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SV Chavan

M.Sc student, Department of Agricultural Botany, Dr. PDKV, Akola, Maharashtra, India

PV Jadhav

Assistant Professor, Department of Agricultural Biotechnology, Dr. PDKV, Akola, Maharashtra, India

SS Mane

Head, Department of Plant Pathology, Dr. PDKV, Akola, Maharashtra, India

SS Nichal

Associate Professor, Regional Research Center on Soybean, Dr. PDKV, Amravati, Maharashtra, India

Correspondence SV Chavan M.Sc student, Department of Agricultural Botany, Dr. PDKV, Akola, India, Maharashtra, India

Morphological characterizations of soybean genotypes in response to charcoal rot disease under sick plot conditions

SV Chavan, PV Jadhav, SS Mane and SS Nichal

Abstract

The present study entitled morphological characterizations of soybean genotypes in response to charcoal rot disease under sick plot conditions was carried out at Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during the year 2018-19 to evaluate various genotypes of soybean for charcoal rot resistance. Charcoal rot disease caused by *Macrophomina phaseolina* is one of the most damaging diseases of soybean resulting to 70 % losses and till date no immune genotype is known for the same. Various limitations inherent in field experiments may have hindered progress toward identifying new source (s) of resistance and breeding resistance in soybean. Field testing under supervised conditions may compliment or help to overcome the losses caused by the disease.

The genotypes were screened under sick-plot during Kh-2018 having virulent colonies of *M. phaseolina*. Disease infection was observed and genotypes were categorized accordingly. Four genotypes including varieties viz., AMS MB 5 -18, AMS MB 5-19, AMS 77 and AMS 1001 were identified as resistant to *M phaseolina* while others ranged from moderately resistant to highly susceptible.

Keywords: Soybean, pulse crop, biotic stress resistance, charcoal rot, resistance breeding

Introduction

Soybean [*Glycine max* (L) Merrill] (2n=40) is the *numero uno* oilseed crop of the world. It contains about 38-44% protein and 18-23% oil on a moisture-free basis. It has innumerable uses as food, feed and fuel (biodiesel) besides limitless industrial and pharmaceutical applications. The soybean meal is used primarily as a protein source for swine, poultry, dairy and fish. It is also used to make protein concentrate, texturized protein and protein-isolates that are used in food products for human consumption. On account of its multifarious uses and limitless benefits, soybean is rightly called as "golden bean", "miracle bean" or "wonder crop" (Orf, 2010)^[5].

In India, soybean was introduced from China in tenth century AD through the Himalayan routes, and also brought in via Burma (now Myanmar) by traders from Indonesia. As a result, soybean has been traditionally grown on a small scale in Himachal Pradesh, the Kumaon hills of Uttar Pradesh (now Uttaranchal), eastern Bengal, the Khasi Hills, Manipur, the Naga Hills, and parts of central India covering Madhya Pradesh. It has also been reported that the Indian continent is the secondary center for domestication of the crop after China (Hymowitz, 1990)^[2] (Khoshoo, 1995)^[3] (Singh and Hymowitz, 1999)^[2]. Soybean plays a very important role in the economy and foreign earnings of our country as it contributes 37% and 25% to the national oilseeds and edible oil production, respectively (Anonymous, 2013)^[1]. Therefore, developing soybean cultivars with higher yield, resistance to major pests and diseases and improved quality has become the major objective of soybean breeding program across the country. Soybean crop can be attacked by more than 100 pathogens (Sinclair and Shurtleff, 1975)^[6].

Among the biotic challenges, charcoal rot disease is the most serious one. It is caused by fungus Macrophomina phaseolina (Tassi) Goid., a soil borne pathogen distributed worldwide with a host range of more than 500 plant species of both monocots and dicots (Mihail and Taylor, 1995)^[4]. It is called as 'charcoal rot' on account of small, black, macroscopically visible sclerotia that forms in shredded, parasitized host tissue and cause an appearance of charcoal (Young, 1949)^[9]. All plant parts of soybean are susceptible to infection. However, primary infection starts in the roots which gradually appear over ground. The yield loss can go up to 80% in severe cases (Yang and Navi, 2005)^[8]. Therefore, development of soybean varieties resistant to charcoal rot disease is an important breeding objective and need of the hour. To facilitate breeding, it is necessary to evaluate the soybean genotypes for levels of resistance.

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The genetic improvement of soybean for charcoal rot resistance has been severely hampered by lack of resistant donors as well as unavailability of effective screening techniques. Therefore, the present study was undertaken with the objective to find out differential response of selected soybean genotypes to the infection with charcoal rot incidence on field conditions.

Material and Methods Plant material

A set of 14 diverse soybean genotypes were used for screening. The collected genotypes included promising varieties, indigenous varieties, mutants, few pre released collections, advanced breeding lines as well as obsolete varieties. It varied in maturity, seed color, flower colour, seed size, and reaction to charcoal rot disease as well as other yield attributing traits. Specific features of the genotypes are presented in (Table 1)

Table 1: Soybean genotypes included in the study

S.N	Genotypes	Parents	Remarks
1	AMS MB 5-19	Mutant of Bragg	Developed by Mutation breeding and characteristically fixed at M8 generation.
2	AMS MB 5-18	Mutant of Bragg	Developed by Mutation breeding and characteristically fixed at M8 generation.
3	AMS – 1001	Mutants	Pre released variety
4	AMS – 77	Mutant of JS 93-05	Developed by Mutation breeding and characteristically fixed at M5 generation.
5	AMS – 353	Mutants	Pre released variety
6	AMS – 358	Mutant of JS 93-05	Developed by Mutation breeding and characteristically fixed at M5 generation.
7	BRAGG	Parental genotype	Parental genotypes
8	AMS – 243	Mutant of Bragg	Developed by Mutation breeding and characteristically fixed at M8 generation.
9	JS - 93-05	Parental genotype	Parental genotypes
10	AMS 99-33	Mutants	Pre released variety
11	AMS 38-24	TAMS 38 x RKS 24	Recombinant breeding, entry fixed at F2 generation.
12	AMS -475	Mutant of JS 93-05	Developed by Mutation breeding and characteristically fixed at M5 generation.
13	JS – 335 (R)	(Check-Resistant)	High yielding variety, most popular
14	TAMS -38 (S)	(Check-Susceptible)	Highly susceptible variety

R=Check Resistant; S=Check Susceptible

On field experimental details and management practices

The field experiment was carried out during kharif - 2018 on the sick plots of RRC Amravati, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experimental details are enlisted in (Table 2). The experimental material consisting of 14 genotypes (9 mutants, 2 parental genotypes, 1 recombinant genotype and 2 checks) were laid out in randomized blocks design (RBD) with three replications. The crop was raised under rainfed condition. The crop stand and the crop growth were satisfactory. All the recommended practices were followed for raising the crop successfully.

Table 2: Experimental details of field (sick plot)

S.N	Component	Result
1.	Crop	Soybean
2.	Genotypes	14
3.	Experimental design	Randomized Block Design (RBD)
4.	Size of Sub plot	3 x1.30m
5.	Total Plot size	3 x 27.25m
6.	Spacing	45 x 5 cm
7.	Replications	Three (3)
8.	Genotypes	14 (9 mutants + 2 parents +1 recombinant + 2 checks) (Check Resistant - JS-335 and Check Susceptible - TAMS-38)
9.	Method of sowing	Dibbling

Results and Discussions

On field (sick plot) screening experiment

A set of 14 genotypes was subjected to field screening for sick plot condition at Regional Research Centre, Amravati, Dr PDKV, Akola during kharif 2018.The data was recorded on five randomly selected plants, from each genotype in each replication for morphological and important quality traits. The characters studied were, days to 50% flowering, plant height (cm), number of pods/ plant, 100 seeds weight (g), grain yield/plant (g). The agro-morphological and quality traits recorded were used to determine the genetic diversity in the experimental material.

The mean performance of all soybean genotypes for different traits is depicted in (Table 3)

a. Days to 50% flowering

The character, days to 50% flowering ranged from 38 to 49 days. Average mean for this character was 46.33 days. The

genotype JS-335 (38 days) was found earliest for days to 50% flowering amongst the selected 14 genotypes under study followed by JS 93-05 (41 days). However, the late genotype for days to 50% flowering was AMS MB 5-18 (49 days) and AMS 243 (49 days) followed by AMS MB 5-19 (48 days), AMS 475(48 days) along with AMS 353(48 days) and AMS 358(48 days). Whereas, two genotypes namely AMS 99-33 and AMS 38-24 both shared same records for flowering (47 days). The genotypes, AMS -1001 and AMS -77 (46 days) followed by BRAGG (45 days) and finally TAMS-38 (44 days)

b. Plant height

The mean values for plant height ranged from 27.42 to 40.64 cm. The minimum plant height was recorded by AMS-243 (27.42 cm) followed by AMS 353 (29.55cm) and maximum plant height was recorded by AMS-77 (40.64 cm) and AMS –

475 (40.64 cm) which was followed by AMS -358 (40.33 cm). The average mean for this character was 34.87 cm.

c. No. of pods per plant

Number of green pods per plant ranged from 32.36 to 52.13. Average mean for the character was 40.42 pods per plant. Minimum numbers of pods were recorded by AMS-358 (32.36) followed by BRAGG (33.68) and TAMS-38 (34.14). Whereas, highest number of green pods per plant were recorded by JS- 335 (52.13) followed by AMS MB 5-19 (49.46).

d. 100 seed weight

100 seeds weight ranged from 9.5 to 16.5 (g) with average

mean 10.42 (g). Minimum 100 seeds weight counted for AMS MB 5-19 (9.5 g) followed by. AMS MB 5-18 (10 g), AMS-1001(10 g), AMS – 243 (10 g) JS-93-05 (10 g) and AMS 99-33 (10 g). Maximum 100 beans weight counted for JS-335 (16.5 g) followed by TAMS-38 (12.5 g).

e. Grain yield per plant

The values for grain yield per plant varied from 40.5 to 72.5 (gm). Average value for this character was 53.9 (g). The minimum value was recorded by AMS-475 (40.5 g) followed by TAMS-38(42.5g) and maximum value was observed for AMS MB 5-19 (72.5 g) followed by AMS MB 5-18 (71.5 g).as well as BRAGG (71.5 g)

Table 3: Mean performance of	genotypes for all	morphological traits
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S.N	Genotype	Days to 50% flowering	Plant height(cm)	No. of pods per plant	100 seed weight (g)	Grain yield per plant (g)
1	AMS MB 5-19	48	33.78	49.46	9.5	72.5
2	AMS MB 5-18	49	30.1	39.85	10	71.5
3	AMS - 1001	46	38.05	40.4	10	58.5
4	AMS - 77	46	40.64	40.95	10.5	57.5
5	AMS - 353	48	29.55	39.3	10	45.5
6	AMS - 358	48	40.33	32.36	10.5	43.5
7	BRAGG	45	31.5	33.68	11	71.5
8	AMS - 243	49	27.42	40.26	10	50.5
9	JS - 93-05	41	32.28	40.69	10	48.5
10	AMS 99-33	47	38.73	42.69	10	48.5
11	AMS 38-24	47	37.9	43.43	12	51.5
12	AMS -475	48	40.64	39.5	10.5	40.5
13	JS – 335 (R)	38	31.42	52.13	16.5	55.5
14	TAMS -38 (S)	44	38.05	34.14	12.5	42.5
٠	Range	38-49	27.42-40.64	32.36-52.13	9.5-16.5	40.5-72.5
•	Mean	46.33	34.87	40.42	10.42	53.9
٠	SE(m)	0.18	0.17	0.08	0.27	0.17
٠	CV	0.69	0.84	0.36	4.6	0.57
٠	CD @5%	0.53	0.51	0.24	0.81	0.71
•	F Test	S	S	S	S	S

R=Check Resistant; S=Check Susceptible

Conclusion

All the genotypes had the disease symptoms varying in degree of intensities. The intensities were much higher in the highly susceptible genotypes like AMS 38-24, TAMS -38 and AMS -475. Based on scoring of the disease infection, 5 genotypes were identified as resistant (Table 4). The resistant genotypes viz., AMS MB 5-19, AMS MB 5-18, AMS – 1001, AMS – 77 and JS – 335 were either high yielding varieties of India, pre released varieties or mutant germplasm collections.

During the trial, 5 genotypes developed disease in lesser intensities than others. Such genotypes were categorized as resistant and moderately resistant. However, no genotypes were found to be immune Three other varieties viz., AMS 38-24, TAMS -38 and AMS -475 were identified as highly susceptible as they showed critical symptoms and eventually died. Two of the remaining genotypes viz., AMS – 353 and AMS - 358 were moderately resistant and rest four genotypes viz. BRAGG, AMS – 243, JS - 93-05 and AMS 99-33 were moderately susceptible.

Table 4: Sick plot field screening disease reactions of the selected soybean genotypes

S.N	Genotype	Parents	Reaction to charcoal rot infection (on field)
1	AMS MB 5-19	Mutant of Bragg	R
2	AMS MB 5-18	Mutant of Bragg	R
3	AMS - 1001	Mutants	R
4	AMS - 77	Mutant of JS 93-05	R
5	AMS - 353	Mutants	MR
6	AMS - 358	Mutant of JS 93-05	MR
7	BRAGG	Parental genotype	MS
8	AMS - 243	Mutant of Bragg	MS
9	JS - 93-05	Parental genotype	MS
10	AMS 99-33	Mutants	MS
11	AMS 38-24	TAMS 38 x RKS 24	HS
12	AMS -475	Mutant of JS 93-05	HS
13	JS - 335 (R)	(check-R)	R
14	TAMS -38 (S)	(check-S)	HS

R=Check Resistant; S=Check Susceptible

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