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Screening for Charcoal Rot Resistance in Newly Developed Sesame (*Sesamum indicum* L.) Genotypes and Multivariate Analysis for the Quantitative Characters

P. Vamshi[1], K.T. Ramya*, M. Santhalakshmi Prasad, J.V. Ramana[1] and S.R. Kumhar[2]

ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-500 030, Telangana

[1]Agricultural College, Bapatla-522 101, Andhra Pradesh;

[2]Agriculture Research Station, Agriculture University, Jodhpur, Rajasthan;

**Corresponding author's Email : ramya.kt@icar.gov.in*

Abstract

In the present investigation thirty sesame genotypes were evaluated for agro-morphological characters to study genetic diversity among newly developed genotypes. First six principal components with eigen value more than one contributed 81.02 % of cumulative variance. The thirty genotypes were categorized into four clusters using agglomerative hierarchical cluster analysis. Among the clusters, cluster I had the most genotypes (13 genotypes) followed by cluster III (11 genotypes) and cluster IV was monogenotypic. Charcoal rot leads to 5 to 60 % yield loss and is distributed in all sesame growing areas of India. The newly developed genotypes were screened for charcoal rot disease. Breeding lines *viz.,* SES-S-19-2102, SES-S-20-3003, SES-S-20-2001 and 2 varieties CUMS-17, Swetha til recorded less than 10 % root rot infection and three moderately resistant lines *viz.,* GT-10, SES-S-20-1038, SES-S-20-1039 recorded 10 - 20 % root rot infection. These resistant sources may serve as donor parents in hybridization programme for the development of disease resistant high yielding varieties in future crop improvement programmes.

Key words : *Charcoal rot, cluster, resistance, sesame.*

Introduction

India holds a premier position in the global oilseeds scenario accounting for 29 per cent of the total area and 26 per cent of production. Globally, sesame is cultivated in an area of 12.82 million hectares with a production of 6.549 million tonnes [1]. Across the country it is grown in an area of 15.8 lakh hectares with an overall production of 7.92 lakh tonnes [2]. Major states like Rajasthan, Gujarat, Madhya Pradesh, Andhra Pradesh, West Bengal and Tamil Nadu account for approximately 72 per cent of total area and 58 per cent of sesame production in the country indicating that there is a dire need to enhance the productivity potential of this crop by producing high yielding varieties suitable for different agro-climatic regions. Despite its prominence among oilseeds, sesame has a low average productivity when compared to other oilseed crops due to its narrow adaptability, non-synchronous maturity, seed shattering, yield instability and lack of high yielding cultivars resistant to major insect pests and diseases. Thus there is a need to enhance the productivity of this crop by developing high yielding genotypes which depends on the availability of variability for seed yield and its component traits in the population. The requirement of high yield and quality edible oil is raising day by day so, there is a need to increase the area, production and productivity of the crop which, is possible through crop improvement strategies.

Genetic upgradation of any crop primarily depends on utilization of existing genetic resource, and hence assessment of genetic diversity gets priority area. The nature and magnitude of genetic divergence in a population is essential for selection of diverse parents which upon hybridization leads to a wide spectrum of gene recombination for quantitatively as well as qualitatively inherited traits. Therefore assessment of genetic diversity would become vital to develop better varieties from a wide range of sesame accessions.

One of the major constraint that limits sesame crop productivity is its high susceptibility to the most devastating disease charcoal rot, caused by *Macrophomina phaseolina* (Tassi.) Goid. In India, this disease incidence was recorded up to 50% [3]. One per cent increase in the incidence of *Macrophomina phaseolina* reduces seed yield by 1.8 kg/ha [4]. Host plant resistance remains the best strategy for disease control as the disease is soil borne. To make the cultivation of sesame more remunerative, it is imperative and necessary to breed cultivars having high yield potential along with inbuilt resistance against charcoal rot. Recently, the development of resistant varieties as a means of controlling disease infection has become an important objective in almost all plant breeding programmes. So, identification of new sesame genotypes resistant to charcoal rot would be more beneficial and safe approach to reduce yield losses. Therefore, the present investigation was formulated to evaluate the genetic diversity in the breeding lines and to identify

superior cultivars having high yield potential along with inbuilt resistance against charcoal rot.

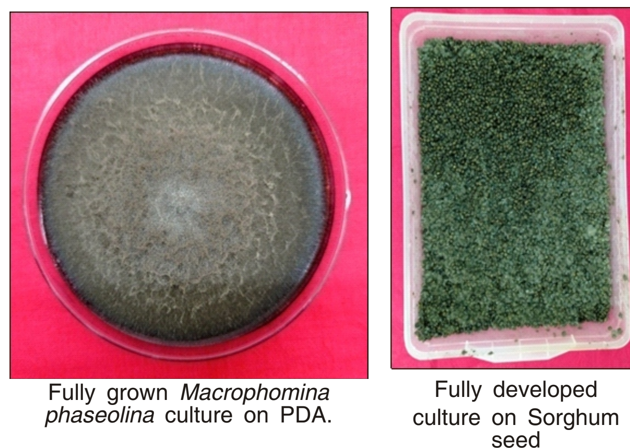
Materials and Methods

The present investigation was carried out during *kharif*, 2020 at experimental farm of ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad. The present study consisted of 27 advance breeding lines developed through pedigree selection from seven different bi-parental crosses, along with three check varieties. Each genotype was sown in two rows of 4.0 m length following a spacing of 45 cm between the rows and 15 cm in between the plants with the plot size of 5.4 m^2. The experiment was laid out in randomized block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. Phenological data on days to 50% flowering, days to maturity were recorded for plots of each genotype. At maturity five plants from each accession were selected randomly for recording data on number of primary branches per plant, number of capsules per plant, capsule length (cm), capsule width (cm), plant height (cm). Plot based data were recorded for harvest index (%), test weight (g), seed weight per capsule (g), seed yield per plot (g) and oil content (%). Different quantitative traits are usually pooled up together in multivariate analysis to reach towards a conclusive outcome of diversity based multivariate analysis is often used in selection of parents for hybridization program in sesame [5, 6]. Multivariate analysis such as principal component analysis (PCA) and cluster analysis using eucledian genetic distances were carried using SAS ver.9.3.

Screening of sesame genotypes against *Macrophomina* root rot disease was carried out adopting sick pot method under pot culture conditions with 31 sesame genotypes (including resistant check GT-10 and susceptible check VRI-1). Initial plant stand was noted after the establishment of the seedlings in the pots and the root rot incidence was recorded at five-day interval from 15 days after sowing (DAS) to 45 DAS for each genotype separately.

Pot Culture Experiment

1. Isolation of the causal pathogen of sesame root rot disease : Infected stem and root of each plant sample were surface sterilized by immersing in 1% sodium hypochlorite solution for 2 min. Disinfected segments after drying were placed onto petri dishes containing potato dextrose agar (PDA) medium supplemented with 400 mg streptomycin sulphate per litre of medium to avoid contamination. Plates were then incubated at 25±5ºC for 4 days to recover axenic cultures (Fig.-1). Axenic cultures of *M. phaseolina* were maintained at 25±5ºC on PDA plates for screening the test genotypes.



Fully grown *Macrophomina phaseolina* culture on PDA.

Fully developed culture on Sorghum seed

Fig.-1 : Innoculum growth of *Macrophomina phaseolina* on PDA plates and Sorghum seed.

2. Preparation of inoculum : *M. phaseolina* inoculum was prepared using clean sorghum seeds devoid of inert material. Boiled sorghum seeds were spread over paper towel to remove excess moisture and filled in tightly sealed poly propylene bags for autoclaving. The autoclaved sorghum seeds were spread in sterile plastic trays (750 g per tray). 90 mm mycelial disc of *M. phaseolina* from 5-day old culture of test pathogen was inoculated in sterile plastic trays containing autoclaved sorghum seed for multiplication and incubated at 25±5ºC for 20 days [7] (Fig.-1).

3. Pathogen inoculation into the pot soil : Formalin-sterilized pots (20 cm diameter) were filled with 1.5 kg autoclaved red sandy loam soil, inoculated with 25 g inoculum per kg soil and irrigated on alternate days until 3 days prior to sowing.

Seed material of the test genotypes were disinfected by dipping in a 2% sodium hypochlorite solution for 3 min, and then rinsed 3 times using sterile water. 30-40 seeds per pot were dibbled into the pot soil. Three pots were sown as replicates for each genotype in a completely randomized design (CRD). The seedlings were thinned on 14 days after sowing (DAS) and 15 plants per pot were maintained. Starting from 15 to 45 DAS *i.e.,* 15, 20, 25, 30, 35, 40, 45 DAS, symptoms of root rot disease were noted and disease incidence was recorded for each genotype separately. The percentage of root rot disease incidence was calculated using the formula [8] :

$$\text{Disease incidence (DI\%)} = \frac{\text{The number of plants infected}}{\text{Total number of plants sown in the pots}} \quad 100$$

The plants showing the typical root rot symptom were pulled out and the causal agent was re-isolated onto PDA plates, incubated at 30 ± 2°C for 5 days. The pathogenicity and symptomatology of the inoculated

culture was compared to the originally isolated axenic culture.

Disease Index Rating Scale : The genotypes were classified into five categories according to the disease incidence % at the end of 45 DAS and were scored 1-9 based on the disease scale represented below [9, 10] :

List 1 : Disease Incidence Percentage with Category.

Percent of infection (%)	Disease scale	Category
1-10	1	Resistant(R)
11-20	3	Moderately resistant (MR)
21-30	5	Moderately susceptible (MS)
31-50	7	Susceptible (S)
51-100	9	Highly susceptible (HR)

Source : Chattopadhyay and Kalpana Sastry (2001); Dinakaran and Mohammed (2001).

Results and Discussion

The analysis of variance exhibited a significant difference for all the traits except for capsule width, indicating sufficient amount of variation present in the material. In order to know with which combination type of agronomic traits the sesame would attain high grain yield, Principal component analysis (PCA) was performed and the analysis identified six principal components with eigen value more than one and 81.02 % of cumulative variance. The first principal component (PC1) contributed maximum towards variability (29.61%) through the characters days to 50% flowering, number of primary branches per plant, harvest index, seed weight per capsule, seed yield per plot and test weight. (Table-1).

Principal components (eigen value greater than one), eigen values (Latent root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table-1. The first five principal components with eigen values greater than one, as well as the sixth component with eigen value 0.96, contributed 87.02 per cent of total variability in the present investigation (Table-1). Therefore, the essential characteristics of the data set had been represented in first six principal components. Three PCs with Eigen-values greater than 1.0 accounting for 73.86% of cumulative variation were obtained in 13 sesame genotypes [11]. Ten Eigen vectors accounting for 65% of the variation were found in 60 genotypes of sesame [12]. 99% of the total variability was explained by the first three PCs in 45 sesame genotypes [13]. Principal Component analysis revealed that first three principal components (PC_1, PC_2 and PC_3) accounted for 70.59 percent of total variability [14].

The PCA simplifies the complex data by transforming the number of associated traits into a smaller number of variables as PCs. The PCA grouped the estimated sesame variables into six main components among which the first principal component (PC_1) contributed maximum towards variability accounting for about 29.61 % of the variation, followed by PC_2 for 15.90 %, PC_3 for 13.01%, PC_4 for 11.20 %, PC_5 for 9.30 % and PC_6 for 8.00 % (Table 1). The first PC was related to number of primary branches per plant and its contributing traits such as plant height, harvest index and seed yield per plot, whereas the second PC was related to number of capsules per plant and its contributing traits such as plant height and capsule width (Table-1).

The traits, which contributed more positively to PC_1, were days to 50 % flowering (0.46), number of primary branches per plant (0.39), number of capsules per plant (0.03), plant height (0.09), harvest index (0.46), seed weight per capsule (0.20) and seed yield per plot (0.41) suggesting that this component reflected the yield potential of each genotype through some yield component aspects. In addition, the traits, which contributed positively to PC_2, were days to 50 % flowering (0.13), days to maturity (0.45), number of capsules per plant (0.58), capsule width (0.34), plant height (0.15), harvest index (0.07), oil content (0.16), seed weight per capsule (0.01) and seed yield per plot (0.35) suggesting that this component reflected the yield potential of each genotype. In addition, the traits, which contributed positively to PC_3, were days to 50 % flowering (0.08), days to maturity (0.45), capsule length (0.10), harvest index (0.17), test weight (0.50), seed weight per capsule (0.60) and seed yield per plot (0.01). The traits days to 50 % flowering (0.23), days to maturity (0.01), number of primary branches per plant (0.29), number of capsules per plant (0.14), capsule length (0.65), capsule width (0.13), oil content (0.43), harvest index (0.33) and seed yield per plot (0.21) contributed positively to PC_4. In addition, the traits, which contributed positively to PC_5, were days to 50 % flowering (0.08), number of primary branches per plant (0.27), number of capsules per plant (0.28), capsule width (0.46) and seed weight per capsule (0.17) suggesting that this component reflected the yield potential of each genotype. The traits days to 50 % flowering (0.03), days to maturity (0.13), number of primary branches per plant (0.11), harvest index (0.04), oil content (0.60) and seed yield per plot (0.05) were positively contributed to PC_6 (Table-1).

The PCA may allow the plant breeder more flexibility in finding the number of plants to be evaluated and the plant breeder could use the multivariate methods by first determining the combination of traits that constitute an ideal plant. By plotting the PCs that are considered to be important, plants close to the ideal plant would be selected [15]. The PCA may be deemed important if their associated coefficients are of relative magnitude with breeding targets and given this apparent potential for

using PCA, further work is required to compare multivariate methods for reaching actual gains.

The PCA thus identified that the maximum contributing traits towards the existing variability were number of capsules per plant, capsule length, plant height, harvest index, test weight and seed weight per capsule. In PCA, the magnitude of relative contribution of a particular trait to total variability is more important rather than the sign (+/-) which only indicates the direction of variability.

The PCA scores of the thirty genotypes for the first three principal components were computed and considered as three axes (x, y and z) and the squared distance of each genotype from these three axes was calculated and presented in Table-2. In PCA, it is important to study the variance as the relative contribution rather than the signs (indicative of direction). The biplot for two PCA scores of thirty genotypes were plotted in a graph to generate two dimensional scattered diagram (Fig.-2), revealing the genotype diversity which can be exploited for generating transgressive segregants in crop improvement programmes.

For yield and its attributes, the PCA biplot revealed that genotypes SES-K-19-3005, SES-R-18-3002, SES-S-1043, SES-S-20-2003, SES-S-20-1039 and RT-323 were divergent. Hybridization between these diverse genotypes can be suggested. However, selecting for yield and its attributes may not be possible simultaneously. So, balanced selection criteria should be followed depending on the objective.

Multivariate analysis uncovered significant genetic divergence among the genotypes grouping them randomly into different clusters. This could be due to differences in population genetic architecture, selection history for the development of these genotypes and the degree of combining ability of the parents used in the development of particular genotype.

Utilizing the genotype principal component scores, Unweighted Pair Group Method with Arithmetic Average (UPGMA) hierarchical cluster analysis, grouped the 30 genotypes into four clusters (Table 4). The dendrogram (Fig. 3) was developed using euclidean distance calculated from genotype PCA scores. Cluster I had the most genotypes, 13 (CUMS-17, GT-10, ISWG-20-05,

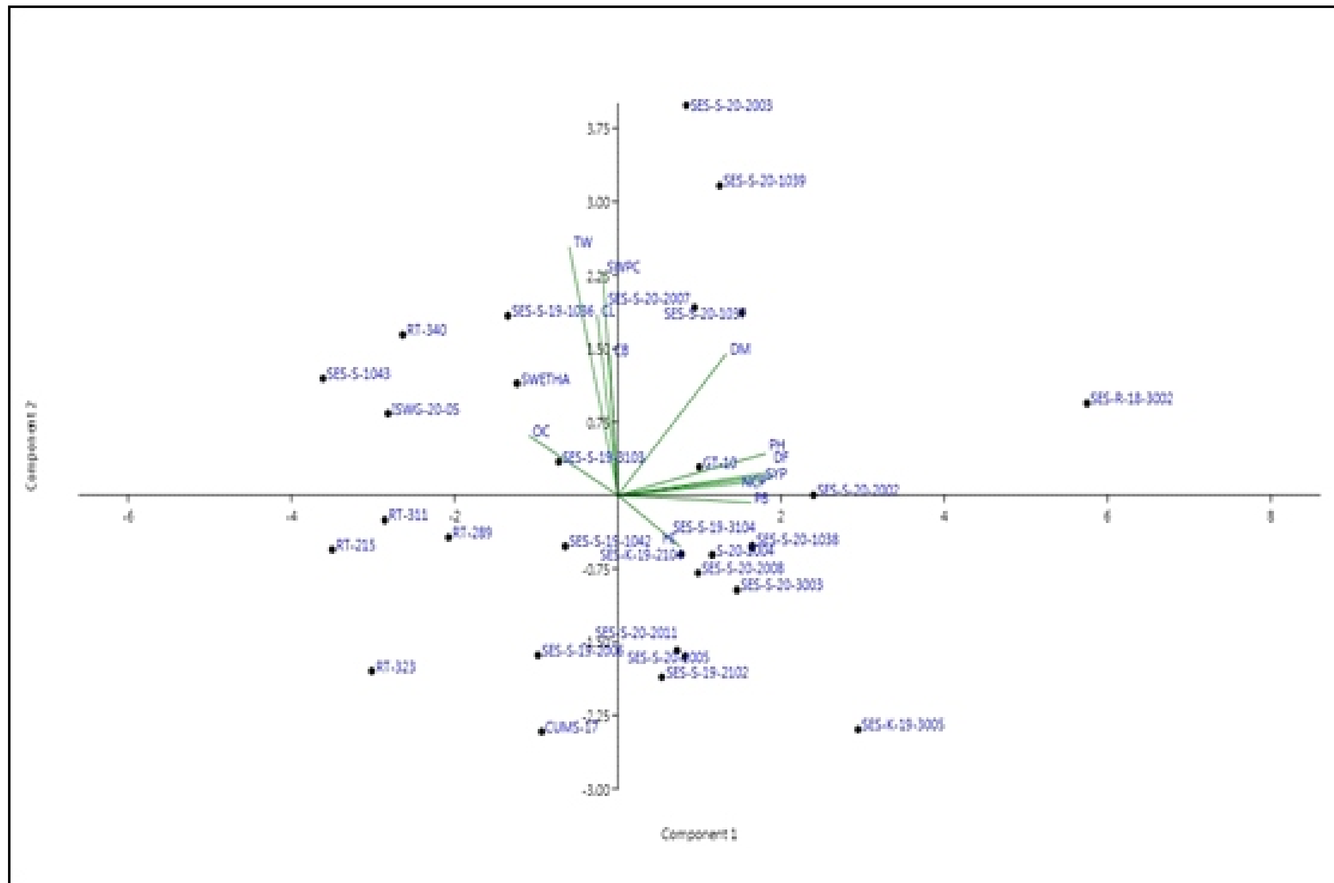


Fig.-2 : Biplot showing relative position of 30 sesame genotypes based on PCA scores for two principal components

RT-289, RT-311, S-20-2004, SES-S-19-1036, SES-S-19-2006, SES-S-19-2102, SES-S-20-2008, SES-S-20-2001, SES-S-20-3003 and Swetha til), followed by clusters III which had 11 genotypes (SES-K-19-2104, SES-K-19-3005, SES-S-19-3103, SES-S-19-3104, SES-S-20-1037, SES-S-20-1038, SES-S-20-1039, SES-S-20-2002, SES-S-20-2003, SES-S-20-2005 and SES-S-20-2007) and cluster II with five genotypes (RT-215, RT-323, RT-340, SES-S-1043 and SES-S-19-1042). The cluster IV was a single genotype (SES-R-18-3002) solitary cluster. The pattern of clusters showed that clustering of germplasm was not associated with the geographical distribution and accessions were mainly grouped due to their morphological differences.

The hierarchical cluster analysis of 52 landraces of sesame for 13 morphological characters grouped the genotypes into four clusters [16]. Thirty six genotypes of sesame were grouped into seven clusters through hierarchical cluster analysis for 10 morphological traits [17]. Diversity assessment using Hierarchical cluster analysis for 19 agro-morphological traits categorized 80 accessions into eight clusters [18]. Thirteen clusters were obtained through hierarchical cluster analysis in 205 sesame genotypes for 8 morphological characters [19].

The average intra-cluster and inter-cluster Euclidean distance values were calculated using UPGMA and are shown in the Table 3. Inter-cluster divergence expresses the diversification among clusters. General notion exists that the larger is the divergence between the parental genotypes, the higher may be the heterosis in crosses [20]. As a result, it would be desirable to attempt crosses between genotypes from distant clusters in order to obtain highly heterotic crosses that are likely to yield a diverse set of segregants for selection. Inter-cluster distances were calculated using twelve characters in this study which ranged from 98.26 (between cluster I and II) to 404.57 (between cluster II and IV) Table-3.

Since varieties with narrow genetic base are more vulnerable to diseases and adverse climatic conditions, therefore, the availability of the genetically diverse genotypes for hybridization programme becomes more important. In the present study the maximum intercluster euclidean distance was found to be 404.57 (between cluster II and IV), followed by 306.80 (between clusters I and IV), 212.82 (between clusters II and III), 194.96 (between cluster III and IV), 115.34 (between clusters III and I) and 98.25 (between clusters II and I) (Table 3). This indicated that there is a high level of genetic diversity among the clusters.

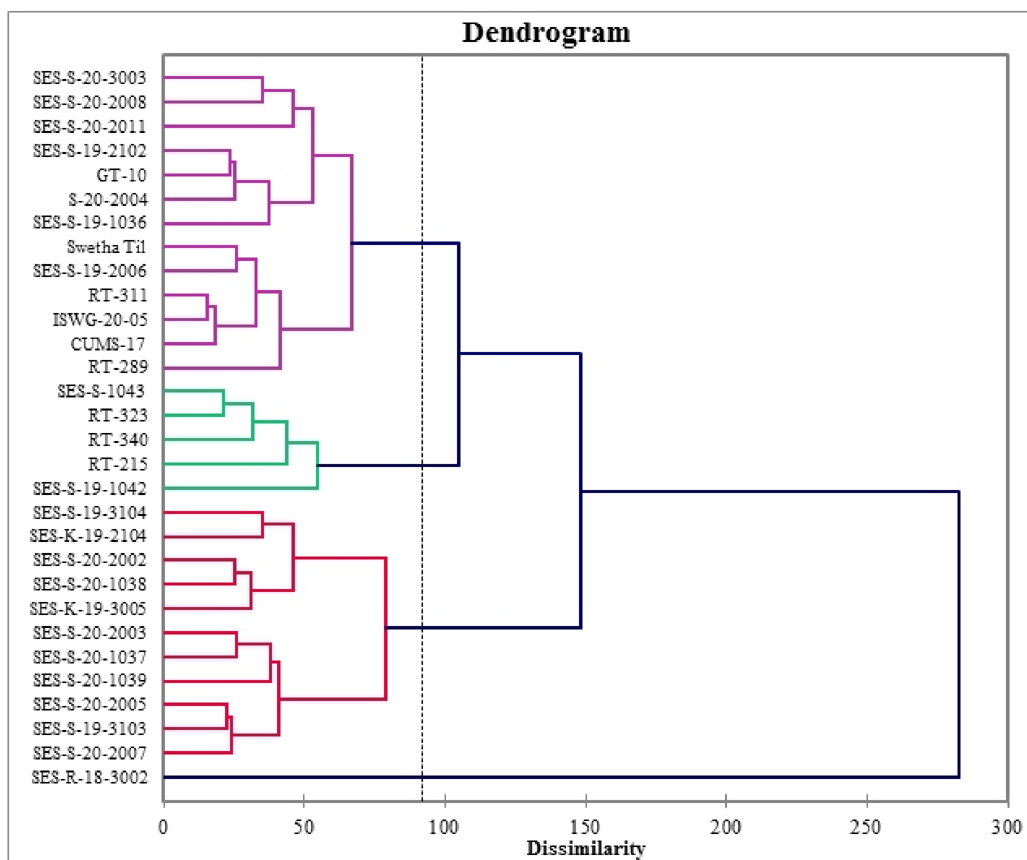


Fig.-3. Dendrogram illustrating the cluster pattern by UPGMA method for quantitative characters of 30 sesame genotypes.

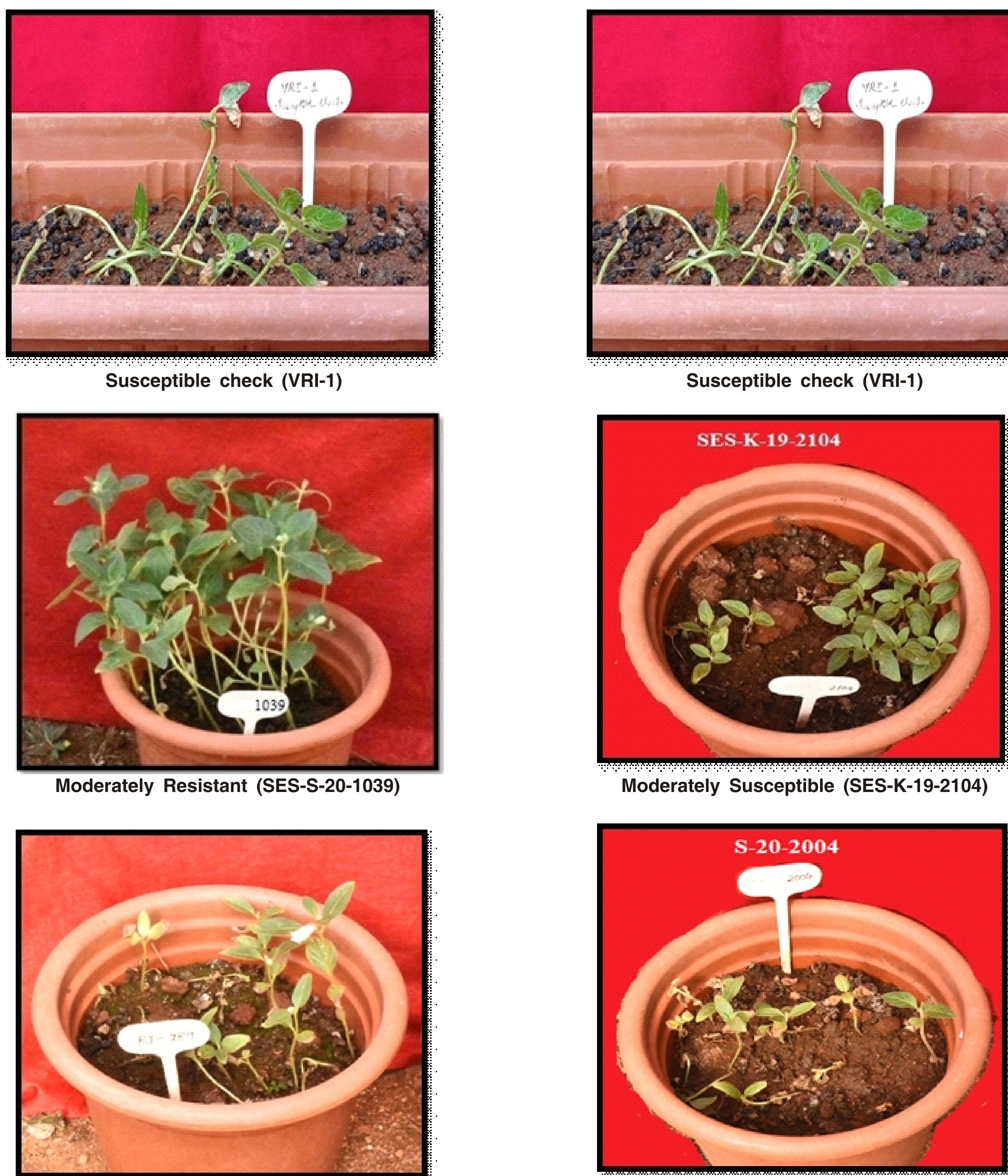


Fig.-4. Reaction of sesame genotypes in screening for Macrophomina root rot resistance.

The cluster mean values representing the average performance of all genotypes in a specific cluster for 12 characters studied by UPGMA are presented in Table-4. The mean values for the characters studied showed a wide range of variation, implying that the clusters formed were distinct.

The cluster means for days to 50 % flowering ranged from 33.50 DAS (cluster II) to 46.0 DAS (cluster IV); days to maturity ranged from 83.6 DAS (cluster I) to 93.0 DAS (cluster IV); number of primary branches per plant ranged from 3.0 (cluster II) to 5.7 (cluster IV); number of capsules per plant ranged from 64.5 (cluster II) to 158.3 (cluster IV); capsule length varied from 2.6 cm (cluster IV) to 2.8 cm (cluster III). The cluster mean for plant height ranged from 112.6 cm (cluster II) to 186.4 cm (cluster IV); harvest

Table-1 : Eigen values proportion of the total variance represented by first six principal components cumulative per cent variance and component loading.

	Principal Component Analysis (PCA)					
	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Eigene Value (Root)	3.55	1.91	1.56	1.34	1.12	0.96
% Var. Exp.	29.61	15.90	13.01	11.20	9.30	8.00
Cum. Var. Exp.	29.61	45.51	58.52	69.72	79.02	87.02
Days to 50 % flowering	0.46	0.13	0.08	0.23	0.08	0.03
Days to maturity	-0.19	0.45	0.45	0.01	-0.18	0.13
No. of primary branches per plant	0.39	-0.24	-0.11	0.29	0.27	0.11
No. of capsules per plant	0.03	0.58	-0.15	0.14	0.28	-0.16
Capsule length (cm)	-0.04	-0.31	0.10	0.65	-0.05	-0.36
Capsule width (cm)	-0.23	0.34	-0.23	0.13	0.46	-0.30
Plant height (cm)	0.09	0.15	-0.25	-0.05	-0.67	-0.53
Harvest index (%)	0.46	0.07	0.17	-0.01	-0.15	0.04
Oil content (%)	-0.22	0.16	-0.06	0.43	-0.27	0.60
Test weight (g)	-0.29	-0.04	0.50	0.33	-0.01	-0.23
Seed weight /capsule (mg)	0.20	0.01	0.60	-0.26	0.17	-0.15
Seed yield per plot (g)	0.41	0.35	0.01	0.21	-0.13	0.05

Table-2 : PCA scores of 30 genotypes of sesame.

S. No.	Genotype	PC_1	PC_2	PC_3
1.	ISWG-20-05	-8.93	16.44	10.11
2.	RT-215	-8.83	16.24	9.85
3	RT-289	-7.77	16.89	9.52
4	RT-311	-8.61	16.24	9.28
5	RT-323	-8.22	16.20	8.82
6	RT-340	-8.84	16.66	10.00
7	S-20-2004	-4.65	15.74	10.33
8	SES-K-19-2104	-4.68	17.12	10.16
9	SES-K-19-3005	-3.20	17.00	8.46
10.	SES-R-18-3002	-3.35	20.24	8.99
11	SES-S-1043	-9.78	15.83	9.60
12	SES-S-19-1036	-7.78	16.70	10.90
13	SES-S-19-1042	-6.82	16.44	9.55
14	SES-S-19-2006	-6.52	16.35	9.22
15	SES-S-19-2102	-5.36	16.06	10.38
16	SES-S-19-3103	-7.09	16.88	9.79
17	SES-S-19-3104	-3.09	15.34	10.40
18	SES-S-20-1037	-5.26	16.79	10.70
19	SES-S-20-1038	-4.62	17.44	8.87
20	SES-S-20-1039	-6.06	17.62	12.14
21	SES-S-20-2002	-3.93	17.17	9.75
22	SES-S-20-2003	-6.28	16.98	12.39
23	SES-S-20-2005	-4.82	16.90	8.97
24	SES-S-20-2007	-4.72	16.13	11.50
25	SES-S-20-2008	-5.10	16.50	8.66
26	SES-S-20-2001	-3.70	14.65	9.37
27	SES-S-20-3003	-4.71	17.06	9.97
28	Swetha til	-7.30	15.58	9.06
29	GT-10	-6.32	17.16	10.11
30.	CUMS-17	-5.32	15.84	9.89

Table-3 : Average intra (diagonal) and inter-cluster Euclidean values among four clusters.

Cluster No.	I	II	III	IV
I	0.00	98.26	115.34	306.80
II	98.26	0.00	212.82	404.57
III	115.34	212.82	0.00	194.96
IV	306.80	404.57	194.96	0.00

Table-4 : Mean values of four clusters estimated by UPGMA method for quantitative characters.

Cluster No.	Days to 50 % flowering	Days to maturity	Primary branches/ plant	Capsules/ plant	Capsule length (cm)	Capsule width (cm)	Plant height (cm)	Harvest index (%)	Oil content (%)	test weight (g)	Seed weight/ capsule (mg)	Seed yield/ plot (g)
I	37.3	83.6	4.1	85.7	2.6	0.6	123.8	27.0	43.7	3.1	133.8	217.1
II	33.5	83.6	3.0	64.5	2.8	0.6	112.6	22.7	47.6	3.2	133.8	122.1
III	40.0	86.4	4.4	93.9	2.8	0.6	141.3	32.2	42.2	3.2	141.5	330.3
IV	46.0	93.0	5.7	158.3	2.6	0.6	186.4	31.4	46.4	3.0	132.1	508.2

Table-5 : Root rot incidence in sesame genotypes under pot culture conditions.

Genotypes	DI %	Category	Disease Score	Genotypes	DI %	Category	Disease Score
SES-S20-2008	44.7	S	7	SES-R-18-3002	35.7	S	7
SES-S-1043	40.0	S	7	SES-K-19-2104	29.0	MS	5
SES-S-19-2102	4.5	R	1	Swetha til	8.9	R	1
SES-S-20-3003	2.2	R	1	SES-S-20-1038	16.7	MR	3
SES-S-20-2001	0.0	R	1	SES-S-20-1039	15.8	MR	3
RT-340	75.8	HS	9	SES-S-20-2003	44.1	S	7
RT-311	31.9	S	7	SES-S-20-2007	24.6	MS	5
GT-10	18.1	MR	3	SES-S-19-1042	29.0	MS	5
ISWG-20-05	49.1	S	7	SES-S-19-2006	44.7	S	7
SES-S19-3103	82.5	HS	9	SES-S-20-2002	31.3	S	7
SES-S-20-2004	71.5	HS	9	SES-K-19-3005	35.7	S	7
CUMS-17	6.7	R	1	RT-289	49.1	S	7
SES-S-20-2005	21.8	MS	5	RT-215	31.3	S	7
SES-S-19-3104	24.6	MS	5	RT-323	75.2	HS	9
SES-S-20-1037	44.7	S	7	SES-S-19-1036	81.4	HS	9
				VRI-1	64.8	HS	9

DI % = Disease incidence percentage; R = Resistant; MR = Moderately resistant; MS = Moderately Susceptible; S = Susceptible; HS = Highly Susceptible.

index ranged from 22.7 % (clusters II) to 32.2 % (clusters III); oil content values ranged from 42.2 % (cluster III) to 47.6 % (cluster II); test weight values ranged from 3.0 g (cluster IV) to 3.2 g (cluster III); Cluster mean values ranged from 132.1 mg (cluster IV) to 141.5 mg (cluster II) for seed weight per capsule. For seed yield per plot cluster mean values varied from 122.1 g (cluster II) to 508.2 g (cluster IV) (Table-4).

Cluster I contained early maturing types with a low mean value (83.6) for days to maturity, while cluster II contained early flowering (33.5) genotypes with the least number of primary branches (3.0) and capsules (64.5), dwarf types (112.6) with a low harvest index (22.7) and seed yield per plot (122.1). Cluster III recorded the lowest mean for oil content (42.2) and the highest mean for capsule length (2.8), test weight (3.2), seed weight per capsule (141.5). Cluster IV's monogenotypic nature resulted in higher cluster mean values for days to 50 % flowering (46.0), days to maturity (93.0), number of primary branches per plant (5.7), number of capsules per plant (158.3), plant height (186.4), oil content (46.4), seed yield per plot (508.2) and minimum for capsule length (2.6), seed weight per capsule (132.1) and test weight (3.0) (Table-4).

Thus the cluster IV (SES-R-18-3002) is useful for generating late maturing types with high oil yield and seed yield per plot by increasing the number of primary branches and capsules per plant, plant height and non-shattering, late flowering traits, while cluster III (SES-S-19-3104) is useful for increasing the seed weight per capsule and test weight. Based on cluster means, cluster IV (SES-R-18-3002) was found to be important for number of primary branches per plant, number of capsules per plant, capsule width, plant height and seed yield per plot. There was no single cluster that contained all the desirable traits, ruling out the possibility of direct selection of genotypes for immediate use.

The genotypes SES-K-19-3005, SES-R-18-3002, SES-S-1043, SES-S-20-2003, SES-S-20-1039 and RT-323 were scattered relatively far away from other genotypes in this biplot for yield and its attributes, confirming the Hierarchical clustering in which the six genotypes were in different clusters namely, cluster II (RT-323 and SES-S-1043), III (SES-K-19-3005, SES-S-20-2003 and SES-S-20-1039) and IV (SES-R-18-3002). Hybridization between these diverse genotypes can be suggested. However, selecting for yield and its attributes may not be possible simultaneously. So, balanced selection criteria should be followed depending on the objective.

***Macrophomina* root rot screening :** In current investigation, level of resistance exhibited by test germplasm ranged from 1-9. Based on resistance reaction recorded during screening in pots, resistant response was evident in SES-S-20-2001 (0%), SES-S-20-3003 (2.2%), SES-S-19-2102 (4.5%), CUMS-17 (6.7%) and Swetha til (8.9%) with less than 10% root rot incidence (Table 5). The reaction of three candidate lines (GT-10, SES-S-20-1038 and SES-S-20-1039) was moderately resistant.

Moderately susceptible response (DI% between 21-30%) was seen in genotypes SES-S-20-2005, SES-S-19-3104, SES-K-19-2104, SES-S-20-2007 and SES-S-19-1042. A total of 12 lines SES-S-20-2008, SES-S-1043, RT-311, ISWG-20-05, SES-S-20-1037, SES-R-18-3002, SES-S-20-2003, SES-S-19-2006, SES-S-20-2002, SES-K-19-3005, RT-289 and RT-215 were found to be susceptible with disease incidence (DI) percentage ranging from 31-50%.

Six genotypes *viz.,* SES-S-19-3103, SES-S-19-1036, S-20-2004, RT-340, RT-323 and VRI-1 were found to be highly susceptible. The susceptible check, VRI-1 recorded 64.8% while resistant check GT-10 showed 18.1% root rot incidence (Table-5 & Fig.-4).

The results indicated the presence of sufficient variation among the genotypes studied for *Macrophomina* root rot resistance and were regarded as resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS) genotypes based on disease incidence % (Table 5).

Root rot disease severity ranging between 8.2% (IVT-17-19) to 56.6% (IVT-17-6) with the lowest root rot incidence (12.3%) for the AVT entry AVT-17-11 and 62.4% for the susceptible check VRI-1 has been recorded [21]. Four genotypes JLS 110-12, HT 9913, T 78 and KMR 60 possessing multiple disease resistance with 0-0.8% disease incidence have been identified after screening 24 sesame genotypes against major diseases *viz.* phyllody, charcoal rot and leaf curl [22].

Conclusion

In this study we conclude that geographical isolation is not the only factor causing genetic diversity in sesame rather forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the fixation of diversity among the germplasm lines. Five genotypes namely, SES-S-19-2102, SES-S-20-3003, SES-S-20-2001, CUMS-17, Swetha til were found to possess resistance against charcoal rot with less than 10% incidence. Our study concludes that these resistant genotypes might be useful as donors for resistance and serve as sources for introgression of resistant genes into more desirable genetic background for developing disease resistant high yielding cultivars. However, further evaluation of these resistant genotypes is still needed over different locations and years to validate them as disease resistant sources.

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