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Data Note

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FIP 1.0 Soybean data: Insights on soybean growth from eight years of high-throughput image field phenotyping

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1 Abstract

Soybean growth is determined by the interaction of genetic, environmental, and management factors. In the context of future climate and climate extremes, understanding genotype by environment interaction (GxE) will be crucial for selecting resilient breeding lines and optimizing management practices to minimize stress. As stress periods occur periodically in a season, in depth knowledge, about causing weather variables and differing responses of genotypes over time is required. In field studies, however, the environment is often treated as a static factor, and the specific effects of weather variability on growth remain poorly understood.

Here, we present a longitudinal dataset comprising 17,247 high-resolution RGB images of soybean breeding line collected over eight years in Eschikon, Switzerland. Top of canopy images were acquired throughout the entire growing seasons and complemented by hourly weather data, enabling a comprehensive analysis of soybean growth dynamics under varying field conditions. High spatio-temporal image resolution enables detailed analysis of growth dynamics and GxE, supporting identification of stress-tolerant genotypes to improve yield prediction and yield stability.

2 Background & Summary

Understanding genotype by environment interaction (GxE) under field conditions is essential for improving crop resilience and yield stability. While distinguishing genotypic effects between different environments is valuable, a more detailed understanding of how weather variables affect the growth of specific genotypes is crucial. Among the weather variables, radiation and water availability play a dominant role in determining photosynthetic efficiency, while temperature influences physiological reactions and enzymatic function [1].

Crop growth models (CGM) such as CROPGRO [2, 3] and APSIM [4, 5] have been widely used to predict crop performance under different environmental scenarios [6]. Kothari et al. (2024) suggest that improving model accuracy requires better input data, particularly for leaf expansion and senescence dynamics [7]. The canopy cover (CC) is often used as a proxy for plant growth and biomass accumulation, and it is commonly assessed using RGB images captured by Unmanned Aerial Vehicles (UAV) [8, 9], while digital repeat photography ("Phenocams") have been used to track crop development and phenological indicators [10]. However, imaging approaches with high spatio-temporal resolution remain underutilized.

High Throughput Field Phenotyping (HTFP) enables a rapid and frequent collection of large-scale phenotypic data, which is crucial for: i) Identifying promising genotypes based on growth traits (including organ segmentation and counting, biomass estimation) that correlate with yield and stress resilience ii) Capturing GxE to specific weather conditions, including extreme temperatures, drought, and varying light intensities. iii) Providing high-resolution

temporal data to refine CGMs and improve their predictive capabilities for different environments. iv) Facilitating real-time decision-making for crop/weed identification or optimizing management practices, such as irrigation and fertilization, based on actual crop conditions [11, 12, 13].

In this data collection, we used a rope-suspended camera system that autonomously captures top-of-canopy images at high spatial and temporal resolution. This Field Imaging Platform (FIP) enables the precise monitoring of plant growth at the plot level with high-frequency measurements over short time intervals [14]. By integrating high-resolution RGB imaging with meteorological data over several years, this data set aims to bridge the gap between genotype and environment (and management, although management and year are confounded in this dataset), enabling valuable insights into soybean growth dynamics.

The benefit of such high-resolution image data was demonstrated by [15] incorporating cultivar-specific models that account for per se temperature responses in a combined soybean and wheat data set including a subset of images (two genotypes, three years) presented in this study. Such detailed phenotypic information is instrumental in refining thermal time concepts and improving the accuracy of genotype-specific predictions in CGM under varying climatic conditions. In wheat, a FIP derived wheat data set was recently made publicly available [16]. Furthermore, images from that data set were used to train a plant segmentation model [17]. In peas, individual flowering detection was successfully performed with high accuracy using FIP images [18].

These advancements are relevant for growth prediction using CGM and improve selection efficiency for new soybean varieties. Such varieties are needed in European agriculture transitioning into more resilient and sustainable agricultural systems.

3 Methods

3.1 Plant material

Soybean breeding lines were obtained from Agroscope Soybean breeding and Delley seeds and plants Ltd. (DSP) for performance evaluation from 2015 to 2022. In total, 72 soybean genotypes were evaluated including 58 breeding lines, 14 varieties as checks and three mixtures of two varieties. The lines included maturity types ranging from the very early (000) type to the intermediate (II) type [19] and most were bred by Agroscope/DSP Supplementary Table 1.

3.2 Field trials

Field trials were carried out at ETH research station of plant sciences in Lindau Eschikon, Switzerland (47.449 N, 8.682 E, 556 m a.s.l.). The soil type is an eutric cambisol with an organic matter content of around 3.5 % and a pH between 6.2 and 7. Soybean was following winter wheat and a green manure in crop rotation.

Common treatments across all years included soil preparation with plowing and harrowing, herbicide applications for weed control, and fertilization based on soil test results. Detailed treatment, dates of sowing and harvest of each trial are shown in Supplementary Table 2. Sowing density varied between 40 to 60 plants m^{-2} .

From 2015 to 2022, eight trials (one trial per year) were carried out including 11 to 36 genotypes in a complete randomized block design. In 2015, eight replicates were used. From 2016 to 2017, three replicates and one to six check varieties with six to twelve replicates were used. The trials from 2018 to 2020 contained three replicates and were described before [20].

3.2.1 Yield and reference traits

The harvest was processed as described in Roth et al. (2022) [20]. Moisture and protein content was measured using near-infrared spectroscopy (NIRS) (A 7200 NIR Diode Array Based Analyzer, Perten Instruments NA, Inc., Springfield, USA) on an approximately 100 g sub-sample of the harvested grain per plot. In 2018 and 2022, both traits were measured in all three replicates. In the remaining years, only one mixed sample of the three replicates was measured. The weighed seed yield and protein content were corrected for moisture content of 11% based on the available values. Handheld chlorophyll meter measurement (SPAD) were taken manually.

Plant heights were measured using a Focus3D S 120 terrestrial laser scanner (TLS) (Faro Technologies Inc., Lake Mary USA) mounted on the FIP in 2016 and 2017. Height was extracted as the 97th percentile of the resulting height profile [21].

3.3 Image acquisition

The images were acquired using the FIP, a rope-suspended imaging platform (**Figure 1**). The images were taken as described in Kirchgessner et al. (2017) from the top view using a EOS 5D Mark II with a 35 mm lens mounted (Canon Inc., Tokyo, Japan) [14]. The camera was positioned 3 m above the canopy, the images were taken at full resolution of 21 MP in raw mode with usually 4 ms exposure time (see Supplementary Table 3). The ground sampling distance was approximately 0.55 mm. For camera parameters and for file name structure (see Supplementary Table 4).

3.4 Image analysis and plot detection

Without geo-referencing of the images, the identification of plots has two main obstacles in images taken over time: The plot location in the image is unknown, and the (unknown) plot position varies due to variation in the camera position (**Figure 2**). To resolve these issues, we developed an algorithm which uses the approximate row distance, the minimum rows (in the plot) and maximum rows (of the image) as parameters. It follows these steps: i) A green-pixel segmentation was performed using color ratio thresholds based on an established leaf area segmentation algorithm [22]. Segmented images are saved as compressed jpg images at 90% quality for potential further use by other users. ii) When plant rows were still visible before canopy closure, clusters were identified using only vertical (y-axis) pixel distribution. This approach grouped pixels into horizontal bands corresponding to plant rows using high-density clustering, effectively ignoring gaps along the x-axis caused by incomplete emergence (Supplementary Figure 1). This resulted in the maximum of five and minimum of three predefined clusters, i.e., rows, in a three-row plot. The cluster nearest to the image center was identified as the middle row, and neighboring clusters were numbered based on their proximity. Excess rows were dropped if they exceed the defined cluster maximum and if they spanned over two or more rows, according to the pre-defined row spacing. This ensured stable row extraction when, e.g., weeds were present within the rows. iii) Rows were then rotated around their midpoint aligning them horizontally and parallel to each other, thereby correcting for both perspective distortion and camera misalignment relative to the plot axis, using robust linear regression. iv) Once processed, plot-level canopy cover was extracted together with pixel counts and positional metadata of the plot (Supplementary Table 5). CC was calculated by determining the proportion of green pixels in the total number of pixels in the plot area (Supplementary Table 6). If more than one row was detected, the upper and lower plot boundary was defined by the median value of the outer rows. If just one row was present (this was used for the nine row plots as they are hard to separate), the upper and lower plot boundaries were set to 1.5 interquantile ranges off-center. For later stages of plant growth, when the canopy was closed and individual rows and/or plots could not be clearly distinguished, plot boundaries were estimated from images earlier in the season. Finally, the two complementary datasets—one based on total green canopy fraction and a row-based data set were merged to get the canopy dynamics over the season (for the resulting csv file see: `data/Soybean_CanopyCover_Raw_data.csv`). An example of the workflow including plot localizing and CC extraction in a single plot over time is shown in **Figure 3**.

3.5 Data Analysis For Technical Validation

Best linear unbiased estimators (BLUEs) for each trait and trial were estimated using the Spatial Analysis of Field Trials with Splines (SpATS) R package [23] as the following:

$$y_{ijk} = \mu + \text{gen}_i + f_{u,v}(\text{col}_j, \text{row}_k) + \varepsilon_{ijk}$$

where y_{ijk} denotes the observed phenotypic plot value for genotype i at column j and row k ; μ is the overall mean; gen_i is a fixed effect of genotype i ; $f_{u,v}(\text{col}_j, \text{row}_k)$ models spatial variation using bilinear polynomial and smoothing spline functions over the column and row positions; and ε_{ijk} is the residual error term. A plot value was removed from the analysis when the residuals of the fitted plot value were larger than ± 3 times the standard deviation as described previously [24, 25]. For heritability calculation, genotype was set as random factor.

4 Data Records

The FIP was successfully deployed to phenotype a wide range of soybean genotypes over entire field seasons (**Figure 1A**). Top-of-canopy imaging was conducted using high-resolution RGB cameras mounted approximately 3 meters above the plots (**Figure 1B**).

Across the eight field trials conducted between 2015 and 2022, a total of 17,247 top-view canopy images were collected, of which 1,098 images were excluded from the subsequent analysis because they showed border plots. The

data set represents 72 soybean genotypes (**Figure 1C**). The number of genotypes per year ranged from 11 to 36, including five standard check varieties that were consistently grown across the trials (**Figure 1D**). Management varied slightly between the years, e.g., from 2015 to 2018 nine planting rows per plot were sown, afterwards plots were sown in three rows (Supplementary Table 2). The associated yield, height and reference trait data is additionally provided.

Weather data was provided by the Swiss Federal Agrometeo (<https://agrometeo.ch/>) station Lindau (47.446 N, 8.680 E, 551 m a.s.l.) in a one-hour resolution. At this station the radiation sensor failed for one season, therefore, from 2020 to 2022, photosynthetic photon fluence rate (PPFR) was taken from a LI-COR sensor placed next to the field. The factor to convert radiation in MJ m^{-2} to PPFR was 2.04 according to [26].

4.1 Data Files and Structure

The dataset presented in this study is available at ETH Research Collection under DOI: <https://doi.org/10.3929/ethz-b-000742401>. The dataset is structured into directories that align with the described data processing pipeline used for extracting and analyzing canopy cover traits from field images. All files are provided in interoperable and widely-used ‘.csv’ and ‘.png’ format.

- **data/Design_2015_2022_Eschikon.csv**: Experimental design file, including plot layout (row and range), genotype names and identifiers, and replication. This file is used to match image-based data to field trials.
- **raw/**: Contains original top-view images acquired from the FIP saved as raw CR2 (**Figure 2**). Each image is uniquely named encoding the date, field trial, and the unique identify of the plot (plot UID; Supplementary Table 4).
- **segmentation/**: Includes binary segmentation masks generated through green channel thresholding, stored as ‘.png’ images. These masks differentiate green canopy from the soil background, and are used for downstream trait extraction (**Figure 3**).
- **data/Soybean_CanopyCover_Raw_data.csv**: Main file containing raw parameters for canopy cover estimates. This includes per-plot row spacing estimates, plot border positions, and extracted green pixel counts within the identified plot area.
- **data/Soybean_CanopyCover_data.csv**: Cleaned and normalized canopy cover data, with each observation tied to a plot identifier, date, time, and genotype. The canopy cover was robustly extracted for each plot corrected by the determined row width (**Figure 4A**).
- **data/Soybean_CanopyCover_BLUEs.csv**: BLUEs of canopy cover for each genotype over time and across environments, computed using spatial models with the SpATS package [23]. Each entry includes standard errors and heritability estimates (**Figure 4B**).
- **data/Weather_data_Lindau_Eschikon.csv**: Hourly weather records (temperature, radiation, PPFR, humidity, precipitation, windspeed) collected at the experimental sites. Aggregated and aligned with image acquisition dates **Figure 4C** and Supplementary Figure 2.
- **data/RefTraits_Soybean_2015_22_BLUEs.csv**: BLUEs for grain yield, protein content, protein yield, Thousand Kernel Weight (TKW) and SPAD calculated for each available genotype and trial. This file enables integration of canopy cover data with agronomic performance indicators (**Figure 5**).

To ensure interoperability, variable names follow MIAPPE [27] naming conventions (Supplementary Table 7). Further harmonization with other public datasets may be achieved using the metadata fields for genotype names and trial dates, e.g., accessing our data via Hugging Face (doi.org/10.57967/hf/6052).

5 Technical Validation

To ensure high quality of the dataset, several validation steps were performed. First, designs were visually checked for the correct position of the genotypes based on the images, especially the lanceolate leaf-type *Opaline* (**Figure 2**). Segmentation performance was visually confirmed by overlaying extracted green canopy areas on the original images and heritability was assessed. Broad-sense heritability of canopy cover was estimated across time points, with values ranging from 0 to 0.98 depending on growth stage and field conditions. Dates with heritability values

lower than 0.2 were then removed as they likely do not add genotypic information (these were six measuring dates in the latest senescence phase). On the remaining data, a high median heritability value of 0.76 ± 0.16 supports the robustness of the phenotyping process (**Figure 4B**). The reference traits reached heritability values ranging from 0.71 to 0.93 for yield and from 0.21 to 0.97 for protein content.

Curves were fitted for CC using generalized additive model (GAM) to assess smoothed temporal trends over time [28]. The model was fitted for each genotype separately in each trial using:

$$y_i = \beta_0 + f(x_i) + \varepsilon_i \quad (1)$$

where y_i is the canopy cover measurement at observation (date and plot) i , β_0 is the intercept term, $f(x_i)$ is a smooth function of the predictor, i.e., the numeric date x_i , $\varepsilon_i \sim \mathcal{N}(0, \sigma^2)$ is the normally distributed error term. The smooth function $f(x)$ is modeled using penalized regression splines. The number of basis functions used to construct each smooth term was set to ten ($k=10$).

The coefficient of determination (R^2) for the smoothed curve was calculated for each field site and year combination, with all R^2 values above 0.92, indicating high temporal coherence of the data (**Figure 4A**).

Additionally, we computed the date when each genotype reached 50% canopy cover by interpolating fitted curves before and after reaching maximal height. The dates when canopy cover declined to 50% after maximal height, i.e., in the senescence phase, was then correlated to yield reaching Pearson’s coefficient of up to 0.73 (**Figure 6**), except in the 2017 season (FPSB007) where most of the lower yielding genotypes showed extreme delayed senescence.

Similarly to CC, canopy height showed an logistic increase over time until reaching its maximum (**Figure 7A**). The heritabilities over the two measured seasons were rather stable and high with a median value of 0.86 ± 0.22 (**Figure 7B**). Until reaching 50% of its maximum, canopy height strongly correlated with extracted CC values reaching Pearson’s correlation coefficient of 0.97 (**Figure 7C**).

6 Usage Notes

The dataset can be readily used by researchers working on high-throughput phenotyping, crop modeling and machine learning.

Users interested in longitudinal canopy development can apply the included timestamp and plot identifiers to construct growth curves. For example, temporal fits using GAM or smoothing splines can reveal genotype-specific differences in growth dynamics.

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8 Data availability

The full FIP 1.0 soybean data set can be accessed from the ETH Zurich’s Research Collection (<https://doi.org/10.3929/ethz-b-000742401>) and as Hugging Face data set card (doi.org/10.57967/hf/6052) allowing interoperability and standardization with other datasets.

9 Code availability

Users with similar data can use the implemented workflow to get canopy cover from their experiments. The code is available on: https://gitlab.ethz.ch/crop_phenotyping/fip-soybean-canopycover

10 Author contributions

BK: Developed algorithm, analyzed data and drafted manuscript; NK, LR, AH, AM: FIP development, BK, NK, CO, LK, LR, OZ, SC, FL, HA, NS, FT, HZ, CAB, CB, AH: Collected and prepared data; Experimental design: BK, LK, LR, AH; all authors improved and approved the manuscript

11 Ethics declarations

The authors declare no competing interests.

12 Figures

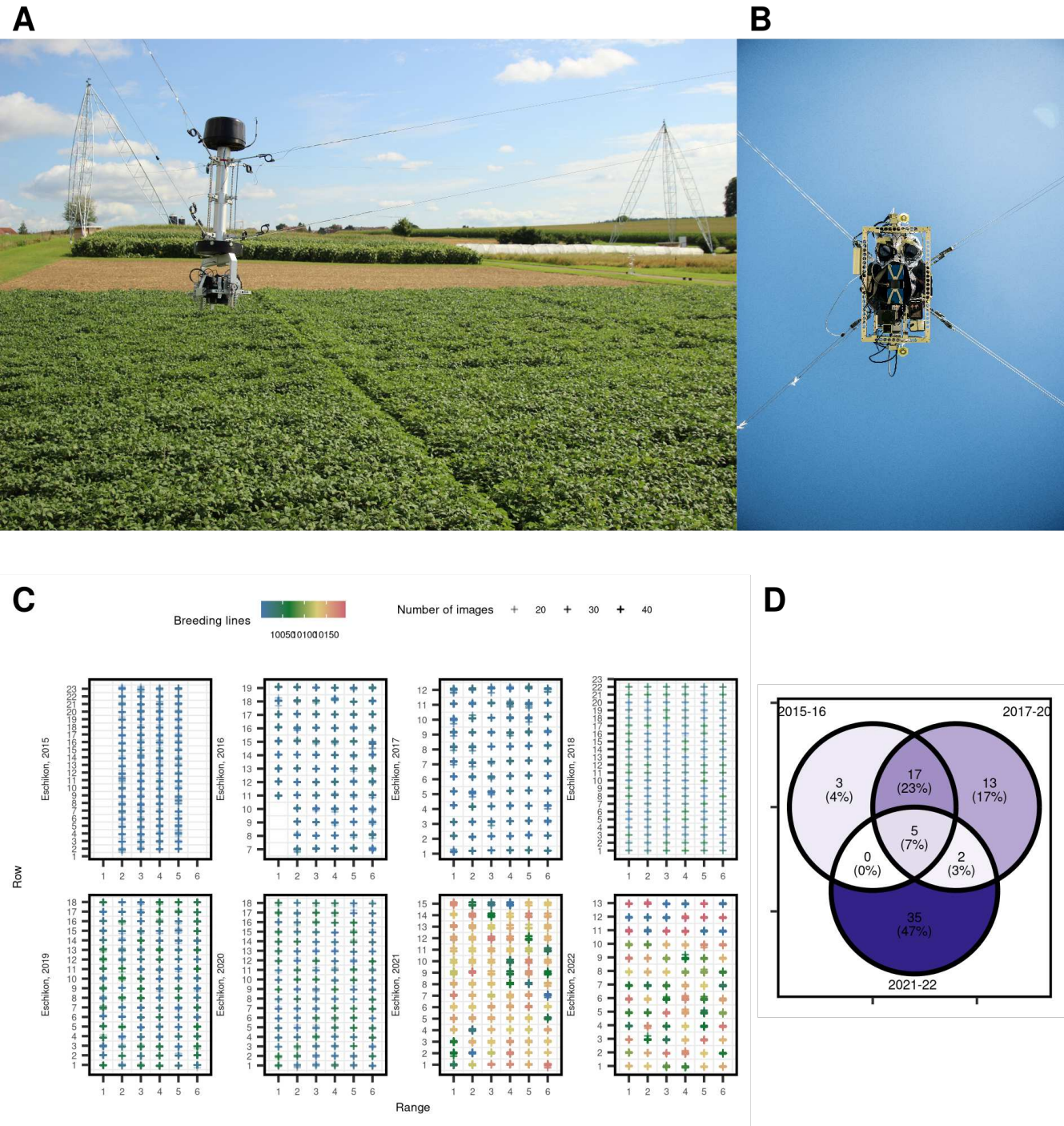


Figure 1: The rope-suspended Field Imaging Platform (FIP) camera head and two towers are shown. A: The FIP cplatform over the soybean field trial. B: The FIP camera head. C: The experimental design of all eight trials. The colors indicate the genotypes and the transparency indicates the number of measuring dates, i.e., the number of images per plot. D: In total, 72 genotypes were tested with various overlap between the years.

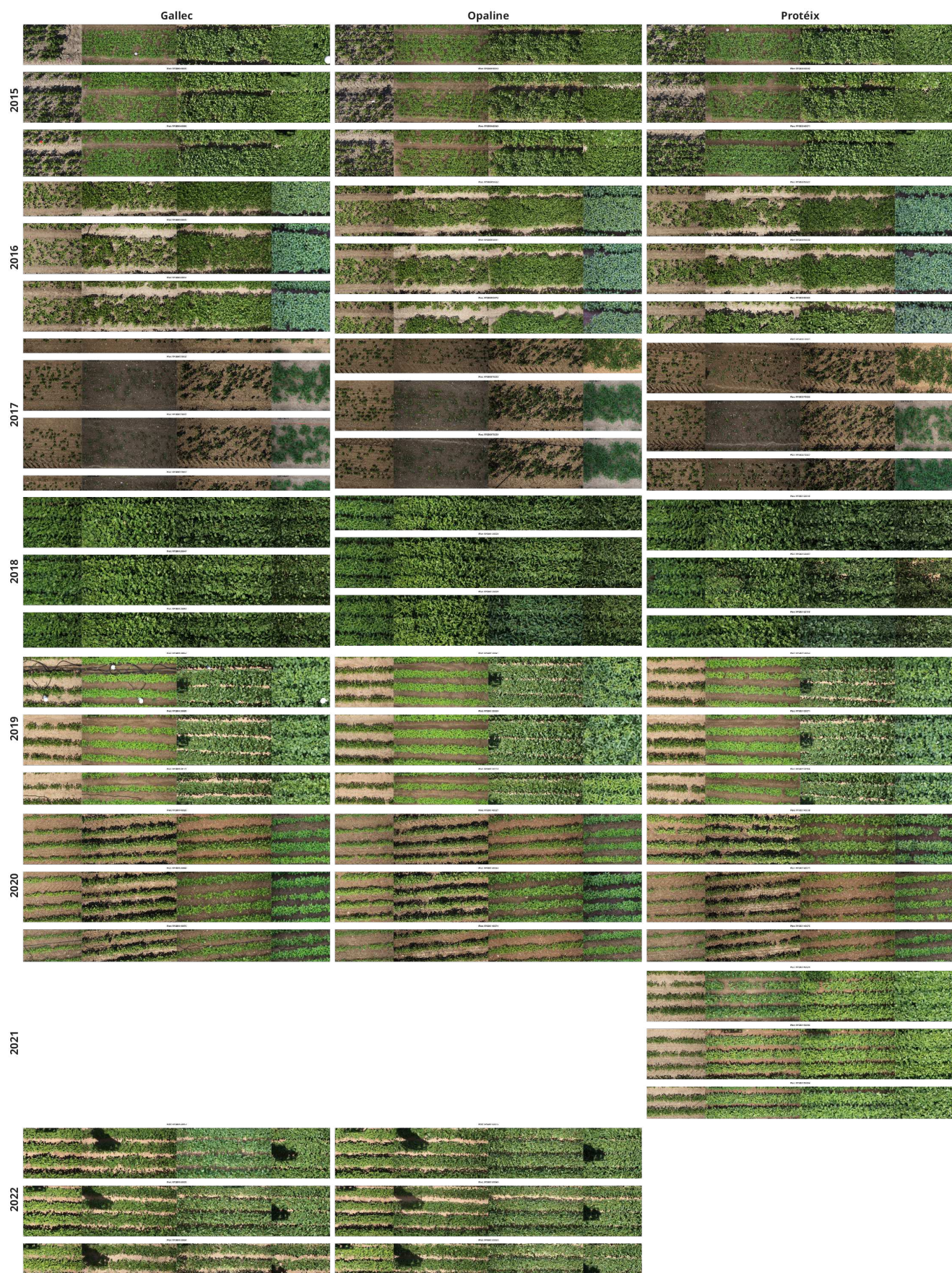
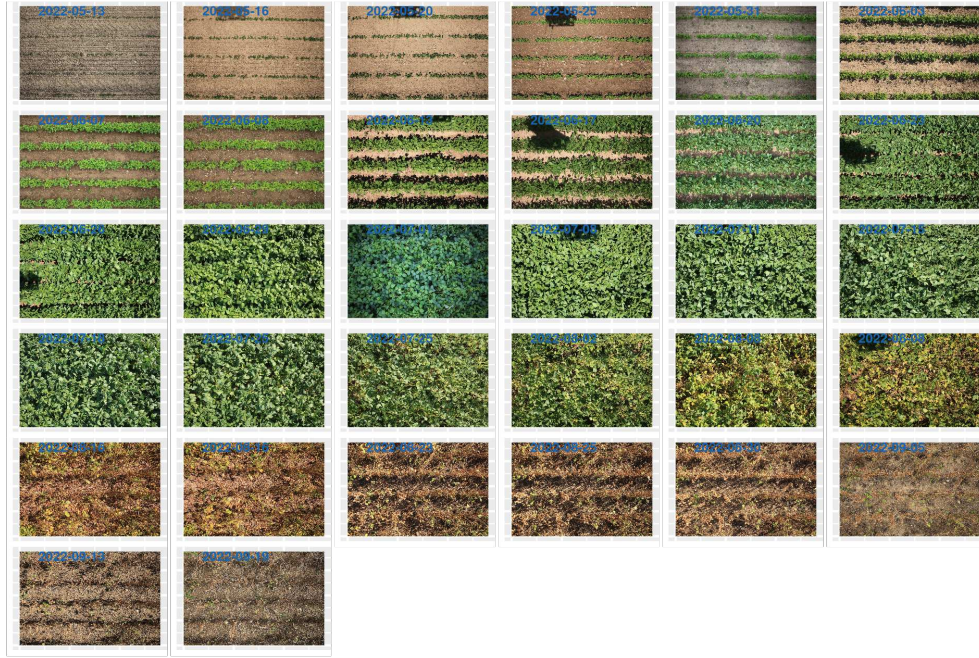


Figure 2: A cutoff of the seasonal data shows three exemplary genotypes evaluated under the Field Imaging Platform (FIP). It includes the lanceolate leaf type variety *Opaline*. Images of four subsequent measuring dates were selected representing different morphological stages in different years.

A

Genotype: *Gallec*

Plot: FPSB0160012



B

Plot: FPSB0160012

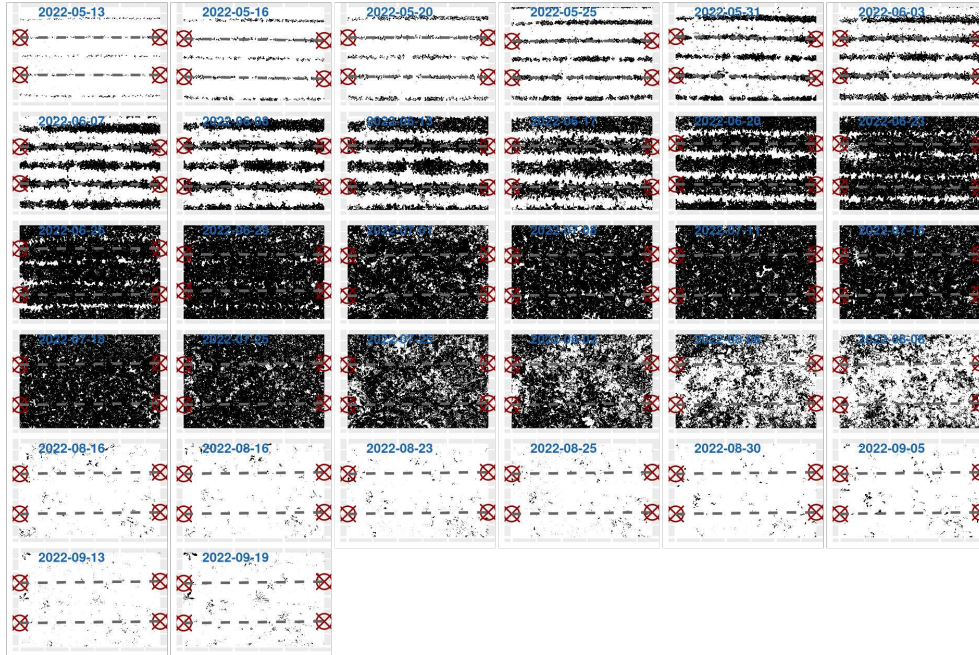


Figure 3: An exemplary plot of variety *Gallec* in 2022 imaged by the Field Imaging Platform (FIP) is shown. A: RGB images. B: Identification of plots and extraction of canopy cover per plot. The plot was defined between the three center rows per plot. For later stages of plant growth, when the canopy is closed and individual rows and/or plots cannot be clearly distinguished, plot boundaries were estimated from images earlier in the season.

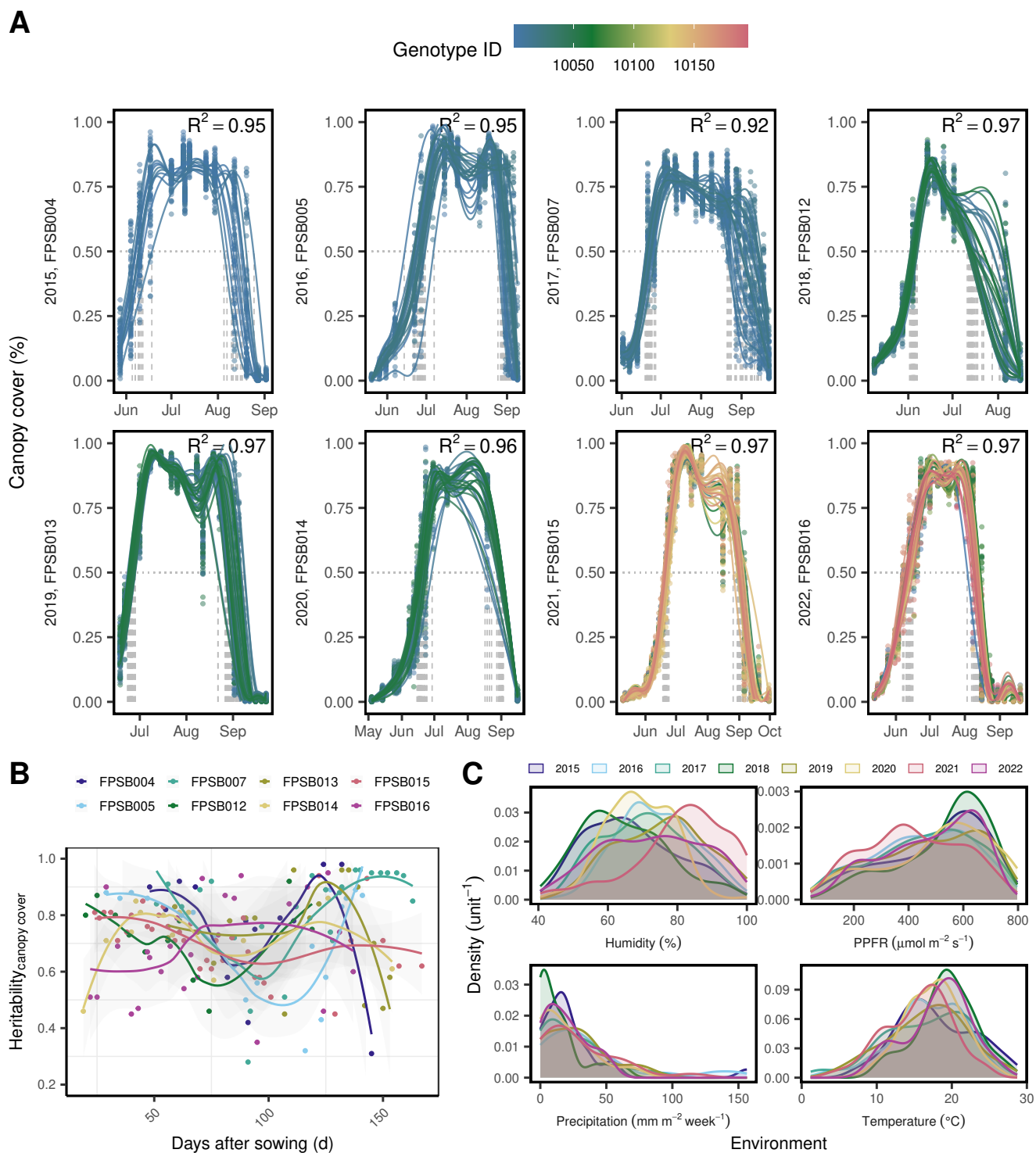


Figure 4: The canopy cover (CC) of genotypes including elite breeding lines and check varieties over eight years. A: The raise and decline of CC is fitted by a generalized additive model (GAM) for each genotype. Vertical dotted lines indicate the reach of 50% CC B: Heritabilities from CC values for each date were derived based on Spatial Analysis of Field Trials with Splines (SpATS). C: Kernel density plots show weather variables during the growing season.

A

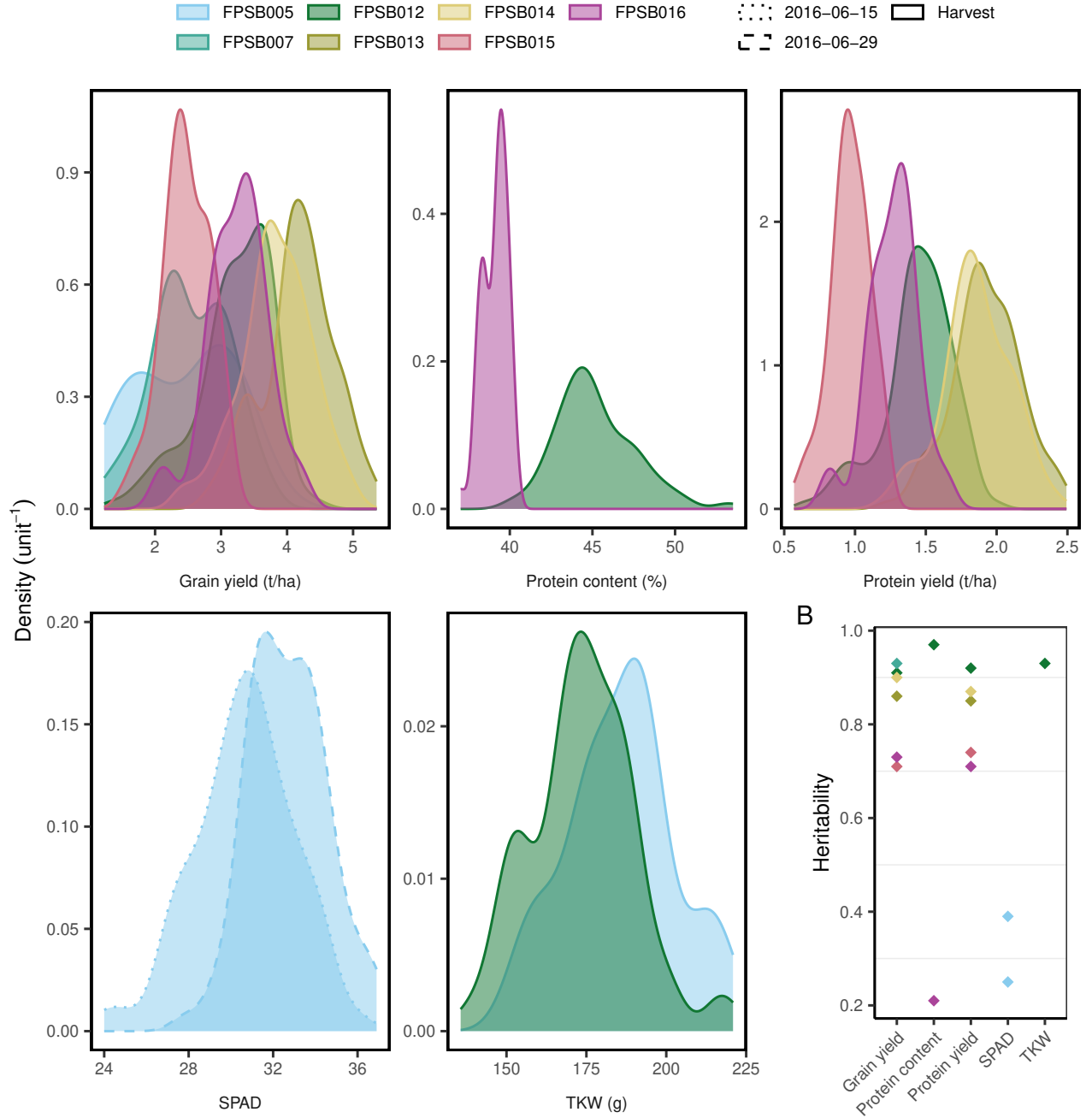


Figure 5: Reference traits. A: Kernel density plot of agricultural traits of the soybean genotypes per trial. The shaded area represents a smoothed estimate of the probability distribution of all plot values for each trial and trait. B: Heritabilities of the traits were derived based on Spatial Analysis of Field Trials with Splines (SpATS).

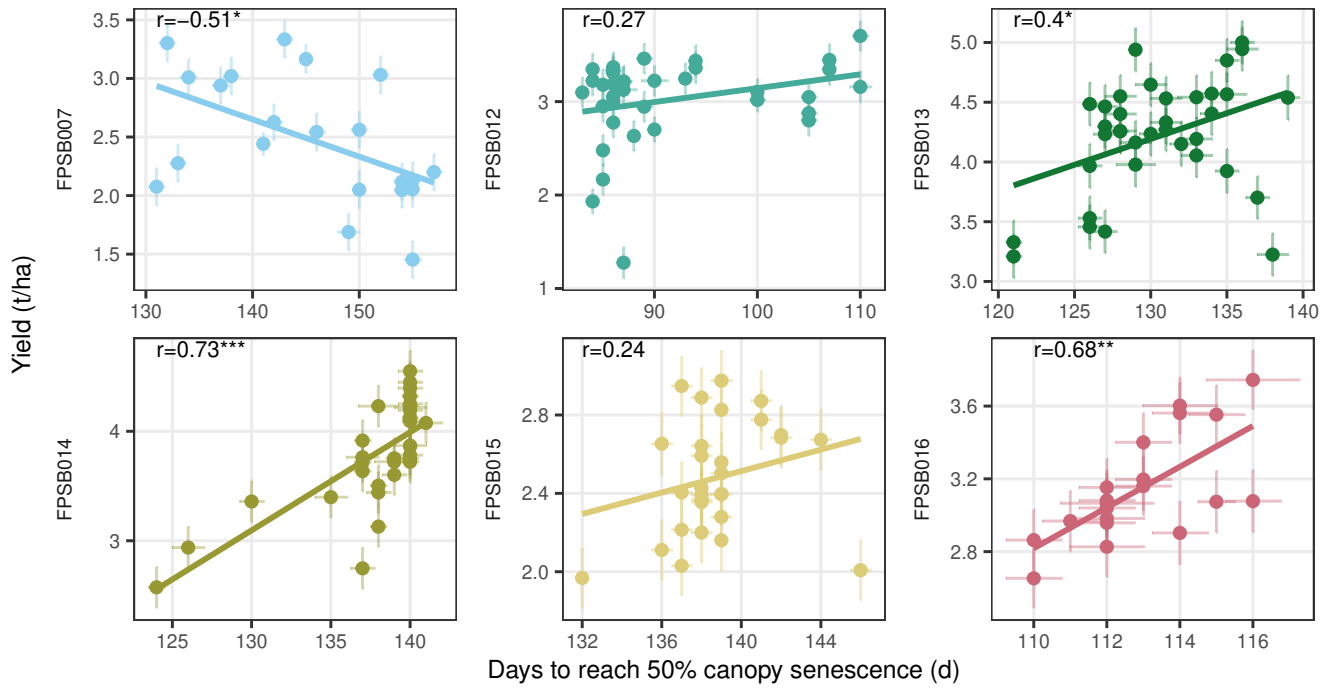


Figure 6: Correlation between threshold date (after 50% canopy cover crossing) and grain yield across environments. Pearson's correlation coefficients (r) with significance levels are shown per environment. Each point represents adjusted genotypic values. Grey error bars show standard error.

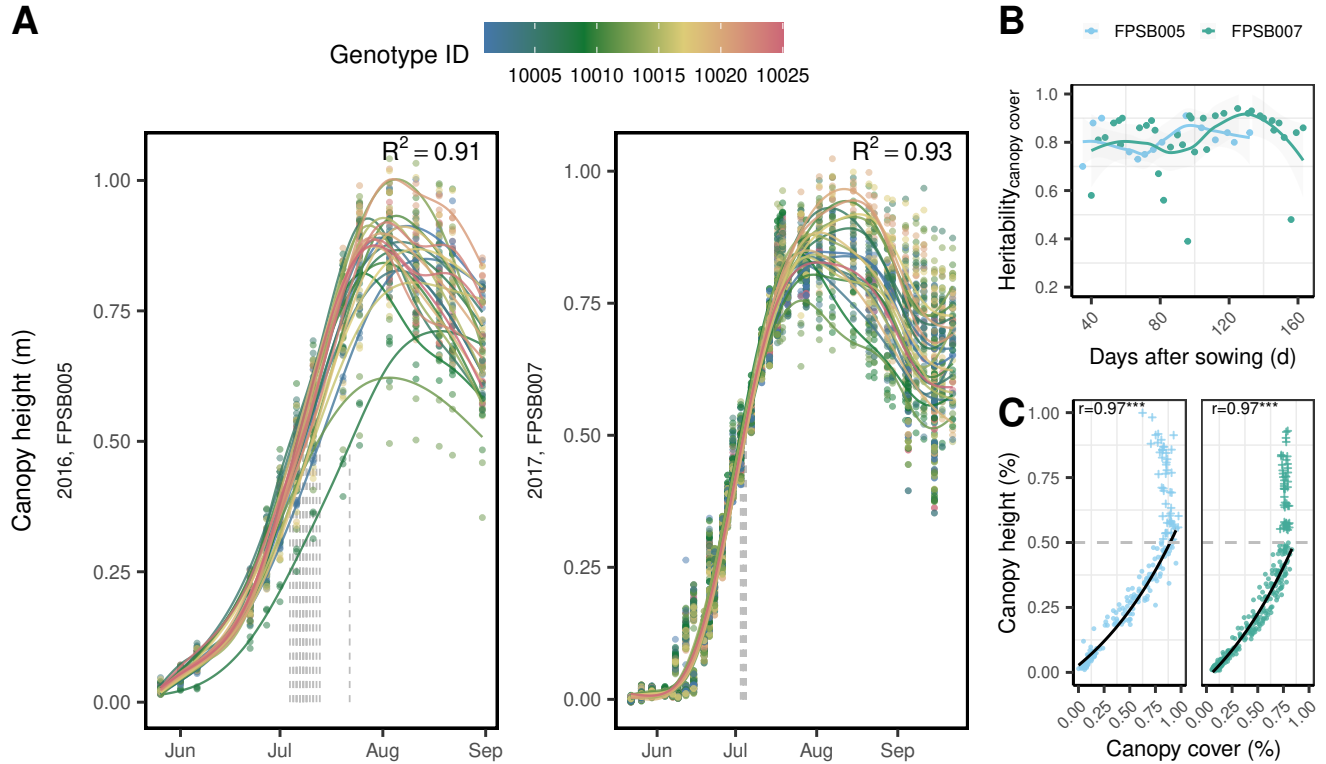


Figure 7: The canopy height of genotypes including elite breeding lines and check varieties over two years. A: The raise and decline of canopy height is fitted by a generalized additive model (GAM) for each genotype. Vertical dotted lines indicate the reach of 50% canopy height B: Heritabilities from canopy height values for each date are shown. C: Correlation between canopy height and canopy height across environments until reaching 50% of canopy height. The threshold is indicated by the grey dashed line. Pearson's correlation coefficients (r) with significance levels for p -values indicated by * $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$ are shown per environment. Each point represents adjusted genotypic value based on the GAM fit.

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Supplemental Materials

1 Supplemental information

1.1 Detailed description of genotypes

Supplementary Table 1: Genotype Information

No.	Genotype ID	Genotype Name	Breeder	Registration	Maturity Type
1	10001	Gallec	Agroscope/DSP	CH:2000	000
2	10002	Lissabon	Saatbau Linz	AT:2012	00
3	10003	Protéix	Agroscope/DSP	CH:2009	00
4	10004	Merlin	Saatbau Linz	AT:2007	000
5	10005	Obelix	Agroscope/DSP	CH:2014	000
6	10006	Aveline	Agroscope/DSP	CH:2005	000/00
7	10007	Tourmaline	Agroscope/DSP	CH:2013	00
8	10008	Amphor	Rustica	FR:2001	00
9	10009	Opaline	Agroscope	CH:2009	00
10	10010	Tiguan	Agroscope/DSP	CH:2014	0000
11	10011	Falbala	Agroscope/DSP	CH:2013	00/0
12	10012	Paradis	Agroscope/DSP	CH:2000	0000
13	10013	Protibus	Agroscope/DSP	CH:2013	00
14	10014	Amarok	Agroscope/DSP	CH:2014	000/00
15	10015	Coraline	Agroscope/DSP	CH:2014	00
16	10016	Galice	Agroscope/DSP	CH:2015	000/00
17	10017	Toutatis	Agroscope/DSP	CH:2015	000/00
18	10018	Tequila	Agroscope/DSP	CH:2013	00/0
19	10019	Bagera	Agroscope/DSP	CH:2007	00/0
20	10020	Idefix	Agroscope/DSP	CH:2002	0
21	10021	Pollux	Agroscope/DSP	CH:2012	00
22	10022	Orion	Agroscope/DSP	NA	0
23	10023	Castétis	Agroscope/DSP	IT:2010	I
24	10024	Paco	Agroscope/DSP	IT:2012	I/II
25	10025	MapleArrow	a	CA:1976	00
26	10044	22460	Agroscope/DSP	NA	000
27	10045	Navaro	Agroscope/DSP	CH:2020	000
28	10046	Paprika	Agroscope/DSP	CH:2020	000/00
29	10047	22511	Agroscope/DSP	NA	00
30	10048	CH90008	Agroscope/DSP	NA	000
31	10049	Amandine	Agroscope/DSP	CH:2012	000
32	10050	Aurelina	SZD	NA	000/00
33	10051	Everest	Agroscope/DSP	UA:2018	000
34	10052	Kalinka	Agroscope/DSP	CH:2017	00
35	10053	Marquise	Agroscope/DSP	AT:2017	00
36	10054	Mentor	NA	NA	00/0
37	10055	Naskia	Agroscope/DSP	CH:2017	000/00
38	10056	Primus	Eurasia	NA	00
39	10057	Xena	Agroscope/DSP	CH:2017	000/00
40	10058	Yakari	Agroscope/DSP	F:2018	00/0
41	10065	Soramax	Agroscope/DSP	CH:2024	00
42	10067	Alambix	Agroscope/DSP	CH:2023	000/00
43	10073	CH90132	Agroscope/DSP	AT:2024	00
44	10074	CH90137	Agroscope/DSP	NA	00
45	10085	CH90139	Agroscope/DSP	NA	00

No.	Genotype ID	Genotype Name	Breeder	Registration	Maturity Type
46	10098	CH22778	Agroscope/DSP	NA	000/00
47	10100	CH22776	Agroscope/DSP	NA	00
48	10121	CH90082	Agroscope/DSP	NA	00
49	10122	CH22725	Agroscope/DSP	NA	00
50	10126	CH22713	Agroscope/DSP	NA	000/00
51	10128	CH22681	Agroscope/DSP	F:2024	00/0
52	10134	CH22707	Agroscope/DSP	CH:2024	000/00
53	10135	CH22706	Agroscope/DSP	NA	00
54	10136	CH22727	Agroscope/DSP	NA	000/00
55	10137	CH22715	Agroscope/DSP	NA	000/00
56	10139	CH22711	Agroscope/DSP	AT:2023	000/00
57	10140	CH22691	Agroscope/DSP	NA	00
58	10143	CH22738	Agroscope/DSP	NA	000
59	10144	CH22645	Agroscope/DSP	CH:2024	000/00
60	10145	CH22654	Agroscope/DSP	NA	000/00
61	10147	CH22751	Agroscope/DSP	NA	00
62	10148	CH22729	Agroscope/DSP	NA	000/00
63	10149	CH22650	Agroscope/DSP	NA	000/00
64	10152	CH22655	Agroscope/DSP	CH:2024	000/00
65	10155	CH22653	Agroscope/DSP	NA	000/00
66	10158	CH22730	Agroscope/DSP	NA	00
67	10163	CH90077	Agroscope/DSP	NA	00
68	10169	CH90075	Agroscope/DSP	CH:2023	00
69	10170	CH22624	Agroscope/DSP	CH:2023	000
70	10172	CH22517	Agroscope/DSP	CH:2024	000/00
71	10178	CH90126	Agroscope/DSP	NA	00
72	10179	Sirelia	Agroscope/DSP	NA	000
73	10192	Gallec.Opaline	NA	NA	NA
74	10193	Tourmaline.Opaline	NA	NA	NA
75	10194	Gallec.Tourmaline	NA	NA	NA

1.2 Detailed description of field trials

Supplementary Table 2: Summary of soybean field trials (2015–2022) in Eschikon, Switzerland (47.449 N, 8.682 E, 556 m a.s.l.).

Year	Task	Date	Treatment	Rate	Rows per plot
2015	Soil Preparation	2014-11-24	Plowing	-	-
	Fertilization	2015-03-11	Superphosphate, Foskal, Dolomit	150 kg/ha, 350 kg/ha, 400 kg/ha	-
	Sowing	2015-04-10	Seeding	60 plants/m ²	9
	Weed Control	2015-04-10	Dual Gold, Molipan Pro	As recommended	-
	Weed Control	2015-04-14	Snail and slug bait	As recommended	-
	Weed Control	2015-05-28	Bolero	As recommended	-
	Weed Control	2015-06-10	Fusilade Max	As recommended	-
	Weed Control	2015-09-21	Roundup Power Max	As recommended	-
	Harvest	2015-09-08	Combine	-	-
2016	Soil Preparation	2016-03-15	Plowing	-	-
	Fertilization	2016-03-07	TSP 46, Kali	250 kg/ha, 350 kg/ha	-
	Sowing	2016-04-21	Seeding	-	9
	Weed Control	2016-04-21	Dual Gold, Molipan Pro	As recommended	-
	Weed Control	2016-04-21	Snail and slug bait	As recommended	-
	Weed Control	2016-06-01	Bolero	As recommended	-
	Weed Control	2016-06-01	Fusilade Max	As recommended	-
	Harvest	2016-09-28	Combine	-	-
2017	Soil Preparation	2017-02-27	Plowing	-	-
	Fertilization	2017-02-23	TSP 46, Kali	300 kg/ha, 400 kg/ha	-
	Sowing	2017-04-12	Seeding	40 plants/m ²	9
	Weed Control	2017-04-13	Dual Gold, Molipan Pro	As recommended	-
	Weed Control	2017-04-18	Snail and slug bait	As recommended	-
	Weed Control	2017-05-19	Snail and slug bait	As recommended	-
	Weed Control	2017-06-01	Bolero	As recommended	-
	Weed Control	2017-06-01	Fusilade Max	As recommended	-
	Weed Control	2017-06-10	Bolero (repeat)	As recommended	-
2018	Soil Preparation	2017-09-27	Combine	-	-
	Soil Preparation	2018-02-09	Plowing	-	-
	Fertilization	2018-02-06	TSP 46, Kali	300 kg/ha, 350 kg/ha	-
	Sowing	2018-04-19	Seeding	55 plants/m ²	3
	Weed Control	2018-04-24	Dual Gold, Molipan Pro	As recommended	-
	Weed Control	2018-04-30	Snail and slug bait	As recommended	-
	Weed Control	2018-05-22	Fusilade Max	As recommended	-
	Weed Control	2018-06-01	Bolero	As recommended	-
	Harvest	2018-08-28	Combine	-	-
2019	Soil Preparation	2019-01-21	Plowing	-	-
	Fertilization	2019-02-27	TSP 46, Kali, Mg-Ammonsalpeter	200 kg/ha, 200 kg/ha, 225 kg/ha	-
	Sowing	2019-04-23	Seeding	55 plants/m ²	3

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Year	Treatment Stage	Date	Treatment	Rate	Rows per Plot
	Weed Control	2019-04-24	Dual Gold, Molipan	As recommended	-
	Harvest	2019-09-24	Pro Combine	-	-
2020	Soil Preparation	2020-01-08	Plowing	-	-
	Fertilization	2020-03-13	TSP 46, Kali, Granumag	200 kg/ha, 200 kg/ha, 200 kg/ha	-
	Sowing	2020-04-15	Seeding	60 plants/m ²	3
	Weed Control	2020-04-16	Cargon S, Successor 600	As recommended	-
	Harvest	2020-09-21	Combine	-	-
2021	Soil Preparation	2021-01-05	Plowing	-	-
	Fertilization	2021-04-09	TSP 46, Kali, Granumag	200 kg/ha, 200 kg/ha, 200 kg/ha	-
	Sowing	2021-04-16	Seeding	60 plants/m ²	3
	Weed Control	2021-04-19	Cargon S, Successor 600	As recommended	-
	Weed Control	2021-06-02	Bolero	As recommended	-
	Harvest	2021-10-01	Combine	-	-
2022	Soil Preparation	2022-02-12	Plowing	-	-
	Fertilization	2022-03-08	TSP 46, Kali, Granumag	100 kg/ha, 150 kg/ha, 200 kg/ha	-
	Sowing	2022-04-21	Seeding	60 plants/m ²	3
	Weed Control	2022-04-22	Successor 600, Cargon S	As recommended	-
	Weed Control	2022-05-30	Bolero	As recommended	-
	Weed Control	2022-06-10	Bolero (repeat)	As recommended	-
	Weed Control	2022-06-10	Fusilade Max	As recommended	-
	Harvest	2022-09-23	Combine	-	-

1.3 Detailed camera acquisition description

Supplementary Table 3: Camera parameters per year, constant settings for all years: ISO = 100, White Balance = Auto white balance, Focal Length = 35 mm, Exposure Mode = Auto exposure, for all other parameters median values are shown.

Year	F number	Aperture Value	Exposure bias value	Exposure program	Exposure time
2018	16	8	-1	Aperture priority	0.016667
2019	4	4	0	Shutter priority	0.004
2020	8	6	-0.5	Shutter priority	0.004
2021	5.6	5	0	Shutter priority	0.004
2022	6.7	5.5	0	Shutter priority	0.004
all years	6.7	5.5	0	Shutter priority	0.004

Supplementary Table 4: Structure of the filenames and the information it contains

Filename structure	Example
Raw file name	FPSB0130031_RGB1_20190618_150650.CR2
Experiment name	FPSB013
Plot number	0031
Sensor name	RGB1
Date	20190618
Time	150650
File extension	CR2

1.4 Detailed description of canopy cover extraction

1.4.1 Segmentation

Green filter to extract canopy cover was applied as described in [22]. The `pixel_check` function analyzes an RGB image to segment green canopy from the background. It loads the images and iterates over each pixel, applying thresholding conditions to classify pixels as leaf, scale, or background based on minimum red (R) and green (G) values as well as ratios between red, green and blue. Identified green pixels are saved as a segmentation image, while the original image is resized and saved with 90% JPEG compression for further processing.

1.4.2 Plot detection without canopy closure

The function `get_row_pixels` processes the segmented images to extract and analyze plant rows based on pixel data. It trims unnecessary parts at the top and bottom based on `cut_above` and `cut_below` input values. It requires information about the maximum rows (`max_cluster`) expected to be visible in one image, the minimum rows (`min_cluster`) which define the rows belonging to the plot, and the expected row distance (`row_distance_min`) in pixels to ensure consistent row detection.

The cleaned dataset is then used to determine the pixel count for the middle row and the row distance. The final output includes extracted row data, row an plot positions, and plant pixel counts within each row section Supplementary Table 5.

Supplementary Table 5: Description of Columns in ‘data/Soybean.CanopyCover.Raw.data.csv’

Column Name	Description
Filename	The name of the processed image file including unique identifier for the plot.
Row_cluster_corr	The assigned cluster label for each detected row.
Sum.Pixel_row	The total number of pixels classified as green canopy cover in the row.
SD.Pixel_row	The standard deviation of the pixel count for every x-axis value within the row.
Row_middle	The median y-coordinate of the detected row.
Lower_row_border	The lower boundary of the detected row (y-coordinate).
Upper_row_border	The upper boundary of the detected row (y-coordinate).
Plot_slope	The estimated slope of the row to correct for image distortion.
min_y_at_x0	The minimum y-coordinate at x = 0 (leftmost edge).
max_y_at_x0	The maximum y-coordinate at x = 0 (leftmost edge).
min_y_at_xmax	The minimum y-coordinate at the maximum x value (rightmost edge).
max_y_at_xmax	The maximum y-coordinate at the maximum x value (rightmost edge).
Sum.Pixel_plot	The total number of plant pixels detected in the entire plot.

1.4.3 Plot detection with canopy closure

When the canopy is closed, individual plots cannot be recognized easily on the presented images. The `get_plot_borders_mean()` function aggregates row-based position data across all measurements in early stages of the plants to determine plot boundaries. The input data is created with the above described `get_row_pixels` function. It cleans and removes outliers, computes upper and lower plot borders, and the average slope of the plot for later correction. This function helps localize the exact plot area in images, ensuring that extracted plant data is correctly positioned.

Then, the `get_green_canopy_plot_cover()` function processes segmented images to compute the green canopy cover for a full plot when the rows have completely covered the soil. It first loads the relevant image from each provided (*folder*) path, adjusts for plot borders and slope using previously estimated border values, and extracts plant pixels by filtering color channels. The total green fraction is calculated as the ratio of green pixels to total pixels. The function then generates visualizations, saves processed images with segmentation overlays, and exports a .csv file containing pixel counts and canopy cover percentages.

Supplementary Table 6: Output variables when detecting plots with closed canopy

Variable	Description
Filename	The name of the processed image file.
x_r	The rounded x-coordinate used for segmentation.
Sum_Pixel_row	The total number of plant pixels detected in the plot.
SD_Pixel_row	Standard deviation of the pixel count within the plot.
Canopy_cover	The percentage of the image covered by green pixels.
Plot_width	The estimated width of the plot in pixels.
min_y_at_x0	Minimum y-coordinate at x = 0 (leftmost edge).
max_y_at_x0	Maximum y-coordinate at x = 0 (leftmost edge).
min_y_at_xmax	Minimum y-coordinate at the maximum x value (rightmost edge).
max_y_at_xmax	Maximum y-coordinate at the maximum x value (rightmost edge).

1.5 Stable extraction of canopy cover

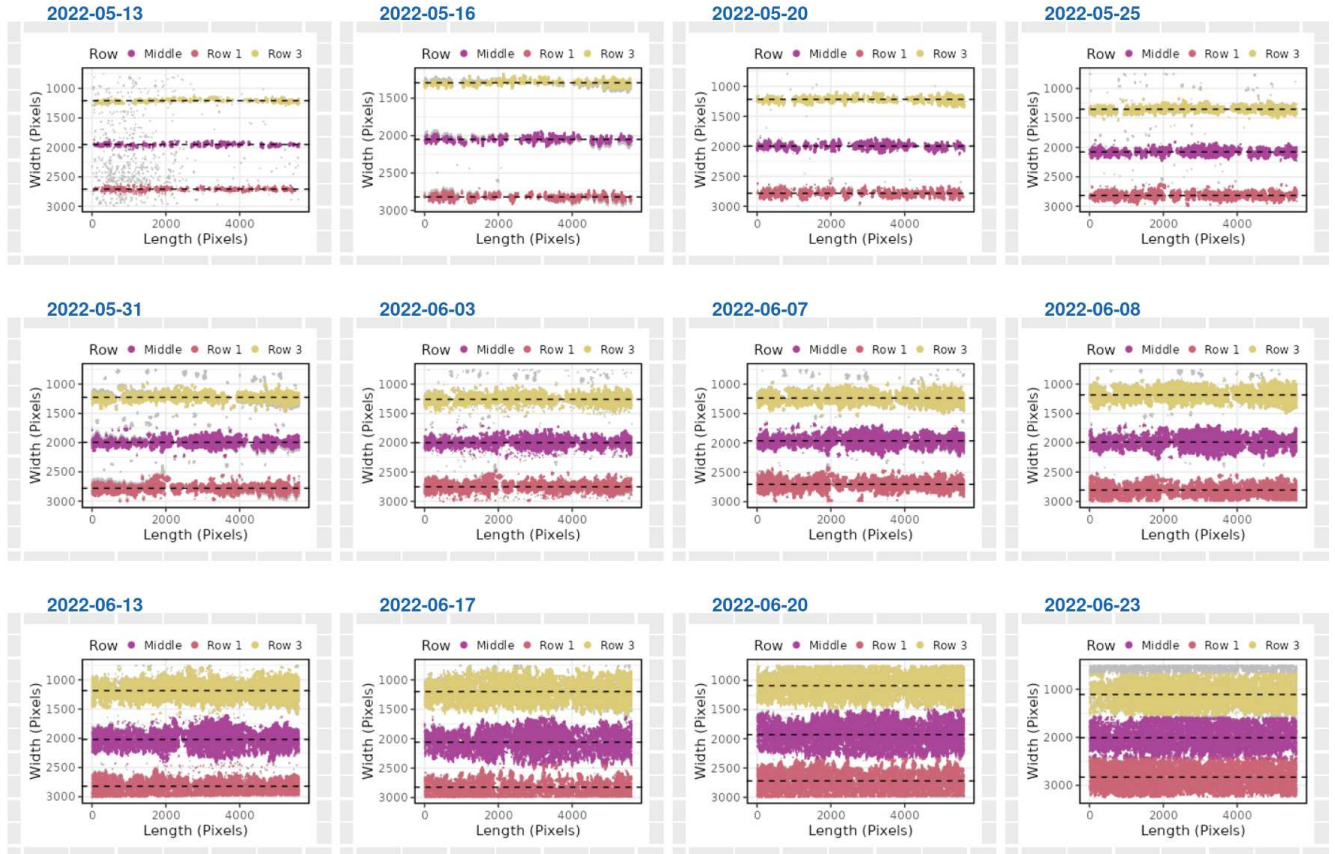
First, a data set for canopy cover is created by previously observed proportion of green pixels compared to the pixels in the entire plot. In parallel, Row_distance analyzes row spacing by detecting individual plant rows and calculating the distances between their middle points. To ensure accuracy, outliers are removed, and a rolling mean is applied to smooth variations in row spacing. Since some plots may have non-uniform plant distributions, it helps to adjust canopy cover estimates by normalizing green pixel counts based on row structure rather than just total pixels. The two datasets are then merged into one, which integrates both total canopy cover and row-based spacing measurements to calculate relative canopy cover. This ensures relative comparisons across genotypes and differences in planting density and row spacing. Outliers are removed before visualization, allowing for clearer growth trend analysis. This final dataset provides a standardized measure of canopy cover, making it more reliable for genotype comparisons and plant growth assessments over time (for the resulting csv file see: data/Soybean_CanopyCover_data.csv).

1.6 Detailed trait description

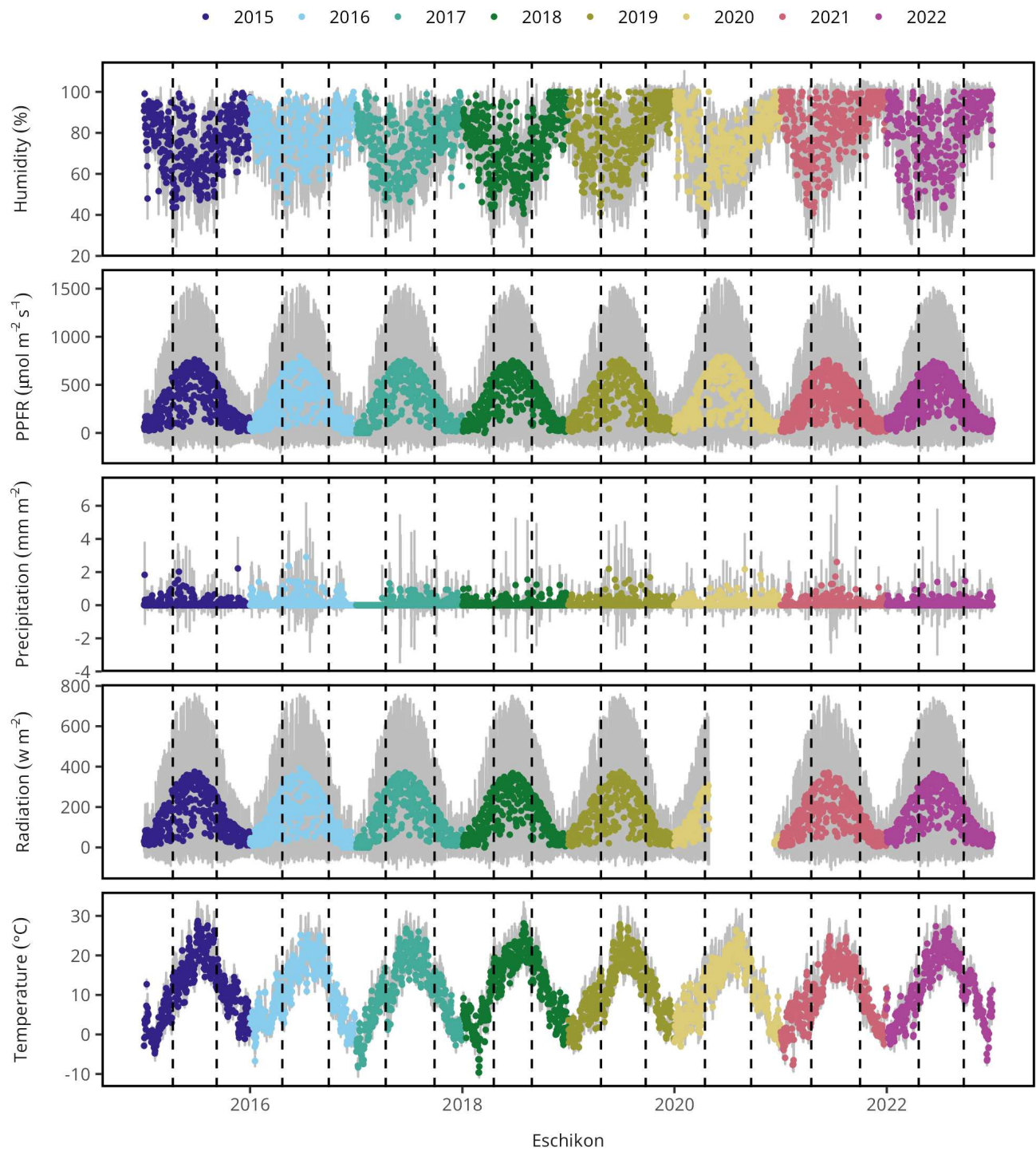
Supplementary Table 7: MIAPPE-compliant trait ontology for soybean phenotyping

Trait Label	Trait Name	SI Unit	Method ID	Method Name
CC	Canopy cover	percent	M01	High-resolution RGB image analysis (top canopy) using FIP platform with loess/spline-based smoothing
SPAD	Chlorophyll content (SPAD)	SPAD unit	M02	Handheld chlorophyll meter measurement (SPAD-502)
TKW	Thousand kernel weight	g	M03	Automatic thousand seed weight determination using seed counter
Protein_content	Protein content	percent	M04	NIRS measurement with Perten 7200 Diode Array (three replicates in 2018 & 2022, single replicate otherwise)
Moisture_content	Moisture content	percent	M05	NIRS moisture content estimation (corrected using averaged 3-rep values where available)
Yield	Grain yield (11% moisture)	t/ha	M06	Weighed grain yield, corrected to a standardized moisture content of 11%

Plot: FPSB0160012



Supplementary Figure 1: Identification of the rows and middle row. Row were detected to localize the plot and determine canopy cover (CC).



Supplementary Figure 2: Weather variables. Vertical dotted lines indicate sowing respective harvest date.