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Genetic variability and selection potential for yield and associated traits in soybean under semi-arid conditions

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Abstract

Soybean productivity depends on the availability of genetically diverse and stable sources for yield improvement, yet substantial genetic variation remains to be effectively exploited in breeding programmes. The present study evaluated 153 soybean genotypes to characterise genetic variability and identify traits and genotypes with potential for improving seed yield. The experiment was conducted during kharif 2024 and 2025 at Zonal Agricultural Research station, Morena, Madhya Pradesh, India, using an augmented block design. Ten quantitative traits encompassing phenology, plant architecture, yield components and productivity were evaluated. Analysis of variance revealed presence of highly significant genotypic differences for all the traits, confirming substantial genetic diversity in the germplasm. In pooled analysis, high genotypic and phenotypic coefficients of variation were observed for number of pods per plant (36.95 and 37.12 %), number of seeds per plant (37.66 and 37.80 %), seed yield (38.25 and 38.46 %), biological yield and number of primary branches per plant. Broad sense heritability was evident very high for all the traits (89.19–99.27 %), while high heritability coupled with higher genetic advance as percentage of mean was observed for seed yield (78.47 %), number of pods per plant (75.90 %), number of seeds per plant (77.41 %) and biological yield (72.14 %), indicating substantial exploitable genetic variation and good prospects for selection. Genotypes JS 21-72, RVSM-35, JS 20-79, JS 21-17, RVSM-2011-35 and JS 20-98 showed superior seed yield with favourable yield-component performance and may serve as promising material for further breeding evaluation. The identified variability and superior genotypes provide useful resources for developing high-yielding soybean cultivars.

Keywords: genotypes; heritability; selection; soybean; variability; yield

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1. Introduction

In the chronicle of agricultural civilisation, few crops have commanded as much biological intrigue, economic consequence and nutritional indispensability as soybean (*Glycine max* (L.) Merr.). Originating as a humble leguminous plant domesticated in ancient northeastern China more than 5000 years ago, soybean has evolved into one of the most extensively cultivated and globally traded commodity crops of the modern era. This transformation has been so profound that soybean now plays a pivotal role in food systems, feed industries and bioenergy economies across six continents (1, 2). At its biochemical core, soybean is an exceptional crop. Its seeds harbour approximately 38–42 % crude protein on a dry weight basis, the highest among all cultivated grain legumes, along with 18–22 % edible oil composed of a nutritionally favourable fatty acid profile dominated by linoleic acid ($C_{18:2}$, ~54 %) and oleic acid ($C_{18:1}$, ~23 %), complemented by α-linolenic acid ($C_{18:3}$, ~8 %), which confers essential omega-3 nutritional value. Beyond macronutrition, its seeds are a reservoir of bioactive compounds including isoflavones (genistein, diadzein, glycitein), saponins, phytosterols and tocopherol molecules with demonstrated roles in modulating cardiovascular risk, hormonal balance and antioxidant defence in human physiology (3–5). This chemical complexity elevates soybean from a mere agronomic commodity to a functional food crop of medicinal relevance.

From an ecological standpoint, it occupies a unique niche as a nitrogen-fixing legume, engaging in a mutualistic symbiosis with *Bradyrhizobium japonicum* through the formation of root nodules capable of biologically fixing nitrogen, thereby enriching soil fertility and reducing dependence on synthetic nitrogenous fertilisers. This attribute imparts substantial sustainability value in diversified cropping systems and aligns with global imperatives for climate resilient, low input

agriculture (6, 7). On the global stage, it has grown across approximately 145 million hectares, with world production exceeding 427 million metric tonnes. The United States, Brazil, Argentina, China and India collectively account for the overwhelming majority of production. In India, soybean cultivation spans over 11.5 million hectares concentrated in Madhya Pradesh, Maharashtra and Rajasthan, where it serves as the dominant kharif oilseed crop and a critical link in the domestic edible oil supply chain (8).

Yet, despite its extraordinary biochemical endowment and agronomical versatility, the yield potential of soybean, theoretically estimated at 7–11 t ha^{-1} under optimal conditions, remains profoundly underexploited in farmer's field, where national average yields frequently languish below 1–2 t ha^{-1} (9, 10). This yield gap is symptomatic of a deeper challenge, the genetic narrowing of commercial cultivars, limited systematic exploitation of the vast untapped diversity residing within global soybean germplasm collections and an incomplete understanding of genetic control of quantitative yield determining traits. It is precisely at this crossroads, between biological potential and realised productivity, that genetic evaluation and quantitative genetics assume strategic primacy. The scientific exploitation of genetic variability is the sine qua non of any meaningful crop improvement programme. Before a breeder can develop a superior genotype, the architecture of variation itself must be comprehensively characterised. This demands a rigorous, multi-parameter analytical framework that transcends simple trait averages and moves toward mechanistic understanding of how genetic and environmental forces interact to shape phenotypic expression (11–13).

The present investigation approaches this challenge by evaluating 153 soybean genotypes for 10 quantitative traits, that collectively encompass morphological development, canopy architecture, reproductive efficiency and harvestable productivity. Descriptive statistics can be used to characterise the phenotypic variation within the soybean germplasm panel by quantifying each trait's range, mean dispersion and distributional pattern (14, 15). Analysis of variance (ANOVA) partitions the observed variation into its genotypic, environmental and interaction components, establishing the statistical significance of genotypic differences as a prerequisite for further genetic inference. Building upon this foundation, the estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) quantifies the relative magnitude of genetic and phenotypic variation, with the GCV to PCV ratio serving as an indirect index of environmental buffering on genetic expression (16–18). Broad sense heritability (h^2b) is the proportion of total phenotypic variance attributable to genotypic differences, defines the fidelity with which phenotypic performance reflects underlying genotypic merit and thereby governs the reliability of selection. Genetic advance (GA) and genetic advance as a percentage of the mean (GAM), estimated at 5 % selection intensity, translate heritability into actionable predictions of breeding progress, distinguishing traits governed by additive gene action, amenable to selection, from those dominated by non-additive effects requiring alternative breeding strategies (19–21).

Together, these parameters constitute a coherent genetic portrait of the germplasm under study, one that does not merely describe variability but decodes its nature, magnitude and practicable exploitability. The insights emerging from this investigation are envisioned to guide the strategic identification of elite donor lines, the prioritisation of target traits for selection and rational design of soybean productivity, quality and adaptability in the target agro-ecosystem.

2. Materials and Methods

Features of experimental site

The field experiment was conducted during the kharif seasons of 2024 and 2025 at the Zonal Agricultural Research Station (ZARS), Morena, under Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior, Madhya Pradesh, India. The experimental site is located in a semi-arid agro-climatic region of Madhya Pradesh (26°05'–26°42' N, 77°05'–78°30' E; 150–300 m above mean sea level) and receives an average annual rainfall of about 862.6 mm, predominantly during the south-west monsoon. The climate is characterised by hot summers, cold winters and variable rainfall patterns. During the study period, kharif 2024, maximum and minimum temperatures ranged between 32 and 36 °C and 19 and 28 °C respectively, with uneven rainfall distribution concentrated during standard meteorological weeks (SMW) 32–38 (Fig. 1). Whereas in kharif 2025, comparatively moderate conditions prevailed, with maximum temperatures ranged from 30 to 36 °C and minimum temperatures from 18 to 26 °C, accompanied by relatively uniform rainfall distribution throughout the crop growth period (Fig. 2). These contrasting meteorological conditions provided a suitable environment for evaluating the performance of soybean genotypes across both years.

Soil characteristics

The general soil characteristics of the experimental area indicate that the soils are predominantly sandy loam in texture, slightly alkaline in reaction (pH around 7.8), with low organic carbon content (approximately 0.28 %) and generally low to medium available nitrogen, phosphorus and potassium (NPK) status (22). These characteristics are typical of alluvial soils of the Morena region and provide a representative environment for evaluating soybean genotypes under central Indian agro-climatic conditions. Since the present investigation was a plant breeding trial aimed at assessing genetic variability and yield related traits, detailed soil analysis of the experimental field was not undertaken.

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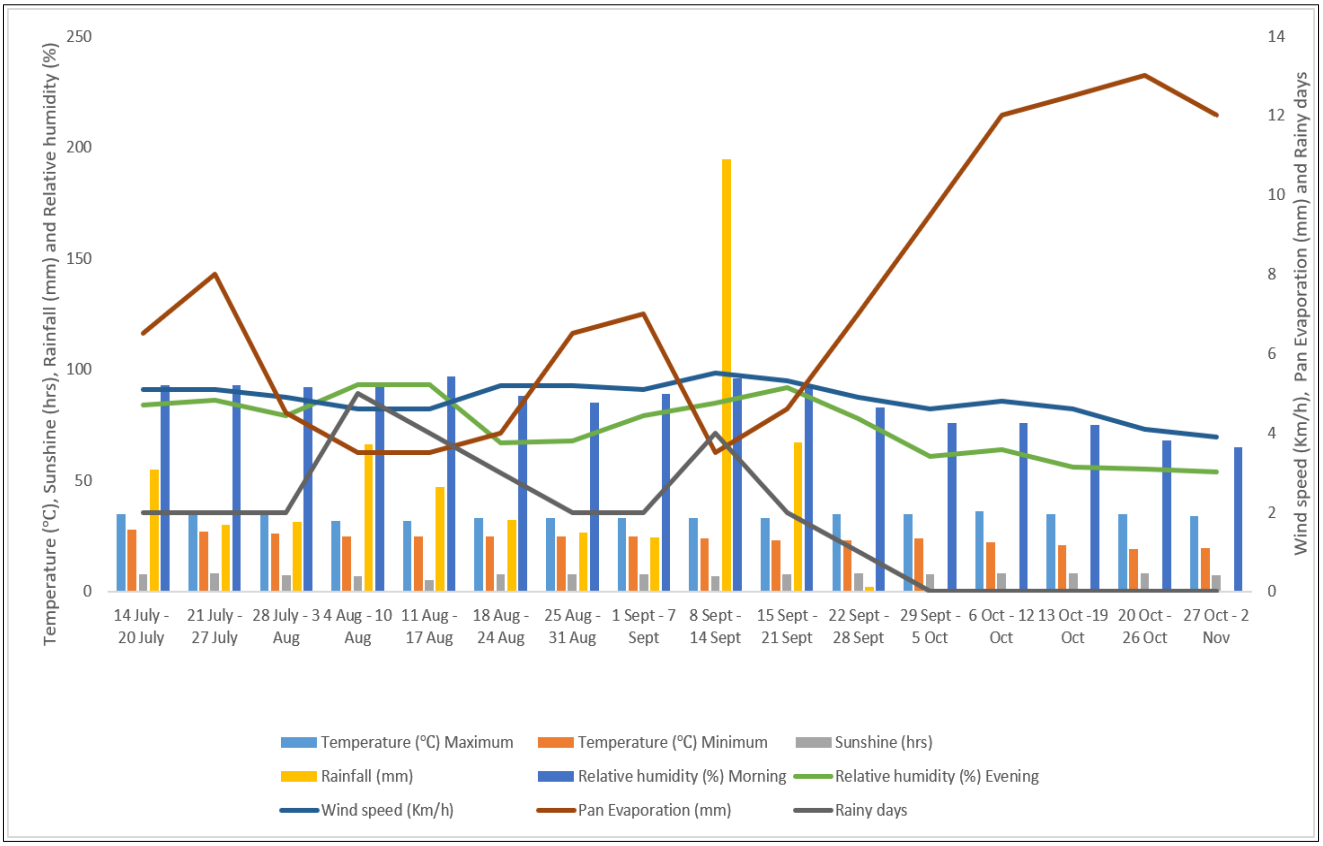


Fig. 1. Meteorological parameters observed during kharif, 2024. [Source: Agrometeorology Observatory, Zonal Agricultural Research Station (ZARS), Morena, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior]

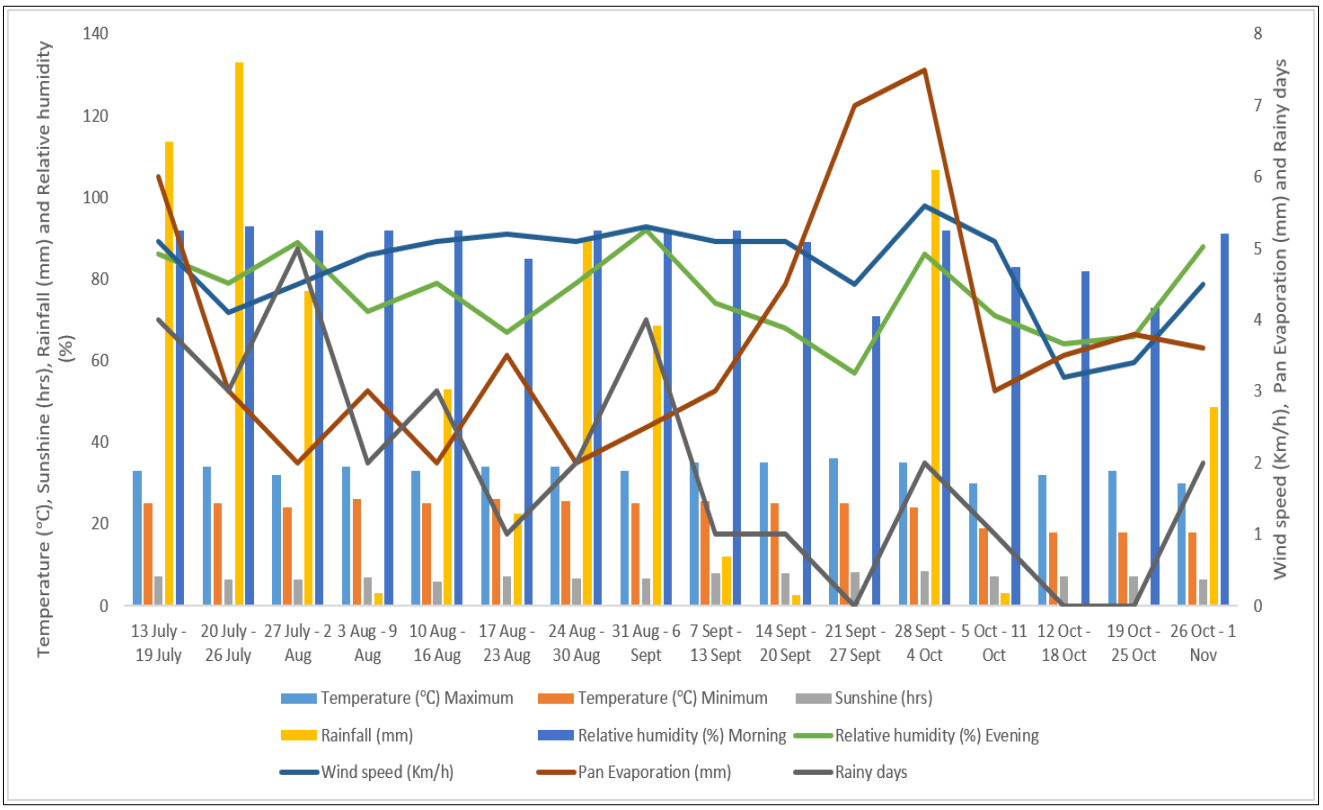


Fig. 2. Weather parameters observed during kharif, 2025. [Source: Agrometeorology Observatory, Zonal Agricultural Research Station (ZARS), Morena, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior]

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Experimental details

The experimental material consisted of 153 soybean (*Glycine max* L. Merr.) genotypes collected from different research institutions, including All India Coordinated Research Project (AICRP) on soybean, ZARS, Morena; Rafi Ahmad Kidwai (RAK) College of Agriculture, Sehore; RVSKVV, Gwalior and the College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, India (Table 1). The experiment was laid out in an augmented block design during kharif 2024 and 2025. The experimental material was distributed across five blocks, with 33 genotypes, including checks in each block. Three checks viz., JS 97-52, JS 20-116 and RVSM-35 were used for yield and its traits. Each genotype was sown in a single row of 3 m length with a spacing of 45 cm between rows and 7-10 cm between plants. The plot size for each genotype was 3.0 m × 0.45 m (1.35 m^2) and the gross experimental area covered 252.45 sq m^2. The genotypes were classified into appropriate maturity groups based on their days to physiological maturity such as early maturing, normal maturing and late maturing.

Crop management

Standard agronomical practices recommended for soybean cultivation were followed to raise a healthy crop (Fig. 3). The experimental field was prepared through deep ploughing with a tractor-mounted cultivar followed by two harrowing to obtain fine tilth. Final levelling was done using a tractor drawn leveller. Prior to sowing, seeds of all soybean genotypes were treated with thiram at 2.0 g kg^{-1} seed 24 hr before sowing. The treated seeds were shade dried before sowing. Sowing was performed manually by hand-dribbling method, maintaining the recommended row-to-row and plant-to plant spacing. A basal fertiliser dose of 20:60:20:20 kg ha^{-1} of nitrogen: phosphorus: potassium: sulphur (N: P: K: S) was uniformly applied to experimental plot. Irrigation was scheduled based on rainfall received during the cropping season, crop growth stage and daily pan evaporation data recorded at the Agrometeorological Observatory, ZARS Morena. The daily pan evaporation observations obtained from the Class A pan evaporimeter were used to assess the atmospheric evaporative demand and soil moisture status for determining the need for supplemental irrigation. Supplemental irrigations were provided whenever prolonged dry spells or high evaporative demand were observed, particularly during the critical growth stages of flowering, pod initiation and seed filling to avoid moisture stress and ensure uniform crop growth. Weed management was carried out through timely intercultural operations. Manual weeding and hoeing were taken as required, particularly during the critical period of crop-weed competition. The experimental plots were regularly monitored for the incidence of insect pests and diseases. No plant protection measures were taken during the crop period to record the crop response under epiphytotic conditions.

Table 1. List of genotypes with their source/origin

Sl. No.	Germplasm	Source/origin
1	JS-26, JS-93-05, JS-97-52, JS-20-29, JS-20-34, JS-20-53, JS-20-69, JS-20-79, JS-20-89, JS-20-94, JS-20-98, JS-20-116, JS-21-05, JS-21-07, JS-21-17, JS-21-72, JS-21-76, JS-21-77, JS-22-01, JS-22-08, JS-22-12, JS-22-16, JS-23-03, JS-23-05, JS-23-09, JS-24-26, JS-24-30, JS-24-34, JS-24-31, JS-25-03, JS-25-05, JS-25-06, JS-25-08, JS-25-02, JS-24-33, JS-25-50, JS-25-52, JS-25-53, JS-25-55	JNKVV, Jabalpur
2	RVS-76, RVS-2001-4, RVS-2011-10, RVS-12-8, RVS-13-20, RVS-15-1, RVS-23-2, RVS-23-5, RVS-23-7, RVS-23-8, RVS-23-9, RVS-23-10, RVS-23-11, RVS-23-12, RVS-23-13, RVS-23-14, RVS-23-15, RVS-23-16, RVS-23-17, RVS-23-19, RVS-23-20, RVS-23-21, RVS-23-22, RVS-23-23, RVS-23-25, RVS-23-26	RVSKVV, Gwalior
3	NRC-130, NRC-138, NRC-142, NRC-150, NRC-152, NRC-166, NRC-192, NRC-201, NRC-254, NRC-255, NRC-258, NRC-259, NRC-264, NRC-265, NRC-266, NRC-267, NRC-269, NRC-271, NRC-859	NSRI, Indore
4	NRCSL-4, NRCSL-7, NRCSL-8, ASB-85, ASB-93, ASB-101, DLSB-5, DLSB-40, PS 1569, PS-1696, Himso 1696, Himso 1695, RVSM-35, RVSM-12-21, RVSM-2011-35, RVSM-2012-4, KSS-213, KSS-225, MAUS-124, MAUS-824, MAUS-791, MAUS-787, Rajsoya-24, CAUMS-3, MACS-1810, MACS-1834, MACS-824, TS-208, TS-156, TS-101, AUKS-212, AUKS-21-5, AS-26, AS-34, AS-55, Cat 492A, Cat 87, KDS-1188, KDS-1193, KDS-1201, KDS-1203, KDSIS-1394, KBSL-23-36, VLS- 104, VLS-106, THPS-6, Lok soya 03, Pusa Sipani BS 8, Pusa Sipani BS 33, Pusa Sipani SPS 433	RAK, Sehore
5	RSC-10-46, RSC-10-52, RSC-11-95, RSC-1165	Raipur
6	DS 1510, DS 1547, DS-1589, DS 1480	Delhi
7	AMS-2021-3, AMS-2021-4, AMS-100-39, AMS- 264, AMS 22-16, AMS-2022-1	PDKV, Akola
8	Jhimka	Landrace
9	EC109563	Exotic collection
10	SL-311, SL-1315	PAU, Ludhiana
11	BAUS(M)-6	Ranchi

JNKVV: Jawaharlal Nehru Krishi Vishwa Vidyalaya; RVSKVV: Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya; NSRI: National Soybean Research Institute; RAK: Rafi Ahmad Kidwai; PDKV: Dr Panjabrao Deshmukh Krishi Vidyapeeth; PAU: Punjab Agricultural University.

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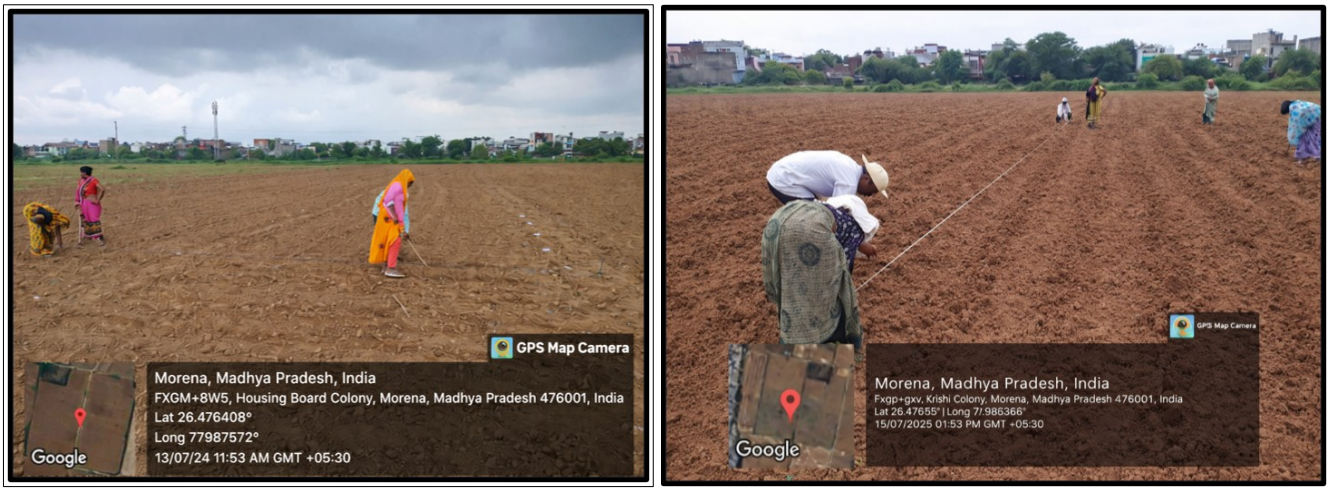


Fig. 3. Standard agronomical practices adopted during the cropping season of kharif, 2024 and kharif, 2025.

Observations recorded

Observations were recorded on five randomly selected competitive plants from each genotype for quantitative traits. Days to 50 % flowering (DFF) and days to maturity (DTM) were recorded on a plot basis. Days to 50 % flowering were counted from sowing to the stage when 50 % of the plants in a plot produced at least one flower, while DTM were recorded when approximately 95 % of the pods turned yellow or brown. The quantitative traits studied included plant height (PH) (cm), number of primary branches per plant (NPB), number of pods per plant (NPP), number of seeds per plant (NSP), 100-seed weight (HSW) (g), biological yield (BY) per plant (g), harvest index (HI) (%) and seed yield (SY) per plant (g). Plant height was measured from ground level to the tip of the plant at maturity. Biological yield was recorded as the dry weight of plants before threshing.

Statistical analysis

The data recorded for 10 different quantitative traits were subjected to pooled statistical analysis across years using an augmented block design (23, 24). Since the test genotypes were evaluated without replication and the checks were replicated within blocks, genotype effects were estimated after adjusting for block effects within each year. Accordingly, adjusted genotype means were obtained by accounting for block-within-year variation and were used for subsequent genotype comparisons and genetic analysis. Before pooling the data across years, homogeneity of error variances for each trait was tested using Bartlett's chi-squared test. Homogeneity of error variances was considered a prerequisite for the use of a common pooled error term in the combined analysis. Bartlett's test indicated homogenous error variances across years for all the traits. Therefore, no variance-stabilising or heterogeneity correction was required and the standard pooled error term was used. A means-based genotype × year (G × Y) analysis was performed using the adjusted genotype means from individual years to test the significance of year, genotype and G × Y interaction effects. The combined analysis therefore enabled assessment of the overall performance of genotypes as well as the consistency of their performance across years. The pooled statistical model for the augmented block design was formulated as follows (Eqn. 1):

$$Y_{ijk} = \mu + Y_i + t_j + B_{j(i)} + G_k + (YG)_{ik} + \varepsilon_{ijk} \quad \text{(Eqn. 1)}$$

Where:

Y_{ijk} = observed value of k^{th} genotype in the j^{th} block during the i^{th} year

μ = overall mean

Y_i = effect of i^{th} year

$B_{j(i)}$ = effect of j^{th} block within the i^{th} year

G_k = effect of the k^{th} genotype

$(YG)_{ik}$ = genotype × year interaction effect

ε_{ijk} = random experimental error associated with the observations.

For the augmented design, the appropriate adjusted treatment and error terms were used for testing the corresponding source of variation. The significance of the sources of variation was tested using the *F*-test at the 5 % and 1 % probability levels. Descriptive statistical parameters including mean, range, standard error and coefficient of variation were estimated using the adjusted genotypic means. Genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance as percent of mean were computed following standard biometrical procedures. The GCV and PCV were calculated using the formulae described in previous studies (25). Whereas, broad sense heritability was estimated using the formula suggested by previous researchers (26). Additionally, genetic advance was estimated using the methods reported in some of the earlier studies (27). Genetic advance as percentage of mean was estimated using the following formula given below (Eqn. 2):

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$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100 \quad \text{(Eqn. 2)}$$

All the statistical analysis was performed using Raisins statistical software (28, 29).

3. Results and Discussion

Descriptive statistics for yield and yield attributing traits

The soybean genotypes exhibited substantial variation for all ten quantitative traits across both years (Table 2–4; Fig. 4). The pooled means ranged from 3.54 for NPB to 95.22 for DTM, with mean seed yield 9.15 g plant^{-1}, biological yield 23.67 g plant^{-1} and harvest index 38.67 % respectively. Seed yield (SY) ranged from 4.54 to 15.02 g plant^{-1}, while substantial variation was also observed for NPP, NSP, HSW and BY. This broad variation indicates existence of adequate phenotypic diversity for selection of contrasting genotypes and parental combinations.

Trait means for the major productivity attributes were found remarkably similar for the years 2024 and 2025. Seed yield was 9.39 and 9.43 g plant^{-1}, BY was 24.35 and 24.44 g plant^{-1} and HI was 38.65 and 38.62 % respectively. This consistency suggests that overall productivity was comparatively stable across the years, whereas greater year-to-year variation in flowering, maturity, plant height and branching indicates stronger environmental influence on phenological and architectural traits. Such differential environmental responsiveness is expected because developmental traits are directly influenced by seasonal temperature and moisture conditions, while yield represents the integrated outcome of growth and reproductive processes.

The relatively low pooled coefficient of variation (CV) (5.11–9.23 %) indicated good experimental precision and limited experimental error. The slightly higher variation for number of primary branches and harvest index suggests greater sensitivity of these traits to environmental conditions and plant-to-plant differences. The wide variation in number of pods and seeds per plant is particularly important biologically, as these traits reflect differences in reproductive sink formation, including flowering intensity, pod retention and assimilate allocation and therefore, provide useful opportunities for indirect improvement of seed yield.

The results of the present study were comparable to those reported by previous researchers (30), who also observed an average of 53.47 ± 11.72 pods plant^{-1}, 111.40 ± 22.54 grains plant^{-1} and 14.57 ± 3.04 g per 100-grains. Similarly, some previous researchers (31) evaluated soybean genotypes during 2008 and 2009. They reported the mean plant heights of 54.78 ± 13.68 and 52.83 ± 13.68 cm and an average of 55.11 ± 14.89 and 53.62 ± 17.24 pods plant^{-1}. The mean number of seeds per pod was 2.36 ± 0.26 and 2.30 ± 0.25, while seed yield averaged 10.45 ± 3.67 and 9.96 ± 3.55 g and 100-seed weight averaged 8.33 ± 2.00 and 8.21 ± 1.72 g during the respective years. Similarly, substantial phenotypic variation among soybean genotypes for several agronomic traits was reported during 2012 and 2013 (32). The 100-seed weight (HSW) ranged from 0.79 to 12.23 g, while the number of effective pods plant^{-1} ranged from 16.67 to 1242.33 and the number of branches plant^{-1} ranged from 1.67 to 11.67 across the two years. The relatively high CV (21–94 %) further reflected wide variability, with seed weight plant^{-1} ranging from 0.38–95.75 g.

Table 2. Descriptive statistical parameters for yield and yield contributing traits in soybean genotypes during kharif, 2024

	DFF	DTM	PH	NPB	NPP	NSP	HSW	SY	BY	HI
Grand mean	39.616	95.590	37.524	3.596	56.162	95.038	9.944	9.393	24.349	38.646
Mean of checks	38.747	97.267	43.227	3.800	64.507	116.520	10.274	12.031	31.752	38.242
Mean of entries	39.703	95.423	36.953	3.576	55.328	92.889	9.911	9.129	23.609	38.686
Min	31.200	84.400	24.900	1.600	26.000	47.600	7.000	4.570	12.140	29.127
Max	49.400	108.600	56.600	5.400	93.000	150.200	14.390	15.120	36.560	44.812
CD at 5 %	4.740	11.187	5.932	0.725	7.351	13.899	1.395	1.478	4.483	7.450
SE(d)	2.397	5.657	3.000	0.367	3.717	7.028	0.706	0.747	2.267	3.767
SE(m)	1.695	4.000	2.121	0.259	2.628	4.970	0.499	0.529	1.603	2.664
CV (%)	6.036	5.925	8.089	10.233	6.697	7.532	7.115	8.141	9.543	9.739
Skewness	0.099	0.289	0.686	0.009	0.160	0.286	0.388	0.289	0.061	-0.418
Kurtosis	-0.140	-0.994	0.005	-0.557	-0.156	-0.743	-0.003	-0.418	-0.880	-0.49

DFF: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); NPB: number of primary branches per plant; NPP: number of pods per plant; NSP: number of seeds per plant; HSW: hundred seed weight (g); SY: seed yield (g); BY: biological yield (g); HI: harvest index (%).

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Table 3. Phenotypic variability for yield and yield contributing traits of soybean genotypes during kharif, 2025

	DFF	DTM	PH	NPB	NPP	NSP	HSW	SY	BY	HI
Grand mean	38.725	94.848	36.794	3.491	56.157	95.022	9.967	9.427	24.438	38.622
Mean of checks	39.240	96.853	42.413	3.827	63.293	116.507	10.289	12.045	31.618	38.391
Mean of entries	38.673	94.648	36.232	3.457	55.443	92.874	9.934	9.165	23.720	38.645
Min	31.000	84.000	24.800	1.400	25.200	45.400	7.190	4.500	12.260	28.996
Max	48.800	110.440	55.200	5.400	96.600	150.200	14.990	14.924	36.930	44.820
CD at 5 %	5.209	12.585	5.870	0.714	7.681	13.198	1.538	1.343	4.215	7.724
SE(d)	2.634	6.364	2.969	0.361	3.884	6.674	0.778	0.679	2.132	3.907
SEm	1.862	4.500	2.099	0.255	2.747	4.719	0.550	0.480	1.507	2.762
CV (%)	6.813	6.719	8.168	10.437	6.988	7.149	7.822	7.360	8.929	10.107
Skewness	0.213	0.407	0.680	0.055	0.199	0.208	0.416	0.224	-0.001	-0.499
Kurtosis	-0.085	-0.749	-0.048	-0.520	0.085	-0.795	0.210	-0.545	-0.843	-0.413

DFF: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); NPB: number of primary branches per plant; NPP: number of pods per plant; NSP: number of seeds per plant; HSW: hundred seed weight (g); SY: seed yield (g); BY: biological yield (g); HI: harvest index (%).

Table 4. Pooled descriptive statistical parameters for yield and yield contributing traits in soybean genotypes across both of the years

	DFF	DTM	PH	NPB	NPP	NSP	HSW	SY	BY	HI
Grand mean	39.170	95.219	37.159	3.544	56.160	95.030	9.955	9.410	24.394	38.634
Mean of checks	38.993	97.060	42.820	3.813	63.900	116.513	10.282	12.038	31.685	38.316
Mean of entries	39.188	95.035	36.593	3.517	55.386	92.881	9.923	9.147	23.665	38.665
Min	31.100	84.300	24.850	1.500	25.600	46.500	7.095	4.535	12.200	29.051
Max	49.100	108.600	55.900	5.200	94.800	149.000	14.690	15.020	36.745	44.609
CD at 5 %	4.422	9.601	5.666	0.628	6.631	12.544	1.226	1.270	4.020	7.057
SE(d)	2.236	4.855	2.865	0.318	3.353	6.343	0.620	0.642	2.033	3.569
SEm	1.581	3.433	2.865	0.225	2.371	4.485	0.438	0.454	1.437	2.523
CV (%)	5.706	5.105	7.805	9.025	6.037	6.796	6.241	6.976	8.535	9.230
Skewness	0.146	0.338	0.694	-0.009	0.174	0.247	0.405	0.257	0.027	-0.465
Kurtosis	-0.056	-0.912	-0.017	-0.589	-0.039	-0.782	0.099	-0.486	-0.871	-0.465

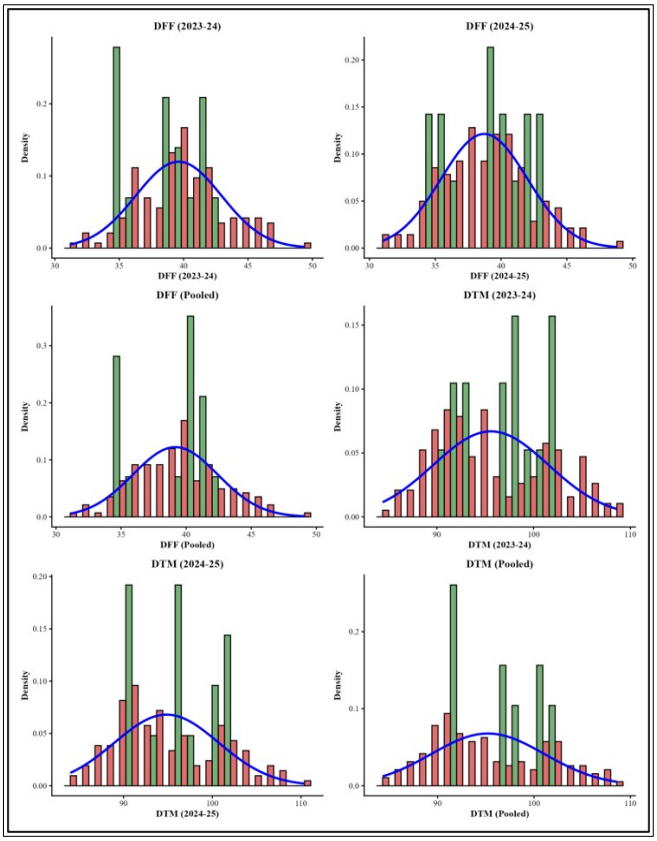
DFF: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); NPB: number of primary branches per plant; NPP: number of pods per plant; NSP: number of seeds per plant; HSW: hundred seed weight (g); SY: seed yield (g); BY: biological yield (g); HI: harvest index (%).

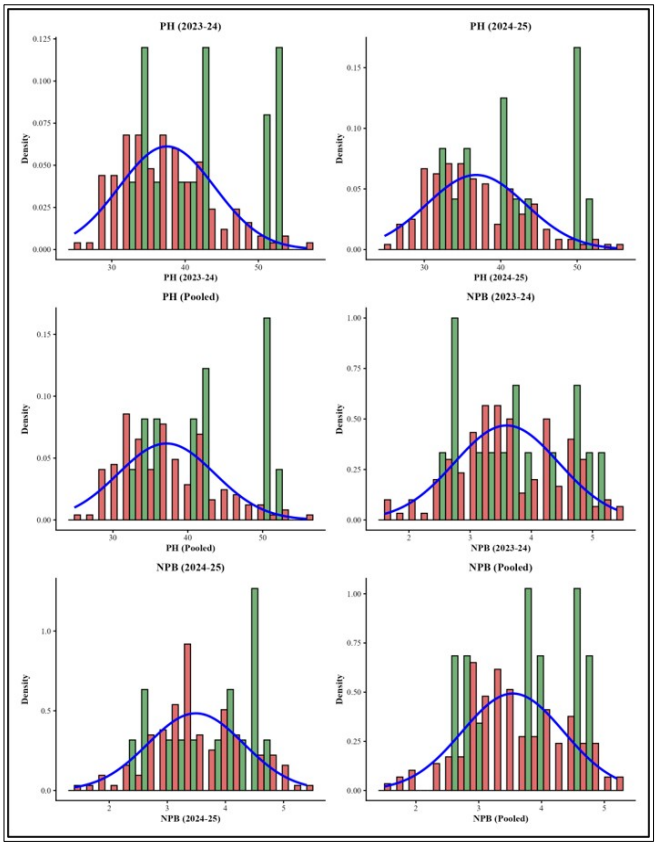
Most traits showed approximately symmetrical distributions, although varying degrees of positive or negative skewness were observed. Positive skewness for seed yield and several yield components indicated an extended upper tail, providing scope for identifying high-performing genotypes. Harvest index showed negative skewness, indicating a comparatively greater concentration of genotypes towards higher values. Most of the traits exhibited negative kurtosis, reflecting relatively broad and flat distributions. These distributional patterns support the presence of substantial phenotypic dispersion, although skewness and kurtosis alone should not be interpreted as evidence of specific type of gene action.

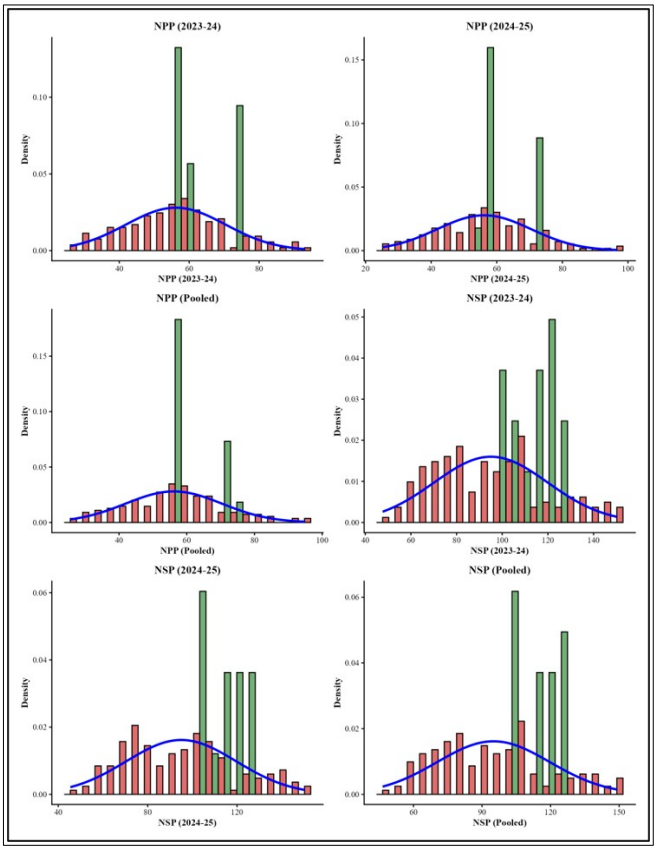
Combined analysis of variance (ANOVA) for yield and yield attributing traits

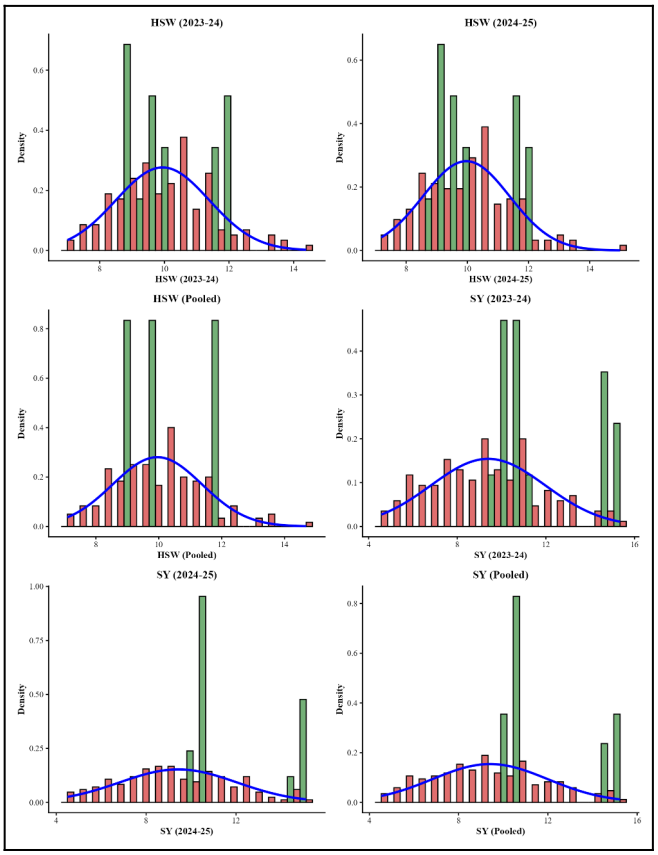
The pooled ANOVA revealed highly significant differences among the evaluated soybean genotypes for all ten quantitative traits (Table 5). This indicates the presence of substantial genetic differentiation among the entries and confirms that the experimental population provided sufficient phenotypic contrast for meaningful selection. Additionally, the significance of genotypic effects was consistent across both of the years, demonstrating that the observed differences were not restricted to a particular growing season.

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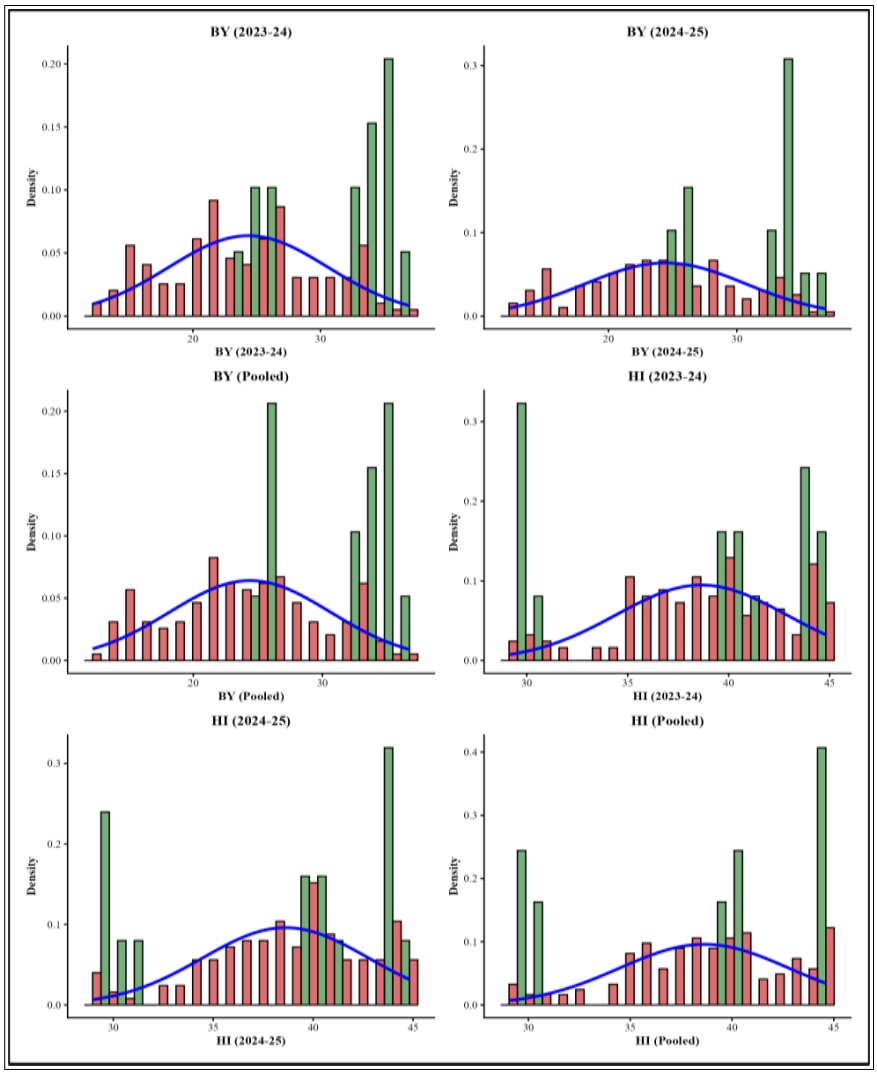


Fig. 4. Comparison of frequency distribution of ten quantitative traits for kharif 2024, kharif 2025 and pooled data across both of the years.

(Note: 2023–24 is kharif 2024 and 2024–25 is kharif 2025)

DFF: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); NPB: number of primary branches per plant; NPP: number of pods per plant; NSP: number of seeds per plant; HSW: hundred seed weight (g); SY: seed yield (g); BY: biological yield (g); HI: harvest index (%).

Table 5. Combined analysis of variance (ANOVA) for yield and yield contributing traits in soybean genotypes for pooled data

Source of variation	DF	SY	DFF	DTM	PH	NPB	NPP	NSP	HSW	BY	HI
Years	1	0.10	76.42**	45.07**	40.00**	1.03**	0.61	0.02	0.04	0.87	0.11
Genotypes + Checks	152	12.63**	22.65**	71.53**	77.37**	1.32**	419.39**	1232.76**	4.12**	72.29**	31.43**
Checks	2	13.08**	21.04**	44.74**	141.96**	1.89**	177.98**	216.45**	4.27**	53.82**	106.23**
Genotypes	149	12.38**	22.82**	72.21**	75.49**	1.32**	422.58**	1232.63**	4.14**	70.49**	30.63**
Genotypes vs. Check	1	49.16**	0.22	24.11**	228.12**	0.52	426.43**	3285.09**	0.76**	378.40**	0.72
Error (G × Y means)	152	0.14	1.36	0.72	1.49	0.14	3.71	8.94	0.05	1.01	0.41

Significance: * indicates significance at 5 % level, ** indicates significance at 1 % level; Mean squares are based on block-adjusted means; Residual = GxY (means-based error term); Abbreviations: DF: degree of freedom; G: Genotype; Y: Year; DFF: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); NPB: number of primary branches per plant; NPP: number of pods per plant; NSP: number of seeds per plant; HSW: hundred seed weight (g); SY: seed yield (g); BY: biological yield (g); HI: harvest index (%).

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The year effect was found significant for DFF, DTM, PH and NPB, whereas it was investigated non-significant for SY, NPP, NSP, HSW, BY and HI. The stronger year influence on flowering, maturity and plant architecture indicates that these traits were more responsive to seasonal environmental variation. Differences in temperature, rainfall distribution and other seasonal conditions can alter the duration of vegetative and reproductive phases and consequently influence plant stature and branching (33). In contrast, the non-significant year effects for seed yield and most yield components suggested that the overall productivity of the genotypes remained comparatively consistent between the two years. This distinction is important because it indicates that the seasonal environment altered crop development to some extent without causing a corresponding large shift in mean yield performance.

The significant genotypic effect for seed yield, together with significant effects for its major component traits, demonstrated that the observed variation in productivity was primarily associated with differences among genotypes. The highly significant genotypic effects for NPP and NSP are particularly relevant because these traits represent important components of reproductive productivity. Likewise, the significant genotypic effect for HSW indicates considerable differentiation among genotype in seed size, while the significant effect for BY reflects differences in total biomass production. The simultaneous significance of genotypic effects for these traits suggested that the material contains contrasting combinations of yield components that can be exploited in breeding programmes.

The partitioning of the genotype + checks source further clarified the nature of the variation present in the experimental material. The replicated checks differed significantly for all investigated traits, indicating that the checks themselves represented distinct phenotypic backgrounds. More importantly, the genotype-versus-check contrast was significant for SY, DTM, PH, NPP, HSW and BY, but not for DFF, NPB and HI. Thus, the test genotypes as a group differed from the standard checks particularly for yield and several of its associated attributes. The significant contrast for SY, NPP, NSP and BY is especially relevant because it indicated that the unreplicated test material included entries with performance differing substantially from the established checks. Conversely, the non-significant contrast for DFF, NPB and HI recommended that the overall performance of the test genotypes for these traits was broadly comparable with the checks.

In alignment with the findings of current study some earlier studies (34) reported significant genotypic variation among 148 soybean recombinant inbred lines (RILs) for most yield and its component traits evaluated under augmented block design. They recorded the mean square of 37.31 for DFF, 87.42 for DTM, 221.99 for PH, 265.41 for pods plant^{-1} and 817.12 for seeds plant^{-1}. Previous studies (35) reported significant genotypic variation among 219 soybean accessions for most of the quantitative traits, with entries showing highly significant mean squares for PH (82.69), NPB (5.31), seeds pod^{-1} (0.26), DFF (12.94) and DTM (17.50). Similarly, some previous research (36) reported highly significant variation among 100 soybean germplasm lines for all ten studied traits, with treatment mean squares ranging from 0.103 for seeds pod^{-1} to 60.112 for plant height. Furthermore, significant variation was observed for SY (mean square (MS) = 2.039), pod plant^{-1} (42.625) and HSW (2.133). Earlier studies (37) also reported highly significant genetic variability among soybean germplasm lines for all yield and its attributing traits with mean squares of 67.86 DFF, 44.95 for DTM, 43.19 for PH and 73.66 for pods plant^{-1}. Significant variation was also observed for the number of seeds pod^{-1} (0.92), HSW (0.59) and SY (3.86), confirming existence of substantial variability and scope for effective selection. From a breeding perspective, the results indicated that seed yield and its principal reproductive components were comparatively robust to seasonal variation, whereas flowering time, maturity, plant height and branching were more environmentally responsive. This has practical implications for further selection.

Genetic variability, heritability and genotype × year interaction

The pooled analysis revealed considerable genetic variability among the soybean genotypes for yield and its associated traits (Table 6). The magnitude of genotypic and phenotypic variances was closely comparable for most of the characters, indicating that phenotypic differences were largely connected with genetic differences rather than environmental variation. This was particularly evident for SY, NPP, NSP and BY, which showed high GCV values of 38.25, 36.95, 37.66 and 35.22 % respectively, with only small differences between GCV and PCV. Such substantial variability provides a broad selection window for improving productivity in the evaluated material.

The high variability observed for NPP and NSP has an important biological basis. Pod and seed production are integrative traits determined by branching and reproductive node development, flower production, pod initiation, flower and pod abortion or retention, assimilate availability during flowering and pod set and the competitive strength of developing reproductive sinks. Genotypic differences in the timing and intensity of these processes can therefore accumulate into large differences in final pod and seed number among soybean genotypes (38, 39). The particularly high genotypic variances for NPP (418.87) and NSP (1223.69) designated that reproductive sink formation was a major source of genetic differentiation in the population. Similar patterns have frequently been observed in soybean, where numbers of pods and seeds per plant are among the most variable yield components and are considered important targets for indirect improvement of seed yield (40, 41).

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Table 6. Estimates of genetic variability parameters and genotype × year variance components for quantitative traits in soybean under pooled augmented block design analysis

Parameter	SY	DFF	DTM	PH	NPB	NPP	NSP	HSW	BY	HI
Grand Mean	9.15	39.19	95.04	36.59	3.52	55.39	92.88	9.92	23.66	38.67
Genotypic Variance (GV)	12.24	21.46	71.49	74.00	1.17	418.87	1223.69	4.09	69.47	30.22
Phenotypic Variance (PV)	12.38	22.82	72.21	75.49	1.32	422.58	1232.63	4.14	70.49	30.63
Error Variance (EV)	0.14	1.36	0.72	1.49	0.14	3.71	8.94	0.05	1.01	0.41
σ^2G × Y (G × Y Variance)	0.10	0.78	0.39	0.80	0.12	3.47	6.43	0.04	0.69	0.30
GCV (%)	38.25	11.82	8.90	23.51	30.81	36.95	37.66	20.39	35.22	14.22
PCV (%)	38.46	12.19	8.94	23.74	32.62	37.12	37.80	20.50	35.48	14.31
ECV (%)	4.04	2.98	0.89	3.34	10.73	3.48	3.22	2.15	4.25	1.65
Heritability (BS) (%)	98.90	94.04	99.00	98.03	89.19	99.12	99.27	98.90	98.56	98.67
Genetic Advance (GA)	7.18	9.27	17.36	17.57	2.11	42.04	71.90	4.15	17.07	11.27
Genetic Advance as % of Mean (GAM)	78.47	23.65	18.26	48.02	60.02	75.90	77.41	41.83	72.14	29.14
σ^2G × Y / σ^2g Ratio	0.08	0.36	0.05	0.11	0.94	0.08	0.05	0.10	0.10	0.10

PV: phenotypic variance estimated from treatment (Test) mean square (ANOVA); GV: genotypic variance = PV – EV; EV: environmental variance (G × Y residual mean square); GCV and PCV indicate extent of variability (High > 20 %, Moderate 10-20 %, Low < 10 %); Broad-sense heritability: higher values indicate stronger genetic control; GA: genetic advance under selection; GAM (%) indicates expected improvement; G × Y to G ratio indicates stability (High = strong interaction, Low = stable performance).

DF: degree of freedom; G: Genotype; Y: Year; DFF: days to 50 % flowering; DTM: days to maturity; PH: plant height (cm); NPB: number of primary branches per plant; NPP: number of pods per plant; NSP: number of seeds per plant; HSW: hundred seed weight (g); SY: seed yield (g); BY: biological yield (g); HI: harvest index (%).

Seed yields also exhibited high GCV (38.25 %) and PCV (38.46 %), with a very small difference between them. This close correspondence indicated that environmental effects contributed relatively little to the observed variation in yield under the successive two test years. The high genetic variance for SY (12.24) therefore provides a favourable basis for direct selection. Nevertheless, because seed yield is a complex trait resulting from the cumulative expression of several component traits, selection based on yield alone may be less efficient than simultaneous consideration of stable yield components such as NPP, NSP and HSW.

The phenotypic and genotypic coefficient of variation were found relatively lower for DTM (8.90 and 8.94 %) and DFF (11.82 and 12.19 %), indicating comparatively restricted variation for phenological traits. This may reflect the relatively narrow adaptation range for flowering and maturity within the breeding material or directional selection for suitable maturity duration in the parental material. In contrast, NPB showed a relatively large difference between GCV (30.81 %) and PCV (32.62 %), indicating that branching was more sensitive to environmental conditions than other traits. Thus, although substantial genetic variation exists for branching, its expression may be less predictable across the years.

Broad sense heritability was investigated very high for all the traits, ranging from 89.19 % for NPB to 99.27 % for NSP. High heritability designated that phenotypic differences among genotypes were largely repeatable under the experimental conditions. However, heritability alone does not establish the underlying nature of gene action because broad sense heritability includes additive, dominance and epistatic components of genetic variance. Accordingly, interpreting broad-sense heritability jointly with predicted genetic advance, particularly genetic advance as a percentage of mean, provides a more useful indication of the likely response of phenotypic selection. High broad-sense heritability coupled with the higher genetic advance is commonly interpreted as evidence that additive genetic effects are important and that direct selection may be effective. In contrast, high heritability with low genetic advance may reflect non-additive gene action and/ or limited exploitable additive variance (42–44).

The combination of high heritability and high genetic advance as a percentage of the mean (GAM) for SY (78.47 %), NPP (75.90 %), NSP (77.41 %), NPB (60.02 %) and BY (72.14 %) suggested that a substantial proportion of genetic variation for these traits is exploitable through selection, with additive genetic effects likely contributing importantly to their inheritance. The particularly high GAM for NPP and NSP indicated that selection for superior reproductive sink capacity could generate considerable improvement. Since these traits are biologically close to yield formation, identifying genotypes with consistent high pod and seed numbers could provide an effective indirect route for improving seed yield (43, 45). High heritability coupled with substantial genetic advance for yield and its components has similarly been interpreted in soybean as evidence of useful transmissible genetic variation and good selection prospects.

In contrast, HI showed a different pattern, with very high heritability (98.67 %) but a comparatively moderate GAM of 29.14 %. This pattern is biologically meaningful because HI is a ratio trait, calculated as the proportion of total above-ground biomass allocated to seed yield and consequently reflects the combined effects of biomass production, assimilate partitioning, reproductive development and seed filling. High heritability indicated that genotype-related differences in HI were consistently expressed under the conditions of the study, whereas moderate GAM indicated a more modest predicted response to phenotypic selection than that observed for NPP, NSP and SY. This pattern may arise from relatively

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limited additive variance, non-additive genetic effects, physiological constraints on biomass partitioning and genotype × environment (G × E) effects on source-sink relations. However, these mechanisms cannot be inferred conclusively from heritability and GAM alone (46, 47). Therefore, high heritability for HI should not be interpreted as evidence of proportionately high selection gain. Selection for HI would be more effective when combined with selection for seed yield and biomass rather than treating HI as an independent target.

The genotype × year variance component further highlighted trait-specific environmental sensitivity. The ratio was low for SY (0.08), DTM (0.05), NPP (0.08), NSP (0.05), HSW (0.10), BY (0.10) and HI (0.10), indicating that genotype × year interaction contributed relatively little compared with genotypic variance. These traits can therefore be considered comparatively stable across the two years. In contrast, the high ratio for NPB (0.94) and the moderate ratio for DFF (0.36) indicate stronger environmental modulation of these traits. This distinction is important for breeding because traits with low genotype × year influence can be selected using pooled performance with greater confidence, whereas branching and flowering behaviour should be evaluated over more environments before making definitive selection decisions.

In agreement with the findings of the present study, substantial genetic variability was reported among 219 soybean accessions in an earlier study (35). The highest PCV and GCV were recorded for number of clusters plant^{-1} (37.04 and 36.94 %) followed by HSW (31.96 and 31.46 %) and NPB (29.56 and 29.18 %). High heritability (> 70 %) coupled with higher genetic advance for several yield related traits further indicated the predominance of heritable variation. Furthermore, another study (48) reported substantial genetic variability among 481 soybean germplasm accessions evaluated under an augmented block design. High PCV and GCV were observed for SY, NPP and PH, while high heritability coupled with higher genetic advance (GA) for SY, NPP, HSW and PH indicated a strong contribution of additive genetic effects. Similarly, another study (34) recorded considerable genetic variability among 148 soybean RILs, with broad sense heritability ranging from 43 % for DFF to 92 % for NPP. High heritability was also observed for HSW (89 %), NSP (69 %) and PH (52 %).

Additionally, based on the pooled block-adjusted means, genotypes were ranked for seed yield while considering their performance for major yield components (Table 7). Genotypes such as JS 21-72, RVSM-35, JS 20-79, JS 21-17, RVSM 2011-35 and JS 20-98 exhibited superior adjusted seed yield together with favourable performance for NPP, NSP and HSW and were therefore identified as promising candidates for further breeding evaluation. The relatively low G × Y to genotype variance ratios for seed yield and major yield components further support the consistency of these entries across the two years.

Table 7. Ranking of soybean genotypes based on pooled adjusted mean performance (mean ± SD) for yield and yield related traits

Sl. No.	Genotype	SY	DFF	DTM	PH	NPB	NPP	NSP	HSW	BY	HI
1	JS-21-72	15.07 ± 0.38	49.93 ± 0.78	108.56 ± 2.40	55.62 ± 1.24	5.08 ± 0.07	94.53 ± 2.58	149.48 ± 2.04	14.68 ± 0.40	36.62 ± 0.07	44.73 ± 0.15
2	RVSM-35	14.99 ± 0.09	47.13 ± 0.78	107.86 ± 1.14	53.79 ± 0.98	5.08 ± 0.02	93.50 ± 3.01	147.41 ± 2.60	13.43 ± 0.02	35.48 ± 0.50	44.60 ± 0.79
3	JS-20-79	14.80 ± 0.38	46.13 ± 1.63	107.36 ± 1.85	53.25 ± 0.34	5.08 ± 0.07	92.77 ± 2.72	147.08 ± 2.77	13.43 ± 0.07	34.94 ± 0.09	44.56 ± 0.11
4	JS-21-17	14.72 ± 0.26	45.93 ± 1.25	106.76 ± 0.70	52.09 ± 0.01	5.05 ± 0.41	88.87 ± 0.43	146.68 ± 3.73	13.35 ± 0.30	34.11 ± 0.42	44.56 ± 0.38
5	RVSM-2011-35	14.58 ± 0.34	45.93 ± 0.50	106.66 ± 0.56	51.52 ± 1.07	4.98 ± 0.12	82.53 ± 1.45	146.51 ± 3.97	13.11 ± 0.24	33.80 ± 0.20	44.56 ± 0.20
6	JS-20-98	14.46 ± 0.12	45.69 ± 1.68	106.56 ± 0.72	50.39 ± 0.43	4.88 ± 0.02	82.53 ± 2.51	142.01 ± 4.58	13.00 ± 0.17	33.76 ± 0.16	44.46 ± 0.16
7	JS-22-01	13.98 ± 0.76	45.53 ± 1.35	106.26 ± 0.10	49.85 ± 2.77	4.88 ± 0.87	82.37 ± 3.38	139.95 ± 2.70	12.40 ± 0.05	33.75 ± 0.49	44.39 ± 0.36
8	DLSB-40	13.98 ± 0.46	45.19 ± 0.44	106.06 ± 0.01	49.35 ± 0.48	4.88 ± 0.58	81.03 ± 0.67	139.95 ± 0.15	12.38 ± 0.22	33.50 ± 0.76	44.35 ± 0.60
9	RVS-23-10	13.88 ± 0.04	45.13 ± 1.25	105.09 ± 2.04	48.69 ± 0.58	4.88 ± 0.02	80.87 ± 2.51	139.88 ± 4.02	12.31 ± 0.30	33.39 ± 2.49	44.34 ± 0.01
10	RVS-23-25	13.01 ± 0.40	44.89 ± 1.68	104.83 ± 0.89	47.12 ± 1.94	4.81 ± 0.02	78.67 ± 0.72	139.78 ± 5.01	12.27 ± 0.49	33.38 ± 0.62	44.34 ± 0.03
11	RVS-12-8	12.81 ± 0.46	44.13 ± 1.25	104.73 ± 0.10	47.09 ± 0.46	4.78 ± 0.44	78.27 ± 0.43	137.61 ± 4.94	12.22 ± 0.07	33.38 ± 0.69	44.29 ± 0.49
12	DS-1589	12.81 ± 0.20	44.03 ± 0.92	104.63 ± 0.81	46.75 ± 2.27	4.78 ± 0.16	77.80 ± 1.38	133.48 ± 4.02	12.05 ± 0.17	33.22 ± 0.23	44.28 ± 0.28
13	SL-311	12.79 ± 0.02	43.99 ± 2.67	104.36 ± 1.28	45.65 ± 0.72	4.78 ± 0.44	77.10 ± 3.50	132.78 ± 0.76	11.90 ± 0.02	33.02 ± 0.77	44.25 ± 0.61
14	RVS-23-21	12.79 ± 0.54	43.86 ± 0.44	104.06 ± 0.01	45.05 ± 2.13	4.78 ± 0.16	75.50 ± 0.18	132.45 ± 1.42	11.90 ± 0.03	32.93 ± 1.41	44.23 ± 0.62

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15	JS-25-53	12.57 ± 0.44	43.86 ± 0.73	104.03 ± 0.24	45.02 ± 1.80	4.74 ± 0.14	74.76 ± 1.98	132.01 ± 1.28	11.66 ± 0.05	32.63 ± 0.73	44.17 ± 0.50
16	KSS-213	12.46 ± 0.16	43.86 ± 0.69	103.49 ± 1.75	44.65 ± 1.28	4.71 ± 0.41	74.67 ± 2.22	130.61 ± 2.04	11.61 ± 0.01	32.63 ± 1.10	44.16 ± 0.35
17	JS-24-31	12.45 ± 0.38	43.56 ± 0.30	103.26 ± 0.58	44.62 ± 1.03	4.68 ± 1.06	74.27 ± 0.72	129.58 ± 0.37	11.54 ± 0.11	32.60 ± 0.29	44.15 ± 0.07
18	JS-20-53	12.42 ± 0.27	43.36 ± 0.26	103.16 ± 0.72	44.32 ± 1.94	4.68 ± 0.02	74.15 ± 0.25	129.21 ± 1.83	11.54 ± 0.05	32.43 ± 1.52	44.11 ± 0.07
19	Cat 87	12.37 ± 0.16	43.26 ± 0.41	102.66 ± 2.65	44.09 ± 0.67	4.58 ± 0.73	73.27 ± 3.64	127.95 ± 3.53	11.50 ± 0.41	32.37 ± 1.00	44.06 ± 0.07
20	JS-25-05	12.33 ± 0.19	43.13 ± 1.35	102.59 ± 2.74	43.55 ± 1.42	4.55 ± 0.30	72.47 ± 4.00	125.92 ± 0.90	11.48 ± 0.07	32.34 ± 0.68	43.97 ± 1.01
21	RVS-23-11	12.15 ± 0.38	42.89 ± 1.68	102.46 ± 0.27	43.42 ± 0.10	4.55 ± 0.55	71.60 ± 2.87	125.75 ± 2.11	11.44 ± 0.19	32.24 ± 0.02	43.78 ± 0.29
22	JS-20-89	12.02 ± 0.03	42.86 ± 0.73	102.29 ± 0.90	43.35 ± 1.42	4.51 ± 0.69	71.17 ± 3.21	124.41 ± 2.13	11.38 ± 0.24	31.69 ± 0.56	43.70 ± 0.27
23	KDS-1201	11.90 ± 0.27	42.76 ± 0.30	102.23 ± 1.38	42.92 ± 0.32	4.48 ± 0.02	70.97 ± 1.41	124.21 ± 4.11	11.37 ± 0.03	31.44 ± 1.98	43.58 ± 0.73
24	AMS-100-39	11.84 ± 1.21	42.16 ± 0.83	102.03 ± 0.81	42.79 ± 0.13	4.48 ± 0.77	70.93 ± 4.28	123.05 ± 2.27	11.32 ± 0.32	31.32 ± 0.56	43.37 ± 1.31
25	ASB-85	11.84 ± 0.46	42.03 ± 0.64	101.96 ± 0.15	42.69 ± 0.39	4.48 ± 0.55	70.30 ± 1.03	122.11 ± 2.82	11.29 ± 0.01	31.24 ± 0.57	43.00 ± 0.88
26	JS-22-16	11.82 ± 0.34	41.99 ± 2.38	101.93 ± 0.67	42.59 ± 0.42	4.45 ± 0.41	69.03 ± 1.31	120.91 ± 1.41	11.29 ± 0.14	31.20 ± 0.23	42.98 ± 0.54
27	Pusa Sipani SPS 433	11.68 ± 0.22	41.99 ± 1.82	101.83 ± 0.81	42.39 ± 0.15	4.38 ± 0.12	67.57 ± 1.03	118.28 ± 1.36	11.29 ± 0.01	30.33 ± 0.65	42.89 ± 0.71
28	MAUS-824	11.68 ± 0.40	41.96 ± 0.02	101.76 ± 0.43	42.24 ± 0.28	4.38 ± 0.22	67.37 ± 1.24	116.41 ± 2.41	11.28 ± 0.05	29.99 ± 1.71	42.86 ± 0.29
29	KDS-1193	11.57 ± 0.41	41.96 ± 1.15	101.76 ± 0.43	42.19 ± 0.98	4.38 ± 0.22	66.93 ± 1.09	116.28 ± 7.13	11.23 ± 0.01	29.98 ± 1.55	42.77 ± 0.59
30	AUKS-212	11.41 ± 0.44	41.93 ± 1.63	101.52 ± 0.40	41.75 ± 2.27	4.38 ± 0.41	66.73 ± 1.94	113.35 ± 1.56	11.23 ± 0.01	29.55 ± 0.88	42.71 ± 0.89
31	NRCSL-7	11.41 ± 0.64	41.89 ± 0.83	101.16 ± 0.81	41.69 ± 0.86	4.31 ± 0.69	66.63 ± 0.95	112.81 ± 2.77	11.22 ± 0.12	29.54 ± 1.35	42.62 ± 0.46
32	DS 1547	11.16 ± 0.14	41.86 ± 0.41	101.06 ± 0.29	41.52 ± 0.81	4.28 ± 0.49	66.60 ± 0.04	110.78 ± 0.65	11.07 ± 0.24	29.05 ± 0.91	42.54 ± 0.65
33	RVS-2011-10	11.11 ± 0.87	41.83 ± 0.64	101.03 ± 0.60	41.29 ± 0.27	4.28 ± 0.55	66.43 ± 3.01	109.35 ± 4.66	11.07 ± 0.10	28.93 ± 0.80	42.51 ± 0.69
34	RVS-23-26	11.03 ± 0.01	41.46 ± 0.44	100.96 ± 0.15	41.19 ± 1.17	4.28 ± 0.26	65.83 ± 1.24	108.55 ± 5.51	11.03 ± 0.14	28.87 ± 0.96	42.20 ± 0.66
35	MAUS-791	10.99 ± 0.03	41.29 ± 1.96	100.86 ± 0.58	41.05 ± 1.85	4.21 ± 0.55	65.20 ± 0.89	108.45 ± 3.38	11.01 ± 0.12	28.83 ± 0.37	42.10 ± 0.51
36	RVS-23-2	10.95 ± 0.74	41.19 ± 1.82	100.76 ± 1.00	40.99 ± 0.53	4.21 ± 0.55	65.10 ± 3.57	108.15 ± 3.26	10.96 ± 0.17	28.31 ± 0.35	42.01 ± 0.05
37	JS-23-03	10.95 ± 0.20	41.16 ± 0.26	100.69 ± 1.19	40.95 ± 2.63	4.18 ± 0.07	65.10 ± 1.24	107.88 ± 1.64	10.92 ± 0.13	28.09 ± 0.64	41.95 ± 0.90
38	NRCSL-8	10.84 ± 0.37	41.12 ± 0.45	100.63 ± 0.89	40.95 ± 1.22	4.18 ± 0.16	64.90 ± 1.03	107.85 ± 1.71	10.78 ± 0.38	28.06 ± 0.47	41.87 ± 0.02
39	JS-24-30	10.81 ± 0.36	41.09 ± 1.43	100.56 ± 2.70	40.89 ± 0.67	4.18 ± 0.16	64.73 ± 2.30	107.61 ± 2.13	10.71 ± 0.11	27.91 ± 0.24	41.59 ± 0.59
40	JS-21-05	10.81 ± 0.10	41.06 ± 0.44	100.53 ± 0.95	40.79 ± 0.53	4.15 ± 0.26	63.80 ± 0.81	106.85 ± 3.12	10.69 ± 0.03	27.82 ± 2.43	41.59 ± 0.23
41	RVS-23-22	10.79 ± 0.42	40.99 ± 0.44	100.39 ± 0.76	40.69 ± 2.25	4.15 ± 0.26	63.47 ± 1.74	106.81 ± 2.13	10.66 ± 0.52	27.65 ± 0.96	41.52 ± 0.10
42	AUKS-21-5	10.78 ± 0.06	40.99 ± 1.82	100.19 ± 1.05	40.55 ± 0.48	4.08 ± 0.83	63.23 ± 0.95	106.58 ± 6.99	10.65 ± 0.01	27.56 ± 0.26	41.12 ± 0.39
43	ASB-93	10.76 ± 0.01	40.93 ± 0.50	99.56 ± 1.00	40.45 ± 1.75	4.08 ± 0.02	62.97 ± 1.69	105.95 ± 4.94	10.61 ± 0.55	27.30 ± 0.66	41.05 ± 1.79
44	MAUS-124	10.74 ± 0.07	40.93 ± 1.25	99.23 ± 1.09	40.42 ± 2.08	4.08 ± 0.83	62.47 ± 2.13	105.75 ± 3.24	10.60 ± 0.15	27.28 ± 0.98	40.91 ± 0.08

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45	RVS-23-16	10.74 ± 0.64	40.89 ± 0.58	99.06 ± 1.14	40.39 ± 1.26	4.08 ± 0.26	62.47 ± 3.15	105.75 ± 2.68	10.60 ± 0.02	27.09 ± 2.10	40.85 ± 0.75
46	VLS- 104	10.72 ± 0.22	40.89 ± 2.81	98.76 ± 1.94	40.09 ± 1.24	3.98 ± 0.35	62.30 ± 1.24	105.34 ± 2.23	10.58 ± 0.07	26.96 ± 0.64	40.78 ± 0.05
47	JS-97-52 (C1)	10.72 ± 0.09	40.89 ± 1.96	98.66 ± 2.56	39.92 ± 3.15	3.98 ± 0.07	62.27 ± 0.32	105.05 ± 1.41	10.58 ± 0.03	26.84 ± 1.03	40.76 ± 0.62
48	Himso 1696	10.69 ± 0.40	40.66 ± 0.41	98.63 ± 1.38	39.85 ± 2.13	3.98 ± 0.41	61.87 ± 0.43	104.85 ± 1.71	10.52 ± 0.08	26.63 ± 0.69	40.74 ± 0.93
49	NRC-259	10.55 ± 0.02	40.60 ± 0.34	98.43 ± 2.79	39.12 ± 1.94	3.98 ± 0.07	61.47 ± 1.28	104.61 ± 0.90	10.49 ± 0.19	26.61 ± 2.66	40.68 ± 0.59
50	JS-20-116 (C2)	10.41 ± 0.21	40.59 ± 1.82	98.16 ± 0.43	39.09 ± 2.84	3.95 ± 0.55	61.37 ± 2.44	104.41 ± 2.41	10.48 ± 0.10	26.39 ± 0.98	40.66 ± 0.30
51	JS-25-55	10.39 ± 0.09	40.53 ± 1.06	97.83 ± 0.81	38.92 ± 1.94	3.90 ± 0.26	60.73 ± 0.24	104.35 ± 2.96	10.46 ± 0.02	26.32 ± 0.57	40.61 ± 0.04
52	DS 1480	10.35 ± 0.32	40.36 ± 0.30	97.76 ± 1.09	38.65 ± 2.41	3.85 ± 0.16	60.63 ± 2.16	103.61 ± 2.77	10.44 ± 0.14	26.32 ± 0.37	40.41 ± 0.81
53	JS-21-77	10.33 ± 0.27	40.13 ± 1.91	97.66 ± 1.88	38.59 ± 1.09	3.85 ± 0.41	59.73 ± 0.24	103.45 ± 2.54	10.42 ± 0.03	26.21 ± 1.07	40.40 ± 0.23
54	RVS-23-12	10.30 ± 0.28	40.13 ± 1.63	97.66 ± 1.14	38.49 ± 2.08	3.81 ± 0.55	59.70 ± 1.80	103.21 ± 0.06	10.41 ± 0.15	26.04 ± 1.88	40.39 ± 0.14
55	JS-23-05	10.17 ± 0.29	40.03 ± 0.64	97.59 ± 1.90	38.29 ± 0.95	3.81 ± 0.55	59.53 ± 0.53	102.85 ± 5.93	10.40 ± 0.17	25.95 ± 0.86	40.32 ± 0.58
56	CAUMS-3	10.15 ± 0.13	40.03 ± 1.40	97.56 ± 0.57	37.99 ± 0.53	3.81 ± 0.55	59.20 ± 0.23	102.25 ± 3.97	10.40 ± 0.34	25.86 ± 1.14	40.25 ± 0.12
57	Himso 1695	10.09 ± 0.01	39.99 ± 0.44	96.63 ± 1.09	37.89 ± 1.71	3.81 ± 0.02	59.00 ± 0.53	101.88 ± 0.62	10.37 ± 0.37	25.77 ± 0.41	40.22 ± 0.68
58	AMS- 264	9.95 ± 0.56	39.99 ± 0.16	96.56 ± 0.04	37.89 ± 0.01	3.78 ± 0.16	58.67 ± 0.70	101.78 ± 2.18	10.34 ± 0.17	25.66 ± 1.31	40.18 ± 0.07
59	RVS-23-23	9.88 ± 0.12	39.99 ± 0.44	96.36 ± 1.66	37.59 ± 0.72	3.71 ± 0.12	58.53 ± 2.02	101.65 ± 4.82	10.33 ± 0.11	25.58 ± 0.83	40.06 ± 0.71
60	PS 1569	9.85 ± 0.41	39.99 ± 1.82	96.23 ± 0.04	37.52 ± 1.38	3.71 ± 0.12	58.50 ± 0.10	100.65 ± 1.97	10.29 ± 0.24	25.58 ± 0.83	40.05 ± 0.38
61	JS-25-02	9.74 ± 0.28	39.96 ± 0.30	96.16 ± 0.24	37.49 ± 0.58	3.68 ± 0.30	58.13 ± 2.22	100.61 ± 2.40	10.29 ± 0.36	25.49 ± 0.34	40.05 ± 0.41
62	KBSL-23-36	9.72 ± 0.03	39.93 ± 0.50	96.16 ± 0.15	37.45 ± 1.28	3.68 ± 0.58	58.03 ± 0.18	99.51 ± 2.06	10.28 ± 0.03	25.46 ± 0.07	40.03 ± 0.05
63	JS-25-52	9.72 ± 0.21	39.93 ± 0.50	95.59 ± 1.05	37.39 ± 0.24	3.65 ± 0.16	58.03 ± 3.29	99.01 ± 0.98	10.26 ± 0.02	25.32 ± 0.70	40.01 ± 0.14
64	NRC-192	9.54 ± 0.59	39.93 ± 1.63	95.16 ± 0.04	37.29 ± 1.99	3.58 ± 0.22	57.74 ± 0.37	98.85 ± 1.12	10.26 ± 0.09	25.14 ± 0.06	39.91 ± 0.49
65	RVS-23-20	9.51 ± 0.84	39.93 ± 0.50	94.99 ± 0.09	37.09 ± 0.46	3.58 ± 0.16	57.67 ± 1.56	97.75 ± 2.41	10.25 ± 0.10	25.13 ± 1.15	39.88 ± 0.46
66	AMS-2021-4	9.47 ± 0.31	39.83 ± 1.40	94.96 ± 0.43	37.02 ± 1.80	3.58 ± 0.16	57.63 ± 0.46	97.61 ± 0.79	10.25 ± 0.20	24.98 ± 2.06	39.88 ± 0.23
67	JS-20-69	9.45 ± 0.29	39.83 ± 1.21	94.86 ± 0.67	36.92 ± 1.38	3.58 ± 0.16	57.17 ± 3.40	97.31 ± 3.10	10.23 ± 0.18	24.90 ± 0.40	39.87 ± 0.42
68	RVS-23-9	9.42 ± 0.06	39.83 ± 1.11	94.69 ± 1.19	36.65 ± 0.98	3.55 ± 0.30	57.17 ± 2.65	97.25 ± 1.69	10.20 ± 0.38	24.70 ± 2.62	39.71 ± 0.13
69	NRC-201	9.36 ± 0.43	39.83 ± 1.11	94.39 ± 0.76	36.59 ± 0.70	3.55 ± 0.02	57.03 ± 2.16	96.41 ± 1.56	10.19 ± 0.13	24.59 ± 1.14	39.67 ± 0.39
70	JS-26	9.35 ± 0.39	39.73 ± 2.38	94.39 ± 0.76	36.59 ± 1.94	3.51 ± 0.69	56.47 ± 0.42	96.15 ± 1.28	10.17 ± 0.07	24.36 ± 1.16	39.64 ± 0.00
71	RVSM-2012-4	9.29 ± 0.04	39.59 ± 0.12	94.16 ± 0.15	36.49 ± 0.29	3.51 ± 0.69	56.43 ± 3.29	94.98 ± 2.06	10.16 ± 0.11	24.31 ± 1.85	39.50 ± 0.75
72	JS-22-08	9.28 ± 0.87	39.36 ± 0.02	94.06 ± 0.18	36.45 ± 0.23	3.48 ± 0.07	56.33 ± 3.07	94.71 ± 4.33	10.13 ± 0.13	24.27 ± 0.97	39.42 ± 0.59
73	TS-156	9.18 ± 0.52	39.33 ± 1.54	94.03 ± 0.81	36.25 ± 1.56	3.48 ± 0.55	56.33 ± 3.43	92.95 ± 2.13	10.09 ± 0.14	24.26 ± 0.87	39.36 ± 0.67
74	JS-25-08	9.18 ± 0.07	39.29 ± 1.43	93.99 ± 1.61	36.25 ± 0.34	3.45 ± 0.16	56.13 ± 0.24	92.51 ± 1.14	10.02 ± 0.49	24.17 ± 0.68	38.77 ± 0.12

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75	RVS-23-5	9.15 ± 0.11	39.29 ± 1.72	93.96 ± 0.24	36.12 ± 0.89	3.45 ± 0.41	56.03 ± 1.59	92.01 ± 0.51	9.97 ± 0.44	24.04 ± 1.40	38.75 ± 0.22
76	RVS-23-7	9.13 ± 0.18	39.29 ± 0.87	93.96 ± 0.72	36.09 ± 0.95	3.45 ± 0.16	55.90 ± 1.59	91.95 ± 2.68	9.96 ± 0.03	24.04 ± 0.01	38.64 ± 1.08
77	JS-24-26	9.13 ± 0.10	39.26 ± 0.16	93.76 ± 1.28	35.65 ± 0.34	3.38 ± 0.07	55.27 ± 1.38	91.88 ± 0.62	9.95 ± 0.34	23.88 ± 0.74	38.62 ± 0.64
78	NRC-152	9.07 ± 0.54	39.06 ± 0.12	93.76 ± 0.43	35.45 ± 1.00	3.38 ± 0.16	55.17 ± 2.65	91.55 ± 1.26	9.93 ± 0.04	23.62 ± 0.66	38.61 ± 0.44
79	AS-55	9.06 ± 0.14	39.03 ± 0.64	93.66 ± 0.58	35.45 ± 0.23	3.38 ± 0.35	54.87 ± 2.30	91.41 ± 1.00	9.90 ± 0.02	23.61 ± 0.94	38.58 ± 0.96
80	JS-25-50	9.03 ± 0.37	39.03 ± 1.21	93.46 ± 0.18	35.39 ± 1.09	3.35 ± 0.26	54.77 ± 1.12	90.85 ± 2.54	9.88 ± 0.01	23.50 ± 0.92	38.58 ± 0.40
81	Lok soya 03	8.96 ± 0.14	39.03 ± 2.24	93.33 ± 0.46	35.35 ± 0.20	3.35 ± 0.55	54.17 ± 1.31	90.18 ± 1.61	9.88 ± 0.47	23.12 ± 1.03	38.57 ± 0.91
82	RSC-1165	8.91 ± 0.33	39.03 ± 0.64	93.16 ± 0.60	35.35 ± 0.37	3.35 ± 0.02	54.07 ± 4.77	89.51 ± 6.03	9.84 ± 0.09	23.05 ± 2.17	38.55 ± 0.94
83	MACS-1834	8.87 ± 0.34	38.99 ± 1.82	93.09 ± 0.62	35.32 ± 1.09	3.35 ± 0.55	54.03 ± 2.37	89.01 ± 0.34	9.75 ± 0.17	23.03 ± 0.99	38.52 ± 0.72
84	RVS-23-19	8.83 ± 0.23	38.96 ± 0.26	93.03 ± 1.94	35.15 ± 1.71	3.35 ± 0.55	53.93 ± 1.45	88.45 ± 1.97	9.67 ± 0.10	22.88 ± 0.59	38.50 ± 0.41
85	NRC-255	8.81 ± 0.52	38.89 ± 0.02	92.93 ± 0.39	35.15 ± 1.42	3.35 ± 0.02	53.73 ± 1.09	88.38 ± 6.99	9.67 ± 0.51	22.81 ± 1.29	38.47 ± 1.07
86	AMS-2021-3	8.68 ± 0.13	38.89 ± 1.68	92.66 ± 1.14	35.15 ± 0.09	3.31 ± 0.41	53.67 ± 0.15	88.18 ± 1.22	9.66 ± 0.03	22.80 ± 0.07	38.24 ± 0.18
87	JS-20-94	8.67 ± 0.65	38.86 ± 0.69	92.46 ± 0.86	34.85 ± 0.70	3.28 ± 0.07	53.57 ± 0.46	86.71 ± 2.27	9.66 ± 0.48	22.74 ± 1.59	38.16 ± 0.31
88	RVS-23-15	8.61 ± 0.30	38.83 ± 0.92	92.36 ± 0.04	34.85 ± 0.06	3.28 ± 0.26	53.43 ± 2.08	84.48 ± 2.04	9.57 ± 0.10	22.70 ± 0.14	38.05 ± 0.40
89	RVS-23-14	8.55 ± 0.33	38.79 ± 0.41	92.26 ± 1.24	34.70 ± 0.37	3.28 ± 0.49	53.33 ± 1.38	84.31 ± 6.59	9.56 ± 0.17	22.57 ± 1.68	38.04 ± 0.13
90	NRC-150	8.54 ± 0.35	38.79 ± 2.38	92.26 ± 0.10	34.59 ± 1.66	3.28 ± 0.26	52.83 ± 2.16	84.05 ± 3.38	9.56 ± 0.03	22.26 ± 0.11	37.98 ± 0.54
91	DLSB-5	8.42 ± 0.55	38.73 ± 2.38	92.26 ± 0.67	34.52 ± 0.32	3.28 ± 0.07	52.53 ± 2.58	83.71 ± 4.61	9.49 ± 0.33	22.24 ± 1.06	37.90 ± 0.00
92	VLS-106	8.41 ± 0.25	38.49 ± 1.15	92.10 ± 0.71	34.22 ± 1.52	3.25 ± 0.41	52.37 ± 0.56	82.71 ± 2.27	9.41 ± 0.09	22.17 ± 0.76	37.67 ± 0.62
93	ASB-101	8.32 ± 0.25	38.49 ± 1.15	92.06 ± 0.29	33.79 ± 0.43	3.25 ± 0.41	52.33 ± 3.15	81.95 ± 2.68	9.36 ± 0.35	21.94 ± 1.46	37.67 ± 0.30
94	NRC-130	8.32 ± 0.16	38.39 ± 1.86	91.96 ± 0.24	33.79 ± 0.70	3.21 ± 0.55	52.10 ± 0.39	81.41 ± 3.90	9.35 ± 0.16	21.86 ± 0.34	37.61 ± 0.21
95	THPS-6	8.22 ± 0.20	38.23 ± 1.68	91.93 ± 0.10	33.75 ± 1.14	3.18 ± 0.22	51.97 ± 3.01	81.35 ± 1.28	9.32 ± 0.04	21.38 ± 0.37	37.53 ± 0.64
96	NRC-166	8.20 ± 0.65	38.16 ± 0.30	91.76 ± 0.72	33.39 ± 0.72	3.18 ± 0.07	51.33 ± 1.94	80.81 ± 1.75	9.32 ± 0.13	21.28 ± 0.41	37.52 ± 0.71
97	JS-21-76	8.16 ± 0.30	38.13 ± 1.82	91.56 ± 0.04	33.22 ± 1.80	3.18 ± 0.41	51.27 ± 4.11	80.48 ± 4.30	9.31 ± 0.47	21.22 ± 0.28	37.41 ± 0.68
98	JS-22-12	8.16 ± 0.52	38.03 ± 0.92	91.46 ± 1.12	33.22 ± 1.52	3.18 ± 0.16	50.53 ± 1.74	79.71 ± 1.14	9.29 ± 0.26	21.18 ± 0.93	37.37 ± 0.68
99	JS-25-03	8.14 ± 0.01	37.99 ± 1.54	91.46 ± 1.24	33.05 ± 1.92	3.18 ± 0.16	50.43 ± 0.67	79.55 ± 6.64	9.28 ± 0.09	21.08 ± 0.89	37.35 ± 1.16
100	RVS-23-17	8.05 ± 0.49	37.96 ± 0.83	91.46 ± 1.88	32.94 ± 0.91	3.13 ± 0.09	50.23 ± 3.57	78.78 ± 0.65	9.27 ± 0.27	21.01 ± 0.89	37.24 ± 0.04
101	JS-24-33	7.99 ± 0.26	37.93 ± 1.25	91.39 ± 0.76	32.82 ± 0.95	3.11 ± 0.41	50.20 ± 2.02	78.75 ± 1.83	9.26 ± 0.01	20.99 ± 1.04	37.20 ± 0.98
102	RVS-2001-4	7.98 ± 0.10	37.93 ± 1.54	91.39 ± 0.76	32.69 ± 1.69	3.08 ± 0.02	50.13 ± 2.30	78.15 ± 2.11	9.24 ± 0.36	20.82 ± 0.26	37.05 ± 0.23
103	KDSIS-1394	7.91 ± 0.37	37.93 ± 1.82	91.29 ± 2.04	32.65 ± 0.70	3.08 ± 0.02	49.93 ± 0.32	77.75 ± 2.41	9.23 ± 0.01	20.80 ± 2.10	36.97 ± 0.44
104	Rajsoya-24	7.88 ± 0.34	37.89 ± 1.15	91.26 ± 0.29	32.55 ± 0.76	3.08 ± 0.02	49.60 ± 0.04	77.61 ± 2.77	9.23 ± 0.17	20.78 ± 0.09	36.84 ± 0.24

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105	SL-1315	7.86 ± 0.64	37.49 ± 1.15	91.16 ± 0.43	32.55 ± 0.20	3.08 ± 0.02	49.27 ± 1.85	76.45 ± 1.99	9.13 ± 0.32	20.77 ± 1.45	36.83 ± 0.34
106	Pusa Sipani BS 8	7.86 ± 0.24	37.19 ± 2.38	91.06 ± 0.01	32.52 ± 1.09	3.08 ± 0.26	49.20 ± 1.74	76.45 ± 2.84	9.11 ± 0.18	20.73 ± 0.52	36.70 ± 0.06
107	MACS-824	7.81 ± 0.54	37.13 ± 1.82	91.06 ± 0.86	32.52 ± 1.09	3.05 ± 0.69	49.07 ± 0.32	76.35 ± 2.13	9.07 ± 0.11	20.70 ± 0.24	36.70 ± 0.09
108	RSC-10-46	7.80 ± 0.41	37.13 ± 1.25	90.99 ± 1.05	32.44 ± 0.74	3.01 ± 0.02	49.03 ± 1.31	75.65 ± 2.25	9.06 ± 0.03	20.66 ± 0.57	36.68 ± 0.03
109	RVS-13-20	7.64 ± 0.14	37.09 ± 1.15	90.99 ± 1.33	32.39 ± 0.15	3.01 ± 0.55	48.67 ± 0.15	75.51 ± 2.74	9.04 ± 0.08	20.47 ± 0.66	36.62 ± 0.04
110	KDS-1203	7.62 ± 0.10	37.03 ± 0.64	90.99 ± 1.33	32.35 ± 0.86	2.98 ± 0.63	48.33 ± 0.24	75.51 ± 1.05	9.03 ± 0.00	20.38 ± 0.73	36.22 ± 0.67
111	PS-1696	7.58 ± 0.37	36.93 ± 0.50	90.96 ± 0.98	32.29 ± 0.95	2.98 ± 0.35	47.87 ± 2.98	75.31 ± 2.84	9.00 ± 0.33	20.37 ± 0.49	36.19 ± 0.68
112	MACS-1810	7.51 ± 0.14	36.89 ± 1.43	90.66 ± 0.10	32.25 ± 0.51	2.98 ± 0.12	45.77 ± 2.27	74.68 ± 1.47	9.00 ± 0.08	20.29 ± 0.28	35.99 ± 0.36
113	NRC-142	7.48 ± 0.44	36.89 ± 2.81	90.56 ± 0.42	32.25 ± 0.23	2.98 ± 0.44	45.53 ± 1.66	73.85 ± 1.42	8.95 ± 0.04	19.90 ± 0.78	35.91 ± 0.45
114	AS-34	7.45 ± 0.41	36.86 ± 0.69	90.46 ± 0.01	32.25 ± 0.42	2.98 ± 0.16	45.43 ± 0.95	73.71 ± 5.46	8.93 ± 0.16	19.89 ± 0.44	35.90 ± 0.62
115	JS-25-06	7.30 ± 0.40	36.86 ± 0.73	90.46 ± 1.24	32.05 ± 0.23	2.98 ± 0.41	45.10 ± 1.03	73.71 ± 2.84	8.92 ± 0.16	19.88 ± 0.82	35.88 ± 0.56
116	AMS-2022-1	7.25 ± 0.53	36.83 ± 1.11	90.43 ± 0.32	31.95 ± 1.61	2.91 ± 0.41	44.93 ± 3.07	72.81 ± 2.13	8.87 ± 0.26	19.80 ± 0.72	35.86 ± 0.70
117	NRC-138	7.20 ± 0.52	36.79 ± 1.82	90.39 ± 0.20	31.85 ± 0.23	2.88 ± 0.07	44.87 ± 3.26	72.81 ± 2.40	8.79 ± 0.13	19.44 ± 0.98	35.83 ± 0.96
118	JS-20-29	7.15 ± 0.33	36.69 ± 0.83	90.19 ± 0.09	31.75 ± 1.05	2.88 ± 0.55	44.13 ± 1.09	72.35 ± 3.07	8.73 ± 0.38	19.33 ± 0.32	35.67 ± 1.53
119	NRC-254	7.08 ± 0.10	36.49 ± 0.87	89.86 ± 0.58	31.72 ± 0.04	2.88 ± 0.02	43.87 ± 0.42	71.80 ± 1.78	8.73 ± 0.21	19.32 ± 0.78	35.62 ± 0.10
120	DS 1510	7.02 ± 0.22	36.43 ± 1.21	89.79 ± 1.61	31.65 ± 2.41	2.85 ± 0.16	43.73 ± 2.30	71.41 ± 3.06	8.70 ± 0.15	19.09 ± 0.35	35.60 ± 0.67
121	JS-23-09	6.98 ± 0.10	36.39 ± 1.29	89.76 ± 0.89	31.59 ± 1.09	2.85 ± 0.41	43.67 ± 1.55	71.11 ± 0.20	8.62 ± 0.22	18.82 ± 1.38	35.57 ± 0.32
122	JS-24-34	6.92 ± 0.17	36.29 ± 2.56	89.69 ± 0.90	31.55 ± 2.27	2.81 ± 0.55	43.03 ± 1.24	70.71 ± 4.61	8.59 ± 0.11	18.49 ± 0.52	35.48 ± 1.10
123	RVS-23-13	6.88 ± 0.29	36.23 ± 1.68	89.63 ± 0.81	31.54 ± 0.65	2.81 ± 0.30	43.00 ± 1.45	70.08 ± 1.47	8.59 ± 0.58	18.37 ± 1.02	35.45 ± 0.89
124	RVS-23-8	6.73 ± 0.60	36.09 ± 1.43	89.59 ± 1.05	31.39 ± 1.74	2.81 ± 0.55	42.83 ± 1.88	70.05 ± 2.27	8.56 ± 0.13	18.35 ± 0.54	35.36 ± 0.73
125	NRCSL-4	6.72 ± 0.06	36.09 ± 1.96	89.56 ± 0.24	31.19 ± 1.74	2.81 ± 0.02	42.67 ± 1.66	70.01 ± 1.26	8.54 ± 0.04	17.73 ± 1.15	35.28 ± 0.77
126	NRC-271	6.72 ± 0.10	36.03 ± 1.40	89.56 ± 0.43	31.15 ± 0.37	2.81 ± 0.02	42.20 ± 0.04	69.25 ± 1.71	8.53 ± 0.06	17.69 ± 0.47	35.25 ± 0.39
127	TS-208	6.71 ± 0.64	36.03 ± 1.11	89.46 ± 0.01	30.95 ± 0.20	2.81 ± 0.02	41.37 ± 1.24	69.05 ± 4.23	8.47 ± 0.04	17.42 ± 1.35	35.23 ± 0.39
128	EC109563	6.66 ± 0.49	35.99 ± 2.95	89.36 ± 0.15	30.69 ± 1.69	2.80 ± 0.06	40.93 ± 1.17	68.85 ± 1.41	8.45 ± 0.08	17.20 ± 0.91	35.05 ± 0.61
129	AS-26	6.45 ± 0.26	35.83 ± 0.36	89.33 ± 0.95	30.49 ± 0.67	2.78 ± 0.35	40.40 ± 0.60	68.25 ± 1.99	8.42 ± 0.03	16.75 ± 0.99	34.81 ± 0.48
130	BAUS(M)-6	6.45 ± 0.26	35.83 ± 1.11	89.23 ± 0.32	30.49 ± 0.67	2.78 ± 0.44	40.13 ± 0.24	67.55 ± 2.68	8.39 ± 0.25	16.32 ± 1.14	34.73 ± 1.48
131	NRC-265	6.44 ± 0.17	35.79 ± 1.29	89.09 ± 0.62	30.35 ± 1.71	2.78 ± 0.92	39.47 ± 2.51	67.41 ± 0.79	8.39 ± 0.02	16.25 ± 1.71	34.72 ± 0.11
132	JS-21-07	6.26 ± 0.56	35.29 ± 1.96	88.96 ± 0.43	30.29 ± 0.95	2.78 ± 0.22	38.60 ± 1.74	66.38 ± 1.22	8.38 ± 0.08	16.22 ± 0.97	34.69 ± 0.44
133	NRC-859	6.12 ± 0.03	35.26 ± 0.26	88.86 ± 0.86	30.25 ± 1.56	2.75 ± 0.55	38.43 ± 1.24	65.28 ± 4.30	8.37 ± 0.23	16.21 ± 0.81	34.68 ± 0.26
134	JS-93-05	6.10 ± 0.03	35.16 ± 0.30	88.66 ± 0.10	29.95 ± 3.40	2.71 ± 0.12	38.37 ± 0.27	64.91 ± 4.33	8.33 ± 0.08	15.50 ± 0.58	34.61 ± 1.04

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135	MAUS-787	6.05 ± 0.44	35.09 ± 2.53	88.53 ± 0.74	29.82 ± 0.74	2.68 ± 0.07	38.30 ± 0.39	64.81 ± 1.26	8.28 ± 0.10	15.46 ± 1.62	34.58 ± 1.06
136	Pusa Sipani BS 33	5.98 ± 0.10	34.99 ± 1.29	88.46 ± 0.95	29.75 ± 1.78	2.68 ± 0.07	38.03 ± 2.44	64.51 ± 4.33	8.24 ± 0.42	15.43 ± 1.18	34.52 ± 0.64
137	Jhimka	5.89 ± 0.07	34.93 ± 1.54	88.29 ± 0.62	29.62 ± 1.52	2.68 ± 0.02	38.00 ± 2.02	63.35 ± 2.40	8.16 ± 0.02	15.08 ± 0.43	34.33 ± 0.37
138	RVS-15-1	5.80 ± 0.06	34.93 ± 1.25	88.16 ± 0.15	29.55 ± 1.14	2.68 ± 0.02	37.53 ± 0.32	63.21 ± 0.06	8.11 ± 0.05	15.01 ± 0.20	33.97 ± 0.30
139	NRC-258	5.79 ± 0.31	34.93 ± 1.25	88.03 ± 0.32	29.52 ± 1.38	2.58 ± 0.44	37.17 ± 1.03	61.58 ± 0.37	8.08 ± 0.06	14.97 ± 1.28	33.87 ± 0.38
140	JS-20-34	5.70 ± 0.20	34.89 ± 0.02	87.86 ± 1.14	29.45 ± 1.92	2.53 ± 0.48	36.70 ± 0.39	61.11 ± 1.69	8.08 ± 0.06	14.97 ± 0.11	32.78 ± 2.25
141	TS-101	5.68 ± 0.10	34.86 ± 0.44	87.86 ± 0.58	29.19 ± 0.89	2.51 ± 0.69	35.17 ± 1.24	60.91 ± 1.14	8.05 ± 0.37	14.94 ± 0.57	32.61 ± 0.99
142	RVSM-12-21	5.62 ± 0.56	34.79 ± 0.73	87.56 ± 0.04	29.05 ± 1.00	2.41 ± 0.55	34.97 ± 2.44	60.15 ± 6.09	8.03 ± 0.32	14.82 ± 0.45	32.06 ± 0.47
143	RSC-10-52	5.55 ± 0.60	34.56 ± 0.26	87.16 ± 0.72	28.79 ± 0.43	2.38 ± 0.35	32.47 ± 2.70	59.88 ± 5.43	8.03 ± 0.16	14.75 ± 0.22	31.78 ± 0.92
144	AMS 22-16	5.43 ± 0.24	33.99 ± 3.23	86.96 ± 1.00	28.75 ± 0.93	2.35 ± 0.26	32.17 ± 2.84	59.58 ± 1.90	7.92 ± 0.16	14.69 ± 0.15	31.60 ± 0.87
145	RVS-76	5.39 ± 0.13	33.93 ± 1.25	86.83 ± 1.17	28.29 ± 0.74	2.28 ± 0.58	31.97 ± 1.42	58.95 ± 1.00	7.77 ± 0.25	14.28 ± 0.25	30.80 ± 1.59
146	KSS-225	5.35 ± 0.03	33.93 ± 1.25	86.83 ± 0.32	28.19 ± 1.09	2.28 ± 0.02	30.67 ± 0.13	56.95 ± 2.13	7.65 ± 0.14	14.19 ± 1.03	30.80 ± 0.75
147	NRC-267	5.18 ± 0.30	33.89 ± 2.53	86.29 ± 0.62	28.15 ± 0.37	2.28 ± 0.26	30.57 ± 0.18	56.45 ± 0.29	7.56 ± 0.13	14.16 ± 0.50	30.22 ± 0.18
148	NRC-269	5.13 ± 0.19	33.39 ± 1.82	86.16 ± 0.43	28.05 ± 2.13	1.95 ± 0.26	30.07 ± 1.74	55.65 ± 2.56	7.55 ± 0.07	13.82 ± 0.78	29.90 ± 0.35
149	NRC-266	5.04 ± 0.49	32.83 ± 1.11	85.96 ± 0.43	27.82 ± 3.21	1.91 ± 0.12	28.53 ± 1.09	55.15 ± 0.43	7.44 ± 0.05	13.71 ± 0.04	29.74 ± 0.13
150	Cat492A	4.89 ± 0.10	31.93 ± 0.50	85.66 ± 1.14	27.49 ± 1.52	1.78 ± 0.41	28.03 ± 1.24	54.91 ± 6.21	7.42 ± 0.07	13.46 ± 1.41	29.52 ± 0.20
151	KDS-1188	4.79 ± 0.44	31.89 ± 1.68	85.36 ± 0.13	27.42 ± 1.24	1.68 ± 0.02	27.83 ± 0.46	53.61 ± 0.06	7.32 ± 0.14	13.31 ± 1.43	29.46 ± 0.81
152	RSC-11-95	4.65 ± 0.02	31.79 ± 1.54	84.56 ± 0.72	26.75 ± 1.14	1.58 ± 0.35	26.33 ± 0.32	51.81 ± 2.77	7.28 ± 0.07	12.65 ± 0.73	29.21 ± 0.12
153	NRC-264	4.48 ± 0.02	31.49 ± 2.24	84.29 ± 0.62	25.44 ± 0.06	1.55 ± 0.26	26.17 ± 0.67	46.55 ± 1.28	7.11 ± 0.14	11.92 ± 0.08	28.84 ± 0.32

4. Conclusion

The findings of present study highlighted the existence of considerable genetic variability among soybean genotypes for seed yield and its associated traits under semi-arid agro-climatic conditions. Highly significant genotypic differences were observed for all ten quantitative traits, while seed yield, number of pods per plant, number of seeds per plant and biological yield exhibited high genetic variability, very high heritability and higher genetic advance as percentage of mean. These traits therefore represent the most useful selection criteria for improving productivity in the evaluated germplasm. In particular, number of pods per plant (NPP) and number of seeds per plant (NSP) should be considered primary selection criteria because of their high genetic variability and substantial expected selection response, whereas biological yield (BY) may be sued as complementary secondary criterion together with direct selection for seed yield (SY). The relatively low genotype × year variance for SY, NPP, NSP and BY further indicated comparatively consistent expression of these traits across the two seasons. Based on pooled block-adjusted performance, genotypes viz., JS 21-72, RVSM-35, JS 20-79, JS 21-17, RVSM 2011-35 and JS 20-98 were identified as promising genotypes, combining superior seed yield with favourable performance for major yield components such as NPP, NSP and 100-seed weight (HSW). These genotypes may therefore be prioritised as potential parents or advanced breeding material. For practical breeding, selection should emphasise high SY supported by superior NPP and NSP, with BY and HSW considered as additional traits for identifying favourable yield-component combinations. The identified genotypes may subsequently be evaluated in replicated multi-environment trials to confirm their yield superiority and stability before their use in advanced breeding programmes.

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Authors' contributions

RM conducted the field investigations, curated and analysed the data and prepared the original manuscript draft. JS, SS, KS, PAG, ST and SST[1] contributed to data collection, field experimentation, recording of observations and preliminary data organisation. SST[2] and MKT conceptualised and designed the study, provided overall supervision and guidance throughout the research and monitored its progress. They also critically reviewed and edited the manuscript. All authors read and approved the final manuscript [SST[1] stands for Swati Singh Tomar and SST[2] stands for Sandeep Singh Tomar].

Compliance with ethical standards

Conflict of interest

Authors do not have any conflict of interests to declare.

Ethical issues

None

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