Brazilian Journal of Biology®

ISSN 1519-6984 (Print)
ISSN 1678-4375 (Online)

Original Article

Increased yield performance of mutation induced Soybean genotypes at varied agro-ecological conditions

Aumento no desempenho de rendimento de genótipos de soja induzidos por mutação em condições agroecológicas variadas

M. S. H. Bhuiyan[a], M. A. Malek[a], R. M. Emon[a], M. K. Khatun[a], Mohammad Moneruzzaman Khandaker[b] and Md. Amirul Alam[c]*

[a]Bangladesh Institute of Nuclear Agriculture, Plant Breeding Division, Mymensingh, Bangladesh

[b]Universiti Sultan Zainal Abidin, School of Agriculture Science and Biotechnology, Faculty of Bioresources and Food Industry, Besut Campus, Besut, Terengganu, Malaysia

[c]Universiti Malaysia Sabah, Horticulture and Landscaping Program, Faculty of Sustainable Agriculture, Sandakan Campus, Sandakan, Sabah, Malaysia

Abstract

In soybean breeding program, continuous selection pressure on traits response to yield created a genetic bottleneck for improvements of soybean through hybridization breeding technique. Therefore an initiative was taken to developed high yielding soybean variety applying mutation breeding techniques at Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture (BINA), Bangladesh. Locally available popular cultivar BARI Soybean-5 was used as a parent material and subjected to five different doses of Gamma ray using Co_{60}. In respect to seed yield and yield attributing characters, twelve true breed mutants were selected from M_4 generation. High values of heritability and genetic advance with high genotypic coefficient of variance (GCV) for plant height, branch number and pod number were considered as favorable attributes for soybean improvement that ensure expected yield. The mutant SBM-18 obtained from 250Gy provided stable yield performance at diversified environments. It provided maximum seed yield of 3056 kg ha^{-1} with highest number of pods plant^{-1} (56). The National Seed Board of Bangladesh (NSB) eventually approved SBM-18 and registered it as a new soybean variety named 'Binasoybean-5' for large-scale planting because of its superior stability in various agro-ecological zones and consistent yield performance.

Keywords: soybean mutant, mutation breeding, yield performance, stability, genetic variance, heritability.

Resumo

No programa de melhoramento da soja, a pressão pela seleção contínua para a resposta das características de rendimento criou um gargalo genético para melhorias da soja por meio da técnica de melhoramento por hibridação. Portanto, foi desenvolvida uma variedade de soja de alto rendimento, aplicando técnicas de reprodução por mutação, na Divisão de Melhoramento de Plantas, no Instituto de Agricultura Nuclear de Bangladesh (BINA), em Bangladesh. A cultivar popular BARI Soybean-5, disponível localmente, foi usada como material original e submetida a cinco doses diferentes de raios gama usando Co60. Em relação ao rendimento de sementes e às características de atribuição de rendimento, 12 mutantes genuínos foram selecionados a partir da geração M4. Altos valores de herdabilidade e avanço genético com alto coeficiente de variância genotípico (GCV) para altura da planta, número de ramos e número de vagens foram considerados atributos favoráveis ao melhoramento da soja, garantindo, assim, a produtividade esperada. O mutante SBM-18, obtido a partir de 250Gy, proporcionou desempenho de rendimento estável em ambientes diversificados e produtividade máxima de sementes de 3.056 kg ha-1 com o maior número de vagens planta-1 (56). O Conselho Nacional de Sementes de Bangladesh (NSB) finalmente aprovou o SBM-18 e o registrou como uma nova variedade de soja, chamada 'Binasoybean-5', para plantio em larga escala por causa de sua estabilidade superior em várias zonas agroecológicas e desempenho de rendimento consistente.

Palavras-chave: soja mutante, melhoramento genético por mutação, desempenho produtivo, estabilidade, variância genética, herdabilidade.

1. Introduction

Worldwide Soybean (*Glycine max* L. Merrill) is a legume that has become the miracle crop of the twenty-first century (Wilson, 2012; Lee et al., 2015; Tandon and Dubey, 2015). It is a unique crop with around 40% protein, 20% polyunsaturated fatty acid-enriched oil, 6%–7% total minerals, 5%–6% crude fiber, and 17–19% carbohydrates (Tefera et al., 2009).

*e-mail: amirulalam@ums.edu.my
Received: August 11, 2021 – Accepted: September 27, 2021

Among the many and varying adaptation strategies aimed at enhancing the livelihoods of the farmers, developing countries have supported the production of soybeans due to its multiplicity uses and positive impacts on soil health (Siamabele, 2021). In addition to human consumption, soybean meal is used in aquaculture, animal feeding, and biodiesel manufacturing (Wilson, 2008).

Without a question, the demand for soybeans and soybean products has risen substantially as the world's population and eating patterns have changed. Today, soybean production is one of the most important crops (nest ot wheat and rice) across the globe, however, developing countries have not fully realized the benefits of soybean yet compared to the developed world. Therefore, it is a favorable moment to expand output in order to lower the imports prices for emerging nations such as Bangladesh. If we judge the world soybean production, we discover that the global average yield is 2.76 tons ha^{-1} (Terzic et al., 2018), whereas average yield in Bangladesh is merely 1.8 ton ha^{-1} (BBS, 2020). As a result, the major goal of Bangladesh's soybean breeding efforts is to create cultivars with high yields. In soybean breeding program, continuous selection pressure on traits response to yield created a genetic bottleneck for improvements of soybean (Valliyodan et al., 2016). Because of all these genetic bottlenecks, rare alleles have been lost, and the genetic diversity of contemporary soybean cultivars has been decreased (Hyten et al., 2006). Whereas genetic improvement of crops is fundamental to long-term success. One of the strategies that can be exploited to increase diversity in crop genome is incorporating mutations techniques. It has recently been utilized as a helpful complement to conventional plant breeding strategies for generating genetic diversity. Due to active promotion of the use of gamma irradiation by the Food and Agriculture Organization of the United Nations and the International Atomic Energy Agency, mutant varieties produced with ionizing radiation, specifically gamma rays, predominate in the database of registered mutant varieties. Physical mutagens also tend to induce larger genomic aberrations than some chemical mutagens, and more dominant or more easily observable traits could be created at a higher frequency of gamma rays (Jankowicz-Cieslak and Till, 2015). The utility of this method is evident in several crops (rice, pulses and oil crops); where induced mutants have been released as new varieties (Khan, 2013). Unlike hybridization and selection, mutation breeding also has the advantage of improving a defect (male sterility, inbreeding depression, increased disease susceptibility, poor grain quality etc.) in an otherwise elite cultivar, without losing its agronomic and quality characteristics (Bhuiyan et al., 2019). However, throughout the globe and in Bangladesh, the use of mutation breeding, particularly for soybean varietal improvement, is still underutilized. Considering the continuous success rate of mutation breeding on self-pollinated crops, an attempt was made to develop higher yield potential soybean varieties utilizing gamma ray induced mutation techniques, which was the goal of this research.

2. Materials and Methods

The seeds of a local improved soybean variety, BARI Soybean-5, were exposed (250 seeds for each dosed) to varying doses of gamma rays (150, 200, 250, 300 and 350 Gy) and M_1 population was cultivated from January to April (2013). Entered seeds were irradiated from the Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. Seeds of the first 10 pods were gathered from each plant and combined using the dosages as a guide. During July to October 2014, dose-wise merged seed was cultivated separately with correct spacing (30 cm x 30 cm) and all other agronomic procedures (weeding, irrigation, pests control etc.) as part of the M_2 population. The first selection pressure was applied to the M_2 population, while the second and third selection pressures were applied to the M_3 and M_4 populations, respectively.

2.1. Genetic variability and genetic diversity study

A total of fifteen soybean genotypes were evaluated for genetic variability, with twelve mutants chosen from the M_4 generation and the remaining three genotypes being the parent BARI Soybean-5 with two local cultivars, BDS-4 and Sohage (Table 1).

2.2. Stability analysis and multiplication yield trial

The M6 and M7 generations were subjected to stability testing and multi-location yield experiments (Table 2). Four soybean mutants (SBM-9, SBM-15, SBM-18, and SBM-22) were chosen for stability study and the best performing two soybean mutants (SBM-18 and SBM-22) were picked for multi-location yield experiments based on their inclusive performance. The parent BARI Soybean-5 and the check variety Binasoybean-1 were both included to the material list in each case.

2.3. Experimental design and way of carrying out

All of the studies had three replications and were set up in a randomized full block design. Each experiment ensured well-drained sandy loam soil. To guarantee proper plant growth and development, recommended management was followed. After 20 days of planting and thinning 600 plants were verified in each case.

2.4. Data collection and statistical analysis

Data on plant height, number of branches $plant^{-1}$, pods $plant^{-1}$, and seeds pod^{-1} were collected from ten randomly

Table 1. List of mutants selected from M_4 generations used for genetic variability study.

Dose (Gy)	No. of mutants	Name of the mutants
150 Gy	3	SBM-9, SBM-12 and SBM-15
200 Gy	2	SBM-16 and SBM-17
250 Gy	2	SBM-18 and SBM-19
300 Gy	3	SBM-20, SBM-21 and SBM-22
350 Gy	2	SBM-23 and SBM-26

Table 2. List of advanced generation and location of the experiment with growing season.

Sl. No	Name of Generation	Location of the Experiments	Growing Season
1	M_5	BINA Headquarters farm, Mymensingh	2017
2	M_6	BINA Headquarters farm, Mymensingh and BINA substation farm Magura and Rangpur and farmers' field at Noakhali and Chandpur	2018
3	M_7	BINA Headquarters farm, Mymensingh, BINA substation farm Magura, farmers' field at Noakhali and Chandpur	2019

Table 3. Assessments of genetic parameters for various yield attributes of 15 soybean genotypes.

Traits	VG	VP	VE	GCV	PCV	h^2b	GA
Days to maturity	7.08	7.83	0.75	2.58	2.71	90.39	5.05
Plant height (cm)	63.75	70.07	6.32	16.64	17.44	90.97	32.69
Number of branches plant^{-1}	0.50	0.59	0.09	5.90	9.23	83.74	67.68
pods plant^{-1}	38.97	48.75	9.78	14.85	16.61	79.92	27.35
Seeds pod^{-1}	0.014	0.024	0.01	6.04	8.38	51.96	8.973
Seed yields	64924	104507	39583	9.71	12.32	62.12	15.76

VG = Genotypic component of variance, GCV = Genotypic coefficient of variance, VP = Phenotypic component of variance, PCV = Phenotypic coefficient of variance, VE=Environmental component of variance, ECV = Environmental coefficient of variance, h^2b = Broad sense heritability GA = Genetic advance

selected plants in each plot. When the plants and pods of each plot became a yellowish-brown hue and virtually all of the leaves were lost, the maturity time was determined. Each plot's seed output was recorded and translated to kg ha^{-1}. Steel et al. (1997) proposed formulae were used for determining genetic parameters. The SPSS software organized the UPGMA dendrogram for the Diversity analysis. Stability analysis of selected genotype with their parent was carried out using Eberhart and Russell model (Eberhart and Russel, 1966) and mean separation was done by Statistix 10 software.

3. Results

3.1. Genetic variability and genetic diversity study

The key yield contributing characteristics of soybean are plant height, branches plant^{-1}, pods plant^{-1}, and seeds plant^{-1}. Table 3 shows all of the genetic parameter components, as well as the coefficient of variability, heritability, and genetic advancement for the intended characteristics. The highest VG (Genotypic component of variance) and VP (Phenotypic component of variance) was found for yield (64924 and 104507) followed by plant height (63.75 and 70.07) and pods plants^{-1} (38.97 and 48.75). Whereas the lowest magnitude of VG and VP was observed in seeds pod^{-1} (0.014 and 0.024) followed by branches plant^{-1} (0.50 and 0.59).

PCV was greater than GCV for each characteristic, and it was highest for yield (9.71 and 12.32). Plant height and days to maturity (99.97 and 99.39, respectively) had the highest heritability, followed by branching plant^{-1} (83.74). Plant height (90.97 and 32.69) was tracked by branching plant^{-1} and found to be associated with strong heritability and genetic progress (83.74 and 67.68).

The UPGMA dendrogram (Figure 1) was used to determine the similarity between genotypes and the examined morphological characteristic. The 15 mutant lines were divided into five groups based on their 100 percent dissimilarity. Clusters I (SBM-26), II (SBM-12), IV (SBM-22), and V (BARI Soybeab-5) each had one accession, whereas cluster III had eleven. SBM-9, SBM-15, SBM-18, and SBM-22 had yield potential more than 2800 kg ha^{-1} (Figure 2). SBM-18 had the highest seed production out of the four, and it took 105 days to mature. SBM-22 matured earlier (101 days) followed by SBM-15, SBM-18 and SBM-09.

3.2. Stability analysis and Multi-location yield trial

Developing genotypes that can resist diversified environmental oscillations are a prerequisite for any crop. The mean square of days to maturity, plant height, pods plant^{-1}, and seed production per hectare (kg ha^{-1}) were all significant for majority of the characteristics, according to pooled data (Table 4, Figure 3). For all characteristics except branches plant^{-1} and seeds pod^{-1}, significant mean squares owing to environments, genotypes x environments (G x E) interactions, and environments + (genotypes x environments) were identified.

For all examined characteristics, substantial variance owing to the linear component of environment was discovered, but significant variance due to genotype x environments (linear) was discovered for days to maturity.

From stability study, we found that SBM-18 and SBM-22 had higher mean values for yield. The environmental retort

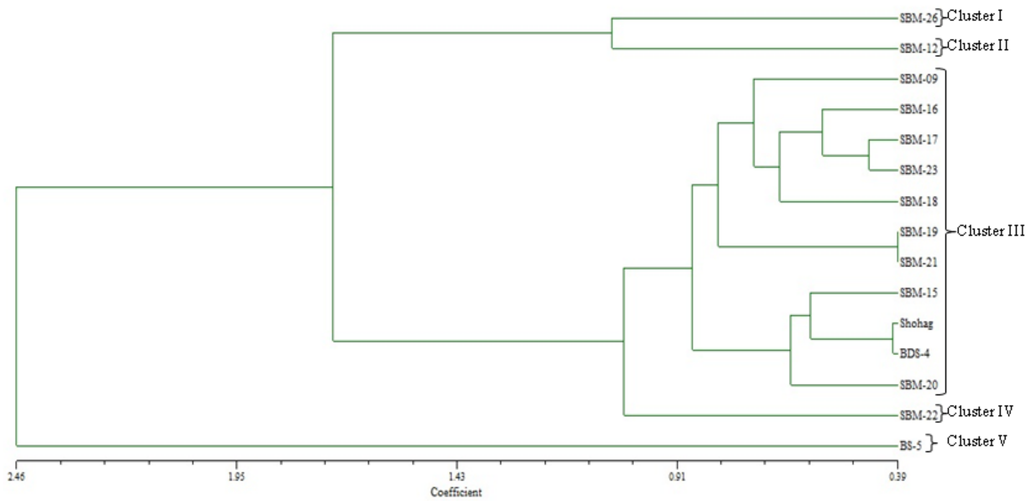

Figure 1. Population structure of 15 soybean genotypes based on morphological traits by UPGMA. In Figure BD-5 represent as BARI Soybean-5.

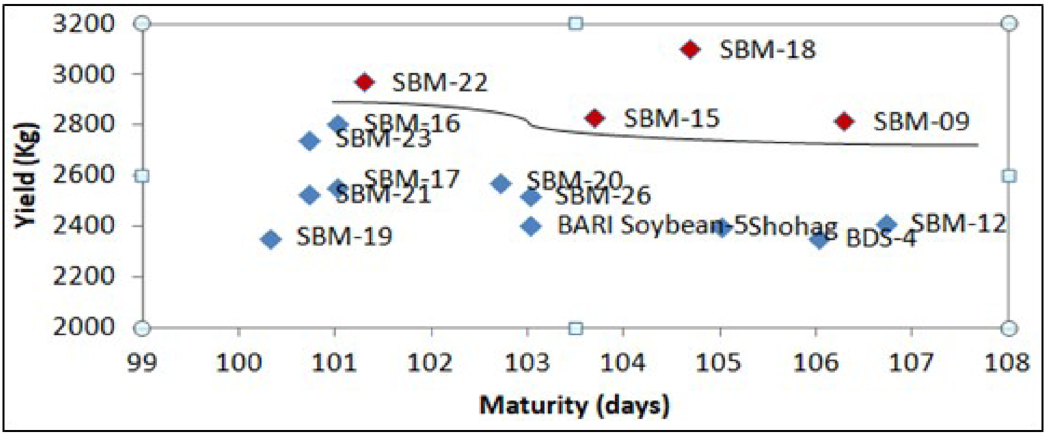

Figure 2. Performance of 15 soybean genotypes based on seed yields and maturity period.

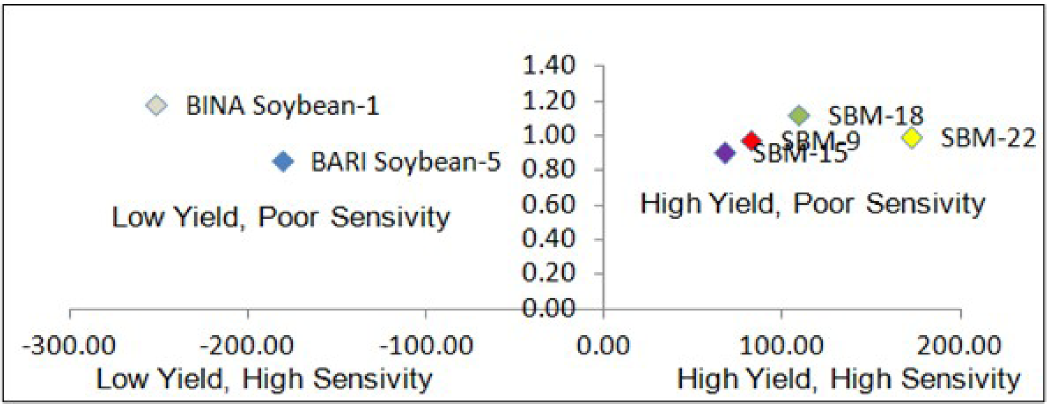

Figure 3. Stability performance of selected soybean mutant regression coefficient models.

of SBM-9 and SBM-15 also paralleled to SBM-18 and SBM-22 but both of them had low yield potentiality.

Multi-location yield trials of SBM-18 and SBM-22 were carried out with their parent and check (Table 5). Maturity periods of the genotypes though significantly varied at a particular location ranging between 110 to 119 days, combined average maturity periods over locations did not differ significantly between the mutants and checks. However, all other parameters significantly varied between the mutants and checks at a particular location, as well

Table 4. Combined analysis of mean square (Variance) for yield and yield controlling characters in a genotype-environment interaction study in soybean genotype used Eberhart and Russell model (1966).

Sources of variation	d.f.	Days to Maturity	Plant Height	Branches plant^{-1}	Pods plant^{-1}	Seeds plant^{-1}	Yields
Genotype	5	10.96**	60.21**	0.08 NS	137.75**	1.58 NS	149238.35**
Environment	4	1177.21**	229.5**	4.40**	68.59**	31.92**	3936776.5**
Genotype X Environment	20	96.60**	166.48**	1.33NS	734.71**	6.72**	989141.32**
Environment +(Genotype X Environment)	24	276.70**	176.98**	0.37 NS	329.54**	0.28 NS	168155.02**
Environment (liner)	1	2415.37**	4046.66**	8.05**	152.16**	4.32*	3942350.8**
Genotype X Environment (liner)	5	827.16**	28.84**	0.17 NS	3133.13**	0.42 NS	8596.19**
Pooled deviation	18	229.76**	8.01*	0.04	83.87**	0.11	2387.83**
Pooled error	50	0.011	0.20	0.13	0.014	0.28	0.22

*indicate 5% level of significant and **indicate 1% level of significant. NS=Not significant

Table 5. Mean performance of soybean mutants along with check varieties for different quantitative characters during Rabi 2019.

Mutants/ varieties	Days to maturity	Plant height (cm)	Branches plant^{-1} (no.)	Pods plant^{-1} (no.)	Seeds pod^{-1} (no.)	100-seed weight (g)	Seed yield (kg ha^{-1})
BINA Hqs. farm, Mymensingh							
SBM-18	114a	80a	2.34ab	52a	2.20b	13.41b	2863a
SBM-22	113b	75b	2.40a	50b	2.30a	13.89a	2758a
Binasoybean-1	110c	80a	2.07b	46bc	2.10c	12.23c	1798b
BARI Soybean-5	113b	74bc	2.31ab	46c	2.22ab	13.62ab	1789b
BINA sub-station farm, Magura							
SBM-18	113b	78a	2.5a	72a	2.45a	14.46a	2920a
SBM-22	117ab	74b	2.3b	69ab	2.30b	13.67b	2796b
Binasoybean-1	118a	78a	2.1c	65b	2.20c	12.61c	2323c
BARI Soybean-5	117ab	75ab	2.1c	67ab	2.25bc	14.38ab	2382bc
Farmer's field, Chandpur							
SBM-18	120b	78b	2.13a	52a	2.10a	13.91a	2850a
SBM-22	123a	79ab	1.8b	47b	1.9b	12.41b	2720b
Binasoybean-1	119bc	81a	1.6c	44c	1.83c	12.54ab	1625c
BARI Soybean-5	117c	75c	1.7bc	47b	1.87bc	13.87ab	1723bc
Farmer's field, Noakhali							
SBM-18	119a	81ab	1.9a	48a	2.10a	13.86ab	2856a
SBM-22	118ab	79b	1.7ab	43ab	1.85b	13.91a	2763b
Binasoybean-1	117b	83a	1.65b	40b	1.73c	12.39ab	1687bc
BARI Soybean-5	118ab	72c	1.68ab	42ab	1.79bc	12.34b	1625c
Combined means over four locations							
SBM-18	117NS	79ab	2.22a	56a	2.23a	13.9a	2922a
SBM-22	118	77b	2.05b	52b	2.09b	13.5ab	2759b
Binasoybean-1	116	81a	1.86c	49c	1.97c	12.4c	1858c
BARI Soybean-5	116	74c	1.96bc	51bc	2.03bc	13.6b	1880bc

Note: mean value with different lower case letters are significantly different at $p \leq 0.05$. NS=Not significant as when the values were combined, and the mutants consistently showed greater performances competed to their parent and check (Table 5). The combined average results over all locations showed that, BINA Soybean-1 had the highest (79 cm) and BARI Soybean-5 had the lowest average plant height (74 cm). Plant heights of the two mutants were intermediate (around 78 cm). Mutant genotype SBM-18 had the highest (2.22) and the two checks had the lowest number of branches per plant (around 1.90). While the other mutant genotype, SBM-22, had around 2 branches per plant which was significantly greater than the checks but significantly lesser than SBM-18. The highest number of pods plant^{-1} were recorded for SBM-18 (56 plant^{-1}), followed by SBM-22 (52 plant^{-1}). The checks genotypes had similarly around 50 pods plant^{-1} which was significantly lesser compared to the mutant genotypes. Similar trends were observed for seeds per pod, having the highest number of seed per pod for SBM-18 (2.23 seeds pod^{-1}) and the lowest for BINA Soybean-1(1.97 seeds pod^{-1}). Regarding 100 seed weight, the two mutant genotypes were comparable (around 14 g) however, significantly greater than BINA Soybean-1. While 100 seed weight of BARI Soybean-5 was comparable to that of SBM-22. The mutant genotype SBM-18 had the highest average seed yield (around 2920 kg ha^{-1}), followed by SBM-22 (around 2760 kg ha^{-1}). BARI Soybean-5 had around 1880 kg ha^{-1} seed yield which was at par with SBM-22 and BINA Soybean-1.

4. Discussion

Parallel to other breeding program, parent selection is the first step of mutation breeding. In this study, the parent BARI Soybean-5 was selected for its broader acceptance to the farmers due to its attractive physical appearance and yield. For successful breeding consequence, heritable variation must exist on the studied genotypes for the yield influence traits and absolutely mutation breeding be able to create this. The recommended dose for quantitative character improvement of soybean, according to the IAEA (International Atomic Energy Agency) is 200Gy (Hanafiah et al., 2010). With increasing irradiation dosages, the variability of essential yield characteristics such as plant height, number of branches plant^{-1}, and number of pods plant^{-1} rises (Hanafiah et al., 2010). Based on these information, the doses of this experiment were selected with ±200Gy. The existence of a higher degree of genetic diversity among the mutants was shown by the predominance of very significant variance among the genotypes for examined characteristics. Yuan et al. (2020) revealed a substantial effect of plant height, pod number, and seed number on yield of soybean mutants. PCV for plant height, branches plant^{-1}, pods plant^{-1}, seeds plant^{-1} and seed yields are scarcely higher than GCV reveal the less influence of environment situation on the countenance of these traits and ensure maxim selection efficiency. Higher hereditary value of yield controlling trait (Table 3) of our study are supported by Ahloowalia et al. (2004), where they found that induced mutation by physical agent are able to develop at least 64% wanted hereditary changes. Selection of these characteristics for soybean development will be more successful if they have higher heritability and GA (percent) as well as a high GCV. Malek et al. (2014) discovered that soybean mutants had a higher hereditary value for morphological characteristics. The presence of a high expected value for wide heritability implies that these qualities are controlled by additive genes, whereas all others are controlled by non-additive gene activity, therefore the combination of these features may be ineffective. We chose twelve genuine mutants based on genetic characteristics, 10 of which were obtained from greater radiation doses. It shows that low-dose irradiation allows for modest gene changes whereas high-dose irradiation allows for significant gene mutations. To optimize the use of both forms of gene mutation, mutants were chosen from both lower and higher classes, and their grouping was based on mean morphological features. The majority of genotypes in our research share their location in cluster III (Figure 1), with around 60% dissimilarity. While BDS-4 and Shohag belong to the same morphological group as other mutants (SBM-15 and SBM-20), their morphological similarities were only 40%. Achina et al. (2019) formed different number groups utilizing comparable morphological features of soybean genotypes. This study established that mutation-induced variation is the most efficient method of generating genetic diversity. It also indicated that all the mutants were also genetically different from the released varieties in Bangladesh. For their performance under a variety of environmental circumstances, genetically identical genotypes must be stable. To assure environmental sensitivity, a stability study was performed, and we discovered statistically significant variance for all investigated characteristics for all sources of variation, which may be attributable to the dominant influence of macro-environmental on regulated agronomic traits. Weather and soil characteristics at different testing locations might cause macro-environmental differences. For days to maturity, plant height, pods plant^{-1}, and yield, fairly significant variation owing to genotype x environments (linear) showed that greater performance of soybean genotypes had linear response to the environmental circumstances for these yield contributing variables. The G × E interaction of yield and its components and other quality characters of soybean studied by other investigators in the past revealed that seed yield remarkably affected by varying locations Mwiinga et al. (2020). In our study, SBM-18 and SBM-22 were chosen for multi-location yield testing because to their extensive adaptability and yield performance and SBM-18 was shown to produce the highest seed yield at all locations. Asadi and Dewi (2020) reported the highest seed yield of mutant lines for soybean, and Mondal and Bhuiyan (2020) reported the highest seed yield of mutant lines for groundnut. Economic analysis showed that SMB-18 can provide Tk. (BD) 71,880.00 net benefit per hectare while BARI Soybean-5 can give Tk. (BDT) 30,200.00 (Table 6). The economic potential of SBM-18 has been analyzed considering only the seed yield with its parent.

5. Conclusions

Based on the results of the investigation, the mutant line SBM-18 produced the highest and most consistent

Table 6. The Economic potential of SBM-18 as compared to check variety BARI Soybean-5.

Name of proposed variety and check	Total production cost ha^{-1} (Tk.)	Gross return ha^{-1} (Tk.)	Net benefit ha^{-1} (Tk.)	Benefit-cost ratio (B/C ratio)
SBM-18	45000/-	1,16,880	71,880	2.53
BARI Soybean-5 (check)	45000/-	75200	30200	1.67

Note; Price of per kg soybean seed = Tk (BDT). 40/-

seed production in a variety of environments. In each scenario, the mean yield of SBM-18 was greater than those of its parent and checked variety. BINA chose to register SBM-18 with the National Seed Board (NSB) of Bangladesh for its registration and release as modern soybean variety and would name it 'Binasoybean-5' if approved based on its yield performance, economical characteristics, and cost-benefit ratio. Eventually, Bangladesh's National Seed Board (NSB) registered SBM-18 as a new soybean variety Binasoybean-5, for large-scale production in Bangladesh.

Acknowledgements

The authors sincerely acknowledge Bangladesh Institute of Nuclear Agriculture (BINA) and the Faculty of Agriculture, Universiti Malaysia Sabah for all the supports for conducting the study and publishing the research findings.

References

ACHINA, T., TWUMASI, P. and QUAIN, M.D., 2019. Use of morphological and molecular profiling for the establishment of relatedness between commercially available and elite soybean genotypes. *European Journal of Biotechnology and Genetic Engineering*, vol. 6, no. 1, pp. 1-17.

AHLOOWALIA, B., MALUSZYNSKI, M. and NICHTERLEIN, K., 2004. Global impact of mutation-derived varieties. *Euphytica*, vol. 135, no. 2, pp. 187-204. http://dx.doi.org/10.1023/B:EUPH.0000014914.85465.4f.

ASADI and DEWI, N., 2020. Agronomic performance of soybean mutant lines based on preliminary and advance yield at dryland area. In: *IOP Conference Series: Earth and Environmental Science, The 1st International Conference on Genetic Resources and Biotechnology, 20-21 August 2018*, Bogor, Indonesia. UK: IOP Publishing Ltd. v. 482, pp. 1-6. https://doi.org/10.1088/1755-1315/482/1/012018.

BANGLADESH BUREAU OF STATISTICS – BBS, 2020. *Statistical Pocket Book of Bangladesh*. Bangladesh: Bangladesh Bureau of Statistics, Ministry of Planning, Government of People's Republic of Bangladesh, pp. 117.

BHUIYAN, M.S.H., MALEK, M., BHUIYAN, S., ISLAM, M. and HASSAN, A., 2019. Mutation determination of rice by using RAPD primers. *International Journal of Agricultural Research, Innovation and Technology*, vol. 9, no. 1, pp. 1-7. http://dx.doi.org/10.3329/ijarit.v9i1.42942.

EBERHART, S.A. and RUSSELL, W.A., 1966. Stability parameters for comparing Varieties. *Crop Science*, vol. 6, no. 1, pp. 36-40. http://dx.doi.org/10.2135/cropsci1966.0011183X000600010011x.

HANAFIAH, D. S., TRIKOESOEMANINGTYAS, YAHYA, S. and WIRNAS, D., 2010. Induced mutations by gamma ray irradiation to Argomulyo soybean (*Glycine max*) variety. *Bioscience*, vol. 2, no. 3, pp. 121-125.

HYTEN, D.L., SONG, Q., ZHU, Y., CHOI, I.Y., NELSON, R.L., COSTA, J.M., SPECHT, J.E., SHOEMAKER, R.C. and CREGAN, P.B., 2006. Impacts of genetic bottlenecks on soybean genome diversity. *Proceedings of the National Academy of Sciences of the United States of America*, vol. 103, no. 45, pp. 16666-16671. http://dx.doi.org/10.1073/pnas.0604379103. PMid:17068128.

JANKOWICZ-CIESLAK, J. and TILL, B. 2015. Forward and reverse genetics in crop breeding. In: J.M. Al-KHAYRI, S.M. JAIN and D.V. JOHNSON, eds. *Advances in plant breeding strategies: breeding, biotechnology and molecular tools*. Switzerland: Springer, vol. 1, pp. 215-240. http://dx.doi.org/10.1007/978-3-319-22521-0_8.

KHAN, H., 2013. A review on induced mutagenesis in soybean. *Journal of Cereals and Oilseeds*, vol. 4, no. 2, pp. 19-25. http://dx.doi.org/10.5897/JCO10.004.

LEE, C., CHOI, M.S., KIM, H.T., YUN, H.T., LEE, B., CHUNG, Y.S., KIM, R.W. and CHOI, H.K., 2015. Soybean [*Glycine max* (L.) Merrill]: importance as a crop and pedigree reconstruction of Korean varieties. *Plant Breeding and Biotechnology*, vol. 3, no. 3, pp. 179-196. http://dx.doi.org/10.9787/PBB.2015.3.3.179.

MALEK, M.A., RAFII, M.Y., SHAHIDA SHARMIN AFROZ, M., NATH, U.K. and MONDAL, M.M.A., 2014. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. *The Scientific World Journal*, vol. 2014, pp. 1-12. http://dx.doi.org/10.1155/2014/968796. PMid:25197722.

MONDAL, M.M.A. and BHUIYAN, M.S.H., 2020. Morphological and reproductive characterization of developed mutants in groundnut. *International Journal of Advanced Geosciences*, vol. 8, no. 1, pp. 21-26. http://dx.doi.org/10.14419/ijag.v8i1.30338.

MWIINGA, B., SIBIYA, J., KONDWAKWENDA, A., MUSVOSVI, C. and CHIGEZA, G., 2020. Genotype x environment interaction analysis of soybean (*Glycine max* (L.) Merrill) grain yield across production environments in Southern Africa. *Field Crops Research*, vol. 256, no. 107922, pp. 107922. http://dx.doi.org/10.1016/j.fcr.2020.107922.

SIAMABELE, B., 2021. The significance of soybean production in the face of changing climates in Africa. *Cogent Food & Agriculture*, vol. 7, no. 1, pp. 1-16, 1933745. http://dx.doi.org/10.1080/23311932.2021.1933745.

STEEL, R.G.D., TORRIE, J.H. and DICKEY, D.A., 1997. *Principles and procedures of statistics. A biochemical approach*. 3rd ed. New York, USA: McGraw Hill Book Co. Inc.

TANDON, S. and DUBEY, A., 2015. Effects of Biozyme (*Ascophyllum nodosum*) Biostimulant on Growth and Development of Soybean [*Glycine max* (L.) Merill]. *Communications in Soil Science and Plant Analysis*, vol. 46, no. 7, pp. 845-858. http://dx.doi.org/10.1080/00103624.2015.1011749.

TEFERA, H., KAMARA, A. Y., ASAFO-ADJEI, B. and DASHIELL, K. E., 2009. Improvement in grain and fodder yields of early-maturing promiscuous soybean varieties in the Guinea Savanna of Nigeria. *Crop Science*, vol. 49, no. 6, pp. 2037-2042. https://doi.org/10.2135/cropsci2009.02.0081.

TERZIC, D., POPOVIC, V., TATIC, M., VASILEVA, V., DEKIC, V., UGRENOVIC, V., POPOVIC, S. and AVDIC, P., 2018. Soybean area, yield and production in world. *XXII Eco-Conference®2018 Ecological Movement of Novi Sad*, vol. 8, no. 4, pp. 135-145. https://doi.org/10.15688/re.volsu.2020.4.14.

VALLIYODAN, B., DAN QIU., PATIL, G., ZENG, P., HUANG, J., DAI, L., CHEN, C., LI, Y., JOSHI, T., SONG, L., VUONG, T.D., MUSKET, T.A., XU, D., SHANNON, J.G., SHIFENG, C., LIU, X. and NGUYEN, H.T., 2016. Landscape of genomic diversity and trait discovery in soybean. *Scientific Reports*, vol. 6, pp. 23598. http://dx.doi.org/10.1038/srep23598. PMid:27029319.

WILSON, R.F., 2008. Soybean: market driven research needs. In: G. STACEY, eds. *Genetics and genomics of soybean. plant genetics and genomics: crops and models*. New York, NY: Springer, vol. 2, pp. 3-15. https://doi.org/10.1007/978-0-387-72299-3_1.

WILSON, R.F., 2012. The role of genomics and biotechnology in achieving global food security for high-oleic vegetable Oil. *Journal of Oleo Science*, vol. 61, no. 7, pp. 357-367. http://dx.doi.org/10.5650/jos.61.357. PMid:22790166.

YUAN, K., RECKLING, M., RAMIREZ, M.D.A., DJEDIDI, S., FUKUHARA, I., OHYAMA, T., YOKOYAMA, T., BELLINGRATH-KIMURA, S.D., HALWANI, M., EGAMBERDIEVA, D. and OHKAMA-OHTSU, N., 2020. Characterization of rhizobia for the improvement of soybean cultivation at cold conditions in Central Europe. *Microbes and Environments*, vol. 35, no. 1, pp. 1-13. http://dx.doi.org/10.1264/jsme2.ME19124. PMid:31996499.