

Plant Archives

Journal homepage: http://www.plantarchives.org DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.2.078

GENETIC VARIABILITY STUDIES IN ADVANCED MUTANT LINES OF SOYBEAN (*GLYCINE MAX* **L. MERRILL)**

Aniket Kumar, Nutan Verma*, Supriya Supal Surin, Sumit Kumar Mishra, Arjun Kumar Agarwal and Shreya Singh

Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi - 834 006, Jharkhand, India. *Corresponding author E-mail : nvbau2022@gmail.com (Date of Receiving- 18-03-2024; Date of Acceptance-08-06-2024)

262 M6 mutants of soybean genotype BSS-2 and 254 M6 mutants of soybean genotype RKS-18 were used in the study conducted in 2019-20. Both genotypes underwent irradiation using five gamma-ray doses [50Gy, 100Gy, 150Gy, 200Gy and 400Gy] in *Kharif* 2014 under the BRNS-BARC project at the Department of Genetics and Plant Breeding, B.A.U., Ranchi. This resulted in 265 M6 mutant plants of BSS-2 and 254 M6 mutant plants of RKS-18 in 2018. Genetic parameters were evaluated. Non-replicated plant-to-progeny rows were grown for all mutants, and observations for quantitative traits were recorded on ten random plants of each mutant progeny of both genotypes. Both BSS-2 and RKS-18 demonstrated unique responses to different gamma-ray doses. RKS-18 displayed notable differences, particularly in the number of pods per plant, 100 seed weight and yield per plant. It indicated low genetic and phenotypic coefficients of variation, suggesting minimal environmental influence on trait expression. **ABSTRACT**

Key words : Soybean, Genetic variability, Heritability, Genetic advance, Gamma-ray.

Introduction

Most of the world's vegetarians depend on pulses, known as the "poor man's meat," for protein. Pulses are highly nutritious and essential for sustainable agriculture due to their nitrogen-fixing abilities. India is a significant pulse producer, accounting for 20% of global production and 37% of consumption, with 28.3 million hectares dedicated to pulse farming in 2020–21. This crop offers triple benefits, comprising approximately 40% proteins with elevated levels of essential amino acids, excluding methionine and cystine, 20% oil abundant in polyunsaturated fatty acids, particularly omega-6 and omega-3 fatty acids, 6 to 7% total minerals, 5 to 6% crude fiber and 17 to 19% carbohydrates (Chauhan *et al*., 1988). Soybeans constitute 61% of global oilseed production and stand as a prominent commercial crop on an international scale (SoyStats, 2016). It is the world's largest oilseed crop, covering 127.19 million hectares globally, with India contributing 10.96 million hectares. (Source: DES, Government of India, Ministry of

Agriculture & Farmers Welfare, 2021-22). Soybeans fulfill the nutritional requirements of both humans and other animals (Malek *et al*., 2014; Ghosh *et al*., 2014). Soybean isoflavones have been discovered to offer health advantages, demonstrating properties such as cancer prevention, alleviation of menopausal symptoms and assistance in diabetes recovery (Chauhan *et al*., 2002).

Soybean cultivation in India thrives in temperatures between 26.5°C and 30°C, requiring annual rainfall of 750-1000 mm and well-drained, loamy soil with a pH range of 6.5 to 7.5. In addition to its capacity for nitrogen fixation, this crop demonstrates versatility in adapting to various environments, mitigating soil erosion, suppressing weed growth and accommodating both intercropping and sequential cropping systems. Understanding genetic variability and heritability is crucial for successful crop improvement, aiding breeders in selecting superior parents to enhance crop yields (Khan *et al*., 2013). Soybeans face challenges such as poor seed viability, absence of early maturation and high-yielding cultivars with stress

resistance (Bhatnagar and Karmakar, 2012). The legume breeder aims to develop genotypes that optimize yield and quality. Today's soybean varieties originate from a narrow genetic base. The genetic variability present in any crop is critical to creating an effective breeding program. In soybeans, the creation of variation through hybridization is a tedious process due to the small, fragile flowers that make it difficult to carry out the process of emasculation even under favorable conditions. Mutation breeding, therefore, plays a vital role in improving soybean plants. The genetic variability generated by induced mutation can undoubtedly contribute to gaining the alleles for higher productivity and better plant types. To effectively choose superior genotypes for hybridization programs aimed at developing enhanced varieties, it's essential to thoroughly investigate genetic variability resulting from both genetic and non-genetic factors, alongside other pertinent genetic parameters (Baisakh *et al*., 2016). Evaluating the genetic makeup is a fundamental step in crop improvement, as it reveals the potential for enhancement. Variability in source populations, genetic progress and heritability are critical for successful breeding. Genetic parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) serve as valuable biometric instruments for assessing genetic variability (Aditya *et al*., 2011). Therefore, before initiating any improvement program, it is crucial to characterize the genetic background of soybeans and assess breeding values (Agong *et al*., 2001). Keeping these in view, the study aimed to identify traits for genetic improvement by manipulating genotypes, considering both heritability and genetic advancement in RKS-18 and BSS-2 mutants. RKS-18 or Pratap Soya-2 mutant's parentage is MACS450 X Monetta. The growth type of RKS-18 is determinate; maturity is medium, flower color is purple, the pod is glabrous, seeds are yellow with black hilum, and it is tolerant to Bacterial Pustules, Girdle Beetle and Leaf Miner. BSS-2 or Birsa Safed Soybean-2 mutant's parentage is JS 335 X MACS 58, the growth type of BSS-2 is semi-determinate, maturity is medium, flower color is white, the pod is pubescent, the seed is whitish-yellow with light brown hilum, it is tolerant to bacterial pustules, Frogeye leaf spot, moderately resistant to Cercospora leaf spot and immune to Target leaf spot disease. It is also tolerant to Blue beetle and Defoliator.

Materials and Methods

The experiment was conducted at the Birsa Agricultural University Research Farm, Ranchi. Row to Row spacing of 0.45 m was taken and the Row length taken was 2.5 m. Materials comprised of seeds from 262 M6 mutants of soybean genotype BSS-2 and 254 M6 mutants of soybean genotype RKS-18 whose seeds were irradiated with five different doses [50 Gy, 100Gy, 150Gy, 200Gy, 400Gy] of Gamma rays in the year 2014 using the Cobalt 60 sources in Gamma Chamber at Bhabha Atomic and Research Centre, Mumbai as part of the BRNS-BARC Project on Soybean in the Department of Genetics and Plant Breeding at BAU, Ranchi. Non-replicated plant-to-progeny rows of all the M6 mutants of BSS-2 and RKS-18 were grown along with their parent genotypes as checks. Observation for quantitative characters was recorded in ten random plants of each mutant progeny of both the genotypes BSS-2 and RKS-18. The analysis of variance was done by the procedures described by Panse and Sukhatme (1967). The methods adopted for calculating GCV and PCV parameters used were described by Burton and de Vane (1953). Heritability (broad sense), genetic advance and genetic advance as a percent of the mean were calculated as per the method suggested by Lush (1949), followed by Johnson *et al*. (1955).

Results and Discussion

The phenotypic coefficient of variation, genotypic coefficient of variation and heritability percentage were estimated along with genetic advance and genetic advance as percent of the mean within treatments of both the genotypes BSS-2 and RKS-18 in the different plant populations of M6 generation.

Mutant Population of BSS-2 and RKS-18 of 50 Gy dose

Table 1 highlights significant variability in BSS-2's yield per plant, with maximum GCV and PCV. In contrast, RKS-18 showed highest GCV in pod length (63.93) followed by plant height (21.66), no of pods per plant (20.37). BSS-2 exhibited lowest GCV value for pod length (0.92) followed by days to maturity (1.24) and days to first flowering (4.27). BSS-2 exhibited lowest PCV valuein days to maturity (1.47) followed by pod length (4.06) and days to first flowering (4.44), while RKS-18 had lowest PCV values for days to maturity (2.39) followed by days to first flowering (3.57) and pod length (5.79). BSS-2 had the highest broad-sense heritability for plant height (97.20) and days to first flowering (92.60) and moderate heritability for 100-seed weight (73.63). RKS-18 showed high heritability for pods per plant (77.63) and moderate for pod length (27.84). BSS-2 has lowest heritability for pod length (5.09) and In RKS-18 lowest heritability was observed for days to maturity (0.94). BSS-2 had the highest genetic advance for plant height (2122.63), while

RKS-18 had the highest for pods per plant (1431.16). Conversely, the lowest genetic advance was in pod length (1.35) for BSS-2 and days to maturity for (4.29) RKS-18.

Mutant population of BSS-2 and RKS-18 of 100 Gy dose

Table 2 highlights significant variability in BSS-2's the number of pods per plant with the highest GCV (17.72), while RKS-18 excels in pod length (63.50) with maximum GCV. Both varieties exhibit low GCV, for BSS-2 days to maturity (0.82) and for RKS-18 (0.51), indicating uniform maturation responses. BSS-2 shows the highest PCV for yield per plant (24.92), emphasizing variability in yieldrelated traits, RKS-18 has maximum PCV for plant height (34.08), reflecting diversity in plant height. BSS-2 has the highest broad-sense heritability for plant height (96.60), while RKS-18 has the highest for 100-seed weight (97.80), indicating strong genetic influence on these traits. The highest genetic advance as a percent of the mean is recorded for plant height in both varieties for BSS-2 (34.21) and in RKS-18 (67.28), suggesting potential for genetic improvement, while the lowest values are in days to maturity, indicating limited scope for genetic enhancement in maturation.

Mutant Population of BSS-2 and RKS-18 of 150 Gy dose

Table 3 highlights significant variability in RKS-18' the pod length with the highest GCV (63.68), while BSS-2 excels in no of pods/plants (42.63) with maximum GCV. Both varieties exhibit low GCV, for BSS-2 days to maturity (0.86) and for RKS-18 (0.23), indicating uniform maturation responses. BSS-2 shows the highest PCV for no of pods/plant (44.47), emphasizing variability in yield-related traits, RKS-18 has maximum PCV for plant height (22.91), reflecting variation in plant height. BSS-2 has the highest broad-sense heritability for days to first flowering (93.62), while RKS-18 has the highest for no of pods/plant (94.18), indicating strong genetic influence on these traits. The highest genetic advance as a percent of the mean is recorded for no of pods/plant in both varieties for BSS-2 (84.19) and in RKS-18 (43.42), suggesting potential for genetic improvement, while the lowest values are in days to maturity, indicating limited scope for genetic enhancement in maturation. Highest variation in BSS2 and RKS-18 ranged observed in days to maturity (104-112), RKS-18 (85-96). In BSS-2, Plant height (cm) shows huge variation ranged from (25-89) and in RKS-18, days to flowering show huge variation ranged from (40-44).

Table 3 : M6 Population of BSS-2 and RKS-18 of 150 Gy dose. **Table 3 :** M6 Population of BSS-2 and RKS-18 of 150 Gy dose.

Mutant Population of BSS-2 and RKS-18 of 200 Gy dose

Table 4 highlights significant variability in both the genotypes for BSS-2 highest GCV was observed in no of pods/plants (16.77), similar results was observed in RKS-18 with high GCV value (19.03). Both varieties exhibit low GCV, for BSS-2 days to maturity (0.09) followed by pod length (4.90) and days to 50% flowering (5.93) and for RKS-18 (1.01), indicating uniform maturation responses. BSS-2 shows the highest PCV for yield/plant (23.96) followed by no of pods/plant (22.11), emphasizing variability in yield-related traits, RKS-18 has maximum PCV for yield/plant (33.52), followed by no of pods/plants (31.96) reflecting variation in yield related traits. BSS-2 has the highest broad-sense heritability for days to first flowering (96.17) followed by plant height (92.12) and 100 seed (71.24), while RKS-18 has the highest for no of pods/plant (97.04) followed by pod length (94.21), indicating strong genetic influence on these traits. The highest genetic advance as a percent of the mean is recorded for no of pods/plant in both varieties for BSS-2 (26.18) and in RKS-18 (63.89), suggesting potential for genetic improvement, while the lowest values are in days to maturity, indicating limited scope for genetic enhancement in maturation. Highest variation in BSS2 and RKS-18 ranged observed in BSS-2 days to maturity (102-107), RKS-18 (84-96). In BSS-2, Plant height (cm) shows huge variation ranged from (40-73) and in RKS-18, days to flowering show huge variation ranged from $(40-45)$.

Mutant Population of BSS-2 and RKS-18 of 400 Gy dose

Table 5 highlights significant variability in both the genotypes for BSS-2 highest GCV was observed in yield/ plant (g) (13.25). In RKS-18 high GCV value was observed in pod length (63.90). Both varieties exhibit low GCV value, in BSS-2 days to maturity (0.16) followed by pod length (4.59) and days to 50% flowering (5.93). BSS-2 shows the highest PCV for yield/plant (21.99) followed by no of pods/plant (19.40), emphasizing variability in yield-related traits, RKS-18 has maximum PCV for no of pods per plant (27.56), followed by yield/ plant (g) (24.79) reflecting variation in yield related traits. BSS-2 has the highest broad-sense heritability for days to first flowering (96.17) followed by plant height (92.12) and 100 seed (71.24), while RKS-18 has the highest for no of pods/plant (97.04) followed by pod length (94.21), indicating strong genetic influence on these traits. The highest genetic advance as a percent of the mean is recorded for no of pods/plant in both varieties for BSS-2

(26.18) and in RKS-18 (63.89), suggesting potential for genetic improvement, while the lowest values are in days to maturity, indicating limited scope for genetic enhancement in maturation. Highest variation in BSS2 and RKS-18 ranged observed in BSS-2 days to maturity (102-107), RKS-18 (84-96). In BSS-2, Plant height (cm) shows huge variation ranged from (40-73) and in RKS-18, days to flowering show huge variation ranged from $(40-45)$.

Similar findings were observed by Osekita *et al* . (2014), Kumar (2003), Baraskar *et al*. (2014), Mulagounda *et al*. (2013) in soybean.

Genotype BSS-2 exhibits minimal difference between GCV and PCV, indicating a predominant influence of genetic factors on observed trait variation. Intermediate heritability suggests a substantial genetic component, allowing for potential genetic improvement through breeding programs, particularly for traits like days to first flowering, plant height, and days to maturity. The high genetic advance in various plant populations further underscores the significant potential for improvement in these traits through selective breeding.

In contrast, genotype RKS-18 shows a moderate difference between GCV and PCV, emphasizing a substantial genetic contribution to the variation in the number of pods per plant. High heritability indicates a strong genetic influence, making this trait amenable to genetic improvement through selective breeding. The observed high genetic advance suggests a significant potential for enhancing the number of pods per plant through selective breeding in the RKS-18 genotype. Moreover, the stability of the character "number of pods per plant" across different gamma-ray doses highlights the robust genetic influence on this trait, with less pronounced effects from environmental conditions or gamma-ray doses.

Conclusion

BSS-2, exposed to varied gamma-ray doses, displays low environmental impact, moderate heritability and significant genetic improvement potential. This is valuable for enhancing traits in BSS-2 through breeding programs. In the M6 generation, RKS-18 shows strong genetic influence on pods per plant, high heritability, and substantial improvement potential, making it a promising candidate for soybean breeding. Traits with high phenotypic variation coefficients are more influenced by environmental factors, cautioning against potential pitfalls in selection programs. This research can develop soybean varieties suited to Jharkhand's conditions, enhancing food security and contributing to economic growth through job creation

and income generation in the soybean sector.

References

- Aditya, J.P., Pushpendra B.P. and Anuradha B. (2011). Genetic variability, heritability and character association for yield and component characters in soybean [*G. max* (L.) Merrill]. *J. Central Europ. Agricult.*, **12(1)**, 27-34.
- Aditya, K., Verma N., Srivastava N., Chakraborty M. and Prasad K. (2017). Effect of gamma rays on seed germination, plant survival and quantitative characters on two varieties of soybean [*Glycine max*.(L.) Merrill.] in M1 generation. *Bull. Environ., Pharmacol. Life Sci.*, **1**, 259– 265.
- Agong, S.G., Schittenhelm S. and Fried W. (2001). Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* Mill.) germplasms. *J. Food Technol. Africa*, **6(1)**, 13-17.
- Arefrad, M., Nematzadeh G., Babaian Jelodar N. and Kazemitabar S.K. (2012). Improvement of qualitative and quantitative traits in Soybean [*Glycine Max* (L.) Merrill] through gamma irradiation. *J. Plant Mole. Breed.*, **1(1)**, 10-15.
- Arshad, M., Ali N. and Ghafoor A. (2006). Character correlation and path coefficient in soybean *Glycine max* (L.) Merrill. *Pak. J. Bot.*, **38(1)**, 121.
- Bai, M., Yuan J., Kuang H., Gong P., Li S., Zhang Z. and Guan Y. (2020). Generation of a multiplex mutagenesis population via pooled CRISPR Cas9 in soya bean. *Plant Biotechnol. J.*, **18(3)**, 721-731.
- Baisakh, B., Swain S.C., Panigrahi K.K., Das T.R. and Mohanty A. (2016). Estimation of genetic variability and character association in micro mutant lines of greengram [*Vigna radiata* (L.) Wilczek] for yield attributes and cold tolerance. *Legume Genomics and Genetics*, **7(2)**.
- Baraskar, V.V., Kachhadia V.H., VachhanI J.H., Barad H.R., Patel M.B. and Darwankar M.S. (2014). Genetic variability, heritability, and genetic advance in Soybean [*Glycine max* (L.) Merrill]. *Elect. J. Plant Breed.*, **5(4)**, 802-806.
- Begum, T. and Dasgupta T. (2010). A comparison of the effects of physical and chemical mutagens in sesame (*Sesamum indicum* L.). *Gen. Mole. Biol.*, **33**, 761–766.
- Bhosale, U.P. and Hallale B.V. (2013). Mutagenic effectiveness and efficiency of gamma rays and ethyl methanesulphonate in black gram [*Vigna mungo* (L.) Hepper]. *Bionano Frontier*, **6(2)**, 271-273.
- Burton, G.W. and Devane D.E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. *Agron. J.*, **45(10)**, 478-481.
- Bhatnagar, P.S. and Karmakar P.G. (2012). Achievements and prospects of breeding researches on soybean (*Glycine max*) in India. *The Indian J. Agricult. Sci.*, **65(1)**.
- Chandel, K.K., Patel N.B. and Patel J.B. (2013). Genetic variability analysis in Soybean [*Glycine max* (L.) Merrill]. *AGRES–An Int. e-J.*, **2(3)**, 318-325.
- Chauhan, G.S., Verma N.S. and Bains G.S. (1988). Effect of extrusion processing on the nutritional quality of protein

in rice-legume blends. *Nahrung*, **32(1)**, 43.

- Chauhan, O.P., Chauhan G.S., Singh G., Kumbhar B.K. and Mishra D.P (2002). Varietal variability in the contents of nutrients and anti-nutrients in different parts of soybean seeds. *J. Rural Agric Res.*, **2(2)**, 42-50.
- Concibido, V., La Vallee B., Mclaird P., Pineda N., Meyer J., Hummel L. and Delannay X. (2003). Introgression of a quantitative trait locus for yield from *Glycine soja* into commercial soybean cultivars. *Theoret. Appl. Gen.*, **106**, 575-582.
- Fisher, R.A. (1919). XV.—The correlation between relatives on the supposition of Mendelian inheritance. *Earth Environ. Sci. Trans. Royal Soc. Edinburgh*, **52(2)**, 399- 433.
- Fisher, R.A. and Yates F. (1938). Statistical tables for biological, agricultural and medical research London. *UK: Oliver and Boyd.*
- Ghosh, J., Ghosh P.D. and Choudhury P.R. (2014). An assessment of genetic relatedness between soybeans [*Glycine max* (L.) Merrill] cultivars using SSR markers. *Amer. J. Plant Sci.*, **05**, 3089-3096.
- Girija, M. and Dhanavel D. (2009). Mutagenesis and efficiency of gamma rays Ethyl Methan Sulphonate and their combined treatments in cowpea (*Vinga anguiculata* L.). *Glob. J. Mole. Sci.*, **4**, 68-75.
- Gopinath, P. and Pavadai P. (2015). Morphology and Yield parameters and Biochemical analysis of Soybean [*Glycine max* (L.) Mrr.] using Gamma rays, EMS and DES treatment. *Int. Lett. Nat. Sci.*, **08**.
- Haneef, I., Khan A.H., Aslam R., Gulfishan M. and Choudhary S. (2013). Assessment of genotoxicity of ethylmethane sulphonate (EMS) in two varieties of Lentil (*Lens culinaris* Medik.). *Biosci. Int.*, **2(1)**, 01-04.
- Hipparagi, Y., Singh R., Choudhury D.R. and Gupta V. (2017). Genetic diversity and population structure analysis of Kala bhat [*Glycine max* (L.) Merrill] genotypes using SSR markers. *Hereditas*, **154**, 1-11.
- Hofmann, N.E., Raja R., Nelson R.L. and Korban S.S. (2004). Mutagenesis of embryogenic cultures of Soybean and detecting polymorphisms using RAPD markers. *Biologia Plantarum*, **48**, 173-177.
- Jaya, R., Lavanaya G.R., Narendra K. and Khedar O.P. (2014). Evaluation of gamma rays induced genetic variability and divergence in M₃ generation of mungbean. *Int. J. Agricult. Innov. Res.*, **3(1)**, 161-164.
- Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agron. J.*, **47(7)**, 314-318.
- Kavithamani, D., Kalamani A., Vanniarajan C. and Uma D. (2008). Mutagenic effectiveness and efficiency of gamma rays and EMS in Soybean [*Glycine max* (L.) Merrill]. *Madras Agricult. J.*, **95**(Jul-Dec), 1.
- Khan, M.H. and Tyagi S.D. (2013). A review on induced mutagenesis in Soybean. *J. Cereals and Oilseeds*, **4(2)**, 19-25.
- Kim, D.G., Lyu J.I., Lee M.K., Kim J.M., Hung N.N., Hong M.J. and Kwon S.J. (2020). Construction of soybean mutant diversity pool (MDP) lines and an analysis of their genetic relationships and associations using TRAP markers. *Agronomy*, **10(2)**, 253.
- Kim, M.Y., Shin J.H., Kang Y.J., Shim S.R. and Lee S.H. (2012). Divergence of flowering genes in Soybean. *J. Biosci.*, **37(5)**, 857-870.
- Kumar, A. (2003). Genetic analysis of yield and its components in Soybean. *M.Sc.(Ag). Thesis*. IGKV, Raipur. 49-51.
- Li, C., Nguyen V., Liu J., Fu W., Chen C., Yu K. and Cui Y. (2019). Mutagenesis of seed storage protein genes in Soybean using CRISPR/Cas9. *BMC Research Notes*, **12**, 1-7.
- Li, Z., Jiang L., Ma Y., Wei Z., Hong H., Liu Z. and Qiu L. (2017). Development and utilization of a new chemically induced soybean library with a high mutation density. *J. Integ. Plant Biol.*, **59(1)**, 60-74.
- Lush, J.L. (1949). Heritability of quantitative characters in farm animals. *Heritability of Quantitative Characters in Farm Animals.*
- Panse, V.G. and Sukhatme P.V. (1967). *Statistical Mthods for Agricultural Workers*. 4th Edn. ICAR, New Delhi, pp. 228-232.
- Mahto, J.L. (2016). Variability, Correlation, and Path Analysis in Fababean (*Vicia faba*) for Drought tolerant in alfisols of Jharkhand. *Madras Agric. J*., **103**.
- Malagouda, Patil, Basamma Kumari and Jagadeesh B.N. (2014). Root dynamics in Soybean (*Glycine max* L.) under two moisture regimes. *Soybean Research*, **12(1)**, 59-68.
- Malek, M.A., Raffi M.Y., Afroj M.S.S., Nath U.K. and Mondol M.M.A. (2014). Morphological characterization and assessment of genetic variability, character association and divergence in soybean mutants. *The Scientific World J.*, 1-12.
- Malek, M.A., Rafii M.Y., Afroz S.S., Nath U.K. and Mondal M. (2014). Morphological characterization and assessment of genetic variability, character association and divergence in soybean mutants. *The Scientific World J.*, *2014*.
- Miranda, C., Scaboo A., Cober E., Denwar N. and Bilyeu K. (2020). The effects and interaction of soybean maturity

gene alleles controlling flowering time, maturity, and adaptation in tropical environments. *BMC Plant Biol.*, **20**, 1-13.

- Naik, S.M., Madhusudan K., Motagi B.N. and Nadaf H.L. (2016). Diversity in soybean (*Glycine max*) accessions based on morphological characterization and seed longevity characteristics. *Progressive Res.–An Int. J.*, **11(03)**, 377-381.
- Osekita, O.S. and Olorunfemi O. (2014). Quantitative genetic variation, heritability and genetic advance in the segregating F³ populations in Soybean [*Glycine max* (L.) Merrill.]. *Intl J Adv Res.*, **2(7)**, 82-89.
- Panse, V.G. and Sukhatme P.V. (1985). *Statistical Methods for Agricultural Workers*. ICAR, New Delhi: 357.
- Patil, A., Taware S.P., Oak M.D., Tamhankar S.A. and Rao V.S. (2007). Improvement of oil quality in Soybean [*Glycine max* (L.) Merrill] by mutation breeding. *J. Amer. Oil Chemists' Soc.*, **84(12)**, 1117-1124.
- Prasad, B., Bahuguna A. and Shukla D.K. (2012). Geno typic variation studies of perilla (*Perilla prutescens* L.) germplasm under north-west Himalayan agrisystem. *Environ. Ecol.*, **30(4)**, 1235-1237.
- Ramteke, R. and Murlidharan P. (2012). Characterization of soybean (*Glycine max*) varieties as per DUS guidelines. *Indian J. Agricult. Sci.*, **82(7)**, 572-577.
- Singh, R.J. and Hymowitz T. (1999). Soybean genetic resources and crop improvement. *Genome*, **42(4)**, 605-616.
- Smit, A. (2019). Yield Stability of Edamame (*Glycine max* L.) Introductions under South African production conditions (*Doctoral dissertation*, University of the Free State Bloemfontein).
- SoyStats (2016). *A Reference Guide to Important Soybean Facts & Figures.* St. Louis, MO: American Soybean Association.
- Sudaric, A. and Vrataric M. (2003). Variability and interrelationships of grain quantity and quality characteristics in Soybean. *Bodenkultur-Wien and Munchen*, **53(3)**, 137-142.
- Tulmann Neto, A. and Alves M.C. (1997). Induction of mutations for earliness in the soybean cultivar Paraná. *Brazilian J. Gen.*, **20**, 45-50.