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Genetic diversity assessment of soybean (*Glycine max* (L.) Merrill) genotypes in Summer season

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ABSTRACT

An extensive evaluation was conducted to assess the genetic diversity, character associations, and yield determinants among fifty drought-tolerant soybean genotypes during the Summer season of 2026. Field experiments conducted at the Agril. Botany Research Farm, MPKV, Rahuri, revealed highly significant genetic variability across all fourteen evaluated agro-morphological and physiological traits. Phenotypic coefficients of variation consistently exceeded genotypic coefficients, indicating environmental influence on trait expression. High heritability coupled with high genetic advance as a percentage of the mean was observed for primary branches, pods per plant, and seed yield, signifying the dominance of additive gene action. Genotypic correlation analysis demonstrated that single-plant seed yield shares a strong positive association with pods per plant, 100-seed weight, and the Normalized Difference Vegetation Index (NDVI). Path coefficient analysis identified 100-seed weight, seeds per pod, and pods per plant as the most critical positive direct drivers of seed yield. Furthermore, D^2 statistical analysis clustered the genotypes into twelve diverse groups, with the number of pods per plant contributing most significantly to the total genetic divergence. Hybridization between highly divergent genotypes, specifically G21 [JS 2098 × EC333901 (F6-25)] and G46 [KDS 1173 × EC 538828 (F6-24)], is highly recommended to isolate superior transgressive segregants for rainfed agro-ecosystems.

Keywords: *Glycine max*, Genetic diversity, Drought-tolerant, Seed yield, D^2 statistical analysis

1. Introduction

Recognized globally as a foundational crop of the modern agricultural framework, soybean (*Glycine max* (L.) Merrill) provides immense economic utility and plays a vital role in global food security. Belonging to the Papilionoideae subfamily of the Fabaceae family, it functions as the world's dominant oilseed crop, contributing to roughly 25% of the international edible oil supply and commanding over 50% of aggregate oilseed production. The unparalleled agricultural value of this legume arises from its highly complementary seed composition, which averages 40-42% premium protein and 18-22% oil. This biological profile makes it an indispensable source of both vegetable protein for global livestock industries and edible oil for human consumption (Verma *et al.*, 2023) [1]. Nutritionally, the protein profile is exceptionally balanced, supplying all eight essential amino acids—including lysine and tryptophan, which are often deficient in standard cereal grains. Furthermore, soybeans are rich in vitamins, essential minerals, and health-promoting phytoestrogens, specifically isoflavones, which help mitigate cardiovascular and bone density ailments. Botanically, the cultivated soybean is a diploidized ancient polyploid with a chromosomal configuration of $2n = 2x = 40$. In India, organized breeding efforts during the 1970s triggered a "yellow revolution," establishing the crop as a crucial kharif-season commodity. Recent production estimates for the 2024-25 season place India's total output at a record 151.80 lakh metric tonnes (LMT) across 126.90 lakh hectares. Maharashtra stands as the premier cultivating state, recording a production of 52.69 LMT across 50.72 lakh hectares during 2023-24. Despite this expansive acreage, national productivity remains constrained at approximately 1.0 to 1.2 tonnes per hectare, severely lagging behind the global average of 2.8 tonnes per hectare. This stagnant productivity is fundamentally driven by cultivation in marginal, rainfed environments prone to drought, which can slash yields by up to 40% during critical pod-filling stages (Marinho *et al.*, 2022) [2]. Additionally, the genetic base of current Indian cultivars is exceptionally narrow, increasing vulnerability to environmental stresses. Consequently, evaluating available germplasm to understand genetic variability and trait associations is a prerequisite for formulating strategic breeding programs aimed at breaking the current yield plateau.

2. Materials and methods

A comprehensive field experiment was executed to evaluate the genetic diversity among 50 distinct drought-tolerant soybean genotypes. The trials were conducted at the Agril. Botany Research Farm, affiliated with the Post Graduate Institute at MPKV, Rahuri, during the Summer season of 2026. The genotypes were sys

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Table 1. List of genotypes along with their crosses of soybean used for present study

Geno type No.	Cross	Geno type No.	Cross
G1	NRC37 × EC 602288 (F6-5)	G26	JS 2098 × EC 602288 (F6-33)
G2	NRC37 × EC 602288 (F6-7)	G27	JS 2098 × EC 602288 (F6-40)
G3	NRC37 × EC 602288 (F6-13)	G28	JS 2098 × EC 602288 (F6-41)
G4	NRC37 × EC 602288 (F6-17)	G29	JS 2098 × TGX 709 50E (F7-1)
G5	NRC37 × EC 602288 (F6-21)	G30	JS 2098 × TGX 709 50E (F7-2)
G6	KDS 1201 × EC333901 (F6-1)	G31	JS 2098 × TGX 709 50E (F7-7)
G7	KDS 1201 × EC333901 (F6-5)	G32	JS 2098 × TGX 709 50E (F7-9)
G8	KDS 1201 × EC333901 (F6-10)	G33	JS 2098 × TGX 709 50E (F7-11)
G9	KDS 1201 × EC333901 (F6-16)	G34	NRC37 × EC 602288 (F6-3)
G10	KDS 1201 × EC333901 (F6-17)	G35	JS 2098 × TGX 709 50E (F7-14)
G11	KDS 1173 × EC 602288 (F6-5)	G36	KDS 1201 × TGX 709 50E (F6-2)
G12	KDS 1173 × EC 602288 (F6-8)	G37	KDS 1201 × TGX 709 50E (F6-6)
G13	JS 2098 × EC333901 (F6-6)	G38	KDS 1201 × TGX 709 50E (F6-7)

Geno type No.	Cross	Geno type No.	Cross
G14	JS 2098 × EC333901 (F6-10)	G39	KDS 1201 × TGX 709 50E (F6-9)
G15	JS 2098 × EC333901 (F6-13)	G40	KDS 1201 × TGX 709 50E (F6-13)
G16	JS 2098 × EC333901 (F6-15)	G41	KDS 1201 × TGX 709 50E (F6-14)
G17	JS 2098 × EC333901 (F6-18)	G42	KDS 1173 × EC 538828 (F6-3)
G18	JS 2098 × EC333901 (F6-22)	G43	KDS 1173 × EC 538828 (F6-12)
G19	JS 2098 × EC333901 (F6-23)	G44	KDS 1173 × EC 538828 (F6-20)
G20	JS 2098 × EC333901 (F6-24)	G45	KDS 1173 × EC 538828 (F6-23)
G21	JS 2098 × EC333901 (F6-25)	G46	KDS 1173 × EC 538828 (F6-24)
G22	JS 2098 × EC 602288 (F6-6)	G47	JS 2098 × TGX 709 50E (F6-16-10)
G23	JS 2098 × EC 602288 (F6-7)	G48	Phule Sangam [c]
G24	JS 2098 × EC 602288 (F6-8)	G49	Phule Kimaya [c]
G25	JS 2098 × EC 602288 (F6-10)	G50	Phule Durva [c]

3.1 Analysis of variance

The analysis of variance confirmed that the mean sum of squares for the genotype treatments was highly significant at the 1% probability level for all fourteen traits, definitively establishing the presence of extensive genetic diversity within the test population.

Table 2. Analysis of variance for 14 yield and yield contributing characters in Soybean

Sr. No	Characters	Mean sum of square		
		Replication (1)	Treatment (49)	Error (49)
1.	Days to 50% flowering	0.36	49.409**	4.503
2.	Chlorophyll content	0.137	8.962**	3.613
3.	Canopy temperature	0.0225	1.597**	0.780
4.	NDVI	0.0004	0.0052**	0.0026
5.	Days to maturity	38.44	62.220**	15.868
6.	Plant height	0.017	124.262**	6.826
7.	Pods/plant	0.593	201.360**	6.036
8.	Primary branches/plant	0.044	2.007**	0.061
9.	Pods/cluster	0.0016	0.428**	0.08
10.	Seeds/pod	0.032	0.082**	0.037
11.	Seed yield/plant	0.327	3.620**	0.169
12.	100-seed weight	0.083	3.654**	0.193
13.	Oil content (%)	0.667	1.936**	0.970
14.	Protein content (%)	2.427	30.595**	3.874

* Significant at 5% level ** Significant at 1% level

3.2 Parameters of genetic variability

To evaluate the true genetic potential of the traits, variability indices were calculated. The phenotypic coefficient of variation (PCV) consistently marginally exceeded the genotypic coefficient of variation (GCV) for all characters, affirming that environmental factors influenced final trait expression. However, the magnitude of variability was highly promising. Traits such as primary branches per plant, seed yield per plant, pods per plant, and plant height exhibited high GCV (above 20%) and PCV values, indicating a robust inherent variance that is highly responsive to direct selection. The characters, primary branches per plant, seed yield per plant, pods per plant, and plant height marked matching results with [Suresh Rao et al. \(2014\)](#) [3] and [Pawar et al. \(2020\)](#) [4] in terms of high GCV and PCV.

Broad-sense heritability serves as a predictive metric for trait transmission. The study documented exceptionally high heritability estimates (greater than 60%) for pods per plant (94.18%), primary branches per plant (94.10%), seed yield (91.08%), and 100-seed weight (89.98%). The characters, pods per plant, primary branches per plant, seed yield per plant, and plant height marked matching results with [Suresh Rao et al. \(2014\)](#) [3] in terms of exceptionally high heritability.

Furthermore, these same parameters demonstrated high genetic advance as a percentage of the mean (GAM), with primary branches

reaching 66.31% and seed yield registering 61.49%. [Neelima et al. \(2018\)](#) [5] and [Kumari et al. \(2022\)](#) [6] reported high amount of genetic advance as percent of mean for 5 traits, viz. primary branches per plant, seed yield per plant, pods per plant, plant height, and 100-seed weight. The concurrence of high heritability and high GAM firmly indicates that these structural yield components are governed by additive gene action, ensuring that conventional breeding methodologies will yield rapid genetic gains.

3.3 Correlation analysis

Correlation coefficient analysis was utilized to quantify trait associations, providing vital insight for indirect selection criteria in crop improvement programs. At the genotypic level, single-plant seed yield exhibited a highly significant positive correlation with the number of pods per plant (0.583), pods per cluster (0.430), 100-seed weight (0.429), the Normalized Difference Vegetation Index (NDVI) (0.411), seeds per pod (0.395), and days to maturity (0.340). It maintained non-significant positive associations with primary branches per plant, days to 50% flowering, protein content, canopy temperature, and plant height. Conversely, chlorophyll content exhibited a significant negative correlation with seed yield (-0.373), indicating a physiological trade-off between prolonged vegetative maintenance and reproductive sink filling.

Table 3. Parameter of genetic variability in 50 genotypes in soybean

S. No.	Character	Grand Mean	Range	GCV (%)	PCV (%)	Heritability, h^2 (bs) (%)	Genetic Advance (GA)	GA as % of Mean (GAM)
1	Days to 50% flowering	48.86	41.5 to 58	9.7	10.63	83.3	8.909	18.23
2	Chlorophyll content (SPAD Index)	40.557	35.95 to 45.65	4.03	6.18	42.54	2.197	5.42
3	Canopy temperature (°C)	24.949	23.15 to 27.35	2.56	4.37	34.38	0.772	3.09
4	NDVI	0.573	0.435 to 0.67	6.3	10.86	33.65	0.043	7.53
5	Days to maturity	95.82	84 to 108.5	5.02	6.52	59.36	7.64	7.97
6	Plant height (cm)	37.215	21.5 to 62.6	20.59	21.75	89.58	14.941	40.15
7	No. of Pods/plant	39.805	22.4 to 65.6	24.83	25.58	94.18	19.756	49.63
8	No. of Primary branches/plant	2.973	0.6 to 4.75	33.18	34.21	94.1	1.971	66.31
9	No. of Pods/cluster	3.248	2.2 to 4.1	12.84	15.52	68.51	0.711	21.9
10	No. of Seeds/pod	2.526	2 to 2.8	5.88	9.65	37.2	0.187	7.39
11	Oil content (%)	17.028	15.075 to 19.165	4.08	7.08	33.26	0.826	4.85
12	Protein content (%)	35.694	26.655 to 44.8	10.24	11.63	77.52	6.63	18.57
13	100-seed weight (g)	8.013	4.99 to 10.625	16.42	17.31	89.98	2.571	32.08
14	Seed yield/plant (g)	4.199	2.405 to 8.975	31.28	32.78	91.08	2.582	61.49

At the phenotypic level, the trend remained largely consistent, with seed yield registering a significant positive correlation with pods per plant (0.549), 100-seed weight (0.424), and pods per cluster (0.356). These associations confirm that pods per plant, cluster density, and individual seed weight act as the dominant yield-contributing characters. Therefore, localized yield improvements in rainfed soybean populations can be effectively achieved by selecting for denser pod clusters and heavier seeds. Furthermore, significant negative correlations were observed between antagonistic biochemical traits, such as protein and oil content (-0.948 genotypically), presenting standard bioenergetic trade-offs that breeders must balance. The data confirms that selecting for robust structural traits like pods per plant will concurrently drive the genetic advancement of complex polygenic traits like seed yield. Jagtap *et al.* (2024) [7] and Tyagi *et al.* (2025) [8] also found a significant positive relationship between seed yield per plant and primary yield-attributing traits such as the number of pods per plant, pods per cluster, seeds per pod and 100-seed weight.

3.4 Path coefficient analysis

Path coefficient analysis was employed to dissect genotypic correlation coefficients into direct and indirect causal effects, explaining 84.40% of the total variation in seed yield (residual effect = 0.3950). The standardized component regression revealed that 100-seed weight exerted the highest positive direct effect on single-plant seed yield (0.7707). This was sequentially followed by strong positive direct contributions from seeds per pod (0.6249), pods per plant (0.6169),

plant height (0.3617), canopy temperature (0.3436), days to maturity (0.1397), and primary branches per plant (0.0049). Conversely, phenological and physiological maintenance traits displayed substantial negative direct impacts on seed yield, most notably days to 50% flowering (-1.5863), chlorophyll content (-0.8578), and NDVI (-0.6059). This dynamic indicates a clear biological trade-off: while prolonged canopy greenness and delayed flowering support initial vegetative endurance under moisture stress, they can restrict the direct remobilization of assimilates into developing seed sinks during reproductive phases. However, traits with negative direct effects often compensated through positive indirect pathways; for example, NDVI channeled positive indirect contributions to yield via 100-seed weight (0.4716) and seeds per pod (0.3670). Similarly, the negative direct effect of oil content (-0.1070) was mitigated by positive indirect contributions through days to 50% flowering. Ultimately, the path analysis firmly validates that direct phenotypic selection for heavier seeds (100-seed weight), increased seed packing per pod, and total pod load are the most reliable strategies for securing yield enhancements in drought-stressed soybean populations. Similar results showing a positive direct effect on seed yield per plant and 100-seed weight, seeds per pod, pods per plant, plant height, days to maturity, and primary branches per plant were reported by Shete *et al.* (2023) [9] and Barpanda *et al.* (2024) [10]. This biological dynamic confirms that while vegetative vigor is necessary for early establishment, the direct mobilization of resources into structural pod and seed parameters is the ultimate driver of soybean productivity.

Table 4. Estimates of genotypic (above diagonal) & phenotypic (below diagonal) correlation coefficients among seed yield & yield contributing characters in 50 soybean genotypes

Character	Days to 50% flowering	Chlorophyll content	Canopy temperature	NDVI	Days to maturity	Plant height	Pods/plant	Primary branches/plant	Pods/cluster	Seeds/pod	Oil content (%)	Protein content (%)	100-seed weight	Seed yield/plant
DF	1.000	-0.927**	0.392**	-0.129	0.785**	0.457**	0.324*	0.211	-0.032	0.391**	-0.623**	0.507**	-0.025	0.112
CHL	-0.524**	1.000	-0.121	0.046	-0.879**	-0.232	-0.418**	-0.242	-0.261	-0.573**	0.982**	-0.391**	-0.121	-0.374**
CT	0.161	-0.075	1.000	-0.714**	0.335*	0.418**	-0.092	-0.069	-0.258	-0.056	-0.164	0.563**	-0.354*	0.058
NDVI	0.002	0.048	-0.163	1.000	0.335*	0.107	0.402**	0.345*	0.707**	0.587**	-0.543**	0.136	0.612**	0.412**
DM	0.541**	-0.565**	0.068	0.034	1.000	0.255	0.259	0.183	0.155	0.470**	-0.658**	0.530**	0.353*	0.340*
PH	0.404**	-0.119	0.267	0.232	0.170	1.000	0.355*	0.309*	-0.062	0.233	-0.212	0.316*	-0.358*	0.022
PP	0.269	-0.234	-0.044	0.233	0.235	0.337*	1.000	0.501**	0.430**	0.274	-0.203	0.077	0.152	0.583**
PB	0.182	-0.171	-0.034	0.262	0.098	0.300*	0.474**	1.000	0.287*	0.444**	-0.131	0.198	-0.123	0.212
PC	0.022	-0.129	-0.161	0.273	0.144	-0.056	0.353*	0.238	1.000	0.535**	-0.355*	0.003	0.252	0.430**
SP	0.290*	-0.243	0.045	0.172	0.251	0.119	0.156	0.229	0.251	1.000	-0.346*	0.246	0.052	0.395**
OC	-0.372**	0.261	-0.061	-0.091	-0.381**	-0.076	-0.118	-0.033	-0.107	-0.128	1.000	-0.948**	-0.275	-0.201
PRC	0.442**	-0.252	0.186	0.056	0.406**	0.236	0.069	0.159	-0.033	0.135	-0.626**	1.000	0.168	0.101
SW	-0.012	-0.033	-0.249	0.253	0.341*	-0.358*	0.160	-0.120	0.209	0.051	-0.220	0.166	1.000	0.429**
SY	0.133	-0.130	-0.033	0.267	0.222	0.020	0.549**	0.218	0.356*	0.207	-0.107	0.104	0.424**	1.000

*, ** significant at 5 and 1 per cent respectively

Table 5. Estimates of genotypic direct (diagonal) & indirect effects (above and below diagonal) of component characters on seed yield in 50 soybean genotypes

Character	Days to 50% flowering	Chlorophyll content	Canopy temperature	NDVI	Days to maturity	Plant height	Pods/plant	Primary branches/plant	Pods/cluster	Seeds/pod	Oil content (%)	Protein content (%)	100-seed weight	Genotypic correlation with yield/plant
DF	-1.586	0.795	0.135	0.078	0.110	0.165	0.200	0.001	0.005	0.244	0.067	-0.082	-0.019	0.112
CHL	1.471	-0.858	-0.042	-0.028	-0.123	-0.084	-0.258	-0.001	0.042	-0.358	-0.105	0.063	-0.093	-0.373**
CT	-0.623	0.104	0.344	0.433	0.047	0.151	-0.057	0.000	0.041	-0.035	0.018	-0.091	-0.273	0.058
NDVI	0.204	-0.040	-0.245	-0.606	0.047	0.039	0.248	0.002	-0.112	0.367	0.058	-0.022	0.472	0.411**
DM	-1.245	0.754	0.115	-0.203	0.140	0.092	0.160	0.001	-0.025	0.294	0.070	-0.086	0.272	0.340*
PH	-0.724	0.199	0.144	-0.065	0.036	0.362	0.219	0.002	0.010	0.146	0.023	-0.051	-0.276	0.022
PP	-0.514	0.359	-0.032	-0.244	0.036	0.129	0.617	0.003	-0.068	0.171	0.022	-0.013	0.117	0.583**
PB	-0.334	0.208	-0.024	-0.209	0.026	0.112	0.309	0.005	-0.046	0.277	0.014	-0.032	-0.095	0.212
PC	0.050	0.224	-0.089	-0.428	0.022	-0.023	0.265	0.001	-0.159	0.334	0.038	0.000	0.194	0.430**
SP	-0.620	0.491	-0.019	-0.356	0.066	0.084	0.169	0.002	-0.085	0.625	0.037	-0.040	0.040	0.395**
OC	0.989	-0.842	-0.056	0.329	-0.092	-0.077	-0.125	-0.001	0.056	-0.217	-0.107	0.154	-0.212	-0.201
PRC	-0.804	0.336	0.193	-0.082	0.074	0.114	0.048	0.001	0.000	0.154	0.101	-0.162	0.130	0.102
SW	0.039	0.104	-0.122	-0.371	0.049	-0.130	0.094	-0.001	-0.040	0.032	0.030	-0.027	0.771	0.429**

Residual effect (R) = 0.395**Table 6.** Estimates of average intra-cluster and inter-cluster distance (D and D^2 values) of 12 clusters across 50 genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	58.83 (7.67)	124.99 (11.18)	87.05 (9.33)	141.85 (11.91)	106.30 (10.31)	87.05 (9.33)	135.72 (11.65)	243.36 (15.60)	124.99 (11.18)	129.28 (11.37)	147.14 (12.13)	221.12 (14.87)
II		86.49 (9.30)	169.26 (13.01)	100.60 (10.03)	184.69 (13.59)	118.81 (10.90)	115.78 (10.76)	184.96 (13.60)	145.44 (12.06)	117.07 (10.82)	259.21 (16.10)	143.76 (11.99)
III			0	179.56 (13.40)	87.24 (9.34)	171.09 (13.08)	197.96 (14.07)	179.56 (13.40)	225.90 (15.03)	54.76 (7.40)	77.26 (8.79)	335.62 (18.32)
IV				0	253.45 (15.92)	108.99 (10.44)	155.75 (12.48)	67.73 (8.23)	192.65 (13.88)	102.62 (10.13)	195.16 (13.97)	190.16 (13.79)
V					85.93 (9.27)	179.02 (13.38)	208.80 (14.45)	325.08 (18.03)	222.31 (14.91)	144.24 (12.01)	153.02 (12.37)	333.79 (18.27)
VI						0	102.62 (10.13)	243.98 (15.62)	166.41 (12.90)	162.56 (12.75)	232.26 (15.24)	255.36 (15.98)
VII							0	300.68 (17.34)	185.23 (13.61)	135.02 (11.62)	348.20 (18.66)	141.61 (11.90)
VIII								0	336.36 (18.34)	84.64 (9.20)	207.94 (14.42)	362.90 (19.05)
IX									0	247.75 (15.74)	353.82 (18.81)	129.28 (11.37)
X										0	147.38 (12.14)	278.22 (16.68)
XI											0	467.42 (21.62)
XII												0

(Values in parenthesis are the square root of D^2 values)**Table 7.** Arrangement of 50 genotypes into different clusters

Cluster No.	No. of genotypes	Name of Genotypes in each cluster
I	25	G33, G34, G16, G40, G39, G14, G47, G27, G45, G43, G23, G7, G18, G30, G10, Phule Durva, G32, G13, G35, G26, G41, Phule Kimaya, G37, G22, G9
II	13	G3, G4, G11, G12, G5, G24, G28, G6, G36, G17, G20, G42, G8
III	1	G38

Cluster No.	No. of genotypes	Name of Genotypes in each cluster
IV	1	G15
V	3	G1, G2, G31
VI	1	G29
VII	1	G25
VIII	1	G21
IX	1	Phule Sangam
X	1	G19
XI	1	G46
XII	1	G44

Table 8. Per cent contribution of 14 characters in divergence

Sr. No.	Character	No. of times ranked 1st	Contribution %
1	Days to 50% flowering	29	2.37%
2	Chlorophyll content	1	0.08%
3	Canopy temperature	0	0.00%
4	NDVI	0	0.00%
5	Days to maturity	3	0.24%
6	Plant height	210	17.14%
7	Number of pods/plant	279	22.78%
8	Number of primary branches/plant	227	18.53%
9	Number of pods/cluster	16	1.31%
10	Number of seeds/pod	2	0.16%
11	Oil Content (%)	1	0.08%
12	Protein Content (%)	33	2.69%
13	100 seed weight	181	14.78%
14	Yield/plant	243	19.84%
	Total		100%

(continued on next page)

3.5 Genetic divergence (D^2 analysis)

Maximizing hybrid vigor requires parents selected from genetically distant backgrounds. The multivariate D^2 analysis grouped the 50 evaluated soybean genotypes into 12 distinct clusters, minimizing intra-cluster variation while maximizing inter-cluster diversity. Cluster I was the largest, comprising 25 genotypes, followed by Cluster II with 13 genotypes and Cluster V with 3 genotypes. The remaining nine clusters (III, IV, VI, VII, VIII, IX, X, XI, and XII) were solitary, containing only a single genotype each. The maximum intra-cluster distance was recorded in Cluster II ($D = 9.30$).

The highest inter-cluster distance was observed between Cluster XI and Cluster XII ($D = 21.62$), signifying the maximum genetic divergence within the test population. Conversely, the lowest inter-cluster distance occurred between Cluster III and Cluster X ($D = 7.40$).

Evaluating the percent contribution of individual parameters revealed that the number of pods per plant exerted the most substantial influence, responsible for 22.78% of the total genetic divergence. This was closely trailed by seed yield per plant (19.84%), number of primary branches (18.53%), plant height (17.14%), and 100-seed weight (14.78%). Conversely, physiological traits like canopy temperature and NDVI contributed nothing (0.00%) to the overall divergence. Based on these maximum inter-cluster spatial distances and superior mean performance, specific cross combinations are recommended to generate elite transgressive segregants. Hybridizing genotype G21 from Cluster VIII with genotype G46 from Cluster XI is strategically recommended to maximize overall seed yield, while crossing G8 with G44 is advised for improving plant architecture and total primary branches.

4. Conclusion

The rigorous evaluation of the fifty drought-tolerant soybean lines established the presence of profound genetic variability across critical agro-morphological and physiological profiles. Traits heavily influencing ultimate productivity, notably primary branches, pod counts, and seed yield, showcased high heritability and additive gene action, rendering them ideal candidates for immediate phenotypic selection. Both correlation matrices and path coefficient analyses conclusively validated that genetic improvement in soybean yield is most effectively achieved by directly selecting for heavier seeds, increased pods per plant, and higher seed packing per pod. Utilizing the established D^2 clustering data to inform parent selection—particularly by hybridizing the highly divergent G21 [JS 2098 $\times$ EC333901 (F6-25)] and G46 [KDS 1173 $\times$ EC 538828 (F6-24)] lines—provides an optimized, strategic pathway for breeders to develop climate-resilient cultivars capable of breaking the productivity barriers currently affecting rainfed agricultural systems.

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