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Response of different soybean genotypes against soybean tobacco caterpillar, *Spodoptera litura* (Fabricus)

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Abstract

A study was conducted in the experimental farm of BAU, Ranchi during *Kharif* 2021 and 2022 in order to screen soybean genotypes for resistance against tobacco caterpillar using two replications. Thirty-five soybean genotypes along with two check varieties were arranged in RBD. The screening studies carried out with thirty-five genotypes against tobacco caterpillar resulted in the identification of some promising genotypes against pest. Among the genotypes, for the *Kharif* 2021, three genotypes (BAUS-110, BAUS-124, JS 97-52) were found to be resistant and in 2022 eight genotypes (BAUS-110, BAUS-124, BAUS-96, RCS-10-46, BAUS-119, BAUS-118, BAUS-BRNS-20, JS 97-52) were found highly resistant against tobacco caterpillar. On the basis of overall pooled mean of *S. litura* infestation, none of the thirty-five genotypes were free from the larval infestation, which ranged between 1.49 and 2.98 larvae/mrl. The lowest larval population was recorded in genotype BAUS-110 which remained at par with JS 97-52 (1.53 larvae/mrl), BAUS-124 (1.54 larvae/mrl), RCS-10-46 (1.54 larvae/mrl) followed by BAUS-96 (1.64 larvae/mrl).

Keywords: Soybean, genotype, caterpillars, screening

1. Introduction

The largest oil-seed legume crop known as "Golden Bean" is soybean (*Glycine max* (L.) Merrill, Leguminosae). Soybeans have a better potential for productivity than other legumes. It is also the most affordable and abundant source of high-quality protein, making it a useful tool for treating protein-calorie deficiency. Aside from minerals and vitamins, it has about 40% protein having all the essential amino acids and 18-20% oil. Soybean crop world production during 2021-22, 380.57 million ton, it contributes more than 90 percent of the world's acreage. In India during the year 2021-22, soybean cultivation reached to 12.50 million ha with productivity of 1.04 ton/ha (Directorate of Economics and Statistics, Department of Agriculture and Cooperation, Ministry of Agriculture, GOI, 2021).

The rich crop development and soft, succulent leaves entice insects, providing them with lots of food, space, and cover. Soybean crop is infested by more than 275 insect pests throughout its growth stages and about a dozen of them have been reported to be causing serious damage to soybean from sowing to harvesting (Jain *et al.*, 2011) ^[3]. About 15–25% of soybean output is lost due to insect pest fauna (Biswas, 2013) ^[1]. Among them tobacco caterpillar (*Spodoptera litura*), semiloopers (*Gastonia game*, *Achaea janata*, *Chrysodeixis acuta*), leaf miner (*Aproaerema modicella* Decanter), stem fly (*Melanagromyza sojae* Zehnter), girdle beetle (*Obereopsis brevis* Sweden board), and sucking insect pests such as white fly (*Bemisia tabaci*) and leaf hopper (*Amrasca biguttula biguttula*) are important.

In addition to environmental pollution, the careless use of pesticides has resulted in issues such as pest outbreaks, resurgences, and pest resistance to insecticides. It has also eliminated natural adversaries and posed health hazards to humans and animals. (Rao *et al.* 2000) ^[5]. The best line of action is to create resistant varieties, which are also more advantageous for the environment and more economical. Current investigation was undertaken with the aim to screen some of the promising soybean genotypes for their resistance against tobacco caterpillar.

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2. Material and Methods

The experiment was laid out in randomized block design (RBD) by using 35 genotypes including two check varieties as resistant check JS 97-52 and susceptible check JS 335, replicated two times with spacing of 45×10 cm and the plot size was 4 m x 3 m. The suggested techniques were followed when it came to field preparation, weeding, fertilizer application, and other crop management procedures. The larval population of tobacco caterpillar were recorded at 15, 30, 45 and 60 days after germination from three randomly selected spots of one meter row length in each plot leaving border rows and mean was recorded in per meter.

2.1 Categorization of the genotypes

After recording data on insect count the genotypes were categorized by the method given by Sharma, 1996^[4] (AICRP method, 1996).

- **HR:** Value < mean CD at 1%.
- **R:** Value between mean CD at 1% and mean CD at 5%.
- MR: Value between mean CD at 5% and mean.
- **LR:** Value between mean and mean + CD at 5%.
- S: Value between mean + CD at 5% and mean + CD at 1%.
- **HS:** Value > mean + CD at 1%.

3. Results and Discussion

The results on the response of the genotypes in the screening trials are mentioned as below.

The Pooled data of two consecutive years on the incidence of *S. litura* on different soybean genotypes at 15 DAG, 30 DAG, 45 DAG and 60 DAG ranged from 0.58 to 2.49, 1.30 to 2.95, 1.78 to 3.40, 1.60 to 3.13 larvae/mrl respectively (Table 1). At 15 DAG, the lowest population 0.58 larvae/ m row length observed in BAUS-124 which remained at par

with JS-97-52 (0.59 larvae/mrl), RCS-10-46 (0.62 larvae/mrl) and BAUS-110 (0.75 larvae/ mrl) but at 30 DAG, least larval count was found in BAUS-110 which was at par with BAUS-124 (1.32 larvae/ mrl) and JS-97-52 (1.36 larvae/ mrl). At 45 DAG, lowest larval population was recorded in genotype BAUS-96 which is followed by JS 97-52 and BAUS-110 with 1.94 larvae/mrl. While at 60 DAG, minimum larval incidence was recorded in genotype RCS-10-46 which remained at par with BAUS-110 (1.61 larvae/mrl) followed by BAUS-124 (1.69 larvae/mrl). On the basis of overall pooled mean of S. litura infestation, it was observed that none of the thirty-five genotypes were free from the larval infestation, which ranged between 1.49 and 2.98 larvae/mrl. The lowest larval population was recorded in genotype BAUS-110 which remained at par with JS 97-52 (1.53 larvae/mrl), BAUS-124 (1.54 larvae/mrl), RCS-10-46 (1.54 larvae/mrl) followed by BAUS-96 (1.64 larvae/mrl) (Table 1).

Based on the reaction of soybean genotypes against *S. litura* infestation during *Kharif* 2021 and 2022, The result showed that for the *Kharif* 2021, three genotypes (BAUS-110, BAUS-124, JS 97-52) were found to be resistant, eighteen genotypes (BAUS-96, RCS-10-46, BAUS-119, BAUS-118, BAUS-BRNS-20, BAUS-120, BAUS-116, BAUS-112, BAUS-121, BAUS-123, BAUS-125, BAUS-6, BAUS- BRNS-18, BAUS- BRNS-19, BAUS-106, BAUS-104, BAUS-40, BAUS-105) were classified as moderately resistant and three genotypes (BAUS-BRNS-31, BAUS-BRNS-14, JS 335) showed highly susceptible (Table 2). While in 2022, eight genotypes (BAUS-110, BAUS-124, JS 97-52).

BAUS-96, RCS-10-46, BAUS-119, BAUS-118, BAUS-BRNS-20, JS 97-52) were found highly resistant, one genotype (BAUS-120) was found to be resistant and nine genotypes (BAUS-BRNS-14, BAUS-101, BAUS-100, BAUS-107, BAUS-113, BAUS-BRNS-14, BAUS-115, BAUS-31, JS- 335) showed highly susceptible (Table 2).

Table 1: Pooled Larval population of Spodoptera litura on different soybean genotypes during Kharif 2021 and 2022

Sr. No.	Genotype	Mean larval population/plant					
		15 DAG	30 DAG	45 DAG	60 DAG	Overall mean	
1.	BAUS-110	0.58 (0.75) ab	2.05 (1.30) a	3.80 (1.95) ab	2.65 (1.62) a	2.27 (1.49) a	
2.	BAUS-124	0.35 (0.59) a	2.30 (1.33) a	4.23 (2.05) abc	3.35 (1.69) ab	2.56 (1.54) a	
3.	BAUS-96	0.70 (0.84) abc	2.95 (1.68) a-d	3.25 (1.79) a	4.03 (1.97) abc	2.73 (1.65) ab	
4.	RCS-10-46	0.40 (0.63) a	2.45 (1.50) ab	3.93 (1.98) ab	3.10 (1.61) a	2.47 (1.55) a	
5.	BAUS-119	0.85 (0.92) bc	3.33 (1.82) a-f	4.18 (2.04) abc	5.28 (2.26) a-f	3.41 (1.84) bcd	
6.	BAUS-118	1.08 (1.04) c	2.80 (1.57) abc	5.30 (2.27) а-е	4.25 (2.02) abc	3.36 (1.8) bc	
7.	BAUS-BRNS-20	1.83 (1.35) de	2.70 (1.62) a-d	4.85 (2.20) a-e	4.90 (2.03) abc	3.57 (1.87) bcd	
8.	BAUS-120	2.05 (1.43) def	3.15 (1.74) а-е	5.00 (2.22) a-e	4.80 (2.08) a-d	3.75 (1.91) cd	
9.	BAUS-116	1.83 (1.35) de	3.95 (1.91) a-f	4.80 (2.19) a-d	6.33 (2.47) a-f	4.23 (2.04) c-f	
10.	BAUS-112	1.18 (1.08) c	3.70 (1.79) a-f	5.95 (2.43) a-e	5.60 (2.19) a-e	4.11 (1.97) c-f	
11.	BAUS-121	1.75 (1.32) d	3.95 (1.96) a-f	5.00 (2.24) a-e	5.79 (2.37) a-f	4.12 (2.02) c-f	
12.	BAUS-123	1.88 (1.36) de	3.70 (1.85) a-f	4.88 (2.21) a-e	4.60 (2.09) a-d	3.76 (1.92) cde	
13.	BAUS-125	2.35 (1.53) d-h	3.90 (1.93) a-f	4.95 (2.22) a-e	5.15 (2.20) a-e	4.09 (2.00) c-f	
14.	BAUS-6	2.60 (1.60) e-i	4.15 (2.00) a-g	4.95 (2.22) a-e	5.30 (2.24) a-f	4.25 (2.05) c-f	
15.	BAUS-117	2.33 (1.52) d-h	5.10 (2.16) a-g	5.90 (2.43) a-e	6.05 (2.41) a-f	4.84 (2.18) e-h	
16.	BAUS-106	2.10 (1.44) def	4.20 (1.98) a-f	5.35 (2.31) a-e	6.20 (2.44) a-f	4.46 (2.1) d-g	
17.	BAUS-BRNS-3	2.23 (1.49) d-g	4.75 (2.16) a-g	6.63 (2.57) a-g	5.65 (2.33) a-f	4.81 (2.18) e-h	
18.	BAUS-108	2.50 (1.58) d-i	4.80 (2.12) a-g	6.75 (2.59) a-g	6.11 (2.45) a-f	5.04 (2.23) fgh	
19.	BAUS-114	2.85 (1.69) f-i	5.30 (2.27) a-g	7.00 (2.64) b-g	6.95 (2.57) b-f	5.53 (2.33) ghi	
20.	BAUS-109	3.00 (1.73) ghi	3.70 (1.91) a-f	6.25 (2.49) a-f	6.50 (2.45) a-f	4.86 (2.18) e-h	
21.	BAUS- BRNS-18	3.10 (1.76) g-j	3.95 (1.98) a-f	6.30 (2.50) a-f	5.80 (2.37) a-f	4.79 (2.18) e-h	
22.	BAUS-BRNS-19	2.85 (1.69) f-i	4.05 (1.99) a-g	6.35 (2.51) a-f	5.60 (2.33) a-f	4.71 (2.17) e-h	
23.	BAUS-105	3.40 (1.84) ijk	4.55 (2.12) a-g	5.05 (2.25) a-e	6.35 (2.47) a-f	4.84 (2.19) e-h	
24.	BAUS-104	3.20 (1.79) hij	5.05 (2.21) a-g	5.20 (2.28) a-e	5.80 (2.37) a-f	4.81 (2.19) e-h	
25.	BAUS-40	2.93 (1.7) f-i	4.90 (2.18) a-g	5.60 (2.36) a-e	6.60 (2.51) a-f	5.01 (2.22) fgh	

26.	BAUS-113	4.05 (2.01) jkl	4.85 (2.19) a-g	6.75 (2.60) a-g	7.50 (2.70) c-f	5.79 (2.40) hij
27.	BAUS-101	4.30 (2.07) klm	5.95 (2.42) b-g	7.70 (2.74) b-g	9.20 (2.98) def	6.79 (2.58) ijk
28.	BAUS-100	4.78 (2.19) lmn	6.35 (2.5) c-g	5.85 (2.42) a-e	8.35 (2.86) c-f	6.33 (2.51) ij
29.	BAUS-107	5.35 (2.31) mn	6.60 (2.56) d-g	8.13 (2.85) c-g	7.90 (2.77) c-f	6.99 (2.64) jkl
30.	BAUS-122	5.35 (2.31) mn	6.40 (2.52) c-g	6.20 (2.49) a-f	7.70 (2.76) c-f	6.41 (2.53) ij
31.	BAUS-115	6.00 (2.45) n	7.20 (2.67) efg	8.45 (2.90) d-g	10.00 (3.13) f	7.91 (2.81) klm
32.	BAUS-BRNS-14	5.90 (2.43) n	7.40 (2.71) efg	9.35 (3.05) efg	9.60 (3.06) ef	8.06 (2.83) lm
33.	BAUS-31	5.95 (2.44) n	9.00 (2.96) g	11.65 (3.41) g	9.35 (3.03) ef	8.99 (2.98) m
34.	JS-335 (SC)	5.73 (2.39) n	7.75 (2.76) fg	10.95 (3.30) fg	10.05 (3.14) f	8.62 (2.92) m
35.	JS 97-52 (RC)	0.40 (0.60) a	2.40 (1.37) a	3.80 (1.94) ab	3.23 (1.77) ab	2.46 (1.54) a
	SE (m) ±	0.815	0.165	0.144	0.156	0.077
	CD at5%	0.234	0.476	0.416	0.449	0.222
	CV %	7.307	11.428	8.457	9.233	5.069

Figures in parentheses are square root transformed values, grading was done by DMRT (Duncan's Multiple Range Test)

		Mean larval population/mrl					
Sl. No.	Genotype	20	21	2022			
		Mean	Category	Mean	Category		
1.	BAUS-110	3.01 (1.73) a	R	1.53 (1.21) a	HR		
2.	BAUS-124	3.10 (1.70) a	R	2.01 (1.37) abc	HR		
3.	BAUS-96	3.34 (1.82) a	MR	2.13 (1.46) a-d	HR		
4.	RCS-10-46	3.39 (1.80) a	MR	1.55 (1.24) a	HR		
5.	BAUS-119	3.93 (1.98) ab	MR	2.89 (1.66) cde	HR		
6.	BAUS-118	4.06 (1.99) ab	MR	2.65 (1.59) b-e	HR		
7.	BAUS-BRNS-20	4.34 (2.06) ab	MR	2.80 (1.65) cde	HR		
8.	BAUS-120	4.25 (2.04) ab	MR	3.25 (1.77) def	R		
9.	BAUS-116	4.58 (2.13) ab	MR	3.88 (1.94) e-j	MR		
10.	BAUS-112	4.56 (2.09) ab	MR	3.65 (1.84) efg	MR		
11.	BAUS-121	4.74 (2.17) ab	MR	3.50 (1.85) e-h	MR		
12.	BAUS-123	4.18 (2.03) ab	MR	3.35 (1.81) efg	MR		
13.	BAUS-125	4.43 (2.08) ab	MR	3.75 (1.92) e-i	MR		
14.	BAUS-6	4.30 (2.07) ab	MR	4.20 (2.03) f-j	MR		
15.	BAUS-117	4.84 (2.19) abc	LR	4.85 (2.16) g-k	LR		
16.	BAUS-106	4.60 (2.14) ab	MR	4.33 (2.04) f-j	MR		
17.	BAUS-BRNS-3	4.94 (2.21) abc	LR	4.69 (2.15) g-k	LR		
18.	BAUS-108	5.18 (2.27) abc	LR	4.90 (2.18) g-k	LR		
19.	BAUS-114	5.68 (2.37) abc	LR	5.38 (2.29) i-m	LR		
20.	BAUS-109	4.90 (2.19) abc	LR	4.83 (2.17) g-k	LR		
21.	BAUS-BRNS-18	4.41 (2.10) ab	MR	5.16 (2.24) i-l	LR		
22.	BAUS-BRNS-19	4.45 (2.11) ab	MR	4.98 (2.22) i-l	LR		
23.	BAUS-105	4.68 (2.16) ab	MR	5.00 (2.21) h-l	LR		
24.	BAUS-104	4.23 (2.06) ab	MR	5.40 (2.29) j-m	LR		
25.	BAUS-40	3.86 (1.96) ab	MR	6.15 (2.43) k-n	S		
26.	BAUS-113	4.93 (2.22) abc	LR	6.65 (2.55) l-o	HS		
27.	BAUS-101	5.6 (2.36) abc	LR	7.98 (2.76) n-q	HS		
28.	BAUS-100	5.39 (2.32) abc	LR	7.28 (2.66) n-q	HS		
29.	BAUS-107	5.14 (2.26) abc	LR	8.85 (2.94) pq	HS		
30.	BAUS-122	6.00 (2.45) abc	LR	6.83 (2.60) m-p	HS		
31.	BAUS-115	7.38 (2.72) bc	S	8.45 (2.88) opq	HS		
32.	BAUS-BRNS-14	7.78 (2.79) bc	HS	8.35 (2.87) opq	HS		
33.	BAUS-31	9.53 (3.07) c	HS	8.45 (2.90) opq	HS		
34.	JS-335 (SC)	8.14 (2.85) bc	HS	9.10 (2.98) q	HS		
35.	JS 97-52 (RC)	3.14 (1.74) a	R	1.78 (1.29) ab	HR		
	SE $(m) \pm$	0.150		0.108			
	CD at 5%	0.434		0.311			
	CV %	9.797		7.217			
	CD at 1%	0.582		0.417			

Table 2: Categorization of different soybean genotypes during Kharif 2021 and 2022

Figures in parentheses are square root transformed values, grading was done by DMRT (Duncan's Multiple Range Test)

4. Conflict of interests

Authors have declared that no competing interests exist.

5. Conclusion

Some of the genotypes were identified as promising types during both the year. However, on the basis of two-year data it is too early to comment or categorized these genotypes as

6. References

be tested in other stations also.

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resistant, highly resistant etc. Further experiments are to be

conducted for their confirmation and those genotypes are to

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