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CHARACTERIZATION AND IDENTIFICATION OF THE SOURCES OF RESISTANCE AGAINST MOSAIC VIRUS IN SOYBEAN (*Glycine max* L.)

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ABSTRACT

Soybean mosaic virus (SMV), a member of genus *Potyvirus* within the family Potyviridae, is an important constraint that influences soybean seed production and seed quality. To ensure steady soybean production, this study sought to assist continuing efforts to increase mosaic resistance through genetic improvement. The present study was carried out during *Kharif* 2020-21 and 2021-22 at the Research Farm of Division of Genetics & Plant Breeding, Faculty of Agriculture, SKUAST-K, Sopore, Jammu & Kashmir. A diverse panel of 154 genotypes of soybean was evaluated to study variability, genetic diversity among yield and its attributing traits, and also resistance to soybean mosaic virus. Genotypes were phenotypically screened for SMV resistance under natural field conditions and classified into different reaction categories based on the disease response. Out of these genotypes, 9 were found resistant, 9 moderately-resistant, 124 susceptible, and 12 highly susceptible. Considerable variation was observed for all agro-morphological traits studied, with a significant magnitude of genotypic and phenotypic coefficient of variation indicating substantial scope for selection. The promising genotypes identified in this study can serve as a vital component and valuable genetic resources for developing varieties with higher yield and enhanced resistance to soybean mosaic virus.

Keywords: GCV, variability, genetic PCV, soybean mosaic virus, resistance

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill), is a diploid, annual, self-pollinated, legume crop belonging to family Fabaceae, with chromosome number (2n) of 40 and genome size of 1.1-1.5 Gb (Kumari *et al.*, 2025). Globally, it is the largest cultivated oilseed crop, with global production of 364.40 million tons in 2019 with USA, Brazil, Argentina, India and China as the main producers (Patil *et al.*, 2025). Recognised as an important oilseed and protein-rich crop, soybean approximately possess 40% protein and 20% oil and essential fatty acids, besides being rich in vitamins, minerals, and other bioactive compounds (Lokurunka, 2010; Mishra and Amrate, 2024). However, its productivity and seed quality are constrained by several pests and diseases including soybean mosaic virus (SMV). SMV, a member of genus *Potyvirus*, is a most destructive viral disease that affects soybean crop (Amrate *et al*., 2023). The SMV is transmitted by whitefly (*Bemisia tabaci*) and disease produces the symptoms of yellow patches, puckered leaves, stunted growth, which eventually leads to significant yield loss (Allen *et al.*, 2017; Widyasari *et al*., 2020). Depending on the stage of infection and the susceptibility of genotype,

the yield losses can range from 30 to 70% (Mishra *et al*., 2022). Under field circumstances, yield losses due to SMV have been observed to range from 50 to 100% (Song *et al*., 2016).

Previous studies have established the genetic complexity of SMV resistance and highlighted the importance of evaluating diverse soybean germplasm (Widyasari *et al.,* 2020). Concurrently, Gaur and Pandey (2020) characterized 10 soybean varieties under natural field conditions and reported distinct trait profiles for 13 qualitative and quantitative markers, showed variations in different traits. Considering the anticipated threat of disease outbreaks to soybean production in Kashmir, the present study aimed to characterize soybean genotypes grown under Kashmir agro-climatic conditions by assessing SMV-associated disease, yield performance, and diverse qualitative and quantitative morphological traits, which may provide a comprehensive basis for germplasm characterization to elucidate phenotypic variability and identify the promising genotypes for further evaluation and potential use in soybean breeding programmes.

MATERIALS AND METHODS

Experimental material

The germplasm comprised of 154 soybean genotypes procured from the Indian Institute of Soybean Research (IISR) Indore (India), besides known susceptible check genotypes *viz*., Shalimar Soybean-1, Shalimar Soybean-101, and two local landraces *viz*., Wadura Local Landrace-1 and Wadura Local Landrace-2. All genotypes were evaluated for yield attributing traits, and screened for the identification of soybean mosaic virus resistant sources under field conditions for two consecutive years.

Experimental site

The study was conducted during two consecutive growing seasons in *Kharif* 2020 and 2021, in SKUAST-Kashmir, Wadura, Sopore, India (latitude 34° 10' N, longitude 74° 30' E). The experiment was conducted under natural conditions in an augmented block design in which four checks were replicated and randomized after every block. Each genotype was sown in a plot size of 1.6 m^2 with row to row and plant to plant spacing of 0.4 and 0.2 m, respectively. The crop was managed as per the recommended agronomic soybean production practices (ICAR-IISR, 2016).

Agro-morphological observations

Traits were recorded on the minimal descriptors for evaluation and characterization issued by the ICAR-Indian Institute of Soybean Research, Indore, India as per the guidelines of the Protection of Plant Varieties and Farmer Right Authority (PPV&FRA, 2009). The agro-morphological traits observed were days to 50% flowering, days to 80% maturity, leaf colour, leaf shape, flower colour, plant height, pod colour, seed coat pattern, and hilum colour. Yield attributing traits were recorded for number of pods $plant^{-1}$, pod length, number of seeds pod^{-1}, seed length, 100-seed weight, and seed yield $plant^{-1}$ from randomly tagged five plants of each accession.

Screening of genotypes against soybean mosaic virus (SMV) disease

The genotypes were assessed for reaction against SMV during reproductive phase. Disease scoring was done at the beginning of maturity and five plants were randomly selected in each genotype for this purpose. Severity of disease was recorded by using a 0-8 disease rating scale, where 0 = no visible disease symptoms, 1 = covering 10 % plant area showing molting and puckering, 2 = 11-30% curling leaf area, 5 = 31-60% plant area affected, 8 = >60% plant area affected, showing molting, puckering and curling of leaves. Disease severity was calculated by using the formula:

$$\text{Disease severity} = [\Sigma(n \times v)/N \times G] \times 100,$$

where n = the number of diseased leaves in each category, v = the numerical value of the category, N = total number of leaves examined, and G = highest grade value, i.e., 8 in this case.

Genotypes were categorized on the basis of disease severity as follows: 0-10% = resistant (R), 10.1-30% = moderately resistant (MR), 30.1-60% = susceptible (S), >60% = highly susceptible (HS) **(**McKinney, 1923).

Statistical analysis

The data recorded for various quantitative traits were analysed as per the augmented block design for various statistical parameters namely, mean, range, variances and cluster analysis using the R-software. Multivariate dissimilarity matrix was obtained by using Mahalanobis' (D^2) statistic (Mahalanobis, 1936). Based on these computed distance values, a hierarchical tree was generated using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) algorithm.

RESULTS AND DISCUSSION

Frequency distribution of qualitative traits

The visual characterization of 154 genotypes based on morphological descriptors revealed substantial phenotypic variation in leaf, flower, pod, and seed traits (Fig. 1). Leaf shape was predominantly broad in 116 genotypes (75.32%); whereas 29 (18.83%) and 9 (5.84%) genotypes exhibited narrow and intermediate leaf shapes, respectively. The variation in leaf colour, observed during early morning at flowering stage, revealed that 100 genotypes (64.94%) were green, while 27 (17.53%) genotypes each were dark green and light green. Flower colour, recorded from freshly opened flowers, was predominantly purple in 111 genotypes (72.08%), followed by white 21 (13.64%), light purple 15 (9.74%) and dark purple 7 (4.55%) genotypes. Similarly, pod colour, assessed at the advanced pod filling stage, was found light brown in a majority of genotypes 121 (78.57%), whereas brown and dark brown pods were observed in 17 (11.4%) and 16 (10.39%) genotypes, respectively. In terms of seed coat pattern, 124 genotypes (80.52%) displayed a light hilum; while the remaining 30 (19.48%) had dark hilum. Hilum colour was diverse, with yellow being the most common in 102 genotypes (66.23%), followed by brown 33 (21.43%), buff 11 (7.14%), and black and grey in 4 genotypes each (2.60%) indicating considerable genetic variability for these traits recorded visually. Characterization of soybean genotypes done by previous researchers also noticed similar phenotypic variations in soybean germplasm (Barela *et al.*, 2022; Naflath *et al*., 2022; Ullah *et al*., 2024), corroborating the morphological diversity observed in the present study.

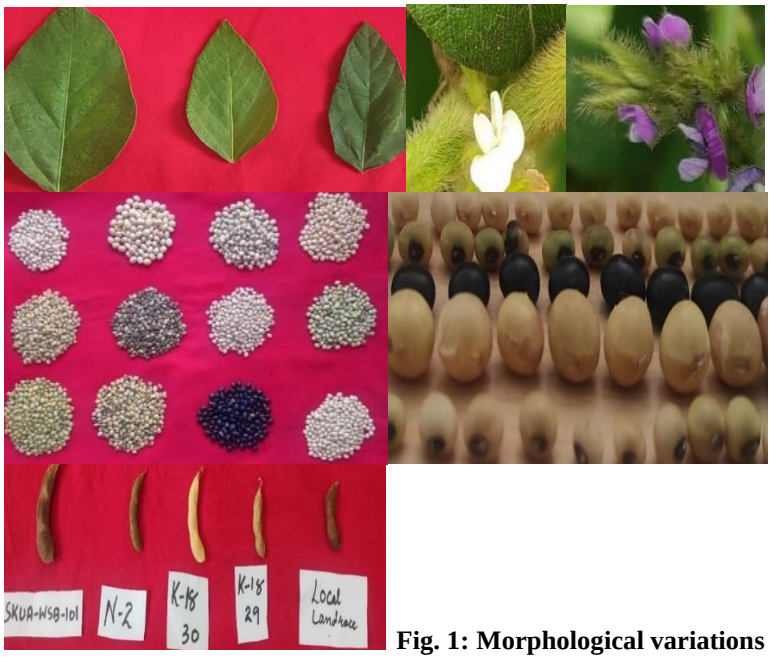


Fig. 1: Morphological variations across the evaluated soybean germplasm in leaf shape and leaf colour (upper left hand side), flower colour (upper middle and right hand side), seed coat colour (middle left hand side), hilum colour (middle right hand side), and pod colour (bottom)

Analysis of variance for yield and yield attributing traits

The pooled analysis of variance for all the traits for both years revealed that the mean sum of squares due to genotypes was highly significant (Table 1) and also showed significant effects for all traits for different sources of variation, thereby indicating the presence of sufficient genetic variability among the genotypes for all the characters studied. Additionally, the critical difference was also computed (Table 2).

Table 1: Pooled mean sum of square for yield and yield attributing traits for year 2020-21 & 2021-22

Source of variation	DF	DTF	DTM	PH	NPPP	NSPP	PL	SL	100-SW	SYPP
Block (ignoring treatments)	9	365.03**	699.11**	131.05**	40.71**	0.07**	1.19**	0.34	2.36*	12.18**
Blocks (eliminating treatments)	9	7.37*	150.04**	16.80**	48.48**	0.01^{ns}	0.44**	0.19*	1.84^{ns}	3.95^{ns}
Treatment (ignoring blocks)	153	122.15**	283.05**	116.01**	63.71**	0.06**	0.37**	0.70**	3.36**	25.93**
Treatment (eliminating blocks)	153	101.12 **	250.75**	109.29**	64.17**	0.06**	0.33**	0.69	3.33**	25.45**
Test entries	149	90.16	213.82	77.55	42.84	0.06	0.29	0.57	1.23	12.49
Checks	3	55.99	102.38	165.42	180.44	0.10	1.41	1.66	8.63	112.23
Test vs Checks	1	5087.63	11139.49	5697.43	2822.91	0.41	8.94	18.05	305.63	1769.64
Error	27	3.25	43.25	4.82	7.69	0.01	0.05	0.06	0.99	2.95

DTF: Days to 50% flowering, DTM: Days to 80% maturity, PH: Plant height (cm), NPP: No of pods plant^{-1}, NSPP: No. of seeds pod^{-1}, PL: Pod length (cm), SL: Seed length (mm), 100 SW: 100 seed weight (g), SYPP: Seed yield plant^{-1}

Table 2: Pooled critical difference (5%) for yield and yield attributing traits for the years 2020-21 and 2021-22 in a set of 154 soybean genotypes

Sources	$CD_{0.05}$								
	DTF	DTM	PH	NPP	NSP	PL	SL	100SW	SYP
Control treatment means	1.65	6.03	2.01	2.54	0.10	0.20	0.23	1.58	0.91
Two test treatments (same block)	5.23	19.08	6.37	8.05	0.30	0.63	0.72	4.99	2.88
Two test treatments (different blocks	5.85	21.34	7.12	9.00	0.34	0.71	0.81	5.58	3.22
A test treatment and a control treatment	4.34	15.82	5.28	6.67	0.25	0.53	0.60	4.13	2.39

DTF: Days to 50% flowering, DTM: Days to 80% maturity, PH: Plant height (cm), NPP: No of pods plant^{-1}, NSPP: No. of seeds pod^{-1}, PL: Pod length (cm), SL: Seed length (mm), 100 SW: 100 seed weight (g), SYPP: Seed yield plant^{-1}

Descriptive statistics

The descriptive statistics of different yield and yield attributing traits recorded in the present study for two consecutive years were pooled and analysed. Significant variations were observed in all the studied traits (Table 3). The coefficient of variation (CV) ranged from 2.80 to 11.57% with highest CV observed for seed yield plant^{-1} and lowest for plant height. The magnitude of phenotypic coefficient of variance was greater than the genotypic coefficient of variance for all the characters studied, indicating an important role of environment in the expression of characters (Jain *et al.*, 2018). Days to 50% flowering varied from 40.92 to 78.84 days, with genotype 'K-51' being the earliest and 'K-13' and 'K-14' the latest to flower, averaging 56.35 days. The days to 80% maturity spanned from 81.8 to 152.8 days, with 'K-44' maturing earliest and 'K-14' latest, with a mean of 113.29 days. Plant height varied between 47.48 cm (SKUA-304) and 106.62 cm (N-2), with an average height of 75.93 cm. The number of pods plant^{-1} ranged from 24.92 (SKUA-315) to 74.75 (N-2), averaging 47.56 pods. Pod length ranged from 3.78 to 6.28 cm, with 'SKUA-10' having the longest pods and a mean length

Table 3: Pooled descriptive statistics for yield attributing traits in a set of 154 soybean genotypes for year 2020-21 and 2021-22

Traits	Min.	Max.	Mean	Std. Error	Std. Deviation	CV (%)
Days to 50% flowering	40.92	78.84	56.35	0.78	9.73	3.34
Days to 80% maturity	81.80	152.80	113.29	1.15	16.06	5.99
Plant height (cm)	47.48	106.62	75.93	0.72	9.37	2.80
No of pods plant^{-1}	24.92	74.75	47.56	0.56	6.96	5.62
No. of seeds pod^{-1}	1.57	2.72	2.18	0.02	0.26	4.70
Pod length (cm)	3.78	6.28	4.97	0.05	0.53	4.31
Seed length (mm)	4.15	7.87	6.11	0.07	0.81	3.99
100 Seed weight (g)	9.07	16.74	12.79	0.08	1.29	7.44
Seed yield plant^{-1} (g)	4.92	27.49	13.48	0.32	3.90	11.57

of 4.97 cm. Seeds pod^{-1} varied from 1.57 (SKUA-05) to 2.72 (N-2), averaging 2.18 seeds. Seed length ranged from 4.15 mm 'SKUA-05' to 7.87 mm 'SG-16', with an average of 6.11 mm. Hundred seed weight ranged from 9.07 g (SG-31) to 16.74 g (SKUA-WSB-101), averaging 12.79 g. Seed yield plant^{-1} ranged from 4.92 g (SKUA-304) to 27.49 g (N-2), with a mean yield of 13.48 g. The present findings are consistent with Vasanth *et al.* (2023) and Hizli *et al*. (2023), who also reported considerable variation for yield and yield-attributing traits in soybean germplasm.

Genotypic and phenotypic coefficient of variation for different traits in soybean

The estimation of genotypic and phenotypic coefficients of variation revealed valuable insights into the extent of variability present among the soybean genotypes. The genotypic coefficient of variation (GCV) was highest for seed yield plant^{-1} (22.91%), suggesting a broad range of genetic diversity for this economically important trait (Table 4). This was followed by days to 50% flowering (16.54%), number of pods plant^{-1} (12.47%), seed length (11.62%), days to maturity (11.53%), plant height (11.23%), number of seeds pod^{-1} (10.23%), pod length (10 %), and 100-seed weight (3.85%). Similarly, the phenotypic coefficient of variation (PCV) was highest for seed yield plant^{-1} (26.2%), followed by days to 50% flowering (16.8%), number of pods plant^{-1} (13.7%), days to maturity (12.9%), seed length (12.3%), plant height (11.6%), number of seeds pod^{-1} (11.2%), pod length (10.9%), and 100-seed weight (8.67%). For all traits examined, PCV values were consistently higher than GCV indicating the role of environment in trait expression. Traits like seed yield plant^{-1}, number of pods, and seed length showed high GCV and PCV, suggesting strong potential for improvement through selection. The close correspondence between GCV and PCV across most traits further emphasizes the reliability of these traits for genetic enhancement in soybean breeding programs. Similar results were recorded by Ali *et al*. (2016), Mehra *et al*. (2020) and Banerjee *et al.* (2020), who reported substantial genetic variation and high heritability for yield-associated traits in soybean, revealing considerable scope for selection and genetic improvement.

Table 4: Pooled mean, PCV, GCV, heritability and genetic advance in a set of 154 soybean genotypes for year 2020-21 and 2021-22

Trait	Mean	PV	GV	PCV	GCV	h^2 (%)	GA	GAM
Days to 50% flowering	56.35	90.16	86.91	16.8	16.54	96.40	18.88	33.51
Days to 80% maturity	113.29	213.82	170.57	12.9	11.53	79.77	24.06	21.24
Plant height (c,)	75.93	77.55	72.74	11.6	11.23	93.79	17.04	22.44
No of pods plant^{-1}	47.56	42.84	35.15	13.7	12.47	82.05	11.08	23.29
No. of seeds pod^{-1}	2.18	0.06	0.05	11.2	10.23	82.29	0.42	19.15
Pod length (cm)	4.97	0.29	0.25	10.9	10.00	83.84	0.94	18.90
Seed length (mm)	6.11	0.57	0.50	12.3	11.62	89.04	1.38	22.63
100 Seed weight (g)	12.79	1.23	0.24	8.67	3.85	19.70	0.45	3.52
Seed yield plant^{-1} (g)	13.48	12.49	9.54	26.2	22.91	76.35	5.57	41.31

Estimation of genetic divergence

Genetic divergence among soybean genotypes was estimated using Mahalanobis D^2 statistic method (Mahalanobis,1936) to group the genotypes into different clusters based on Euclidean distances. A dendrogram was generated using hierarchical clustering to visualize the genetic relationships among the studied genotypes and the distribution pattern of genotypes into various clusters (Table 5; Fig. 3). One hundred and fifty-four genotypes, including four check varieties and two land races, were grouped into four main clusters with cluster-III having maximum number of genotypes (69), followed by cluster-I (47), cluster-II (29) and cluster-IV (9). Similar genetic differentiation has been reported by Beyene and Jalata (2022), who grouped 100 soybean genotypes into nine clusters. Clusters IX and IV had the highest number of genotypes, while clusters II and VII had the least but exhibited desirable yield traits. Ullah *et al*. (2024) reported significant diversity among soybean genotypes for agro-morphological, yield, and quality traits, concordant with the divergence observed in present study.

Screening for soybean mosaic virus resistance

The field screening of soybean genotypes for resistance against SMV revealed the presence of

Table 5: Distribution of soybean genotypes into different clusters

Clusters	No. of genotypes	Name of the genotypes
I	47	Shalimar Soybean 1, SKUA-WSB-101, C3, C4, N-2, SKUA-19, SKUA-307, SKUA-311, SG-18, SG-20, SG-20, SG-27, SG-32, SG-33, SG-34, SG-35, SG-37, SG-38, SG-39, SG-41, SG-42, SB-51, SB-49, SG-52, SG-54, SG-55, SG-56, SG-58, SG-59, K-1, K-3, K-4, K-5, K-6, K-7, K-9, SB-48, SB-10, K-29, K-44, K-45, K-46, K-47, K-48, K-49, K-50, K-51.
II	29	SKUA-44, SKUA-321, SKUA-323, SKUA-325, SKUA-327, SKUA-331, SKUA-304, SKUA-306, SKUA-318, SG-16, SG-30, SKUA-37, SKUA-01, SKUA-04 SKUA-05, SKUA-09, SKUA-20, SKUA-34 SKUA-35, SG-31, SG-36, SG-40, K-2, K-25, K-31, K-32, K-40, K-41
III	69	SKUA-02, SKUA-08, SKUA-06, SKUA-07, SKUA-10, SKUA-11, SKUA-13, SKUA-14, SKUA-15, SKUA-16, SKUA-17, SKUA-22, SKUA-23, SKUA-24, SKUA-25, SKUA-26, SKUA-27, SKUA-28, SKUA-29, SKUA-31, SKUA-33, SKUA-36, SKUA-38. SKUA-39, SKUA-40, SKUA-43, SKUA-319, SKUA-320, SKUA-322, Sk-53, SKUA-330, SKUA-301, SKUA-305, KUA-308, SB-52, SKUA-316, SG-1, SG-5, SG-10, SG-14, SG-17, SG-19, SG-21, SG-28, SB-51, SG-60, K-8, K-11, K-12, K-13, K-17, K-18, K-19, K-20, K-21, K-22, K-23, K-24, K-26, K-27, K-28, K-30, K-33, K-34, K-35, K-36, K-37, K-38, & K-39
IV	9	SKUA-41, SKUA-315, SG-4, SG-13, K-14, K-15, K-42,K-43, K-52

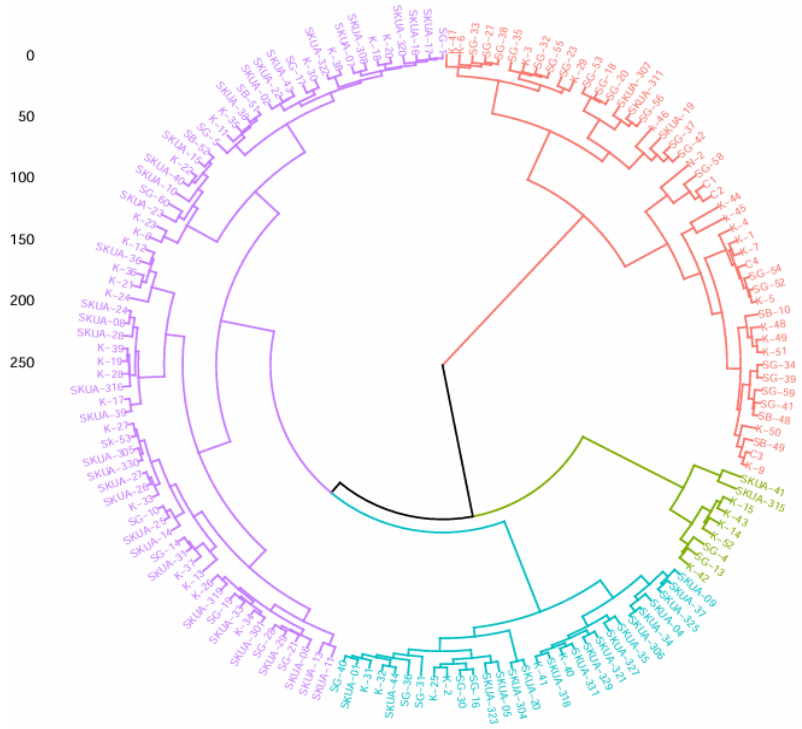


Fig. 3: UPGMA dendrogram showing hierarchical clustering of soybean genotypes into four groups: Red (cluster I, 47 genotypes), cyan (cluster II, 29 genotypes), purple (cluster III, 69 genotypes), and green (cluster IV, 9 genotypes). In the dendrogram, branch lengths represent the genetic distance between genotypes. Four clusters were found: Purple is the largest group with maximum divergence, cyan is the second largest cluster, red and green indicate closely related lines. This clustering directs parental selection for maximizing hybrid vigour and genetic variation.

characteristic symptoms of SMV ranging from mosaic to leaf discolouration, puckering and yellowing. Out of 154 genotypes, field screening revealed that only nine genotypes *viz*., N-2, SG-16, SG-39, SG-56, SG-58, SG- 59, K-21, K-28 and SKUA-05 exhibited resistant reaction to SMV. Other nine genotypes namely 'SG-13', 'SB-10', 'K-11', 'K-12', 'K-13', 'K-14', 'K-15', 'K-17', and 'K-18' showed moderate resistance to SMV, and the remaining genotypes were either susceptible or highly susceptible (Table 6; Fig. 2). Bachkar *et al*. (2019) screened 36 genotypes under natural and glass-house conditions and found genotypes in resistant to moderately resistant category. Likewise, Usovsky *et al*. (2022) reported differential responses of soybean germ-



N2 SKUA-39 SKUA-28

Fig. 2: Resistant vs susceptible soybean genotypes

plasm to SMV and highlighted the availability of diverse genetic sources of resistance, supporting the potential exploitation of genetic variability for developing virus-resistant soybean cultivars.

Conclusion: The present study demonstrated substantial agro-morphological and genetic diversity among 154 soybean genotypes, revealing significant variation in yield and yield-contributing traits, and response to SMV.

Table 6: Categorization of soybean genotypes on the basis of disease severity

Categories	Genotypes	No. of genotypes
Resistant (R)	N-2, SG-16, SG-39, SG-56, SG-58, SG- 59, K-21, K-28, SKUA-05	9
Moderately resistant (MR)	SG-13, SB-10, K-11, K-12, K-13, K-14, K- 15, K-17, K-18	9
Susceptible (S)	SKUA-01, SKUA-02, SKUA-06, SKUA-07, SKUA-08, SKUA-09, SKUA-10, SKUA-11, SKUA-13, SKUA-15, SKUA-16, SKUA-17, SKUA-19, SKUA-20, SKUA-22, SKUA-23, SKUA-24, SKUA-26, SKUA-27, SKUA-28, SKUA-29, SKUA-30, SKUA-34, SKUA-35, SKUA-36,, SKUA-39, SKUA-40, SKUA-41, SKUA-43, SKUA-44, SKUA-320, SKUA-321, SKUA-322, SKUA-325, SKUA-327, SK-53, SKUA-329, SKUA-330, SKUA-301, SKUA-305, SKUA-307, SKUA-308, SKUA-311, SB-52, SKUA-316, SG-1, SG-4, SG-5, SG-10, SG-14, SG-17, SG-18, SG-19, SG-20, SG-21, SG-23, SG-27, SG-28, SG-30, SG-30, SG-31, SG-32, SG-33, SG-35, SG-36, SG-37SG-38, SG-40, SG-41, SG-42, SB-51, SB-49, SG-52, SG-53, SG-54, SG-55, SG-60, K-1, K-2, K-3K-4, K-5, K-6, K-7, K-8, K-9, SB-48K-19, K-9, K-20, K-22, K-23, K-24, K-25, K-26, K-27, K29-30, K-31, K-32, K-33, K-34, K-35, K-36, K-37, K-38, K-389, K40, K41, K-42, K-43, K-44, K-45, K-46, K-47, K-48, K-49, K-50, K-51, K-52, SC1, SC2, SC3, SC4	124
Highly susceptible (HS)	SKUA-04, SKUA-14, SKUA-31, SKUA-33, SKUA-37, SKUA-38, SKUA-319, SKUA-331, SKUA-304, SKUA-306, SKUA-315, SKUA-318	12

The identified SMV-resistant genotypes, together with genetically divergent and agronomically superior lines, represent valuable genetic resources for enhancing crop productivity and promoting sustainable soybean cultivation in virus-prone regions. Furthermore, the integration of agro-morphological characterization with disease screening enabled the simultaneous identification of disease-resistant and high-performing genotypes. These findings provide a strong foundation for the selection of promising parental lines and their effective utilization in future soybean breeding programmes aimed at improving yield and disease resistance.

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