.035	0.121	-0.147	0.354*	-0.204	-0.037	-0.150	-0.063	0.350*	0.072
NRI	0.019	-0.156	-0.116	0.072	-0.042	-0.063	-0.113	0.107	-0.322*	0.172	0.305*	-0.186	0.045
CI	-0.104	0.031	0.205	-0.099	0.189	-0.075	0.443**	-0.207	0.161	-0.208	-0.212	0.487**	0.106
REIP	-0.120	0.126	0.232	-0.099	0.100	0.064	0.445**	-0.211	0.081	-0.075	-0.121	0.475**	0.098
PSSRa	-0.062	-0.098	0.132	-0.041	0.136	-0.132	0.352*	-0.179	-0.053	-0.138	-0.051	0.346*	0.064
PSSRb	-0.002	-0.048	0.098	-0.008	0.150	-0.151	0.380**	-0.202	0.129	-0.270	-0.226	0.411**	0.039
MA1_R	-0.202	-0.137	0.070	-0.094	-0.056	0.075	-0.155	0.164	-0.535**	0.435**	0.558**	-0.264	0.062
WI	-0.123	0.058	0.388**	-0.122	-0.087	0.346*	0.322*	-0.040	-0.311*	0.202	0.400**	0.269	0.144
WI_1	-0.016	-0.201	-0.126	0.009	0.254	-0.504**	-0.235	0.115	0.127	-0.183	-0.289	-0.215	0.021
WI_2	0.149	0.047	-0.359*	0.118	-0.129	-0.158	-0.402**	-0.011	0.306*	-0.120	-0.369*	-0.353*	-0.185
WI_3	0.118	0.147	-0.238	0.091	-0.416**	0.201	-0.326*	-0.124	0.233	0.029	-0.239	-0.290	-0.282
NWI_1	0.115	-0.060	-0.381**	0.108	0.084	-0.350*	-0.339*	0.036	0.308*	-0.200	-0.395**	-0.286	-0.140
NWI_2	0.073	-0.153	-0.267	0.051	0.219	-0.513**	-0.363*	-0.031	0.183	-0.117	-0.397**	-0.334*	-0.133
NWI_3	0.120	-0.017	-0.401**	0.115	0.036	-0.280	-0.307*	0.031	0.336*	-0.224	-0.390**	-0.249	-0.149
NWI_4	0.091	-0.147	-0.314*	0.079	0.203	-0.495**	-0.350*	0.016	0.222	-0.154	-0.391**	-0.314*	-0.112
NWI_5	0.116	0.021	-0.369*	0.042	-0.158	-0.020	-0.340*	-0.082	0.355*	-0.215	-0.333*	-0.280	-0.185

ttf: time to flowering; ttm: time to maturity; SPAD: SPAD value; lsize: leaf size; podse: pod set score; plh: plant height; yield: grain yield; tsw: 1000-seed weight; prot: seed protein content; oil: oil content; sucr: sucrose content; proty: protein yield. For description of spectral reflectance indices see Appendix Table 1.