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Article

Screening of soybean genotypes for the source of soybean mosaic resistance

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Abstract: Soybean mosaic virus (SMV) is the major constraints for soybean cultivation in many parts of the country. Experiments were carried out to study the seed transmission of SMV and to identify the resistant sources through screening of 30 promising soybean genotypes obtained from different sources under natural infections conditions in between 2000 and 2001. Indirect-ELISA was performed against TRSV, TMV, CPMV, CMV, BBSV, BBTMV and SMV in leaf materials, both from healthy and diseased plant materials and the results showed that the seeds and the plants in the field were free from those 6 viruses. The highest seed transmission was found in Gaurab (15.07%) followed by G-2120 and the lowest (1.5%) seed transmission was found in TG-893 followed by BS-32, CM and AGS-129. Seed mottling was found related to seed transmission. No disease incidence was found in AGS-129 but there were seed mottling (1.25%). On the other hand, genotype AGS- 160 was free from mottled seeds but produced infected seedlings. Mosaic symptom became apparent 15 days after sowing (DAS), highest at 60 DAS and disappear after 90 DAS. Seeds from seed lot containing up to 20% mottled symptom could not hamper production. Screening of 30 soybean genotypes based on the natural infections revealed that AGS-129 was identified as resistant and grading 1, 10 were identified as moderately resistant (MR) considered as grading 3 and the remaining genotypes were susceptible (S) and moderately susceptible (MS) considered as grading 7 and 5, respectively. The 10 genotypes *viz*. CM, BS-32, ACAGS-154, G-2261, AGS-129, Durga, Williams, AGS-160, EC-1178 and PR-164 could be used for further study to locate resistant genes against soybean mosaic virus and varietal improvement in breeding purpose.

Keywords: resistant; soybean genotypes; soybean mosaic

1. Introduction

Soybean [*Glycine max* (L.) Merr.] is the leading oilseed crop produced and consumed in the world (Wilcox, 2004). It has exceptional nutritional value, provides the richest source of protein of any crop (similar to levels found in cow's milk and meat, fish or poultry) and is able to serve as the core protein supplement to human diets. Soybean, including processed soybean products like tofu, constitutes good nutritional quality for adult humans, containing a high amount of protein (40%–50%), lipids (20%–30%) and carbohydrates (26%–30%), with more than eighty-five percent of its protein content made up of β-conglycinin and glycinin (Gibbss *et al*., 2004). The USDA reports much lower levels of protein (13%), lipids (6.8%), carbohydrates (11%) and dietary

fiber (4%) in raw green soybeans (USDA, 2018a) but higher levels in mature raw soybean seed (36.5%, 20%, 30% and 9 %, respectively) (USDA, 2018b).

It improves soil fertility because it fixes nitrogen (94 kg of nitrogen per hectare per season) as a legume crop (Satter, 2001). Bangladesh uses soybean primarily as a poultry feed, but it is also used in the preparation of a variety of healthy dishes and confections (Mondal and Wahhab, 2001). As linoleic and linolenic acids, which are found in soybeans, help the body absorb essential nutrients and regulate smooth muscle contraction, blood pressure, and cell growth, soybeans are an excellent source of these two fatty acids. In addition, it contains 3% lesithine, which is beneficial for brain development (Rahman, 1982).

Worldwide, the total annual production of soybean is 365.79 million tons from an area of land totaling 130.90 million hectares (FAOSTAT 2017). In Bangladesh, total annual production is 96,921 tons from a cultivated area of 62,870 hectares – at 1.54 tons/ha, this is much lower than the world average of 2.79 tons/ha . Much neglected until just a couple of years ago, soybean is gradually gaining popularity as a cash crop, especially among farming households in the country's southern belt (Noakhali, Lakshmipur and Bhola districts). The socio-economic condition of these farming communities could be potentially enhanced through the establishment of small soy-based food manufacturing industries, producing milk, curd (yoghurt), flour/breads, meat, halwa, biscuits and assorted snacks, all from soybean. In Bangladesh, there are ample opportunities to increase both the area and productivity of oilseed crops such as soybean because of the availability of short-duration improved varieties and suitable agro-climatic conditions. At the same time, at the production and post-harvest processing levels there is some potential for mechanical interventions. These might enhance current oilseed production and processes and allow farmers to earn more from soybean cultivation (Miah *et al.*, 2017).

Soybean Mosaic Disease (SMD) is one of the most serious, devastating, and widespread diseases of *Glycine max* (L.) Merry. caused by Soybean Mosaic Virus (SMV) belongs to the genus Potyvirus and the family Potyviridae. It reduces soybean yields from 8 to 35% and occurs in virtually all soybean production areas of the world (Hill, 1999).SMV only infects six plant families, including Fabaceae, Amaranthaceae, Chenopodiaceae, Passifloraceae, Schrophulariaceae, and Solanaceae, with its narrow host range. Both *Glycine soja* and *Glycine max* are common hosts for the parasite and with 160 species, the Potyvirus genus is the most diverse in the plant RNA virus world (Hajimorad, 2018). Only the soybean mosaic potyvirus has been found to cause 50% yield loss in experimentally inoculated plants, with yield reductions as high as 93% (Sinclair, 1994). Foliar symptoms range from mild leaf mottling to severe leaf distortion, necrosis, and general stunting, with the infected plants sometimes dying. Most infections occur after flowering and have a negligible effect on seed quality or yield (Bowers and Goodman, 1979; Song *et al.*, 2016). SMV is an aphid-transmitted and seed transmitted virus. Seed transmission rates range from 0% to 64% depending on the virus genotype and soybean variety (Bowers and Goodman, 1991; Domier *et al*., 2007).

Soybean cultivation is relatively insignificant in Bangladesh, with an area (acres) of 154396, and a production of 110785 (M. Ton), despite the widespread use of soybean oil in cooking. However, the yield losses caused by the attack of soybean mosaic viruses are a major obstacle to successful soybean production in this area and Bangladesh must import 1.20 million metric tons of edible oil each year at a cost of nearly Tk 40 billion to meet its rising demand (Miah *et al*., 2017). It has thus taken precedence over everything else in the selection of soybean lines for high yield and viral disease resistance. Agricultural studies in Bangladesh have shown how soybean production systems in the districts of Noakhli and Laxmipur are actually working (Salam and Kamruzzaman, 2015). Till date, no specific study has been conducted on screening soybean for SMV. SMV is controlled primarily by the application of sound agricultural practices and the production of resistant cultivars through breeding and genetic engineering (Galvez *et al*., 2014). Consequently, this paper has utilized soybean to identification the source(s) of SMV resistance in the genotypes that have been chosen and to investigate in vitro the connection between soybean seed mottling and SMV seed transmission while exploring in vivo the relationship between yield and the incidence and severity of soybean mosaic disease.

2. Materials and Methods

Thirty different genotypes of soybean were studied. These were collected from Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. Two genotypes ST-2 and Tampomus were used for check and planted as border crop collected from Pulse Research Centre, Bangladesh Agricultural Research Institute, Gazipur. The name and origin of the genotypes are presented in Table 1.

2.1. Laboratory Experiment

2.1.1. Seed health test

Detection of viruses on leaves and seed samples were performed in the Virology Laboratory, Professor Golam Ali Fakir Seed Pathology Laboratory, Department of Plant Pathology, Bangladesh Agricultural University (BAU) through Indirect-ELISA. Ten samples of symptom bearing seed and ten symptom bearing leaf samples of different genotypes were used to detect viruses. Indirect-ELISA was performed against the following viral antisera: Tobacco ring spot virus (TRSV), Tobacco mosaic virus (TMV), Cowpea mosaic virus (CPMV), Cucumber mosaic virus (CMV), Broad bean strain virus (BBSV), Broad bean true mosaic virus (BBTMV).

2.1.2. Dry inspection of seeds and transmission study of SMV by seedling symptom test

Sorting of mottled seeds were done from 400 randomly taken seeds from the seed lot and counted the symptom bearing seeds and healthy-looking seeds in the laboratory. The percentage of symptom bearing seeds in the seed lot for every genotype under study was calculated. In addition, 100 seed weight of symptom bearing seeds and healthy-looking seeds were taken by an electric balance and calculated out the reduction of seed weight (%) due to SMV infection. The experiment was conducted in the net house and the soil was collected from BAU, Mymensingh. After drying the soil, decomposed cow dung was mixed with collected soil (1:1) and earthen pots of 30 cm dia. were filled two third portions with the mixture. Chemical fertilizers were not used in the pot soil. The pots were arranged in RCBD with 3 replications. The soybean seeds were sown on December 15, 2000. Twenty-five seeds were sown in each pot. As check, five pots were planted with only symptom bearing seeds and three pots with apparently healthy seeds, sowing 10 seeds per pot. Irrigation was done regularly in the pots by supplying water in the trays on which the pots were placed in the net house.

The data recorded for each variable was averaged to obtain mean values and analysis of variance was performed using these mean values. Duncan's Multiple Range Test (DMRT) was performed for all the variables to locate the difference between them following Steel and Torrie (1960). Multiple regression model was also used to estimate the disease incidence, yield per plant, yield of healthy-looking plant, yield of symptom bearing plant and yield per plot.

For the estimation of disease incidence, the multiple regression model was:

$Yi = a + \sum bjXij + ei$

Where, i = 1 ..... 90; j = 1 15

$Yi(k) = a + \sum bjXij + ei$

Where, i = 1 ..... 90; j = 1 ..... 12; k = 1 4

k = 1, 2,3 and 4 represents yield /plant, yield of healthy-looking plant, symptom bearing plant and yield /plot respectively, whereas, X=1,2,3,4,5,6,7,8,9,10,11 and 12 represents Disease incidence, Plant height, No. of effective nodules per plant, Pod/plant, Pod length, Seeds/pod, 100 seed weight, Days to maturity, Germination (%), Seed transmission (%), Seed infection (%), Reduction in seed weight (%) respectively. In addition, a = Constant; b = Regression coefficient; c = Random error distributed as N (0, 2).

2.2. Field Experiment

2.2.1. Experimental site and layout

The field experiment was conducted at the experimental field laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh during the period from November 2000 to April 20. Urea, Triple Super Phosphate (TSP), Muriate of Potash (MoP), Gypsum, Zinc Sulphate were applied to @ 40, 120, 60, 25 and 5 kg/ha respectively. All fertilizers except half portion of urea were applied at the time of final land preparation. The remaining half of urea was applied as top dressing at vegetative stage. Rhizobial inoculum was mixed with the seeds @ 25g/Kg seeds just before sowing. The entire field was divided into 90-unit plots for this study. The plots were arranged following Randomized Complete Block Design (RCBD) with 3 replications. The plot size was 3m × 2m with 10 rows of 3 m long each. For each material there were ten rows of plants having 30 cm distance between the rows and aprox. 5 cm distance between the plants. The distance between the blocks were 50 cm. The genotypes were designated as treatment.

2.2.2. Intercultural Operations and Harvesting

Thinning out of seedlings was done 15 days after sowing (DAS) after taking account of the symptom bearing seedlings. Two times weeding was done in the crop field, one at 30 DAS and another at 50 DAS. No irrigation

was done in the field. The plants were harvested at the physiological maturity stage. Such maturity came with yellowing of leaves with completion of leaf shedding and the pod color mostly became dark brown. The varieties were harvested at different dates as they reached maturity. Plants were harvested leaving the root part in the field.

2.3. Data collection

2.3.1. Disease incidence and Disease severity

To record the incidence of mosaic diseases in the experimental plots 6 times regular inspection of the plots was made at 15 days interval starting from 15 DAS. Three lines from each unit plot were selected randomly and number of symptoms bearing plants from the total plants were recorded each time. The data were averaged for each plot and finally the result was expressed as % plant infection indicating the incidence of disease. Soybean mosaic virus disease severity was recorded at 60 DAS (flowering stage) following a 1-9 disease rating scale used for scoring MYMV (Mughbean Yellow Mosaic Virus) by Singh *et al*. (1988). Ten affected plants of each unit plot were randomly selected for collecting the data on diseases severity. Mottling of leaves on 0.1-5% and 5.1-10% of the plants were found resistant and moderately resistant respectively. Meanwhile, mottling and yellow discoloration of leaves on 10.1-25% and 25.1-50% of the plants were moderately susceptible and susceptible respectively. Severe yellow mottling on more than 50% and up to 100% of the plants were found to be stunted of plants as well as failure of flowering and fruit set occurred in highly susceptible plants. To investigate the mosaic disease progress in the field average of date wise disease incidence was made. From this data a disease progress curve was prepared.

2.3.2. Yield and yield contributing characters

Ten plants were randomly selected from each unit plot except the border lines for collection of data and the plants were tag-marked. Data for the designated yield and yield contributing characters were taken on plot and individual plant basis. The plant heights were measured from ground level to the tip of the main stem after harvest. It was expressed in cm. Number of effected nodules were counted from ten randomly selected plants of each plot and were averaged over per plant. Both fertile and empty pods from each of the sample plant per plot were counted and averaged. Average pod length was collected from the harvested pods of ten randomly selected plants. The pod length was expressed in cm. The average number of seed per pod was determined by counting seeds derived from randomly taken fifty pods per sample handled above. One hundred seeds were taken randomly from the seed lot of each plot and weighted in gram using an electric balance. Recorded from date of sowing to date when most of the plants of a plot were ready to harvest. Weight of the total grains of the sample plants in a plot were taken and averaged to determine the yield per plant data. Five healthy looking and five symptom bearing plants were randomly selected from each of the unit plot. The yield of each of the plant was recorded and finally the yields per healthy looking and symptom bearing plant were calculated. Weight of the total harvested grains per plot was calculated in grams.

3. Results and Discussion

3.1. Laboratory experiment

3.1.1. Seed health test

Indirect-ELISA confirmed that all genotypes were from TRSV, TMV, CPMV, CMV, BBSV and BBTMV (Table 2). Unfortunately, antiserum for SMV was not available in the Plant Virology Laboratory, Professor Golam Ali Fakir Seed Pathology Centre, Bangladesh Agricultural University, Mymensingh during the study (2000-2001). Thus, SMV was confirmed by ELISA at DGISP at Copenhagen, Denmark. The results of ELISA carried out with dried leaf materials; both from healthy and diseased plant confirmed the presence of SMV in different genotypes.

3.1.2. Percentage of SMV symptoms bearing seeds in different genotypes

Among 30 genotypes highest (64%) symptoms bearing seed was found in BS-14 followed by THINUNG-154 (28.25%), G-2261 (26.75%), GAURAB (24.25%) while AGS-160 showed no symptoms bearing seed followed by AGS129 (1.25%), PR-164 (1.25%), DURGA (1.75%), BS-16 (2%) and remaining others genotype revealed lower moderate level of symptoms bearing seeds. Above mentioned results were calculated based on the data obtained from number of symptom bearing seed and number of healthy looking seed (Table 2). In this

experiment, results of ELISA tests showed that the seeds and the plants in the field were free from TRSV, TMV, CPMV, CMV, BBSV and BBTMV. However, visual symptoms were confirmed by indirect ELISA and results from Andayani *et al*. (2011) indicated that soybean plants infected with SMV produced mosaic symptom as shown by positive reaction in indirect ELISA with SMV antiserum (Table 2).

3.1.3. Performance of soybean genotypes depending on seed germination, transmission, infection and reduction in seed weight

Considering germination percentage, BS-14 was recorded highest (98.33%) germination followed by Acadian (97.66%), Williams (97.66%), Sau-Luis (96.67%), G-2261 (96.67%), G-2120 (96.67%), ACAGS-154 (96.67%), EC-1178 (95%) and Gaurab (95%) exhibiting statistically similar. BS-29 showed lowest (36.67%) germination while others were in moderate amount of germination (Table 3). With a view to percent seed transmission, highest (15.07%) seed transmission was found in Gaurab which was statistically similar to G-2120 and the lowest was found in TG-893 (1.5%) which was statistically similar to AGS-129, BS-32, and CM (Table 3). According to Balgude *et al*. (2012), SMV was accounted for 6-8% seed transmission in soybean, whereas in our case seed transmission was found 1.3 to 16%. Despite the presence of mottled or symptom bearing seeds (1.25%) in the working sample of AGS-129 (Table 6) there was no disease incidence in the field. The reason is that when the seed coat is only infected (producing typical mottling symptom) the seed transmission to seedling does not take place as Khetarpal *et al*. (1992) showed, to transmit from seed to seedling, an embryo must be infected. On the other hand, AGS-129 may be a very good tolerant genotype, not really resistant. That's why it did not produce any symptom. A positive correlation was found between the percentage of symptom bearing seed and seed transmission indicating one percent increase in symptoms bearing seed leads to 0.075 percent seed transmission, when symptoms bearing seed was more than 60% then seed transmission was 19.314 (Figure 2E). Moreover, a negative correlation was found between the percentage of symptom bearing seed and seed germination revealing one percent increase in symptoms bearing seed accounted for 0.160% reduction of germination (Figure 1A). In terms of percent seed infection, BS-29 was responsible for highest (64%) infection while minimum seed infection was found in AGS-160 followed by AGS-129 (1.25%), PR-164 (1.25%). The highest reduction in seed weight was recorded in Gaurab (56.65%) and the lowest seed weight reduction was found in AGS-160 followed by PB-1 (0.36%), others genotypes were recorded moderate to lower reduction in seed weight. Negative correlation was observed between the percentage of reduction in seed weight and yield (g/plant) showing one percent decrease of reduction in seed weight resulted in 0.0089% decrease of yield (Figure 2D). Earlier research revealed that identifying sources of YMV resistance is a viable strategy for addressing this viral disease. Numerous researchers have previously identified similar types of genotype analyses (Kumar *et al*., 2008; Talukdar *et al*., 2013; Baruah *et al*., 2014).

3.2. Field experiment

3.2.1. Disease incidence and disease severity

The highest (15.3%) disease incidence was calculated in G-2120 followed by Bs-29 (9%) and BS-23 (8.3%) which were statistically similar. No disease incidence was recorded in AGS-129 and rest of the genotypes showed lower to moderate level of incidence (Table 6). Disease incidence differences among the genotypes were found highly significant which is in an agreement with the findings of Bachkar *et al*. (2019) as well. On the other hand, AGS-129 may be a very good tolerant genotype, not really resistant. That's why it did not produce any symptom. It was also interesting to note that genotype AGS-160 did not have mottled seeds in the working sample but disease incidence (1.5%) due to seed transmission was observed (Table 6).This reveals the fact that, unmottled seeds of seeds producing without seed coat symptom are not necessarily healthy. Similar findings were obtained by Parakh *et al*. (1994). Leaves showing different levels of severity as compared with the healthy leave [Figure 1 (A-E)]. Disease severity was recorded according to Singh *et al*. (1988) which conceded that out of 30 genotypes only one genotype (AGS-129) showed resistance with a grading scale one while ten genotypes (PR-164, AGS-160, G-2261, Williams, Durga, Ec-1178, ACAGS-154, BS-32, BS-10 and CM) were under the group of grading three exhibiting moderately resistance (MR). Ten genotypes (Colombus, BS-11, THINUNG-154, G-2120, BS-23, BS-15, BS-16, BS-60, Sau-Luis and TG-893) were recorded as moderately susceptible having grading scale five while nine (Gaurab, Acadian, PB-1, BS-13, BS-14, Cobb, BS-29, CH-1 and BS-17) genotypes were recorded as susceptible having grading scale seven (Table 5). Bachkar *et al*. (2019) screened 36 varieties against the disease, among them two were resistant, seven moderately resistant;

twenty moderately susceptible, five susceptible while two varieties recorded highly susceptible reaction to SMV. Akhtar *et al*. (1992) conducted an SMV resistance screening on twelve cultivars. Four cultivars (Crow ford, Cico, Zane, and 80-B4007) were shown to be viral resistant. Zheng *et al*. (2000) evaluated 348 soybean accessions for resistance to soybean mosaic virus (SMV) using SMV3, a highly pathogenic strain from north east China. 113 accessions were found to be very resistant, 113 to be moderately resistant, and 122 to be vulnerable. Shrirao *et al*. (2009) tested 16 genotypes and discovered that 14 were completely resistant to soybean mosaic virus (SMV) and two were extremely resistant. Positive correlation was observed between the percentage of disease incidence and seed transmission which showed one percent increase of seed transmission resulted in 0.547 percent increases of disease incidence (Figure 2B). SMV strain, soybean cultivar, soybean development stage, and the incidence of infection all play a role in the magnitude of yield loss caused by SMV (Ross, 1983).

3.2.2. Yield of healthy-looking plant and symptom bearing plant

Highest yield of healthy-looking plant was found in CM (9.977%) followed by TG-893 (9.943%), ACAGS-154 (9.897%), BS-10 (9.723%), BS-32 (9.573) and G-2261 (9.387%) exhibiting statistically identical while the lowest was found in BS-29 (3.330%). Highest yield of symptom bearing plant was found in BS-10 (8.74%) and lowest yield was found in BS-29 (0.903%) followed by BS-16 (1.720%) (Table 6). A negative correlation was observed between seed transmission and yield conceded that one percent increase in seed transmission reduces 0.245 g yield/ plant (Figure 2B). Understanding the relationship between grain yield and other characteristics aids in selecting the most suitable plant type (Adiya *et al*., 2011). There is considerable genetic variation across soybean genotypes in terms of leaf area (cm), days to flowering initiation, days to blooming, and days to maturity, Plant height (cm) Pods/plant, Branches/plant, 100-seed weight (g), Seed yield/ plant (g) Oil content (%) were observed by various researchers in different countries (Sihag *et al*., 2004, Chettri *et al*., 2005, Muhammad *et al*., 2003, Malik *et al*., 2006).

3.2.3. Plant height and Number of effective nodules per plant, Pod/plant, Pod length and Seeds per pod

Considering plant height, the top most height (69.60 cm) was recorded in Gaurab followed by THINUNG-154 (64.13cm), BS-11 (59.32%), EC-1178 (56.82%) and ACAGS-154 (56.82%) representing statistically identical data while the minimal plant height (12.63 cm) was found in PB-1 which were statistically similar to BS-60, BS-23, BS-16, BS-29, Acadian, BS-10 and BS-13. Moreover, others genotype exhibited moderate plant height (Table 7). PR-164 showed best (32.23) number of effective nodules per plant while the lowest was found in AGS-129 (3.95), remaining genotypes showed lower to moderate number of effective nodules per plant. Highest number of pods per plant was found in ACAGS-154 which was statistically similar to EC-1178, Williams, Acadian, G-2261, Gaurab, Thinung-154, Sau-Luis, G-2120 and CM. The lowest number of pods per plant was found in PB-1 which was statistically similar to BS-16 and BS-29 (Table 7). The highest (4.747) pod length was found in BS-32 followed by BS-15 (4.653), BS-11 (4.643), AGS-160 (4.593), Durga (4.520), AGS-129 (4.467), BS-29 (4.373), Cobb (4.330), PR-164 (4.300), BS-60 (4.277) and TG-893 (4.23) while the lowest was found in PB-1 (2.897), rest of the genotypes resulted moderate pod length(Table 7). The highest number of seeds per pod was found in Williams (3.023) which was statistically similar to G-2120, G-2261, Acadian, ACAGS-154, Thinung-154, Gaurab and CM whereas the lowest was found in BS-17 (1.167). Genotypes were accounted for insignificant results considering plant height and number of effective nodules per plant, pod/plant, pod length and seeds per pod, as these genotypes showed moderate susceptible (MS) to susceptible (S) reaction which is in accordance with the results of Naveesh *et al.* (2020), they also observed susceptible genotypes showing pronounced yellow mottling discolouration of leaves, reduction in leaf size and stunting of plants and reduction in pod size. According to Baruah *et al*. (2014), found Pod weight was substantially and positively linked with the number of seeds and pods/plant. Malik *et al*. (2011) found a similar result in terms of days to maturity and days to flowering. Baruah *et al*. (2014) also revealed that increased seed yield/plant was associated with increase in 100-seed weight which in turn showed negative correlation with number of pods/plant and seeds/plant.

Table 1. List of soybean genotypes with their country of origin.

Serial No.	Genotypes	Country of Origin	Indirect ELISA	ELISA for SMV
1	COLOMBUS	USA	+	+
2	BS-11	Bangladesh (BCSRP)	+	+
3	PR-164	USA	+	+
4	GAURAB	India	+	+
5	THINUNG-154	AVRDC	+	+
6	G-2120	AVRDC	+	+
7	AGS-160	AVRDC	+	+
8	BS-23	Bangladesh (BCSRP)	+	+
9	BS-15	Bangladesh (BCSRP)	+	+
10	ACADIAN	USA	+	+
11	G-2261	AVRDC	+	+
12	WILLIAMS	USA	+	+
13	BS-16	Bangladesh (BCSRP)	+	+
14	BS-60	Bangladesh (BCSRP)	+	+
15	PB-1	India	+	+
16	BS-13	Bangladesh (BCSRP)	+	+
17	DURGA	India	+	+
18	EC-1178	USA	+	+
19	SAU-LUIS	Philippines	+	+
20	ACAGS-154	AVRDC	+	+
21	BS-32	Bangladesh (BCSRP)	+	+
22	BS-14	Bangladesh (BCSRP)	+	+
23	COBB	USA	+	+
24	BS-29	Bangladesh (BCSRP)	+	+
25	BS-10	Bangladesh (BCSRP)	+	+
26	CH-1	USA	+	+
27	TG-893	Thailand	+	+
28	CM	AVRDC	+	+
29	BS-17	Bangladesh (BCSRP)	+	+
30	AGS-129	AVRDC	+	+

Table 2. Percentage of symptom bearing seeds in different genotypes of soybean.

Sl. No.	Name of genotypes	No. of symptom bearing seed	No. of healthy-looking seed	% Symptoms bearing seed
1	COLOMBUS	24	376	6
2	BS-11	15	385	3.75
3	PR-164	5	395	1.25
4	GAURAB	97	303	24.25
5	THINUNG-154	113	287	28.25
6	G-2120	104	296	26
7	AGS-160	0	400	0.000
8	BS-23	7	393	1.75
9	BS-15	20	380	5
10	ACADIAN	45	355	11.25
11	G-2261	107	293	26.75
12	WILLIAMS	37	263	9.25
13	BS-16	8	392	2
14	BS-60	18	382	4.5
15	PB-1	15	385	3.75
16	BS-13	14	386	3.5
17	DURGA	7	393	1.75
18	EC-1178	88	312	22
19	SAU-LUIS	35	365	8.75
20	ACAGS-154	60	340	15
21	BS-32	80	320	20
22	BS-14	38	362	9.5
23	COBB	30	370	7.5
24	BS-29	256	144	64
25	BS-10	50	350	12.5
26	CH-1	24	376	6
27	TG-893	16	384	4
28	CM	7	393	1.75
29	BS-17	15	385	3.75
30	AGS-129	5	395	1.25

Each sample contain 400 seeds

Table 3. Performance of 30 selected soybean genotypes: percentage of seed germination, transmission, infection and reduction in seed weight.

Sl. No.	Name of genotypes	% of germination	% of seed transmission	% Seed infection	% Reduction in seed weight
1	COLOMBUS	65.00 gh	5.000 k	6.000 jkl	11.67 hijk
2	BS-11	76.67 def	6.000 j	3.750 lmno	43.47 c
3	PR-164	56.67 h	3.033 mn	1.250 op	50.16 b
4	GAURAB	95.00 a	15.07 a	24.25 cd	56.65 a
5	THINUNG-154	91.67 ab	7.000 i	28.25 b	7.770 klm
6	G-2120	96.67 a	14.97 a	25.67 bc	2.243 mn
7	AGS-160	81.67 cde	2.333 no	0.000 p	0.000 n
8	BS-23	80.00 def	12.57 b	1.750 nop	32.90 ef
9	BS-15	78.33 def	13.00 b	5.000 klm	31.03 efg
10	ACADIAN	97.66 a	11.00 c	11.25 gh	11.19 hijk
11	G-2261	96.67 a	3.500 lm	26.75 bc	8.903 kl
12	WILLIAMS	97.66 a	4.067 l	9.250 hi	5.533 klmn
13	BS-16	58.33 h	7.000 i	2.000 mnop	9.930 ijkl
14	BS-60	73.33 efg	11.00 e	4.500 lmn	4.503 lmn
15	PB-1	75.00 ef	8.967 fg	3.750 lmno	0.360 n
16	BS-13	92.00 ab	8.033 h	3.500 lmno	27.27 fg
17	DURGA	85.00 bcd	3.767 lm	1.750 nop	16.42 h
18	EC-1178	95.00 a	3.067 mn	22.00 de	7.070 klm
19	SAU-LUIS	96.67 a	7.167 i	8.750 hij	38.58 cd
20	ACAGS-154	96.67 a	3.100 mn	15.00 f	9.340 jkl
21	BS-32	90.00 abc	1.733 o	20.00 e	15.50 hi
22	BS-14	98.33 a	12.97 b	9.500 hi	15.18 hij
23	COBB	85.00 bcd	8.633 gh	7.600 ijk	16.55 a
24	BS-29	36.67 i	11.13 c	64.00 a	28.56 efg
25	BS-10	60.00 h	9.567 ef	12.50 fg	4.483 lmn
26	CH-1	78.33 def	10.53 cd	5.980 jkl	33.94 de
27	TG-893	80.00 def	1.500 o	4.000 lmno	26.73 g
28	CM	93.33 ab	1.900 o	1.750 nop	25.17 g
29	BS-17	71.67 fg	9.867 de	3.750 lmno	29.52 efg
30	AGS-129	80.00 def	1.600 o	1.250 op	43.29 c
CV		173.46	173.17	173.52	173.44
LSD		3.0212	0.5814	1.072	1.275

Table 4. Performance of 30 selected Soybean genotypes: yield and yield contributing characters.

Sl. No.	Name of genotypes	100 seed weight (g)	Days to maturity	Yield/plant (g)	Yield/plot (g)
1	COLOMBUS	12.33 klm	140.0 e	5.200 defghij	783.3 ghijk
2	BS-11	16.67 defg	140.0 e	6.500 bcdefgh	791.7 ghij
3	PR-164	17.00 def	160.0 e	6.667 abcdefgh	858.3 fgh
4	GAURAB	6.667 o	121.0 j	6.900 abcdefgh	865.0 fgh
5	THINUNG-154	7.000 o	121.0 j	6.750 abcdefgh	870.0 fgh
6	G-2120	6.333 o	121.0 j	6.317 cdefgh	693.3 ijkl
7	AGS-160	21.00 a	149.3 a	7.033 abcdefg	1083.0 cd
8	BS-23	13.00 jklm	117.0 k	3.823 hij	820.0 ghi
9	BS-15	16.33 efjh	140.0 k	6.633 abcdefgh	790.0 ghij
10	ACADIAN	5.333 o	135.0 g	7.483 abcde	980.0 def
11	G-2261	5.667 o	132.0 h	8.300 abcd	115.0 bc
12	WILLIAMS	6.667 o	124.3 i	8.217 abcde	1083.0 cd
13	BS-16	14.33 hijk	122.0 j	2.753 ij	795.0 ghij
14	BS-60	13.67 ijkl	121.0 j	4.017 ghij	753.3 hijkl
15	PB-1	11.00 mn	145.3 c	5.660 defghi	646.7 kl
16	BS-13	17.00 def	138.7 ef	4.200 fghij	613.3 l
17	DURGA	21.00 a	146.0 bc	7.167 abcdefg	1103.0 bcd
18	EC-1178	6.000 o	122.0 j	7.367 abcdef	1017.0 cde
19	SAU-LUIS	9.667 n	121.0 j	7.733 abcde	906.7 efg
20	ACAGS-154	6.667 o	121.0 j	9.050 abc	1155.0 bc
21	BS-32	20.67 ab	138.7 ef	9.250 abc	1233.0 ab
22	BS-14	14.67ghij	120.0 j	5.317 defghij	710.0 ijkl
23	COBB	18.33 cde	140.0 e	6.937 abcdefgh	916.7 efg
24	BS-29	14.67 ghij	117.0 k	2.333 j	450.0 m
25	BS-10	18.67 bcd	146.0 e	9.533 ab	1313.0 a
26	CH-1	13.00 jklm	118.0 k	5.120 defghij	738.0 hijkl
27	TG-893	20.33 abc	148.0 ab	9.167 abc	993.3 def
28	CM	12.00 lm	147.0 bc	9.833 a	1327.0 a
29	BS-17	15.33 fghi	137.3 f	5.017 efghij	670.0 jkl
30	AGS-129	20.33 abc	143.3 d	8.033 abcde	1143.0 bc
CV		173.59	173.36	169.46	173.09
LSD		1.154	2.634	0.8	1.549

Table 5. Disease severity of different genotypes of soybean.

SL No.	Name of genotypes	Grading	Disease incidence (%)	Reaction
1	COLOMBUS	5	1.8 gh	MS
2	BS-11	5	1.9 gfh	MS
3	PR-164	3	2.3 fgh	MR
4	GAURAB	7	7.9 bc	S
5	THINUNG-154	5	3.0 fg	MS
6	G-2120	5	15.3 a	MS
7	AGS-160	3	1.5 gh	MR
8	BS-23	5	8.3 b	MS
9	BS-15	5	5.9 cde	MS
10	ACADIAN	7	3.6 efg	S
11	G-2261	3	2.3 fgh	MR
12	WILLIAMS	3	2.6 fg	MR
13	BS-16	5	4.1 efg	MS
14	BS-60	5	4.5 def	MS
15	PB-1	7	3.1 fg	S
16	BS-13	7	3.6 efg	S
17	DURGA	3	2.1 fgh	MR
18	EC-1178	3	2.2 fgh	MR
19	SAU-LUIS	5	3.5 efg	MS
20	ACAGS-154	3	2.6 fg	MR
21	BS-32	3	2.2 fgh	MR
22	BS-14	7	6.7 bcd	S
23	COBB	7	2.8 fg	S
24	BS-29	7	9.0 b	S
25	BS-10	3	6.8 bcd	MR
26	CH-1	7	3.7 efg	S
27	TG-893	5	3.2 fg	MS
28	CM	3	2.4 fgh	MR
29	BS-17	7	3.1 fg	S
30	AGS-129	1	0.0 h	R
CV			173.34	
LSD			0.9462	

Table 6. Performance of 30 selected Soybean genotypes: percentage of disease incidence, Yield of healthy-looking and symptom bearing plant and plant height.

Sl. No.	Name of genotype	Disease incidence (%)	Yield of healthy-looking plant (g)	Yield of symptom bearing plant (g)
1	COLOMBUS	1.8 gh	5.837 g	4.253 mm
2	BS-11	1.9 gfh	7.600 def	4.860 kl
3	PR-164	2.3 fgh	7.423 ef	5.693 i
4	GAURAB	7.9 bc	8.397 bc	4.570 lm
5	THINUNG-154	3.0 fg	7.320 f	5.560 ij
6	G-2120	15.3 a	7.197 f	4.313 mm
7	AGS-160	1.5 gh	7.257 f	6.497 h
8	BS-23	8.3 b	8.623 b	5.680 i
9	BS-15	5.9 cde	7.200 f	5.140 jk
10	ACADIAN	3.6 efg	7.657 cdef	5.290 ijk
11	G-2261	2.3 fgh	9.387 a	7.587 de
12	WILLIAMS	2.6 fg	8.357 bcd	7.327 ef
13	BS-16	4.1 efg	3.377 j	1.720 s
14	BS-60	4.5 def	4.330 i	3.127 q
15	PB-1	3.1 fg	5.830 g	4.103 n
16	BS-13	3.6 efg	4.593 hi	2.433 r
17	DURGA	2.1 fgh	7.637 cdef	6.657 gh
18	EC-1178	2.2 fgh	7.797cdef	6.967 fg
19	SAU-LUIS	3.5 efg	8.327 bcd	6.607 gh
20	ACAGS-154	2.6 fg	9.897 a	8.453 ab
21	BS-32	2.2 fgh	9.573 a	8.087 bc
22	BS-14	6.7 bcd	5.913 g	3.617 o
23	COBB	2.8 fg	7.870bcdef	5.353 ij
24	BS-29	9.0 b	3.330 j	0.903 t
25	BS-10	6.8 bcd	9.723 a	8.740 a
26	CH-1	3.7 efg	6.137 g	3.583 op
27	TG-893	3.2 fg	9.943 a	7.740 cde
28	CM	2.4 fgh	9.977 a	7.943 cd
29	BS-17	3.1 fg	5.120 h	3.173 pq
30	AGS-129	0.0 h	8.107 bcde	7.677 cde
CV		173.41	173.34	173.57
LSD		0.9256	0.9462	0.9345

Table 7. Performance of 30 selected Soybean genotypes: plant height, no. of effective nodules per plant, pods per plant, pod length and seeds per pod.

Sl. No.	Name of genotypes	Plant height (cm)	No. of effective nodules/plant	Pod/plant	Pods length (cm)	Seeds/pod
1	COLOMBUS	49.66 bcdefg	25.37 cde	29.87 bcd	3.710 hijk	2.233 fghijk
2	BS-11	59.32 abc	17.90 hij	28.59 cde	4.643 ab	2.000 ijkl
3	PR-164	50.30 bcdef	32.23 b	20.73 def	4.300 abcdef	2.367 defghijk
4	GAURAB	69.60 a	12.63 efgh	44.00 ab	3.647 ijk	2.667 abcdefg
5	THINUNG-154	64.13 ab	18.40 hij	43.17 ab	3.707 hijk	2.700 abcdef
6	G-2120	51.01 bcdef	16.67 ij	40.88 abc	3.743 ghijk	2.990 ab
7	AGS-160	44.40 cdefg	28.73 e	22.73 def	4.593ab	2.440 cdefghijk
8	BS-23	25.88 hi	21.43 fgh	18.33 def	4.020 cdefghij	2.067 hijk
9	BS-15	42.92 cdefg	17.03 ij	22.65 def	4.653 ab	2.233 fghijk
10	ACADIAN	34.80 fghi	14.84 jk	46.44 a	3.633 ijk	2.833 abcd
11	G-2261	47.57 cdefg	18.30 hij	44.93 a	3.630 ijk	2.933 abc
12	WILLIAMS	44.24 cdefg	17.87 ghi	47.13 a	3.693 hijk	3.023 a
13	BS-16	32.87 ghi	26.50 cd	12.30 fg	3.377 k	1.923 kl
14	BS-60	25.13 hi	24.93 def	19.40 def	4.277 abcdefg	2.287 efghijk
15	PB-1	12.63 i	8.90 l	3.50 g	2.897 l	1.567 l
16	BS-13	35.98 fghi	18.87 ghi	19.78 def	3.883 efghijk	1.933 kl
17	DURGA	47.35 cdefg	19.00 ghi	20.43 def	4.520 abc	2.233 fghijk
18	EC-1178	56.82 abcd	19.50 ghi	47.44 a	3.497 jk	2.500 bcdefghi
19	SAU-LUIS	46.93 cdefg	22.73 efg	43.00 ab	3.800 fghijk	2.167 ghijk
20	ACAGS-154	55.83 abcde	18.27 hij	52.93 a	3.803 fghijk	2.767 abcde
21	BS-32	45.70 cdefg	24.90 def	30.13 bcd	4.747 a	1.9667 jkl
22	BS-14	44.97 cdefg	18.60 hij	26.40 def	3.940 defghij	2.267 efghijk
23	COBB	39.91 defgh	14.63 ji	28.43 cde	4.330 abcdef	2.100 hijk
24	BS-29	34.68 fghi	17.80 hij	14.63 efg	4.373 abcde	2.100 hijk
25	BS-10	35.92 fghi	20.53 ghi	23.80 def	4.183 bcdefghi	2.233 fghijk
26	CH-1	41.532 defgh	20.53 ghi	24.77 def	4.110 bcdefghi	2.000ijkl
27	TG-893	44.07 cdefg	27.67 cd	30.47 bcd	4.233 abcdefgh	2.433 cdefghijk
28	CM	48.08 bcdefg	12.33 kl	40.78 abc	3.997 cdefghij	2.550 abcdefgh
29	BS-17	39.23 efgh	9.28 l	20.12 def	4.030 cdefghij	1.167 ghijk
30	AGS-129	40.90 defgh	3.950 a	25.47 def	4.467 abcd	2.483 cdefghij
CV		173.31	171.64	173.76	173.48	173.30
LSD		1.1662	1.037	0.9188	0.6324	0.4744

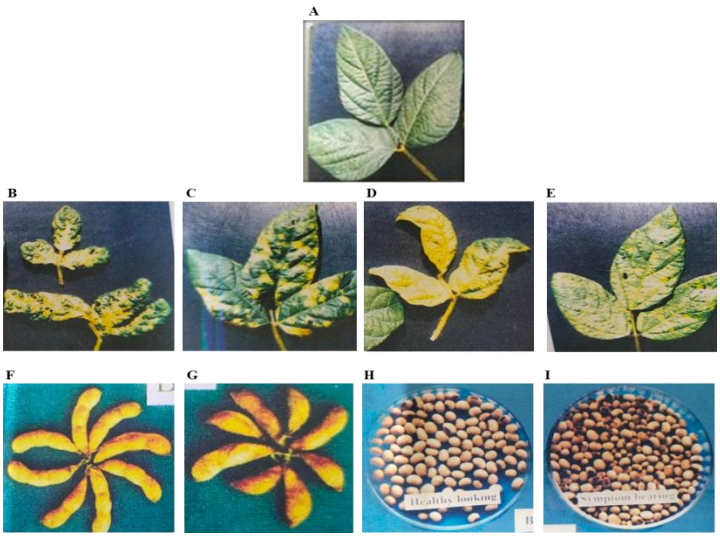

Figure 1. Soybean leaves showing mosaic symptoms of different levels of severity (B-E) compared to healthy looking leaves (A), healthy looking (F) and symptoms bearing pods (G) that are smaller, discolored, mottled and having less number of seeds, healthy looking (H) and symptoms bearing mottled seeds (I) of BS-29 genotype.

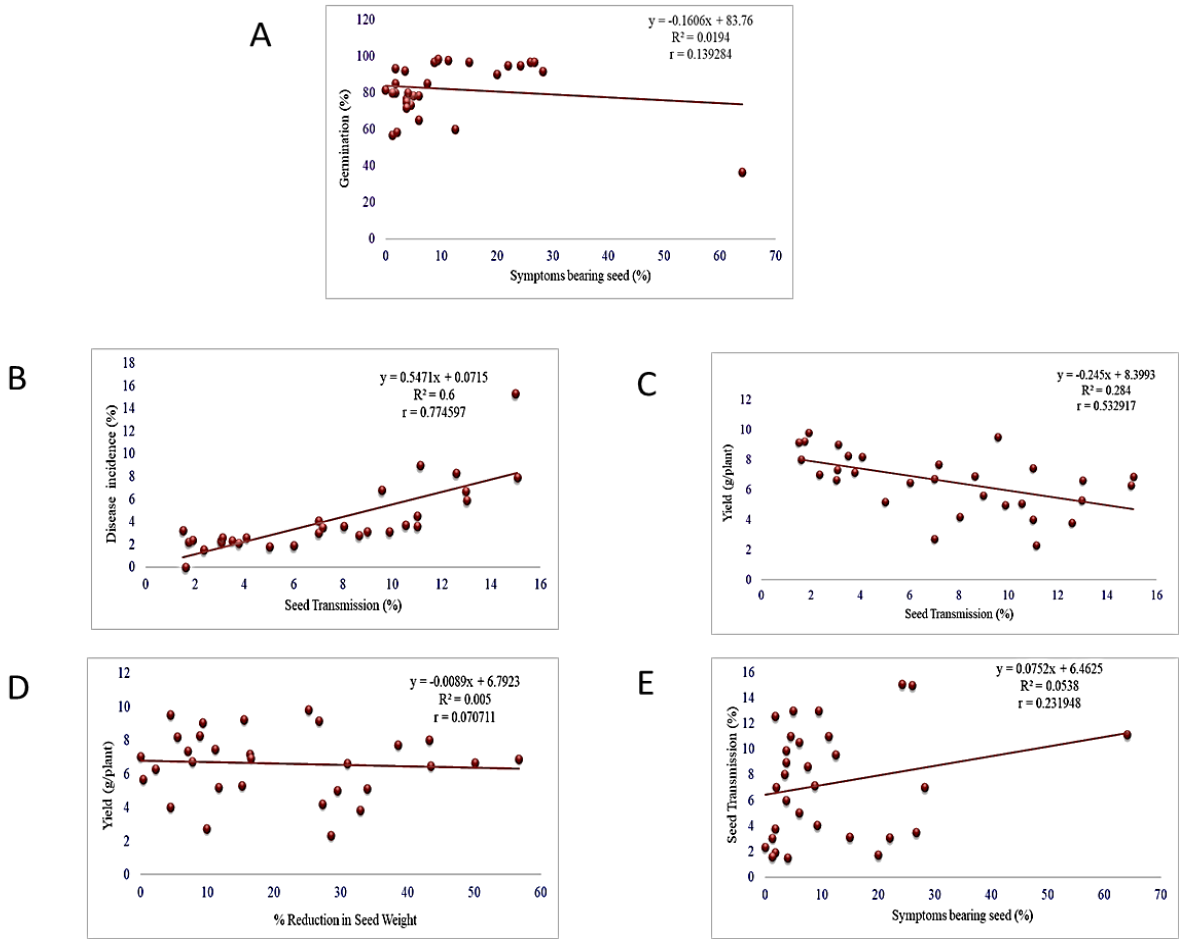

Figure 2. Regression analyses showing the relationship a) between % of symptom bearing seed and germination, b) % of seed transmission and disease incidence, c) % of seed transmission and yield (g/plant) d) % of reduction in seed weight and yield (g/plant) and e) % of symptom bearing seed and seed transmission.

4. Conclusions

SMV's growing impact on soybeans underscores the importance of introducing SMV resistance into Bangladeshi soybeans.11 genotypes *viz.* AGS-129, AGS-160, G-2261, Williams, CM, Durga, EC-1178, ACAGS-154, BS-32, BS-10 and PR-164 cultivars can be selected to locate resistant genes against SMV while the remaining cultivars experienced an increase in disease severity and incidence. However, more research is needed to identify the resistance sources of these soybean genotypes and to further validate them before they can be applied in breeding programs.

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Conflict of interest

None to declare.

Authors' contribution

Uttam Kumar Mozumdar: methodology, data collection, analysis and draft manuscript writing; Md. Mostafa Masud: draft manuscript writing and revision; Mamuna Mahjabin Mita: draft manuscript writing; Samrin Bashar: draft manuscript writing; Md. Mahboob Hossain: conceptualization and supervision; M. Ashrafuzzaman: conceptualization and supervision; Md. Rashidul Islam: supervising the draft writing and final editing. All authors have read and approved the final manuscript.

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