



RESEARCH ARTICLE

Assessing genetic variability and identifying stable soybean (*Glycine max* L.) genotypes across rainfed and irrigated planting conditions using multi-trait stability index (MTSI)

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Abstract

This study assessed genetic variability and identified stable soybean (*Glycine max* L.) genotypes suitable for rainfed and irrigated conditions in central India to enhance soybean breeding programs. Advanced breeding lines were evaluated using a randomized complete block design, with phenotypic assessments analyzing genetic variability, associations, and stability through multiple regression and multi-trait stability index (MTSI). The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits. High heritability combined with significant genetic advance was observed for pods per plant, seeds per plant, seed weight, biological yield, and seed yield. Positive associations of biological yield and harvest index with seed yield were consistent across conditions. Path analysis identified biological yield as having the highest direct effect on seed yield. MTSI identified JS 22-101 as the most stable genotype for both conditions, with JS 22-77 and JS 22-78 performing well under rainfed and irrigated conditions, respectively. Biological yield emerged as the primary yield-contributing trait, highlighting the need to refine selection criteria for soybean breeding programs.

Keywords soybean, multi-environments, genetic variability, selection, stability.

Introduction

Soybean (*Glycine max* L.), globally acknowledged for its unparalleled economic importance, stands as the preeminent legume, serving as a crucial source of vegetable protein and contributing essential constituents to various chemical products. It is renowned for its nutritional richness and plays a vital role in the human body by bestowing health benefits and contributing to disease prevention (Ramlal, 2022). Soybean's nutritional profile comprises 37-42% high-quality protein, 6% ash, 29% carbohydrates, and 17-24% oil (Rajendra et al. 2022). Moreover, it serves as an essential cover crop that symbiotically facilitates soil nitrogen fixation and augments soil fertility (Mohamed et al. 2018). Soybean is primarily a rainy season crop grown within the rainfed agro-ecosystems of central and peninsular India, with cultivation extending to various tropical and subtropical regions worldwide despite genetic variability historically driving soybean improvement through breeding efforts; its decline has been evident over time due to the selective pressure for specific traits. Consequently, this trend has led to the development of modern cultivars characterized by a narrow genetic base and restricted adaptability. Recognizing the risks posed to future breeding efforts by a narrowed gene pool, this study delves into a comprehensive analysis

aimed at expanding the potential of soybean genotypes for future breeding programs. By studying variability, breeders can access diverse germplasm sources, overcoming bottlenecks and introducing fresh genetic material to unlock new potential (Pal et al. 2023). The limitations of a narrowed genetic base in soybeans, evidenced by declining variability and limited adaptability, underscore the urgency and importance of this research endeavour (Rani et al. 2023).

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Several researchers (Wojcik et al. 2022; Raza et al. 2023 and Evaristo et al. 2024) assessed genetic variability in soybean germplasm. Traits such as days to flowering initiation, maturity, seed and pod numbers per plant, primary branches, plant height, hundred seed weight, biological yield, seed yield, and harvest index were previously studied by Raza et al. (2023), and Evaristo et al. (2024). Traditionally, MET analysis focuses on a single trait, typically grain yield. However, the reliability of genotype recommendations improves when multiple traits are considered. Olivoto et al. (2019); Olivoto et al. (2021) introduced a method for Multi-environment trial (MET) analysis that integrates stability selection across multiple traits into a single, interpretable index, which is multi-trait stability index. Lee et al. (2023); Patel et al. (2023) conducted research indicating that simultaneous selection of MTSI and weighted average of absolute score index (WAASB) facilitates the identification of recommended cultivars, guiding breeders in selecting ideal parents for rice breeding. Additionally, the multi-trait stability index (MTSI) index, based on multiple traits, serves as a robust tool for developing improved treatments and genotypes, benefiting both breeders and agronomists, as previously reported (Lima et al. 2022), and has a tremendous potential to combine morpho-physiological and yield traits aiming at selecting hybrids under optimal and stress conditions. Moreover, Nataraj et al. (2021) recommend applying MTSI to identify high-yielding, stable, and drought-tolerant soybean genotypes.

The objective of this study was to ascertain the stable soybean genotype using a multi-trait stability index while simultaneously elucidating the genetic framework of soybeans through the estimation of parameters related to genetic variability, trait association, direct and indirect effects and multiple regression analysis. Through integrating diverse analytical approaches, we attained a comprehensive understanding of the genetic potential and interrelationships within soybean germplasm, with the ultimate goal of developing high-yielding, resilient, and adaptable cultivars for future breeding programs.

Materials and methods

Experimental material

Forty-eight elite, high-yielding soybean advanced breeding lines, along with two checks from diverse crosses, were developed at Jawaharlal Nehru Krishi Vishwa Vidyalyaya, Jabalpur (Table 1). The F7, F8, and F9 generations were evaluated during *Kharif* 2019, 2020, and summer 2021. The *Kharif* trials (E1, E2) relied on rainfall, while the summer trial (E3) was irrigated.

Experimental design and experimental site

The experimental material was planted in randomized complete block design with three replications at the

soybean breeding farm of the Plant Breeding Department, College of Agriculture, JNKVV, Jabalpur, India (latitude 22°49' to 20°80' N, longitude 78°21' to 80°58' E, altitude 411.78 m). The soil was medium-deep black with good drainage, neutral pH (7.5), and consisted of 25.3% sand, 18.9% silt, and 55.8% clay. It had a high cation exchange capacity (30.24 Cmol kg⁻¹), low salt content (EC - 21 dSm⁻¹), and low organic carbon (0.52 g kg⁻¹). Basal fertilizer (20:60:20 kg/ha NPK) and recommended practices were used. Maximum and minimum temperatures were 34.9 to 18.0°C (2019), 34.2 to 16.7°C (2020), and 42.4 to 7.5°C (2021). The rainfall pattern is shown in Fig. 1. Annual rainfall was 1572.3 mm (2019), 1137.6 mm (2020), and 119.2 mm (2021).

Phenotypic characterization

Fifty soybean genotypes, including two checks, were characterized. Phenotypic data for eleven traits were recorded from five randomly chosen plants per plot: days to flower initiation (DTFI), days to 50% flowering (DTF), days to maturity (DTM), plant height (PH), number of primary branches per plant (PBPP), number of pods per plant (NPPP), number of seeds per plant (NSPP), biological yield per plant (BYPP), hundred seed weight (HSW), harvest index (HI), and seed yield per plant (SYPP).

Statistical analysis

The combined analysis of variance (ANOVA) was conducted, treating genotypes as fixed factors and environments as random variables. The components of genetic variability were estimated for all the studied traits. Phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated using the formula provided by Burton and Devane (1952) and classified into three categories: high (>15%), moderate (10–15%), and low (<10%). Broad sense heritability was estimated according to Singh and Chaudhary (1985) and classified into high (>80%), moderate (50–80%), and low (<50%). The expected genetic advance (GA) was calculated using the formula provided by Allard (1960). Correlation coefficients for all character combinations at the phenotypic level were estimated as per Miller et al. (1958). Path coefficient analysis was conducted using the methods suggested by Wright (1921) and Dewey et al. (1959). Regression analysis followed the methods suggested by Draper and Smith (1998). The weighted average of absolute scores (WAASB) and the multi-trait stability index, as proposed by Olivoto et al. (2019), were computed. All statistical analyses were performed using R software version 4.2.

Results

Analysis of variance

A pooled analysis of variance (ANOVA) was conducted to detect significant interactions among the sources of

Table 1. Pedigree detail of advanced breeding lines

Genotype	Pedigree	Genotype	Pedigree
JS 22-63	JS 20-30 X JS 95-60	JS 22-88	JS 20-63 X JS 20-35
JS 22-64	JS 97-52 X JS 95-60-5-12-1	JS 22-89	JS 20-29X JS 93-05
JS 22-65	JS 20-53 X JS 20-34	JS 22-90	JS 20-82 X JS 95-60
JS 22-66	JS 20-71 X JS 20-22	JS 22-91	JS 20-74 X JS 20-22
JS 22-67	JS 20-53 X JS 20-34	JS 22-92	JS 20-88 X JSM 196
JS 22-68	JS 20-71 X JS 20-22	JS 22-93	JS 20-63 X JS 95-60
JS 22-69	JS 20-88 X JS 20-34	JS 22-94	JS 20-53 X JS 20-34
JS 22-70	SL 738 X JS 95-60	JS 22-95	JS 20-98 X JS 20-34
JS 22-71	JS 20-53 X JS 20-34	JS 22-96	JS 20-53 X JS 20-34
JS 22-72	JS 20-98 X JS 20-34	JS 22-97	JS 20-29 X JSM 275
JS 22-73	JS 20-29 X JSM 275	JS 22-98	JSM 226 X JS 20-34
JS 22-74	JS 20-63 X JS 20-35	JS 22-99	JS 97-52 X JS (IS) 90-5-12-1
JS 22-75	JS 20-75 X JS 20-14	JS 22-100	JS 20-29 X JS 93-05
JS 22-76	JS 20-79 X JS 335	JS 22-101	SL 738 X JS 95-60
JS 22-77	JS 20-53 X JS 20-34	JS 22-102	JS 20-69 X JS 335
JS 22-78	JS 20-63 X JS 20-35	JS 22-103	JS 20-88 X JSM196
JS 22-79	JS 20-09 X PS1475	JS 22-104	JS 20-53 X JS 20-34
JS 22-80	JS 20-82 X JS 95-60	JS 22-105	JS 20-79 X JS 335
JS 22-81	JS 20-29 X JS 20-22	JS 22-106	JS 20-71 X JS 20-22
JS 22-82	JS 20-63 X JS 95-60	JS 22-107	JS 20-29 X JS 20-22
JS 22-83	JS 20-29 X JS 20-22	JS 22-108	JS 20-09 X JSM 258
JS 22-84	NRC 86 X JS 20-34	JS 22- 109	JS 20-29 X JSM 275
JS 22-85	JS 20-71 X JS 20-22	JS 22- 110	SL 738 X JS 20-88
JS 22-86	JS 20-63 X JS 20-35	JS 20-98(c)	JS 97-52 X SL 710
JS 22-87	JS 20-29 X JS 93-05	JS 20-34(c)	JS 98-63 X PK 768

variation. The combined ANOVA results for seed yield and its components, presented in Table 2, showed significance at the 0.001% level for genotype (G), environment (E), and their interactions (G x E) and (E x R) across all characters.

Components of genetic variability

Traits exhibited a wide range across all environments (Table 3). Seed yield varied from 3.60 to 16.10 (E1), 3.90 to 17.30 (E2), 5.00 to 25.10 (E3), and 5.40 to 14.80 (pooled data), with mean values of 7.69 (E1), 8.44 (E2), 10.98 (E3), and 9.03 (pooled data). The phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) across all traits in each environment and the pooled data (Table 3). GCV and PCV ranged from 3.66 to 37.19 (E1), 3.93 to 37.03 (E2), and 3.14 to 34.66 (E3). Hundred seed weight (HSW) showed high to moderate consistency across environments. In the pooled analysis, seed yield per plant (SYPP) exhibited high GCV and PCV values across E1, E2, and E3, while other traits showed low to moderate values (2.31 to 19.64). SYPP had a high GCV and PCV estimate of 21.68. High GCV and PCV estimates were noted for SYPP, HI, HSW, BYPP, NPBP, NSPP, and NPPP. Lower GCV and PCV estimates were observed for DTFI, DTF, DM, and PH across environments, with the lowest values for DTFI (3.64), DTF (3.43), DM (2.22), and PH (7.72) in the pooled analysis.

High heritability (72.34–97.79%) was observed for all traits across E1 and E2, except for DTFI, DTF in E2, and NPBP in E3 (60.46–68.88%). Seed yield heritability was 94.4%, 94.8%, and 86.07% for E1, E2, and E3, respectively. PBPP heritability was higher in E1 (81.33%) and E2 (77.14%) compared to E3 (60.46%). Traits like HSW, NSPP, NPPP, and SYPP consistently exhibited very high heritability (87.93–97.79%) across all environments. Genetic advance as a percentage of the mean (GAM) varied from very high for traits like SYPP, PBPP, NSPP, NPPP, HSW, HI, and BYPP across all environments to moderate for DTFI, DTF, and PH in E3 (10.34–12.91). Seed yields consistently displayed high genetic advance (61.45–72.38%) across environments. High heritability coupled with substantial genetic advance was noted for NSPP, NPPP, HSW, HI, and BYPP across all environments and pooled years.

Trait association

Correlation analysis was performed for each year (2019, 2020, 2021) and on aggregated data. Table 4 presents the findings. In Environment E1, biological yield per plant (BYPP) and harvest index (HI) showed high positive correlations

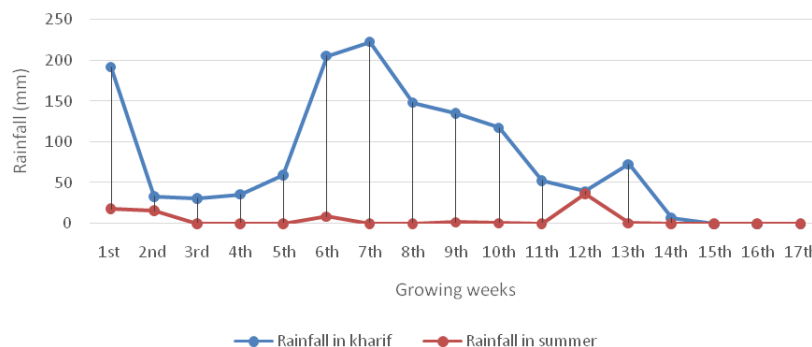


Fig. 1. Pattern of rainfall during kharif and summer trails

Table 2. Combined analysis of variances for soybean genotypes

Traits	Genotypes (G)	Environment (E)	Replication (R)	G x Y	Y x R	Residual
D.F.	49	2	2	98	4	294
DTFI	29***	43362***	29***	23***	10***	1
DTF	29***	41668***	3	22***	7***	1
DTM	53***	32240***	5*	34***	5*	2
NPPP	531.2***	8834.2***	3.2	263.9***	8.0*	2.9
NSPP	3388***	38555***	1	1749***	9	4
PBPP	1.231***	22.832***	0.011	1.210***	0.114	0.051
PH	225.802***	18.788**	2.068	124.758***	11.722*	3.7
HSW	24.744***	3.698***	2.045***	9.970***	0.500**	0.147
BYPP	81.8***	3434.6***	15.5***	71.6***	7.5**	1.9
HI	685.17***	1523.83***	50.77***	604.95***	8.92	4.93
SYPP	32.26***	494.86***	0.1	32.02***	0.85	0.49

PH = Plant height, PBPP = Primary branches per plant, PBPP = Number of pods per plant, NSPP = number of seeds per plant, HSW = Hundred seed weight, BYPP = Biological yield per plant, HI = Harvest index, DTFI = Days to flower initiation, DTF = Days to 50% flowering, DTM = Days to maturity, D.F. = Degree of freedom, GxY = Genotype x Year, YxR = Year x Genotype * $p < .05$. ** $p < .01$. *** $p < .001$.

with seed yield ($r = 0.657$ and $r = 0.795$, respectively). The HI also showed significant correlations in E2, E3, and the pooled data ($r = 0.79, 0.69$). Moderate to high correlations for BYPP were observed in E2 ($r = 0.30$) and E1 ($r = 0.66$). HI consistently displayed a significantly high correlation with seed yield across all years ($r = 0.79, r = 0.795, r = 0.57$, and $r = 0.69$). Among the secondary traits, DTFI exhibited a highly positive and significant association with DTF ($r = 0.67, r = 0.99, 0.99, 0.92$), while NPPP showed positive and significant associations with NSPP ($r = 0.81, r = 0.82, r = 0.99$) and BYPP ($r = 0.42, r = 0.30, r = 0.19, r = 0.28$) in each environment and pool data respectively. In Environment E1, seed yield showed significant positive associations with NPPP, NSPP, HSW, BYPP, and HI ($r = 0.44, r = 0.44, r = 0.46, r = 0.66, r = 0.79$). In E2, BYPP and HI correlated significantly with seed yield ($r = 0.30, r = 0.79$). In E3, seed yield had positive correlations with all traits ($r = 0.23$ to $r = 0.57$). Across pooled data, all traits except PH and PBPP were significantly positively associated with seed yield.

Path analysis

Path analysis in individual years (2019, 2020, 2021) and pooled data (Table 5) showed that biological yield per plant (BYPP) consistently had the highest direct positive contribution to seed yield across all environments (0.59 to 0.92). In E1, NPPP, BYPP, and HI made direct positive contributions (0.34, 0.59, and 0.65). In E2, DTF, NPPP, HSW, and BYPP contributed directly (0.99, 0.35, 0.56, and 0.92). E3 showed direct positive contributions via NSPP and BYPP (0.47 and 0.82). Pooled data revealed direct positive contributions through DTF, NPPP, BYPP, and HI (0.38, 0.69, 0.74, and 0.78). However, NSPP had negative direct contributions in E1, E2, and pooled data

(-0.32, -0.36, -0.73), while NPPP showed negative direct contributions in E3 (-0.47). NSPP indirectly contributed positively in E1, E2, and pooled data, while NPPP indirectly contributed positively in E3 towards seed yield.

Multiple regression analysis

The study conducted multiple linear regression analysis for all studied traits in environments E1, E2, E3, and pooled data across cropping years 2019–2020 and 2020–2021. Table 6 presents the results of the multiple linear regression analysis used to predict seed yield per plant (SYPP) based on soybean plant variables. Positive contributions to SYPP were observed from. E1: NPPP, HSW, BYPP, HI; E2: DTFI, DTM, NPPP, PBPP, PH, BYPP, HI; E3: DTFI, DTM, NSPP, BYPP, HI; Pooled data: DTM, NSPP, PBPP, PH, BYPP, HI. The DTF showed a negative contribution to SYPP across all environments and pooled years. BYPP and HI consistently exhibited positive contributions across all three environments and pooled years.

Multi-trait stability index (MTSI)

WAASBY values for eleven traits were grouped into six factors (FA). The genotypic ranking based on MTSI identified eight soybean genotypes with the lowest values: JS 22-101 (2.07), JS 22-96 (2.25), JS 22-97 (2.36), JS 22-93 (2.53), JS 22-83 (2.54), JS 22-82 (3.00), JS 22-103 (3.08), and JS 22-91 (3.12) (Fig. 2). The MTSI cut-off at 3.00 (red circle) marked optimal genotypes. These selected genotypes outperformed the overall average (X_o) for most traits, except for HI and PBPP (Table 7). A positive selection differential (SD) was observed for all traits except HI (-3.89, -7.43) and PBPP (0.115, -0.115). FA2 contributed approximately 53% to the distance from JS

Table 3. Parameters of genetic variability for seed yield and its component traits in soybean genotypes

Traits	Env.	Mean	Range	PCV (%)	GCV (%)	h ² (%)	GAM (5%)
DTFI	E1	38.88	32–45	7.04	6.64	89.09	12.91
	E2	37.77	30–46	5.85	4.86	68.88	8.30
	E3	67.747	58–77	5.75	5.37	87.22	10.34
	Pooled	48.13	42–52.67	3.93	3.64	85.56	6.93
DTF	E1	42.02	36–49	6.24	5.64	81.76	10.51
	E2	40.10	33–48	5.52	4.60	69.30	7.89
	E3	69.88	60–79	5.61	5.30	89.25	10.32
	Pooled	50.67	45.33–55	3.71	3.43	85.41	6.53
DTM	E1	98.62	92–106	3.66	3.50	91.27	6.89
	E2	100.45	89–111	3.93	3.65	86.16	6.97
	E3	124.88	115–134	3.14	2.97	89.25	5.78
	Pooled	107.98	103–116.33	2.31	2.22	92.46	4.40
NPPP	E1	42.13	22–76.30	24.82	24.35	96.3	49.23
	E2	41.17	22.60–62.55	20.91	19.82	89.88	38.71
	E3	54.02	30.30–100	25.22	24.17	91.86	47.73
	Pooled	45.87	26.74–65.01	17.26	16.81	94.85	33.73
NSPP	E1	105.33	55–190.80	24.82	24.36	96.31	49.24
	E2	3.95	56.50–156.25	20.91	19.82	89.88	38.71
	E3	135.09	75.8–250	25.21	24.17	91.86	47.71
	Pooled	114.44	66.86–162.53	17.17	16.75	95.24	33.68
PBPP	E1	2.316	0.70–3.70	30.30	27.32	81.33	50.76
	E2	2.99	5.70–1.00	23.87	20.97	77.14	37.93
	E3	2.32	1.00–4.00	29.41	22.86	60.46	36.62
	Pooled	2.54	1.63–3.47	16.42	14.13	73.98	25.03
PH	E1	65.17	45.30–79.20	9.96	9.27	86.53	17.76
	E2	64.71	44.70–87.40	11.94	11.08	86.05	21.17
	E3	64.42	42.80–82.50	13.30	12.37	86.6	23.72
	Pooled	64.92	49.91–76.52	8.09	7.72	91.09	15.18
HSW	E1	10.48	5.00–16.10	24.28	24.01	97.79	48.91
	E2	10.22	4.98–13.96	21.65	21.32	96.94	43.24
	E3	10.62	6.40–15.90	19.18	17.99	87.93	34.75
	Pooled	10.44	5.93–14.29	16.26	15.94	96.09	32.18
BYPP	E1	17.86	9.10–26.80	21.55	20.32	88.85	39.45
	E2	17.39	10.40–28.30	21.62	20.34	88.53	39.42
	E3	26.24	11.40–43.60	28.34	26.90	90.14	52.62
	Pooled	20.53	14.43–27.83	15.73	14.83	88.88	28.80
HI	E1	42.85	16.60–78.80	26.63	24.48	84.51	46.36
	E2	49.67	20.54–126.96	37.79	36.29	92.2	71.78
	E3	43.17	20.20–101.70	31.02	26.39	72.34	46.23
	Pooled	45.23	28.10–76.68	19.64	18.19	85.81	34.72

SYPP	E1	7.69	3.60–16.10	37.19	36.15	94.47	72.38
	E2	8.44	3.90–17.30	37.03	36.05	94.8	72.31
	E3	10.98	5.00–25.10	34.66	32.15	86.07	61.45
	Pooled	9.03	5.40–14.81	21.68	20.75	91.61	40.91

PH = Plant height, PBPP = Primary branches per plant, PBPP = Number of pods per plant, NSPP = number of seeds per plant, HSW = Hundred seed weight, BYPP = Biological yield per plant, HI = Harvest index, DTFI = Days to flower initiation, DTF = Days to 50% flowering, DTM = Days to maturity, DF = Degree of freedom, E1 = 2019, E2 = 2020, E3 = 2021.

Table 4. Phenotypic correlation coefficient among characters in soybean in the environment E1, E2, E3 and pooled years

Trait	Env.	DTFI	DTF	DTM	NPPP	NSPP	PBPP	PH	HSW	BYPP	HI
DTF	E1	0.67**									
	E2	0.99**									
	E3	0.99**									
	Pooled	0.94**									
DTM	E1	0.03	0.19								
	E2	0.38**	0.38**								
	E3	0.99**	0.69**								
	Pooled	0.67**	0.79**								
NPPP	E1	0.28**	0.39**	0.24**							
	E2	0.42**	0.42**	0.32**							
	E3	0.18*	0.19*	0.19*							
	Pooled	0.38**	0.45**	0.28*							
NSPP	E1	0.28**	0.39**	0.24**	0.78**						
	E2	0.42**	0.42**	0.32**	0.81**						
	E3	0.18*	0.19*	0.19*	0.06						
	Pooled	0.38**	0.44**	0.28*	0.99**						
PBPP	E1	0.05	0.12	0.07	0.06	0.03					
	E2	0.19*	0.19*	-0.04	0.03	0.03					
	E3	0.02	0.03	-0.03	0.35**	0.35**					
	Pooled	0.11	0.11	-0.23	0.11	0.10					
PH	E1	0.01	0.21*	0.21**	0.21*	0.21*	0.04				
	E2	0.31**	0.33**	0.25**	0.20*	0.20*	0.15				
	E3	0.41**	0.42**	0.42**	0.32**	0.34**	0.06				
	Pooled	0.54**	0.63**	0.45**	0.40**	0.38**	0.40**				
HSW	E1	0.02	0.01	0.04	-0.11	-0.11	0.11	-0.27			
	E2	0.14	0.14	0.03	0.06	-0.06	-0.06	-0.14			
	E3	-0.03	-0.05	-0.05	-0.05	-0.05	0.05	-0.23			
	Pooled	-0.04	-0.08	-0.08	-0.16*	-0.15*	0.07	-0.34**			
BYPP	E1	0.26**	0.34**	0.09	0.42**	0.42**	0.13	0.06	0.34		
	E2	0.31**	0.31**	0.01	0.30**	0.30**	0.10	0.01	0.11		
	E3	0.44**	0.43**	0.43**	0.19*	0.19*	0.07	0.25**	0.21*		
	Pooled	0.42**	0.36**	0.35*	0.32*	0.33*	0.04	0.24	0.21**		

HI	E1	-0.18	-0.11	0.03	0.24**	0.25**	0.07	-0.11	0.36**	0.09	
	E2	-0.13	-0.13	-0.12	0.02	0.02	0.18*	-0.01	0.17*	-0.29**	
	E3	0.06	0.06	0.06	0.21**	0.21**	0.26**	0.01	0.17*	-0.34**	
	Pooled	-0.04	0.09	0.07	0.19*	0.19*	0.14	0.03	0.21**	-0.27**	
SYPP	E1	0.02	0.13	0.08	0.44**	0.44**	0.10	0.05	0.46**	0.66**	0.79**
	E2	0.07	0.07	0.07	0.15	0.15	0.14	0.06	0.11	0.30**	0.79**
	E3	0.47**	0.47**	0.47**	0.36**	0.36**	0.17*	0.23**	0.30**	0.55**	0.57**
	Pooled	0.24**	0.34**	0.21**	0.41**	0.41**	0.16	0.20	0.07	0.47**	0.69**

PH = Plant height, PBPP = Primary branches per plant, PBPP = Number of pods per plant, NSPP = number of seeds per plant, HSW = Hundred seed weight, BYPP = Biological yield per plant, HI = Harvest index, DTFI = Days to flower initiation, DTF = Days to 50% flowering, DTM = Days to maturity, DF = Degree of freedom, E1 = 2019, E2 = 2020, E3 = 2021, * $p < .05$. ** $p < .01$. *** $p < .001$.

Table 5. Genotypic path coefficient showing direct and indirect effects of different contributing characters on seed yield per plant in soybean

Trait	Env.	DTFI	DTF	DTM	NPPP	NSPP	PBPP	PH	HSW	BYPP	HI
DTFI	E1	-0.10	0.04	0.00	0.11	-0.11	0.00	0.04	0.00	0.20	-0.12
	E2	-0.02	0.99	0.02	0.19	-0.18	-0.01	0.03	0.24	-0.11	0.01
	E3	0.04	0.04	0.03	0.78	0.59	-0.30	0.13	-0.46	0.21	0.25
	Pooled	-0.27	0.35	0.00	0.27	-0.29	-0.02	-0.08	0.33	-0.01	-0.01
DTF	E1	-0.08	0.06	0.00	0.08	-0.07	-0.01	0.02	0.00	0.03	0.03
	E2	-0.02	0.99	0.02	0.19	-0.18	-0.01	0.03	0.24	-0.11	0.01
	E3	-0.01	-0.02	-0.03	-1.70	-0.56	0.45	-0.04	0.55	-0.34	-0.40
	Pooled	-0.25	0.38	0.00	0.33	-0.34	-0.02	-0.09	0.29	0.11	0.00
DTM	E1	-0.01	0.01	0.00	0.08	-0.07	-0.01	0.00	0.00	0.03	0.03
	E2	-0.51	0.52	0.04	0.13	-0.14	0.00	0.02	-0.02	-0.13	0.00
	E3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	Pooled	-0.18	0.26	0.00	0.18	-0.21	-0.03	-0.07	0.26	-0.07	0.00
NPPP	E1	-0.03	0.03	0.00	0.34	-0.32	0.00	0.04	0.00	0.27	0.13
	E2	-0.70	0.68	0.01	0.35	-0.36	0.00	0.02	0.21	0.01	0.00
	E3	-0.31	-0.30	-0.30	-0.47	-1.42	-0.42	-0.49	0.15	-0.31	-0.31
	Pooled	-0.11	0.18	0.00	0.70	-0.72	0.01	-0.07	0.24	0.21	0.02
NSPP	E1	-0.03	0.03	0.00	0.34	-0.32	0.00	0.04	0.00	0.27	0.12
	E2	-0.42	0.40	0.01	0.35	-0.36	0.00	0.02	0.19	-0.04	0.00
	E3	0.28	0.28	0.28	1.42	0.47	0.57	0.49	-0.09	0.28	0.29
	Pooled	-0.11	0.18	0.00	0.69	-0.73	0.01	-0.06	0.26	0.19	0.02
PBPP	E1	-0.01	0.01	0.00	-0.02	0.03	-0.04	0.01	0.00	0.05	0.08
	E2	-0.87	0.89	0.00	-0.01	-0.02	-0.03	0.01	0.04	-0.23	0.00
	E3	0.01	0.02	0.02	-0.10	-0.13	-0.33	0.03	-0.05	0.02	-0.08
	Pooled	0.05	-0.08	0.00	0.09	-0.06	0.10	-0.01	-0.10	0.16	0.00
PH	E1	0.11	-0.04	0.00	-0.43	0.40	0.01	-0.03	-0.01	-0.38	-0.62
	E2	-0.07	0.07	0.01	0.09	-0.10	-0.01	0.06	0.05	-0.03	0.00
	E3	0.03	0.04	0.04	0.03	0.03	-0.01	0.08	-0.02	0.02	0.00
	Pooled	-0.15	0.24	0.00	0.32	-0.31	0.01	-0.15	0.23	0.00	0.02
HSW	E1	-0.01	0.00	0.00	-0.03	0.03	-0.01	0.01	0.02	0.18	0.28
	E2	-0.09	0.10	0.00	0.13	-0.12	0.00	0.01	0.56	-0.22	0.00
	E3	0.01	0.01	0.01	0.02	0.01	-0.03	0.05	-0.21	-0.05	-0.05
	Pooled	-0.04	-0.02	0.00	-0.27	0.26	-0.01	0.04	-0.06	0.10	-0.16

BYPP	E1	-0.03	0.02	0.00	0.15	-0.15	0.00	0.02	0.01	0.59	0.09
	E2	0.60	-0.61	-0.01	0.01	0.02	0.01	0.00	-0.14	0.92	0.00
	E3	0.39	0.37	0.37	0.18	0.15	-0.05	0.22	0.20	0.82	-0.28
	Pooled	-0.12	0.15	0.00	0.22	-0.26	-0.01	-0.05	-0.01	0.74	-0.17
HI	E1	0.02	-0.01	0.00	0.07	-0.06	0.00	0.03	0.01	0.08	0.65
	E2	-0.01	0.98	0.00	-0.03	0.03	0.00	-0.01	0.06	-0.15	0.03
	E3	0.03	0.06	0.06	0.25	0.22	0.29	0.06	0.28	-0.39	0.15
	Pooled	0.00	0.05	0.00	-0.27	0.26	-0.01	0.04	0.10	-0.16	0.78

PH = Plant height, PBPP = Primary branches per plant, PBPP = Number of pods per plant, NSPP = number of seeds per plant, HSW = Hundred seed weight, BYPP = Biological yield per plant, HI = Harvest index, DTFI = Days to flower initiation, DTF = Days to 50% flowering, DTM = Days to maturity, Env. = Environments, DF = Degree of freedom, E1 = 2019, E2 = 2020, E3 = 2021, * $p < .05$. ** $p < .01$. *** $p < .001$.

Table 6. Regression coefficient (b), standard error (SE), t value, and probability of the estimated variables to predict seed yield by multiple linear regression analysis for the environment E1, E2, E3 and pooled

Traits	Environments	Regression coefficient (b)	SE	t-value	p-value
DTFI	E1	-0.013	0.051	-0.249	0.804*
	E2	1.240	3.397	0.365	0.717
	E3	1.143	0.383	2.986	0.005**
	Pooled	-0.033	0.137	-0.238	0.813
DTF	E1	-0.032	0.061	-0.512	0.612
	E2	-1.450	3.399	-0.427	0.672
	E3	-0.982	0.382	2.570	0.014*
	Pooled	-0.043	0.160	-0.268	0.790
DTM	E1	-0.008	0.026	-0.313	0.756
	E2	0.125	0.052	2.382	0.022*
	E3	0.059	0.039	1.035	0.756
	Pooled	0.142	0.048	2.953	0.005**
NPPP	E1	0.070	0.069	1.006	0.321
	E2	0.120	0.079	1.519	0.137
	E3	-0.103	0.045	-2.296	0.027*
	Pooled	-0.020	0.052	-0.385	0.702
NSPP	E1	-0.019	0.028	-0.686	0.497
	E2	-0.048	0.030	-1.575	0.123
	E3	0.047	0.018	2.704	0.010*
	Pooled	0.014	0.021	0.680	0.500
PBPP	E1	-0.014	0.132	-0.109	0.914
	E2	0.050	0.275	0.181	0.857
	E3	-0.479	0.286	-1.675	0.102
	Pooled	0.342	0.236	1.448	0.156
PH	E1	-0.003	0.016	-0.194	0.847
	E2	0.046	0.023	2.024	0.059*
	E3	-0.015	0.022	-0.692	0.493
	Pooled	0.006	0.023	0.244	0.808

HSW	E1	0.002	0.043	0.055	0.956
	E2	-0.024	0.073	-0.333	0.741
	E3	-0.072	0.097	-0.741	0.463
	Pooled	-0.029	0.057	-0.514	0.610
BYPP	E1	0.453	0.031	14.715	0.001***
	E2	0.477	0.049	9.774	0.001***
	E3	0.416	0.029	14.222	0.001***
	Pooled	0.379	0.033	11.574	0.001***
HI	E1	0.168	0.009	18.500	0.001***
	E2	0.167	0.010	17.393	0.001***
	E3	0.230	0.014	16.979	0.001***
	Pooled	0.186	0.011	16.184	0.001***

PH = Plant height, PBPP = Primary branches per plant, PBPP = Number of pods per plant, NSPP = number of seeds per plant, HSW = Hundred seed weight, BYPP = Biological yield per plant, HI = Harvest index, DTFI = Days to flower initiation, DTF = Days to 50% flowering, DTM = Days to maturity, DF = Degree of freedom, E1 = 2019, E2 = 2020, E3 = 2021, * $p < .05$. ** $p < .01$. *** $p < .001$.

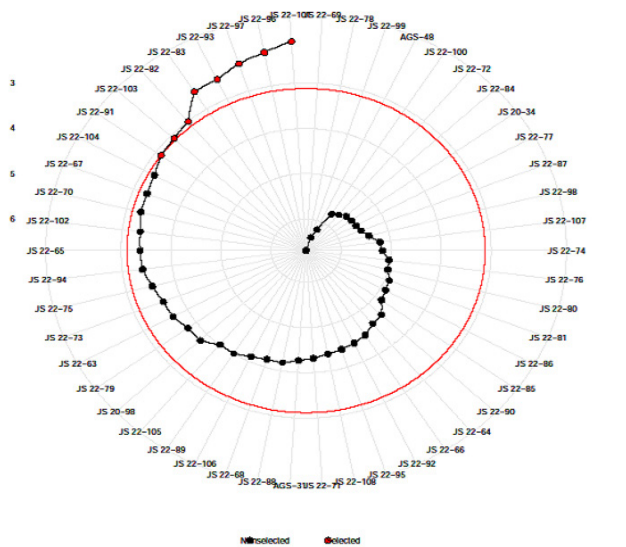


Fig. 2. Genotype ranking and selected genotypes for the multi-trait stability index (MTSI) of 50 soybean genotypes based on eleven traits. The selected genotypes shown in the red and the red spiral depict the cut-point according to the selection differential of 10%.

22-101 to the ideotype, highlighting the need to improve traits in FA1 (DTFI, DTF), FA2 (NPPP, NSPP), and FA3 (HI, SYPP) for industrial quality. The WAASBY index showed a negative selection differential for all traits except DTM, with an overall mean of -28.243%, the lowest for PBPP (-41.400) and the highest for DTM (6.330).

Discussion

Substantial variability among advanced soybean lines, as highlighted by Raza et al. (2023), underscores the critical importance of effective selection processes. The

estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) components is essential for gauging genetic variation across studied traits. Typically, PCV values exceed GCV values, indicating the significant influence of the environment on trait expression (Hizli et al. 2023). High GCV and PCV values reflect the diverse performance of each genotype under varying environmental conditions (Deshmukh et al. 1986). High heritability denotes trait stability across environments, whereas inconsistent broad-sense heritability suggests a strong environmental influence (Belay et al. 2022). Traits exhibiting high heritability combined with high genetic advance are promising candidates for selection in soybean improvement programs (Belay et al. 2022).

Correlation and path analysis studies are invaluable for identifying yield-contributing traits assisting plant breeders in selecting superior genotypes from diverse genetic pools (Raza et al. 2023; Poudel et al. 2023). Notably, Yildirim et al. (2023); Zafar et al. (2023) and Nasir et al. (2023) found a positive relationship between seed yield and harvest index. Path analysis reveals that biological yield per plant exerts the highest positive direct influence on the dependent trait (Machado et al. 2017). Multiple regression analysis indicated that both biological yield per plant and harvest index positively contributed to the overall variation of dependent traits (Wojcik et al. 2022; Foronski et al. 2023). Therefore, indirect selection might be performed via harvest index and biological yield.

Recent studies have highlighted the significance of the multi-trait stability index (MTSI) as a sophisticated tool for breeders, facilitating the evaluation of distances between ideotypes and genotypes to identify desirable traits (Munda et al. 2023). Truncated selection, commonly utilized in breeding programs, relies on data from a limited

Table 7. Selection differential for mean of the traits and WAASBY index for eleven traits of soybean genotypes across three environments

Traits	Factor	Mean performance			Traits	Factor	WAASBY		
		Overall (X0)	Selected genotype (Xs)	SD (%)			Overall (X0)	Selected genotype (Xs)	SD (%)
DTFI	FA1	48	48.30	0.35	DTFI	FA1	0.5	0.4	-26.0
DTF	FA1	51	51.00	0.66	DTFF		0.5	0.4	-27.0
NPPP	FA2	46	48.80	5.23	NPPP	FA2	1.0	0.7	-29.0
NSPP	FA2	113	119.00	4.94	NSPP		1.5	1.1	-26.0
HI	FA3	46	44.60	-3.90	HI	FA3	1.1	1.0	-15.0
SYPP	FA3	9.1	9.19	0.83	SYPP		0.6	0.4	-37.0
DTM	FA4	108	109.00	0.94	DTM	FA4	0.5	0.6	6.33
BYPP	FA4	20	21.60	5.85	BYPP		0.7	0.4	-44.0
PH	FA5	65	67.20	3.55	PH	FA5	0.8	0.5	-30.0
PBPP	FA6	2.5	2.31	-7.40	PBPP		0.2	0.1	-41.0
HSW	FA6	10	10.50	1.71	HSW	FA6	0.4	0.2	-43.0

PH = Plant height; PBPP = Primary branches per plant; PBPP = Number of pods per plant; NSPP = number of seeds per plant; HSW = Hundred seed weight; BYPP = Biological yield per plant; HI = Harvest index; DTFI = Days to flower initiation; DTF = Days to fifty percent flowering; DTM = Days to maturity; Xo = mean; SD = selection differential.

number of environments, potentially leading to the loss of valuable alleles for other desirable traits (Olivoto et al. 2019). However, with the advancement of breeding programs and the modernization of production systems, there is a growing demand for the simultaneous improvement of multiple traits through multivariate approaches (Zuffo et al. 2020). One such approach gaining prominence is the MTSI. Recommendations derived from MTSI-based analyses are considered more reliable than those from single-trait evaluations, especially when traits exhibit high correlation. The MTSI index allows for genotype-ideotype selection based on Euclidean distance by considering multiple traits. Researchers have observed that genotypes with lower MTSI values tend to indicate higher stability across measured traits, making them desirable candidates for selection. Furthermore, the utilization of the WAASB statistic has been employed to characterize ideal genotypes based on both yield performance and stability findings supported by Zuffo et al. (2020). Yue et al. (2022).

Authors' contribution

Experimentation and writing the original draft of the manuscript (MS); Provides the resource and conceptualization of the experiment (MKS); Investigation and validations (PKA, YS); Data curation, data analysis and framing of the manuscript (VK).

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