

Integrative Genetic Diversity and Disease Resistance Analysis for Identification of superior Genotypes in soybean

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Abstract

A field experiment was conducted during kharif 2024 at Birsa Agricultural University, Ranchi, to evaluate 30 soybean genotypes for genetic divergence, yield, quality traits, and resistance to *Rhizoctonia* aerial blight and bacterial blight under natural field conditions. The experiment was laid out in a randomized block design with three replications, and data were analysed using Mahalanobis D^2 statistics, Tocher's clustering, and percent disease index (PDI). The genotypes were grouped into four clusters, showing substantial genetic variability, with Cluster I found early maturing and Cluster IV high yielding. The maximum inter-cluster distance between Clusters II and III indicated good scope for hybridization. Branches per plant contributed most to divergence, followed by days to maturity and plant height. BAUS(M)-15 showed complete resistance to both diseases, while BAUS(M)-11 recorded the highest yield with good oil and protein content. The study identified BAUS(M)-15, BAUS(M)-11, BAUS-102, MACS-1140, and BAUS-103 as promising parents for soybean improvement.

Key Words: *Rhizoctonia* aerial blight, Bacterial Blight, Disease resistance, Genetic Diversity

Introduction

Soybean (*Glycine max* L. Merrill) ranks as a premier oilseed and protein-rich legume crop globally, for its 40% protein and 20% oil content. The crop is a good source of essential fatty acids viz., linolenic acid, linoleic acid and oleic acid. Soybean (*Glycine max* L.), a self-fertilizing diploid species ($2n = 40$) belonging to the family *Fabaceae*, is one of the most economically important legume crops, prized globally for its exceptional edible oil content and high-quality protein, sustains global food security as the fifth-largest produced oilseed (151.8 Lakh tones) in India, 2024-25). Yet India's productivity lags at 1172 kg/ha—far below the USA's 3000+ kg/ha—due to narrow genetic bases, photoperiod sensitivity, and diseases causing 20-50% losses. Enhancing soybean productivity under diverse and disease-prone agro-climatic conditions requires the systematic identification and utilization of genetically diverse genotypes possessing superior yield potential with early maturing and stable resistance to multiple economically important diseases.

In Jharkhand with production of 0.144 thousand ton and productivity 1189 kg/ha during the year 2024-25, RAB (*Rhizoctonia* aerial blight) caused by *Rhizoctonia solani* and Bacterial Blight (*Pseudomonas syringae* pv. *glycinea*) thrive in monsoon humidity (20-30°C, 80-90% RH), defoliating canopies and shrivelling pods. *Rhizoctonia* aerial blight is characterized by the appearance of light to dark brown lesions, the development of web-like mycelial growth on foliage, and the formation of sclerotia on above-ground plant parts (Verma and Thapliyal, 1976) and Bacterial leaf blight of soybean, is a major threat to crop yield and quality. The disease begins as tiny, angular water-soaked spots on the foliage, which gradually develop yellow halos. As the infection progresses, these spots darken to brown or black and merge, forming extensive necrotic patches that damage the leaves. The pathogen survives in infected plant debris across seasons and can also be carried through seeds, making it a persistent and challenging adversary for soybean cultivation therefore, in view of

the increasing incidence of these diseases, the present field experiment was conducted under hotspot conditions to assess the resistance levels of different genotypes and to identify high-yielding genotypes possessing effective resistance for minimizing disease-induced yield losses.

In this context, the integration of field-based disease screening with robust genetic diversity analysis provides a comprehensive approach for identifying elite genotypes capable of combining productivity with resilience. Genetic diversity analysis, particularly through multivariate techniques such as Mahalanobis D² statistics, enables the assessment of divergence among genotypes and facilitates the selection of genetically distant yet agronomically superior parental lines. Therefore, the present investigation aims to evaluate soybean genotypes through simultaneous disease screening and genetic divergence analysis in order to identify high-yielding, multi-disease-resistant genotypes that can be effectively exploited in future breeding programmes for the development of improved and sustainable soybean cultivars.

Materials and Methods

The field trial was executed during *khari*f 2024 at the Western Research Plot, Department of Genetics and Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand evaluating 30 *Glycine max* (L.) Merrill genotypes—comprising diverse advanced breeding lines, mutants, and three comparator checks: National Check (NC), Zonal Check (ZC) and Local Check (LC). Experimental plots followed a Randomized Block Design (RBD) with three replications, each genotype established in four 3-m rows (45 cm inter-row, 10 cm intra-row spacing). A basal fertilizer dose of 20:40:40:40 kg ha⁻¹ (N:P:K:S) was applied at sowing. The experimental material was cultivated under standard agronomic practices, and observations were recorded from five randomly selected plants per plot. Nine quantitative traits—days to 50% flowering, days to maturity, plant height, number of branches per plant, 100-seed weight, seeds per pod, pods per plant, grain yield per plant, and grain yield per plot—were measured, along with two quality traits, oil and protein content, facilitating robust Mahalanobis D² analysis (Mahalanobis, 1936) and Tocher-mediated clustering to delineate genetic divergence and nominate elite parental genotypes for targeted breeding advances in earliness, yield potential, and nutritional profiling.

Also, thirty soybean genotypes were screened against Rhizoctonia aerial blight and bacterial blight under natural epiphytotic conditions in the field. Disease severity was recorded at weekly intervals throughout the crop season using the standard (0-9) rating scale as described by Mayee and Datar (1986). The disease

scoring was later used to calculate percent disease index using the formula given by Wheeler (1969) as follows in (Table 1 & 2) :

$$\text{PDI (\%)} = \frac{\text{sum of all ratings}}{\text{number of ratings} \times \text{maximum grade}} \times 100$$

Observation for RAB and bacterial blight was taken on randomly selected thirty plants from each genotype populations. Each selected plants were graded on the basis of symptoms for scoring disease severity and later categorised into disease reaction based on PDI% as mentioned in Table 3.

Result and Discussion

The genotypes were grouped into four clusters according to their genetic distances using a method suggested by Tocher (Rao, 1952) is presented in Table 4. Among four clusters, with Cluster I being the largest (13 genotypes), followed by Cluster IV (7 genotypes), Cluster III (6 genotypes), and the smallest Cluster II (4 genotypes). This pattern shows clear heterogeneity among groups based on trait performance rather than geographic origin. Cluster I contained early-flowering (42.59 days) and early-maturing genotypes (109.69 days), ideal for short-season areas, while Cluster IV featured late-flowering, tall plants (69.59 cm) with the highest grain yield per plant (12.26 g), marking them as prime yield parents.

Intra-cluster distances varied from 8.52 (most uniform Cluster IV) to 11.49 (highly diverse Cluster II), while inter-cluster distances were substantially larger, ranging from 21.05 (Clusters I-IV) to a maximum of 27.82 between Clusters II and III—indicating these groups are genetically most distinct. This suggests crosses between Cluster II (high pods/plant: 62.20) and Cluster III (high protein: 40.2%) genotypes would maximize heterosis and generate superior progeny, consistent with findings from Joshi *et al.* (2018) and Patil *et al.* (2011). Crosses between Cluster I and Cluster IV would effectively combine early maturity with superior yield potential (similar findings from Roja *et al.*, 2022; Zatybekov *et al.*, 2023), (Table 5 & 6).

The per cent contribution of each character towards divergence is presented in Table 7. It was observed that branches per plant contributing most to divergence (37.60%), followed by days to maturity (24.62%) and plant height (21.28%), while yield per plant and seed weight had minimal influence.

Table 1 Rating scale (0-9)/ description of symptoms for scoring disease severity (Mayee and Datar 1986).

Rating Scale	Bacterial pustule/ RAB/ CLS/ ALS/ MLS/ TLS/FLS	Pod blight/BB
0	No lesions/Spot	No lesion / spot
1	0.01 -1% leaf area covered with lesion/ spot	0.01-1% leaf area covered with lesion
3	1.1-10% leaf area covered with lesion/ spot	1.1-10% leaf area covered with lesion
5	10.1-25% leaf area covered, no defoliation	10.1-25% leaf area covered with lesion
7	25.1-50 % leaf area covered some leaves drop, death of few plants	25.1-50 % leaf area covered with lesion/ spot/ discoloration
9	More than 50% area covered, defoliation common, death of plants common	More than 50% area covered with lesion/ spot/ discoloration

Table- 2 Categorization of disease reaction based on PDI%

% Disease index (PDI)	Reaction
0	Immune (absolute resistant)
0.1 – 1.0	Highly resistant (HR)
1.1-10.0	Moderate resistant (MR)
10.1- 25.0	Moderate susceptible (MS)
25.1 - 50.00	Susceptible (S)
>50.01	High Susceptible (HS)

Table 3 Disease incidence and reaction (0-9 scale) of soybean genotypes against RAB and Bacterial blight.

S. No.	Genotype	Mean PDI (%) (arc sin)			
		RAB	Reaction	Bacterial blight	Reaction
1.	B.S 4	0 (0)	(I)	1.34 (6.55)	(MR)
2.	B.S 3	7.47 (15.79)	(MR)	1.35 (6.55)	(MR)
3.	RKS -18	31.47 (34.08)	(S)	0.00 (0)	(I)
4.	RSC 10-46	29.21 (32.71)	(S)	0.00 (0)	(I)
5.	B.S.S -2	2.59 (9.10)	(MR)	3.43 (10.63)	(MR)
6.	RSC 11-42	4.55 (12.25)	(MR)	0.00 (0)	(I)
7.	B.S -1	0.10 (1.81)	(HR)	1.60 (7.27)	(MR)
8.	J.S 20 -116	2.17 (8.33)	(MR)	23.42 (28.93)	(MS)
9.	RSC 11-35	9.47 (17.85)	(MR)	22.94 (28.59)	(MS)
10.	BAUS(M)-5	0.00 (0)	(I)	5.06 (12.92)	(MR)
11.	AMS 2014-1	5.04 (12.92)	(MR)	7.03 (15.34)	(MR)
12.	BAUS(M)-1	1.70 (7.49)	(MR)	1.36 (6.55)	(MR)
13.	JS 335	24.37 (29.53)	(MS)	16.41(23.89)	(MS)
14.	BAUS (M)-11	1.57 (7.04)	(MR)	2.59 (9.10)	(MR)
15.	JS 97-52	15.87 (23.42)	(MS)	8.14 (16.54)	(MR)
16.	BAUS(M)-15	0.00 (0)	(I)	0.00 (0)	(I)
17.	NRC -128	13.17 (21.22)	(MS)	8.02 (16.43)	(MR)
18.	MACS 1140	10.36 (18.72)	(MS)	4.93 (12.79)	(MR)
19.	RAUS 5	0.00 (0)	(I)	7.65 (16.00)	(MR)
20.	MACS 1407	0.00 (0)	(I)	4.44 (12.11)	(MR)
21.	BAUS 100	3.90 (11.39)	(MR)	0.00 (0)	0.00 (I)
22.	BAUS 134	5.50 (13.56)	(MR)	6.41 (14.65)	(MR)
23.	BAUS 194	0.00 (0)	(I)	7.40 (15.79)	(MR)
24.	BAUS 103	2.43 (8.91)	(MR)	2.46 (8.91)	(MR)
25.	BAUS 141	1.80 (7.71)	(MR)	9.62 (18.05)	(MR)
26.	BAUS 140	0.00 (0)	(I)	8.64 (17.05)	(MR)
27.	BAUS 138	0.00 (0)	(I)	3.44 (10.63)	(MR)
28.	BAUS 135	11.08 (19.37)	(MS)	6.91 (15.23)	(MR)
29.	BAUS 136	12.10 (20.36)	(MS)	5.30 (13.31)	(MR)
30.	BAUS 102	1.23 (6.29)	(MR)	4.19 (11.54)	(MR)

Table- 4 Composition of genotypes in different clusters based on yield components

S. No.	Cluster	No. of genotype	Name of genotypes
1	I	13	B.S 4, B.S.S -2, RSC 11-42, J.S 20 -116(ZC), RSC 11-35, JS 335, BAUS(M)-15, MACS 1407, BAUS 100, BAUS 103, BAUS 135, BAUS 136, BAUS 102.
2	II	4	B.S 3 (LC), RKS -18, RSC 10-46, JS 97-52
3	III	6	B.S -1, AMS 2014-1, NRC -128 (NC), MACS 1140, RAUS -5, BAUS 138
4	IV	7	BAUS(M)-5, BAUS(M)-1, BAUS (M)-11, BAUS 134, BAUS 194, BAUS 141, BAUS 140

Table- 5 Average Intra and Inter-Cluster distance based on yield and yield components

S. No.	Cluster	I	II	III	IV
1	I	8.89	24.24	23.38	21.05
2	II		11.49	27.82	25.35
3	III			10.66	23.61
4	IV				8.52

Table- 6 Intra-Cluster group means of different yield contributing characters

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches /plant	100 seed weight (g)	No. of seeds/ pod	No. of pods/ plant	Grain yield/plant (g)	Protein (%)	Oil (%)	Grain yield /plot (kg/plot)
I	42.59	109.69	66.67	4.23	11.67	2.74	60.15	12.07	40.12	17.59	0.74
II	43.08	114.83	57.78	3.48	10.45	2.92	62.20	9.61	40.04	18.36	0.56
III	46.94	115.94	64.31	3.13	10.24	2.17	52.67	8.99	40.61	17.06	0.54
IV	48.76	119.00	69.59	4.00	11.29	3.00	50.16	12.26	40.63	17.20	0.70

Table- 7 Contribution of different traits to total divergence

S. No.	Characters	Contribution (%)
1.	Days to 50% flowering	11.85
2.	Days to maturity	24.62
3.	Plant height (cm)	21.28
4.	No. of branches /plant	0.32
5.	100 seed weight (g)	0.59
6.	No. of seeds/ pod	0.14
7.	No. of pods/ plant	37.60
8.	Grain yield /plant (kg)	3.20
9.	Protein (%)	0.11
10.	Oil (%)	0.27
11.	Grain yield /plot (kg/plot)	0.01

Observation and grouping of resistance Rhizoctonia Aerial Blight (RAB)

All the genotypes were observed critically during entire crop period. The symptoms of RAB start appearing after 15th of august and highest severity was noticed in the month of September.

Thirty soybean genotypes, including resistant check MACS-1407 and susceptible checks JS-335/JS-20-116, were evaluated under field conditions. Eight genotypes exhibited immune reactions (PDI=0%): BS-4, BAUS(M)-5, BAUS(M)-15, RAUS-5, MACS-1407, BAUS-194, BAUS-140, and BAUS-138. BS-1 showed highly resistant (HR; PDI=0.10%) response, while 13 genotypes displayed moderate resistance (MR),

including BSS-2, RSC-11-42, and AMS-2014-1. Six were moderately susceptible (MS), led by JS-335 (24.37% PDI), and RKS-18/RSC-10-46 proved most susceptible (S; 31.47% and 29.21% PDI, respectively). High-yielding BAUS-102 maintained low RAB severity (1.23% PDI) alongside 0.91 kg/plot yield, consistent with Amrate *et al.* (2020) who classified JS-335 as MS.

Bacterial blight

Disease developed early in the growing seasons where warm and humid conditions promote bacterial blight development, while wind-driven rainfall facilitates canopy dispersal of inoculum, triggering severe epidemics. Screening of blight including resistant check RKS-18 and susceptible checks JS-335/JS-20-116—identified five immune reactions (PDI=0%): RKS-18, RSC-10-46, RSC-11-42, BAUS(M)-15, and BAUS-100. Twenty-one genotypes exhibited moderate resistance (MR; PDI 1.34-9.62%), including BS-4, BSS-2, AMS-2014-1, and MACS-1407. Three were moderately susceptible (MS): JS-20-116, RSC-11-35, and JS-335. No highly resistant, susceptible, or highly susceptible reactions occurred, consistent with Surbhi *et al.* (2022).

CONCLUSION

D² analysis confirmed substantial genetic divergence among soybean genotypes, identifying AMS-2014-1 and MACS-1407 as most distinct, with Cluster II (high pod number) × Cluster III (quality traits) crosses promising superior productivity-quality hybrids. Cluster I excelled in early flowering/maturity, branches/plant, 100-seed weight, and plot yield, while Cluster IV led plant height, seeds/pod, plant yield, and protein content; mutant BAUS(M)-15 (Cluster I) uniquely combined elite yield traits with earliness, contrasting its parent RKS-18 (Cluster II), while other mutants BAUS (M)-5, BAUS (M)-1, and BAUS (M)-11 performed strongly in Cluster IV. Disease screening revealed BAUS(M)-15 have complete immunity to both Rhizoctonia aerial blight and bacterial blight, positioning it as the premier donor for early-maturing, high-yielding, disease-resistant cultivars. Also, BAUS (M) 11 was found most high yielding genotype along with high oil and protein content. High-yielding BAUS-102, protein-rich MACS-1140, and oil-rich BAUS-103 provide additional valuable parental germplasm for targeted soybean breeding programs.

REFERENCES

- Anonymous (2024). Agricultural Statistics at a glance 2024, Ministry of Agriculture and Department of Agriculture, Animal Husbandry & Co-operative Jharkhand.
- Verma, H. S., & Thapliyal, P. N. (1976). Rhizoctonia aerial blight of soybean.
- Rao, C. R. (1952). Advanced statistical methods in biometric research.
- Joshi, D., Singh, P., & Adhikari, S. (2018). Study of Genetic Divergence in Soybean Germplasm. *Chemical Science Review and Letters* 7(26): 533–539.
- Patil, S. S., Patil, P. P., Lodam, V. A., & Chaudhari, M. H. (2011). Genetic diversity in soybean. *Journal of Phytology* 3(2): 95–102.
- Roja, K. S., Kavuri, S. R., & Rani, P. R. (2022). Genetic diversity studies in soybean (*Glycine max* (L.) Merrill) germplasm lines based on Mahalanobis D² distance. *Biological Forum – An International Journal* 14(2): 11–16.
- Zatybekov, A., Karimov, K., Sarsenbekova, A., Ibragimov, T., Abugalieva, A., & Turuspekov, Y. (2023). Genetic diversity and population structure analysis of soybean (*Glycine max* (L.) Merrill) genotypes using agro-morphological traits and SNP markers. *Genes* 14(11): 1373.
- Amrate, P. K., Shrivastava, M. K., & Singh, G. (2020). Screening of genotypes to identify the resistance source against major diseases of soybean under high disease pressure conditions. *Int. J. Curr. Microbiol. App. Sci*, 9(5), 1739–1745.
- Surbhi, K., Singh, K. P., & Jeena, H. (2022). Evaluation of soybean genotypes for resistance against bacterial leaf blight under field conditions. *The Pharma Innovation Journal* 11(8): 1111–1114.
- Mayee, C. D., & Datar, V. V. (1986). Phytopathometry, Technical Buletien-1 (Special Buletein-3), Marathwada Agric. Univ. Parbhani, India, 218.