Genetic parameters and yield potential of Indonesian soybean varieties (*Glycine max* L.) in wetland during dry season

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Abstract

Cultivating soybean in wetland areas presents unique challenges, particularly during water-limited conditions like dry season, where yield performance can vary significantly among genotypes. This research aimed to assess the yield potential of Indonesian soybean varieties in wetland during dry season, to estimate genetic parameters, and to determine the relationship among traits. Twenty soybean genotypes were evaluated using Randomized Complete Block Design (RCBD) with three replications. Yield components measured included seed weight per plot, number of seeds per plant, and overall yield potential (tons per hectare). The results revealed significant variation among the genotypes. The estimation of genetic parameters indicates that traits comprising plant height, 100-seed weight, and the number of seeds per plant have high heritability and significant CV_G/CV_P ratios, suggesting efficient genetic selection potential and opportunities for genetic improvement through breeding. Pearson's correlation network plot shows positive associations between traits, including plant height (PH), weight of biomass (WB), weight of seed per plot (WSP) and yield. 'Deja 1' variety exhibited the highest yield potential at 1.75 tons per hectare, while 'BS 99' variety showed the lowest at 0.18 tons per hectare. These findings underscore the importance of genotype selection in enhancing soybean productivity in water-limited environments. The study offers valuable insights for future breeding programs aimed at improving soybean yields in challenging conditions, such as dry season in wetlands, thereby contributing to sustainable agricultural practices in Indonesia.

INTRODUCTION

Soybean (*Glycine max* L. Merr.) is one of the main food crops that play a significant role in meeting the demand for plant-based protein in Indonesia. In addition, its high nutritional content, such as protein (40–45%), fat (18–21%), and carbohydrates (26–30%), has led to an increase in soybean consumption (Tanwar and Goyal, 2020). Soybean protein has several advantages, including its low cost, non-animal origin, relatively long shelf life, and classification as a globular protein containing conglycinin and glycinin (Montanha

et al., 2022). The high nutritional content of soybeans makes it a viable alternative food source in Indonesia.

Soybean productivity in Indonesia is still relatively low. The national demand for soybeans continues to increase each year in line with population growth and rising demand from the food industry (Terryana et al., 2020). The 2020 Pusdatin projection showed that soybean productivity in 2023 was 1.76 tons/ha. This figure was lower compared to the average soybean productivity over the past five years in the three major global soybean exporting countries, namely Brazil (4 t/ha), United States (3.4 t/ha), and Argentina (2.8

t/ha) (United States Department of Agriculture, 2023). According to Harsono et al. (2022), Indonesia's total soybean production in 2023 was 576,278 tons, while the national demand for soybeans was 3,163,759 tons. The high demand for soybeans has led to continuous large-scale imports, making Indonesia dependent on soybean imports (Ardiansyah and Faridatussalam, 2023). Therefore, reliance on soybean imports will impact Indonesia's overall food security.

The increasing demand for soybeans has made enhancing their productivity a priority in the agriculture sector. Soybean yield is affected by factors such as agroclimatic conditions, land management, and the genetic characteristics of each variety (Mburu et al., 2022; Rychel-Bielska et al., 2024). Basically, wetlands have the ability to store water longer compared to drylands (Grenfell et al., 2022). Research conducted by Adie et al. (2022) found that some soybean varieties showed better performance when planted in wetlands compared to drylands. Understanding the interaction between soybean and the growing environment, especially in wetlands, is crucial to increase yield.

The dry season can be utilized as an alternative for crop cultivation to meet national food needs and has great potential in diversifying planting times and extending the annual production period. However, drought stress leads to a reduction in photosynthetic carbon assimilation capacity, which seriously affects soybean seed weight (Du et al., 2020a). The accumulation of photosynthetic products varies greatly between plant species (Onder et al., 2022). Additionally, long-term drought stress decreases biomass allocation to reproductive organs, alters photosynthetic pigments, weakens antioxidant capacity, and reduces seed weight (Du et al., 2020b; Markulj Kulundžić et al., 2022). Therefore, selecting drought-tolerant soybean varieties is necessary to ensure optimal growth even under limited water supply conditions.

Hence, the evaluation of Indonesian soybean varieties with high yield potential and drought tolerance during the dry season is imperative. This research aimed to assess the yield potential of Indonesian soybean varieties under wetland conditions during the dry season, to estimate genetic parameters, and to determine the relationship among traits. Understanding these genetic factors and trait correlations allows breeders to develop varieties that are high-yielding and resilient to water stress. This study also provides valuable insights into the genetic variability within the soybean population, essential for designing effective breeding strategies.

MATERIALS AND METHODS

The planting materials used in this study consisted of 20 soybean genotypes, including registered 16 yellow soybean varieties and four black soybean genotypes, which are crossbreed lines from the Plant Breeding Laboratory, Universitas Padjadjaran (presented in Table 1).

This research was conducted at the Ciparanje Experimental Field, Faculty of Agriculture, Universitas Padjadjaran, from April to June 2023 planting season. The experimental design used was a Randomized Complete Block Design (RCBD) with 20 treatments (representing 20 genotypes) and three replications. The soybean genotypes were planted on former wetland, with plot dimensions of 1.2 m × 5 m and a planting space of 40 cm × 15 cm. In each row of a plot, there were 33 planting holes, so a three-row plot consisted of 99 planting holes. The total number of experimental plots was 60, representing 20 genotypes made into three replications each. The number of samples taken for observation was five plants from each treatment in each replication.

The observed traits in this study consisted of nine yield components, including plant height (cm), generative growth phase (R1–R8), seed filling period (SFP), biomass weight (g), number of seeds per plant, seed weight per plant (g), 100-seed weight (g), weight of seeds per plot (g) and potential seed yield (tons/ha). Plant height (PH) was measured using a ruler or measuring tape from the soil surface to the tip of the main stem at full maturity (R8 stage). Generative growth phase (R1–R8) was observed based on the Fehr and Caviness phenological scale, covering the stages from beginning bloom (R1) to full maturity (R8), with daily or weekly recordings to determine its duration. Seed filling period (SFP) was calculated as the difference between the beginning seed stage (R5) and physiological maturity (R7). Biomass weight (WB) was measured by drying the entire plant in an oven at 70°C for 72 hours until a constant weight was achieved, followed by weighing with an analytical balance. Number of seeds per plant (NSP) was manually counted from randomly selected plants within the plot, while seed weight per plant (WSP) was determined by weighing the total seeds of each plant using a precision scale. 100-seed weight

Table 1. List of 20 Indonesian soybean genotypes

Genotype	Pedigree	Status
Argomulyo	Introduction of Nakhon Sawan soybeans	Released (1998)
Anjasmoro	Mass selection of the population of pure lines of MANSURIA	Released (2001)
Biosoy	M-B-2896-1 line selection	Released (2017)
Dega 1	Single cross between Grobogan x Malabar	Released (2016)
Deja 1	Single cross of the Tanggamus x Anjasmoro variety	Released (2017)
Deja 2	single cross of the Sibayak x local variety of central java	Released (2017)
Gepak kuning	Selection of local varieties of Gepak Kuning	Released (2008)
Demas 1	Mansuria x SJ cross selection	Released (2014)
Dena 1	Selection of crosses Agromulyo x IAC 100	Released (2014)
Dena 2	IAC 100 x Ijen cross selection	Released (2014)
Derap 1	G511H x Anjasmoro cross selection	Released (2017)
Dering 1	Single cross of the superior variety Davros x MLG	Released (2012)
Detap 1	G511H x Anjasmoro cross selection	Released (2017)
Devon 1	Selection of Kawi varieties x IAC 100 strains	Released (2015)
Devon 2	G511H x Anjasmoro cross selection	Released (2015)
Grobogan	Purification of the local population of Malabar	Released (2008)
BS 79	Cross between UP106 x UP 122	F6
BS 87	Cross between UP106 x UP 122	F6
BS 99	Cross between UP106 x UP 122	F6
BS 114	Cross between UP106 x UP 122	F6

Table 2. Average climate and soil properties of the experimental environment

Temperature (°C)	Rain fall (mm)	Humidity (%)	Soil texture	pH H$_2$O	Organic C (%)	N (%)	C/N (%)
23.13	52.33	87.66	Silty Clay Loam	6.34	3.32	0.34	10.00

(W100) was measured by randomly selecting 100 seeds from the harvested sample and weighing them using a digital balance. Weight of Seeds per Plot (WSP) was obtained by harvesting all plants within the plot, separating the seeds, drying them to 13% moisture content, and weighing them with a digital scale. Fertilization was applied when the plants were 14 days after planting (DAP). The fertilizer used was NPK Phonska at a dose of 250 kg/ha or 150 g/plot. The soil properties at the experimental site were characterized prior to planting, with composite sampling conducted at a soil depth of 15−30 cm. Soil properties and climate conditions of the wetland during dry season are presented in Table 2.

The soybean yield potential was calculated based on Triyanti (2020) using the following equation:

Yield potential (ton ha^{-1}) = (number of plants per hectare × number of seeds per plant × seed wight per plant (kg))/1,000 ....(1)

Genotypic coefficient of variation and phenotypic coefficient of variation were calculated with the following equation (Kearsey and Pooni, 1996):

$$CV_G = \frac{\sqrt{\sigma^2_G} \times 100}{\overline{x}} \quad \text{.....................................(2)}$$

$$CV_P = \frac{\sqrt{\sigma^2_P} \times 100}{\overline{x}} \quad \text{.....................................(3)}$$

Broad-sense heritability was calculated based on the following equation:

$$H^2_b (\%) = \frac{\sigma^2_G}{\sigma^2_G + \sigma^2_E} \quad \text{.....................................(4)}$$

Where σ^2_E = environmental variance; σ^2_G = genetic variance; σ^2_P = phenotypic variance; H^2_b = broad sense heritability; CV_G = genotypic variation coefficient; CV_P = phenotypic variation coefficient; $\overline{x}$ = mean of the trait being measured.

All the statistical analyses were performed using R Studio, R version 4.4.1. Data analysis was conducted using Analysis of Variance (ANOVA). Estimation of variance components and genetic parameters were performed by using "lme4" package version 1.1−35.5

(Bates et al., 2024). The correlation matrix was performed as network plot, constructed by using "corrr" package version 0.4.4 (Kuhn et al., 2022).

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) results for various observed traits are presented in Table 3. All the genotypes showed a significant variation in all the traits at a 5% significance level. This result signifies substantial genetic variability among the genotypes based on the observed traits. According to Valliyodan et al. (2021), a phenotypic variation is caused by differences in genetic structures, relationships, and linkage disequilibrium. The coefficient of variation (CV%) provides insight into the relative variability of each trait, with WSP exhibiting the highest CV at 19.18%, indicating that weight of seed per plant exhibits the greatest degree of variation compared to the other variables. This elevated variability is attributed to suboptimal experimental environmental conditions, which likely disrupt key physiological processes in the plants, thereby affecting potential seed yield (Vogel et al., 2021). Significant genetic variability in yield and yield components between the genotypes was observed, indicating the impact of genetic differences and non-optimal environmental conditions on yield potential.

Results of the Scott-Knott Test on yield components and soybean yield are presented in Table 4. Significant variation in plant height (PH) was observed across the 20 soybean genotypes tested. The highest plant height was observed in Deja 1 (47.17 cm), followed by Dena 1 (42.22 cm), indicating better vertical growth compared to the other genotypes. In contrast, Dena 2 exhibited the lowest plant height (20.17 cm), suggesting limited vegetative growth potential under the tested conditions. The variation in plant height could be attributed to genetic differences or environmental interactions, impacting the plant's ability to compete for light and resources (Ghorbani et al., 2019), which may further influence yield components (Majidian et al., 2024). A study conducted by Palaniyappan et al. (2023) reported that the plant height was positively correlated with total biomass production. The biomass weight significantly varied between the genotypes, ranging from 0.33 g (BS 79) to 1.20 g (Dena 1). Genotypes like Dena 1 and Deja 2 exhibited higher biomass production, suggesting better growth performance and potential for increased photosynthetic capacity, which could be favorable for yield.

The weight of 100 seeds (W100) reflects the size and density of the seeds, serving as an indicator of seed quality and potential yield of the soybean plants. The Biosoy genotype showed the highest weight (24.80 g), while Gepak Kuning had the lowest weight (10.06 g). In addition, the number of seeds per plant (NSP) was the highest in Demas 1 (204.94), but it had a relatively low W100. Similarly, the Grobogan genotype had the lowest NSP (32.72) but a relatively high W100. The research conducted by Sehgal et al., (2018) found that an increase in 100-seed weight is associated with larger seed, as shown in Figure 1. However, a larger seed size tends to lead to a reduction in the number of seeds produced. This is likely due to an interruption during the critical period for determining seed number, which spans from the R1 growth stage (initial bloom) to the period between the R5 (the beginning of seed filling) and R6 stages (Egli, 2017), particularly during dry seasons. A higher number of seeds and larger seed size usually contribute directly to an increase in total yield, although other factors, such as seed size and environmental conditions, also play a role. Genotypes with a higher weight of seeds per plot (WSP), such as Deja 1 (0.99 kg) and Gepak Kuning (0.58 kg), demonstrated the efficiency of these genotypes in

Table 3. The F-test results for yield components and yield of 20 soybean genotypes

Source	Df	PH	WB	W100	WSP	WST	SFP	NSP	R1–R8	Yield
GEN	19	19.7**	14.0**	72.1 **	7.6**	4.7**	58.6**	33.7 **	3.1**	8.6**
REP	2	17.6**	62.0**	1.2 ns	19.1**	461.6**	99.6**	2.6 ns	103.1**	16.8**
Residual	38	10.0	0.02	0.88	13916.6	0.009	0.39	122.9	0.36	0.01
CV (%)		9.74	15.65	5.69	19.18	7.41	2.57	13.98	0.98	11.5

Remarks: PH = Plant Height; WB = Weight of Biomass; W100 = Weight of 100 Seeds; WSP = Weight of Seeds per Plot; WST; Weight of Seeds per Plant; SFP = Seed Filling Period; NSP = Number of Seeds per Plant; ** = Significant at 5% significance level; ns = non-significant.

Table 4. Results of the Scott-Knott Test on yield components and yield of 20 soybean genotypes

Genotype	PH	WB	W100	NSP	WST	WSP	SFP	R1-R8	YIELD
Argomulyo	37.42 c	0.82 c	18.62 c	49.56 a	1.19 a	0.71 d	20.33 a	62.67 b	1.07 d
Anjasmoro	26.56 b	0.62 b	23.67 d	37.02 a	1.21 a	0.41 b	19.81 a	62.67 b	0.81 c
Biosoy	22.92 a	0.66 b	24.80 d	65.78 b	1.42 b	0.57 c	19.31 a	62.33 b	0.90 c
Dega 1	27.09 b	0.77 b	22.65 d	42.17 a	1.22 a	0.64 c	19.81 a	62.33 b	0.90 c
Deja 1	47.17 e	1.11 d	16.06 b	91.94 d	1.46 b	0.99 e	26.00 b	61.00 a	1.31 d
Deja 2	41.05 d	1.19 d	15.91 b	71.83 c	1.32 a	0.81 d	27.00 b	62.00 b	1.14 d
Gepak kuning	36.78 c	0.89 c	10.06 a	103.60 d	1.35 a	0.58 c	26.00 b	62.67 b	0.96 c
Demas 1	35.23 c	0.89 c	11.79 a	204.94 e	1.60 b	0.72 d	25.67 b	61.67 a	1.08 d
Dena 1	42.22 d	1.20 d	17.46 c	104.35 d	1.41 b	0.75 d	26.00 b	62.00 b	1.11 d
Dena 2	20.17 a	0.67 b	14.83 b	103.94 d	1.47 b	0.59 c	26.00 b	61.67 a	0.98 c
Derap 1	26.84 b	0.75 b	19.30 c	49.00 a	1.22 a	0.58 c	26.31 b	62.67 b	0.96 c
Dering 1	40.05 d	1.14 d	13.09 a	98.29 d	1.43 b	0.75 d	26.33 b	61.67 a	1.09 d
Detap 1	40.54 d	0.99 c	18.19 c	57.56 b	1.29 a	0.64 c	26.00 b	61.33 a	1.09 d
Devon 1	36.88 c	1.00 c	16.56 b	75.39 c	1.35 b	0.72 d	26.33 b	61.33 a	1.08 d
Devon 2	40.93 d	0.92 c	17.95 c	82.06 c	1.44 b	0.69 d	27.00 b	62.33 b	1.07 d
Grobogan	28.99 b	1.07 d	23.34 d	32.72 a	1.13 a	0.57 c	20.33 a	62.67 b	0.96 c
BS 79	22.01 a	0.33 a	10.99 a	67.00 b	1.15 a	0.28 b	25.67 b	61.00 a	0.65 b
BS 87	27.85 b	0.67 b	11.24 a	80.44 c	1.23 a	0.58 c	25.81 b	62.00 b	0.98 c
BS 99	22.73 a	0.43 a	11.75 a	77.84 c	1.24 a	0.12 a	26.00 b	61.33 a	0.42 a
BS 114	26.91 b	0.52 a	11.88 a	90.11 d	1.28 a	0.54 c	26.00 b	61.00 a	0.93 c

Remarks: PH = Plant Height; WB = Weight of Biomass; W100 = Weight of 100 Seeds; NSP = Number of Seeds per Plant; WST= Weight of Seeds per Plant; WSP = Weight of Seeds per Plot; SFP = Seed Filling Period. Means followed by the same lowercase letters in the same column are not significantly different based on Scott-Knott multiple range test at 5 %..

Figure 1. Seed phenotype variation among 20 soybean genotypes

producing seeds in wetland during dry season. Significant variation in yield component across genotypes was caused by decreased soil water content in wetlands during the dry season.

Reproductive Stage 1 to Reproductive Stage 8 (R1–R8) indicates the total duration from the R1 stage (initial flowering) to the R8 stage (physiological maturity). Variation among genotypes shows that some, such as Deja 1 (61.0 days) and Demas 1 (61.7 days), have a shorter reproductive cycle compared to others, such as Argomulyo and Anjasmoro (62.7 days), which have a longer reproductive period.

This where seed development (Saryoko et al., 2017) and pod filling occur (Rahimi-Moghaddam et al., 2023). This phase is directly related to the final yield, as a longer R1–R8 stage allows the plants to optimize seed filling (Rani et al., 2023). SFP (Seed Filling Period) measures the duration from the start of seed filling to seed maturity (Nakagawa et al., 2020). Genotypes with a longer seed filling period, such as Deja 1 (26.0 days) and Demas 1 (25.7 days), tend to produce higher-quality seeds, as they have more time to accumulate biomass in the seeds (Kang et al., 2016). However, genotypes like Gepak Kuning, with a shorter SFP (20.3 days), may result in smaller seeds or suboptimal seed filling. This period is crucial

as it is the stage where seed size and quality are actively determined.

The estimation of variance components (Table 5) indicates that the phenotypic variance is greater than the genotypic variance, but the difference is not statistically significant. Consequently, the heritability estimates for the traits are relatively high, such as for W100 (0.95) and NSP (0.91), suggesting that the inheritance pattern of these traits is not influenced by environmental factors. These findings align with previous research on black bean (Ambrósio et al., 2024). According to Resende (2002), heritability is classified as low (h < 0.15), median (0.15 < h < 0.50), and high magnitude (h > 0.50). The genotypic

Table 5. Estimated variance components and genetic parameters

Component	PH	WB	W100	WSP	WST	SFP	NSP	R1–R8	Yield
σ_G	62.73	0.05	20.95	0.03	53.75	3.36	1341.96	0.25	0.09
σ_E	10.03	0.02	0.88	0.01	380.62	4.19	122.86	0.36	0.06
σ_P	72.77	0.08	21.83	0.04	434.37	7.55	1464.83	0.61	0.16
H^2_b	0.86	0.67	0.95	0.68	0.12	0.44	0.91	0.40	0.58
Accuracy	0.92	0.82	0.97	0.83	0.35	0.66	0.95	0.63	0.76
CV_G	24.35	28.09	27.72	28.53	21.79	7.40	46.20	0.80	31.06
CV_P	9.74	19.36	5.69	19.13	57.98	8.27	13.98	0.97	26.18
CV_G/CV_P	2.50	1.45	4.86	1.49	0.37	0.89	3.30	0.82	1.18

Remarks: SFP = Seed Filling Period; W100 = Weight of 100 Seeds; NSP = Number of Seeds per Plant; PH = Plant Height; WST= Weight of Seeds per Plant; WSP = Weight of Seeds per Plot; WB = Weight of Biomass.
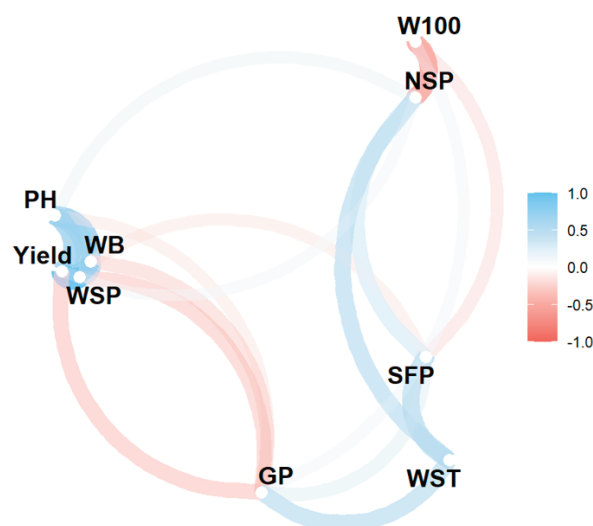
Figure 2. Pearson's correlation network plot between traits

Remarks: SFP = Seed Filling Period; W100 = Weight of 100 Seeds; NSP = Number of Seeds per Plant; PH = Plant Height; WST= Weight of Seeds per Plant; WSP = Weight of Seeds per Plot; WB = Weight of Biomass, GP = Generatif Phase (R1–R8).

Table 6. Yield potential of soybean genotypes in wetland during dry season

Genotype	Yield per plot (kg)	Yield potential (ton ha^{-1})
Argomulyo	0.69	1.14
Anjasmoro	0.40	0.67
Biosoy	0.39	0.65
Dega 1	0.50	0.83
Deja 1	1.05	1.75
Deja 2	0.79	1.32
Gepak kuning	0.57	0.95
Demas 1	0.72	1.20
Dena 1	0.76	1.26
Dena 2	0.58	0.97
Derap 1	0.55	0.92
Dering 1	0.71	1.19
Detap 1	0.74	1.24
Devon 1	0.71	1.18
Devon 2	0.69	1.15
Grobogan	0.56	0.94
BS 79	0.26	0.43
BS 87	0.58	0.97
BS 99	0.11	0.18
BS 114	0.52	0.87

coefficient of variation (CV$_G$) is lower than the residual coefficient of variation (CV$_P$) for the traits WST, SFP, and R1–R8, indicating that these traits are less effective for selecting superior genotypes at this stage of the breeding program.

Pearson's correlation analysis among traits is presented in a network plot. Blue colors represent positive correlations, while red colors indicate negative correlations. Figure 2 shows that yield is positively correlated with PH, WB, and WSP, whereas W100 is negatively correlated with NSP. The network plot reveals that yield, PH, WB, and WSP are in close proximity in one cluster. Similarly, GP, SFP, and WST are in close proximity in another cluster, while W100 and NSP form a separate cluster. The proximity of traits in the plots was determined by using multidimensional clustering (Almeida et al., 2017). Similar Pearson's correlations were performed on maize (Singamsetti et al., 2023) and pearl millet (Khandelwal et al., 2024). Visualization of correlations using a network plot facilitates rapid interpretation of the analysis results.

The yield potential of soybeans is shown in Table 6. Deja 1 has the highest seed weight than other genotypes with a potential yield of 1.75 tons ha^{-1}. This means that genotype can adapt to limited water. The research on soybean yield potential during dry season emphasizes the importance of genotype

selection in optimizing agricultural productivity. For instance, Elmerich et al. (2023) conducted a study on soybean genotypes in France, highlighting the significant influence of genotype-environment interactions on yield potential under drought stress. Similar studies were also reported on other plants, such as cowpea (Mekonnen et al., 2022; Gerrano et al., 2020), mung bean (Islam et al., 2021), sweet potato (Mahaman et al., 2023) and barley (Ahakpaz et al., 2021). Identifying superior genotypes based on yield potential, such as Deja 1, is critical for improving productivity through breeding program, particularly in regions facing similar climatic challenges.

CONCLUSIONS

The study on Indonesian soybean varieties grown in wetlands during dry season reveals significant variability in yield potential among 20 genotypes tested. The Deja 1 demonstrated the highest yield potential of 1.75 tons ha^{-1}. This genotype exhibited adaptability in water-limited conditions. The heritability estimates (H^2_b) indicate that weight of 100 Seeds (W100) and the number of seeds per plant (NSP) have high heritability values (0.95 and 0.91), suggesting a strong genetic influence. The traits that have a positive correlation with yield based on the Pearson's

correlation network plot are plant height (PH), weight of biomass (WB), and weight of seeds per plot (WSP). This study highlights the importance of selecting genotypes that are tolerant to water stress to improve soybean productivity in wetlands during dry season. This research provides an important contribution to soybean breeding programs aimed at enhancing drought tolerance and achieving optimal yields in Indonesia.

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REFERENCES

Adie, M. M., Baliadi, Y., Yusnawan, E., Wijanarko, A. and Krisnawati, A. (2022). Performance of Soybean Genotypes in the Acidic Dryland and Wetland. *International Journal on Advanced Science, Engineering and Information Technology*, 12(5), pp. 1812–1817.

Ahakpaz, F., Abdi, H., Neyestani, E., Hesami, A., Mohammadi, B., Mahmoudi, K. N., Abedi-Asl, G., Noshabadi, M. R. J., Ahakpaz, F. and Alipour, H. (2021). Genotype-by-environment interaction analysis for grain yield of barley genotypes under dryland conditions and the role of monthly rainfall. *Agricultural Water Management*, 245(October 2020), 106665.

Aldri, V. A and Sitti, R.F. (2023). Analisis Pengaruh Harga Kedelai Lokal, Produksi Kedelai Lokal, Kurs, Dan Konsumsi Kedelai Dalam Negeri Terhadap Tingginya Impor Kedelai Di Indonesia Tahun 1997–2021. *JEMSI (Jurnal Ekonomi, Manajemen, Dan Akuntansi)*, 9(4), pp. 1354–1358.

Almeida, F. R., Brayner, A., Rodrigues, J. P. C. and Bessa Maia, J. E. (2017). Improving multidimensional wireless sensor network lifetime using pearson correlation and fractal clustering. *Sensors (Switzerland)*, 17(6), pp. 1–24.

Ambrósio, M., Daher, R. F., Santos, R. M, Santana, J. G. S., Vidal, A. K. F., Nascimento, M. R., Leite, C. L., de Souza, A. G., Freitas, R. S., Stida, W. F., Farias, J. E. C., de Souza Filho, B. F., Melo, L. C. and dos Santos, P. R. (2024). Multi-trait index: selection and recommendation of superior black bean genotypes as new improved varieties. *BMC Plant Biology*, 24(1), pp. 1–12.

Bates, D., Maechler, M., Bolker, B., Walker, S., Christensen, R. H. B., Singmann, H., Dai, B., Scheipl, F., Grothendieck, G., Green, P., Fox, J., Bauer, A., Krivitsky, P. N., Tanaka, E. and Jagan, M. (2024). Linear Mixed-Effects Models using "Eigen" and S4. *In The R Project for Statistical Computing,* 1.1–35.5, pp. 50–51.

Du, Y., Zhao, Q., Chen, L., Yao, X. and Xie, F. (2020). Effect of drought stress at reproductive stages on growth and nitrogen metabolism in soybean. *Agronomy*, 10(2), 302.

Du, Y., Zhao, Q., Chen, L., Yao, X., Zhang, H., Wu, J. and Xie, F. (2020). Effect of drought stress during soybean r2–r6 growth stages on sucrose metabolism in leaf and seed. *International Journal of Molecular Sciences*, 21(2), pp. 1–19.

Egli, D. B. (2017). Seed biology and yield of grain crops. In *Seed biology and yield of grain crops*. CABI.

Elmerich, C., Boulch, G., Faucon, M. P., Lakhal, L. and Lange, B. (2023). Identification of Eco-Climatic Factors Driving Yields and Genotype by Environment Interactions for Yield in Early Maturity Soybean Using Crop Simulation. *Agronomy*, 13(2), 322.

Gerrano, A. S., Jansen van Rensburg, W. S., Mathew, I., Shayanowako, A. I. T., Bairu, M. W., Venter, S. L., Swart, W., Mofokeng, A., Mellem, J. and Labuschagne, M. (2020). Genotype and genotype × environment interaction effects on the grain yield performance of cowpea genotypes in dryland farming system in South Africa. *Euphytica*, 216(5), pp. 1–11.

Ghorbani, R., Alemzadeh, A. and Razi, H. (2019). Microarray analysis of transcriptional responses to salt and drought stress in Arabidopsis thaliana. *Heliyon*, 5(11), e02614.

Grenfell, S., Grenfell, M., Tooth, S., Mehl, A., O'Gorman, E., Ralph, T. and Ellery, W. (2022). Wetlands in drylands: diverse perspectives for dynamic landscapes. Wetlands Ecology and Management, 30(4), pp. 607–622.

Harsono, A., Harnowo, D., Ginting, E. and Elisabeth, A. A. D. (2022). Soybean in Indonesia: *Current Status, Challenges and Opportunities to Achieve Self-Sufficiency*. Legumes Research - Volume 1. IntechOpen.

Islam, M. R., Sarker, B. C., Alam, M. A., Javed, T., Alam, M. J., Zaman, M. S. U., Azam, M. G., Shabbir, R., Raza, A., Habib-ur-rahman, M.,

Dessoky, E. S. and Islam, M. S. (2021). Yield stability and genotype environment interaction of water deficit stress tolerant mung bean (Vigna radiata l. wilczak) genotypes of Bangladesh. *Agronomy*, 11(11), 2136.

Kang, Y., Li, M., Sinharoy, S. and Verdier, J. (2016). A snapshot of functional genetic studies in Medicago truncatula. *Frontiers in Plant Science*, 7.

Kearsey, J. M. and Pooni, S. H. (1996). The Genetical Analysis of Quantitative Traits. *Journal of Medical Genetics*, 33(11), 976.

Khandelwal, V., Patel, R., Choudhary, K. B., Pawar, S. B., Patel, M. S., Iyanar, K., Mungra, K. D., Kumar, S. and Satyavathi, C. T. (2024). Stability Analysis and Identification of Superior Hybrids in Pearl Millet [Pennisetum glaucum (L.) R. Br.] Using the Multi Trait Stability Index. *Plants*, 13(8), pp. 1–22.

Kuhn, M., Jackson, S. and Cimentada, J. (2022). *Correlations in R Package ' corrr ' (0.4.4)*. CRAN.

Mahaman, M. I. Z., Oselebe, H. O., Baina, D. jimo, Nwankwo Innocent, I. M., Houdegbe, A. C., Oumarou, S., Chukwu, S. C. and Moussa, B. (2023). Selection of new sweetpotato hybrids for West Africa using accelerated breeding scheme and genotype × environment interaction under drought stress. *Scientific Reports*, 13(1), pp. 1–13.

Majidian, P., Masoudi, B., Hezarjaribi, E., Razmi, N., Peyghamzadeh, K. and Gholizadeh, A. (2024). Deciphering genotype-by-environment interaction in new soybean lines based on multiple traits using different adaptability and stability methods. *Food Science and Nutrition*, 12(5), pp. 3295–3308.

Markulj Kulundžić, A., Josipović, A., Matoša Kočar, M., Viljevac Vuletić, M., Antunović Dunić, J., Varga, I., Cesar, V., Sudarić, A. and Lepeduš, H. (2022). Physiological insights on soybean response to drought. *Agricultural Water Management*, 268.

Mburu, S. W., Koskey, G., Njeru, E. M., Ombori, O., Maingi, J. and Kimiti, J. M. (2022). Genetic and phenotypic diversity of microsymbionts nodulating promiscuous soybeans from different agro-climatic conditions. *Journal of Genetic Engineering and Biotechnology*, 20(1), 109.

Mekonnen, T. W., Mekbib, F., Amsalu, B., Gedil, M., and Labuschagne, M. (2022). Genotype by environment interaction and grain yield stability of drought tolerant cowpea landraces in

Ethiopia. *Euphytica*, 218(5), 1–13.

Montanha, G. S., Perez, L. C., Brandão, J. R., de Camargo, R. F., Tavares, T. R., de Almeida, E. and de Carvalho, H. W. P. (2022). May mineral composition trigger or limit the protein content in soybean (Glycine max (L.) Merrill) seeds? Insights from a survey on 95 varieties cultivated in Brazil. *BioRxiv*.

Nakagawa, A. C. S., Ario, N., Tomita, Y., Tanaka, S., Murayama, N., Mizuta, C., Iwaya-Inoue, M. and Ishibashi, Y. (2020). High temperature during soybean seed development differentially alters lipid and protein metabolism. *Plant Production Science*, 23(4), pp. 504–512.

Onder, S., Erbas, S., Onder, D., Tonguc, M. and Mutlucan, M. (2022). Seed filling. *IntechOpen*, 11(tourism), 13.

Palaniyappan, S., Ganesan, K. N., Manivannan, N., Ravichandran, V. and Senthil, N. (2023). Multi trait genotype-ideotype distance index - A tool for identification of elite parental inbreds for developing heterotic hybrids of fodder maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, 14(3), 841–849.

Rahimi Moghaddam, S., Amiri, S. and Eyni-Nargeseh, H. (2023). Assessing chickpea attainable yield and closing the yield gaps caused by agronomic and genetic factors. *Field Crops Research*, 303, 109137.

Rani, R., Arif, M., Rahman, S. U., Hammad, M., Mukhtar, Z., Rizwan, M., Shimelis, H. and Raza, G. (2023). Field Screening of Diverse Soybean Germplasm to Characterize Their Adaptability under Long-Day Condition. *Agronomy*, 13(9), pp. 1–17.

Resende, M. D. V. (2002). Genética biométrica e estatística no melhoramentode plantas perenes. *Pesquisa Agropecuaria Brasileira,* 10.

Rychel-Bielska, S., Książkiewicz, M., Kurasiak-Popowska, D., Tomkowiak, A., Bielski, W., Weigt, D., Niemann, J., Surma, A., Kozak, B. and Nawracała, J. (2024). Molecular selection of soybean towards adaptation to Central European agroclimatic conditions. *Journal of Applied Genetics*, 66, pp. 29–45.

Saryoko, A., Homma, K., Lubis, I. and Shiraiwa, T. (2017). Plant development and yield components under a tropical environment in soybean cultivars with temperate and tropical origins. *Plant Production Science*, 20(4), pp. 375–383.

Sehgal, A., Sita, K., Siddique, K. H. M., Kumar, R., Bhogireddy, S., Varshney, R. K., HanumanthaRao, B., Nair, R. M., Prasad, P. V. V. and Nayyar, H.

(2018). Drought or/and heat-stress effects on seed filling in food crops: Impacts on functional biochemistry, seed yields, and nutritional quality. *Frontiers in Plant Science*, 871, pp. 1–19.

Singamsetti, A., Zaidi, P. H., Seetharam, K., Vinayan, M. T., Olivoto, T., Mahato, A., Madankar, K., Kumar, M. and Shikha, K. (2023). Genetic gains in tropical maize hybrids across moisture regimes with multi-trait-based index selection. *Frontiers in Plant Science*, 14, pp. 1–16.

Tanwar, B. and Goyal, A. (2020). *Oilseeds: Health Attributes and Food Applications.* Springer Singapore.

Terryana, R. T., Safina, N. D., Suryani, S., Nugroho, K. and Lestari, P. (2020). Analisis Keragaman Genetik Aksesi Kedelai Introduksi Dari Wilayah Subtropis Berbasis Morfologi Dan Molekuler. *Berita Biologi*, 19(3B).

Triyanti, D. R. (2020). *Outlook Kedelai 2020*. Pusat Data Dan Sistem Informasi Pertanian Sekretariat Jenderal Kementerian Pertanian, pp. 1–84.

United States Department of Agriculture. (2023). *Production - Soybeans* [online]. Available at: https://www.fas.usda.gov/data/production/commodity/2222000 [Accessed 25 February 2025].

Valliyodan, B., Brown, A. V., Wang, J., Patil, G., Liu, Y., Otyama, P. I., Nelson, R. T., Vuong, T., Song, Q., Musket, T. A., Wagner, R., Marri, P., Reddy, S., Sessions, A., Wu, X., Grant, D., Bayer, P. E., Roorkiwal, M., Varshney, R. K., and Nguyen, H. T. (2021). Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. *Scientific Data*, 8(1), pp. 1–9.

Vogel, J. T., Liu, W., Olhoft, P., Crafts-Brandner, S. J., Pennycooke, J. C. and Christiansen, N. (2021). Soybean Yield Formation Physiology – A Foundation for Precision Breeding Based Improvement. *Frontiers in Plant Science*, 12(November), pp. 1–15.