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Genetic variability studies in mutant PVK 801 genotype of sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract

The present investigation was undertaken on “Study on induced mutations in *Kharif* sorghum (*Sorghum bicolor* L.)”. The experimental material comprised of different mutagenic treatments treated with different concentrations *viz.*, 0.1%, 0.2%, 0.3% were EMS treatments and 10 kR + 0.1% EMS, 20 kR + 0.1% EMS, 30 kR + 0.1% EMS and 40 kR + 0.1% EMS were combination treatments and dry and wet control treatments of sorghum cultivar “PVK 801”. All these treatments were grown in randomized block design with three replications during *kharif* 2019. The genetic variability was significant for yield and yield contributing characters among the M₂ generation. The better mean performance in 20 kR + 0.1% EMS treatment was recorded for most of the characters. The GCV and PCV estimates showed wide variation for most of the characters in segregating M₂ generation. The high GCV, PCV, heritability and GAM were observed for number of grains per primary and grain yield per plant.

Keywords: Sorghum, genetic variability, mutation, heritability, gamma rays, EMS

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is an important staple food crop for more than 300 million people and feed for cattle in Asia and Africa. Sorghum is often cross pollinated, diploid ($2n = 2x = 20$) and belongs to the family Poaceae. Sorghum is the fourth most important cereal crop followed by rice, wheat and maize. Cultivated sorghums originated about 5000-7000 years ago or earlier in Northern East Africa, probably in Sudan or Ethiopia. After domestication these moved to other parts of India, Africa, Europe and China. Sorghum was introduced into the Western hemisphere during the 17th and 18th centuries. Mutation breeding is an important method to generate variability for quantitatively inherited traits in different plants and is considered as an alternative method for raising genetic variability in plant breeding (De Oliveira Camargo *et al.*, 2000) [4]. Genetic variations induced by mutation represent a more efficient source of genetic variability than gene pools conserved by nature. Gamma radiation and EMS are important tool for inducing the genetic variability, enhancing yield and yield contributing traits. Genetic variability for economic traits or characters is the pre-requisite for any good breeding programmer as the degree of response to selection depends on the quantum of variability. The present investigation was undertaken to study the effect of physical and chemical mutagens on induction of viable mutation.

Material and Method

The present study was undertaken at the field of Department of Agricultural Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The pure seed of PVK 801 variety of sorghum (*Sorghum bicolor* (L.) Moench) was selected for mutagenic treatment. Seven different mutagenic treatments of PVK 801 *viz.*, T1 (0.1%), T2 (0.2%), T3 (0.3%) EMS treatments and T4 (10kR+0.1% EMS), T5 (20kR+0.1% EMS), T6 (30kR+0.1% EMS) and T7 (40kR+0.1% EMS) combination treatments obtained from B.A.R.C. Trombay, Mumbai, along with two control treatments *viz.*, T8 (dry control) and T9 (wet control) were sown in *Randomized Block Design* with 3 replications, at spacing of 15 cm within plants and 45 cm between plants in M₂ generation. The observations were recorded on following eleven characters. Days to panicle initiation, days to 50% flowering, days to maturity, plant height (cm), number of primaries per panicle, number of grains per primary, panicle length (cm), panicle width (cm), flag leaf area (cm²), grain yield per plant (g) and 100 seed weight. The mean values were used for statistical analysis. The data was analyzed statistically for genotype and phenotype coefficients of variation (Burton, 1952) [3], Heritability (Allard, 1960) [1] and genetic advance (Johnson *et al.*, 1955) [5].

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Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2) and genetic advance as percentage of mean (GAM) were calculated using the following equations.

$$GCV (\%) = [(\sigma^2g)^{1/2}/\bar{X}] \times 100$$

$$PCV (\%) = [(\sigma^2p)^{1/2}/\bar{X}] \times 100$$

$$h^2 (\%) = (\sigma^2g/\sigma^2p) \times 100$$

$$GAM = (k \times \sigma p \times h^2) / \bar{X}$$

Where; \bar{X} = mean value, σ^2g = genotypic variance, σ^2p = phenotypic variance, σp = phenotypic standard deviation, k = 2.64, constant for 1% selection intensity.

Results and Discussion

The results of analysis of variance for M_2 generation of *kharif* sorghum are evaluated in Table 1. Highly significant differences among the genotypes were observed for eleven characters indicating presence of sufficient amount of variability among genotypes for these eleven characters. Variation for yield and some yield contributing character was also reported earlier by Khaing wah htun *et al.* (2015) [6].

The genetic components *viz.*, genotypic variance, phenotypic variance, genotypic co-efficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance (GA) and genetic advance as the per cent of mean (GAM) were worked out using appropriate statistical formulae for all sixteen characters in M_2 generation of *Kharif* sorghum. The results are presented in Table 2.

In the present investigation, though the phenotypic coefficient of variation was greater than genotypic coefficient of variations, the differences between them were of lower magnitude i.e. they were more or less close to each other. This indicates that there is small effect of environment on characters and selection may be effective. GCV and PCV values were categorized as low (0- 10%), moderate (10-20) and high (20% and above) as indicated by Sivasubramanian and Menon (1973) [11].

The higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) for all the characters was studied by Khaing Wah Htun *et al.*, (2015) [6] in sorghum. According to Johnson *et al.*, (1955) [5] the expected genetic advance is categorized into less than 10% as low, 10-20% as moderate and more than 20% as high expected genetic advance.

The low GCV (2.83) and PCV (3.01) were recorded for days to panicle initiation in the M_2 generation with high heritability (88.25) and low genetic advance (3.55). These type of similar

results are in accordance with the findings Khaing Wah Htun *et al.* (2015) [6].

The low genotypic (3.41) and phenotypic coefficient of variation (3.79) were observed for days to 50% flowering in M_2 generation. Similar results were reported by Wani (2011) in chick pea. High heritability (80.91) coupled with low expected genetic advance (4.69). Low estimates of genotypic (2.10) and phenotypic (2.31) coefficient of variation were observed for days to maturity. High heritability (82.78) coupled with low expected genetic advance (4.52) was observed for days to maturity.

The moderate estimates of genotypic (10.41) and phenotypic (11.05) coefficient of variation were observed for plant height. These results are in accordance with the findings of Sanjeevsingh (2009) [10] exhibited moderate phenotypic and genotypic coefficient of variation for plant height. High heritability (88.62) with high expected genetic advance (34.43) were observed for plant height and this type of similar results were reported by Nang Htwe Kham *et al.* (2015) [8] sorghum. Low estimates of genotypic (5.38) and phenotypic (6.15) coefficient of variation were observed number of primaries per panicle with high heritability (76.71) with low expected genetic advance (5.12). Similar results of low GCV, PCV, heritability and genetic advance were also reported by Potdukhe *et al.* (1994) [9].

High estimates of genotypic (20.51) and phenotypic (21.06) coefficient of variation were observed with high estimates of heritability (94.87) with moderate expected genetic advance (14.03) and high GAM (41.16) were observed for number of grains per primary. The results obtained are in agreement with the observations of Mahajan *et al.* (2011) [7] in Sorghum. The low genotypic and phenotypic coefficient of variation were observed with high estimates of heritability with low expected genetic advance were observed for panicle length and width.

In the flag leaf area observed low genotypic (5.58) and phenotypic (6.25) coefficient of variation with high heritability (79.85) and high expected genetic advance (24.71). The high estimates of genotypic (106.16) and phenotypic (113.31) coefficient of variation were observed for grain yield per plant, similar result were observed by Anand and Kajidoni (2014) [2] and high heritability (93.69) and high genetic advance (20.54) similar result were observed by Nang Htwe Kham *et al.*, (2015) [8] in sorghum.

The low estimates of genotypic (7.73) and phenotypic (9.27) coefficient of variation were observed for 100 seed weight with the high heritability (69.68) and low expected genetic advance (0.35). Similar findings were reported by Anand and Kajidoni (2014) [2] and Khaing Wah Htun *et al.*, (2015) [6].

Table 1: Analysis of variance for various characters in M_2 generation of PVK 801 sorghum genotype

Source of variation	D.F.	Mean sum of squares										
		Days to panicle initiation	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primaries per panicle	Number of grains per primary	Panicle length (cm)	Panicle width (cm)	Flag leaf area (cm ²)	Grain yield per plant (g)	100 seed weight (g)
		1	2	3	4	5	6	7	8	9	10	11
Replication	2	20.91	4.23	2.77	45.29	2.75	4.34	0.52	0.44	27.69	22.27	0.013
Treatment	8	84.72**	165.81**	149.49**	986.56**	213.31**	149.36**	78.44**	2.19**	586.43**	325.65**	0.15**
Error	16	7.19	24.16	19.27	40.49	39.26	2.64	25.29	0.20	45.48	7.14	0.019

*and ** indicates significance at 5% and 1% level, respectively

Table 2: Genetic variability parameters for yield and yield contributing characters in M_2 generation of PVK 801 sorghum genotype

Sr. No.	Characters	Range	GM	GV (%) (σ^2g)	PV (%) (σ^2p)	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	GAM (%)
1	Days to panicle initiation	61.73-67.60	64.84	3.38	3.83	2.83	3.01	88.25	3.55	5.48
2	Days to 50% flowering	69.93-77.33	72.22	6.40	7.91	3.41	3.79	80.91	4.69	6.31
3	Days to maturity	109.86-117.46	114.49	5.82	7.03	2.10	2.31	82.78	4.52	3.95
4	Plant height (cm)	165.00-175.60	170.57	315.35	355.84	10.41	11.05	88.62	34.43	20.18

5	No. of primaries per panicle	48.00-56.13	52.74	8.07	10.52	5.38	6.15	76.71	5.12	9.71
6	No. of grains per primary	31.26-36.20	34.09	48.90	51.54	20.51	21.06	94.87	14.03	41.16
7	Panicle length (cm)	19.93-24.06	21.87	2.74	4.32	7.57	9.50	63.42	2.71	12.41
8	Panicle width (cm)	6.04-7.49	6.86	0.66	0.87	11.87	13.61	76.03	1.46	21.32
9	Flag leaf area (cm ²)	232.60-250.93	240.40	180.31	225.80	5.58	6.25	79.85	24.71	10.28
10	Grain yield per plant (g)	47.00-56.00	51.08	106.16	113.31	20.17	20.83	93.69	20.54	40.22
11	100 seed weight (g)	2.58-2.94	2.70	0.04	0.06	7.73	9.27	69.68	0.35	13.30

Reference

- Allard RW. Principal of Plant Breeding. John Wiley and Sons, Inc., New York 1960, P84-85.
- Anand Y, Kajidoni ST. Genetic enhancement of grain size and other productivity related traits through induced variability in *kharif* sorghum. Karnataka Jr. Agric. Sci 2014;27(2):121-124.
- Burton GW. Quantitative inheritance in grasses. Proc. Sixth Int. Grassland Cong 1952;1:227-283.
- De Oliveira Camargo CE, Neto AT, Ferreira Filho AW, Felicio JC. Genetic control of aluminum tolerance in mutant lines of the wheat cultivar Anahuac. Euphytica 2000;114(1):47-53.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agron J 1955;47:314-318.
- Khaing Wah Htun, Myat Min, Nay Chi Win. Evaluation of genetic variability for agronomic traits in M₂ generation of sorghum through induced mutation. International Journal of Technical Research and Applications 2015;3(6):145-149.
- Mahajan RC, Wadikar PB, Pole SP, Dhuppe MV. Variability, correlation and path analysis studies in sorghum. Res J Agric. Sci 2011;2(1):101-103.
- Nang Htwe Kham, Nay Chi Win, Myat Min. Study on the variability of induced mutation for improvement of local cultivar sorghum (shweni-15). International Journal of Technical Research and Applications 2015;3(6):139-144.
- Potdukhe NR, Shekar VB, Thote SG, Wanjari SS, Ingle RW. Estimates of genetic parameters, correlation coefficients and path analysis in grain sorghum (*Sorghum bicolor* (L.) Moench). Crop Res., Hisar 1994;7(3):402-406.
- Sanjeevsingh SR. Variability studies for yield and downy mildew in F₂ segregating material of *kharif* Sorghum [*Sorghum bicolor* (L.) Moench] M. Sc. (Agri.) Thesis, Univ. Agric. Sci., Dharwad (India) 2009.
- Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agric J 1973;60:1139.