**Induction of genetic variability through mutagenesis in *rabi* sorghum [*Sorghum bicolor* (L.) Moench]**

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**Abstract**

The 'TSV-32' *rabi* sorghum genotype was exploited to create a mutation by electron beam. The experimental material included several electron beam dosages viz., 100 Gy, 200 Gy, 300 Gy, 400 Gy, and 500 Gy as well as wet and dry control seeds. Individual plants were selfed, harvested and recorded for putative mutations that might have been present in the M1 generations. During rabi 2022-23, the M2 generation, which comprised total of 36 mutant progenies from seven different treatments, was assessed using random block design with three replications. Among M2 generation, genetic variability was significant for yield and yield contributing traits. In most of the treatments, relative higher mean performance was seen as compared to control for all traits, with the exception of days to 50% flowering, days to maturity, number of grains per primary, panicle width and 100 seed weight. For the majority of the characters in the segregating M2 generation, the GCV and PCV values revealed significant variability. Moderate GCV, PCV, heritability and GAM values were found for grain yield per plant,100 seed weight.

**Keywords:** *rabi* Sorghum, Electron beam, mutation, genetic variability, heritability.

**Introduction**

Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most significant cereal in the world in terms of area and production. It is an often cross-pollinated, diploid (2n = 2x = 20) plant that is a member of the Poaceae family. The primary jowar producing states in the nation include Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Gujarat, Rajasthan, Uttar Pradesh (Bundelkhand region) and Tamil Nadu.

 Mutation breeding has played a beneficial role in sustainable agriculture, since it is a complementary strategy for crop development that promotes unselected genetic variability for useful breeding application. Due of the extremely low frequency of natural mutation, induced mutations are employed to increase genetic variability for both quantitative and qualitative parameters. Among various physical mutagens such as x-rays, fast neutrons, thermal neutrons, ultraviolet and beta radiation, gamma rays, electron beam in particular are well known with their effect on the plant growth and development by inducing cytological, physiological and morphological changes in cells (Thapa, 2004). Several reports are available, where breeders are used gamma radiations as a source for inducing genetic variability in quantitative characters for enhancing yield and yield contributing traits. Recently, high power linear electron accelerators in the range of 500 keV – 10 MeV energy have gained importance for various applications. The accelerators work in switch-on-off mechanism like in X-ray facilities. It produces electron beam, which can be used for irradiating materials in a high-throughput manner. Electron beam radiation is an important tool for inducing the genetic variability, enhancing yield and yield contributing traits.

 Genetic variability for economic traits is the pre-requisite for any successful breeding programmers as the degree of response to selection depends on the quantum of variability. In any crop, yield being a complex character influenced by many of its contributing characters controlled by polygene and the environmental factors. So, an understanding of genetics of yield and its component traits.

 ‘TSV-32’ *rabi* sorghum genotype was choosen as base material. It was selection from CSV-20 X Phule Anuradha. This is the early maturing (47-55 days to 50% flowering) sorghum genotype. The variability present in this segment is very low. Under these circumstances, creating variability through induced mutation will add more scope for improvement in *rabi* sorghum. The primary focus of the current research on the inducing genetic variability in sorghum (TSV-32) through Electron beam.

**Materials and Method**

 The present investigation was undertaken in sorghum (*Sorghum bicolar* (L.) Moench) at Dept. of Agricultural Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. during *rabi* 2022-23. which is situated at the latitude of 19o 24' N, longitude of 76o 78' E and altitude of 458.38 m above mean sea level (msl), with the soil type of shallow to medium black.

Pure selfed seeds (1200) of TSV-32 with 10 per cent moisture content were exposed to 100, 200, 300, 400 and 500 Gy dose of electron beam radiation from electron accelerator at Nuclear Agriculture & Biotechnology Division, BARC Trombay, Mumbai and sown as M1 generation along with the same number of untreated seeds of each variety served as control seeds during *rabi* 2021-22.

Dominant mutations observed in the M1 generations were recorded and individual plants were selfed, harvested, and used to raise the M2 generation during *rabi* 2022-23. A total thirty Six (36) selfed progeny selected from each treatment was grown in head to row progeny in M2 generation in randomized block design with seven treatments including 2 control and three replications. The observations were recorded on 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 (g), 100 grain weight (g), grain yield per plant (g) and fodder yield per plant (g), Relative water content (%), Chlorophyll content (SPAD values), Leaf area (cm2), Flag leaf area (cm2)*.*The standard statistical approach for the Random block design (RBD) described by Panse and Sukhatame (1954) was used to analyse the variance for differences between and within families. According to the method recommended by Burton (1952) and Allard (1960), **t**he variability parameters, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance were estimated.

**Results and Discussion**

The results of analysis of variance for M2 generation of *rabi* sorghum are furnished in Table 1. Highly significant differences among the genotypes were observed for fourteen characters indicating presence of sufficient amount of variability among genotypes for these fourteen characters.

For all fourteen of the traits under consideration, the mean sums of squares due to progenies within families were found to be highly significant, demonstrating that progenies within the family differ from one another. Anand and Kajjidoni (2014), Ambli and Mullainathan (2015), Htun et al. (2015), Kham et al. (2015), Suthakar and Mullainathan (2015) and Takele et al. (2021) have all observed such variation for yield and yield attributing traits. The outcome of the variability parameters is shown in (Table 2). For each of the fourteen characters in the M2 generation of sorghum, the genetic components; genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (in broad sense), genetic advance (GA) and genetic advance as the percent of mean (GAM) were calculated using the proper statistical formulas. The results are presented in Table 2.

(PCV) was found to be higher than the genotypic coefficient of variation (GCV) for all the characters with extremely minor differences, indicating a substantial genetic influence. Anand and Kajiidoni (2014), Kham et al. (2015), Shivaprashad et al. (2019), Htun et al. (2015) and Thange et al. (2021) were in agreement with these findings. GCV and PCV values for grain yield per plant were moderate (15.97% and 18.19%, respectively), indicating moderate variability across progenies for this character and greater possibility for improving this character by selection in the appropriate direction. Additionally, the progeny showed moderate GCV and PCV values for the 100 seed weight (8.36% and 13.25%), and flag leaf area (6.08% and 10.38%). The other variables such as days to 50% flowering (1.32% and 1.99%), plant height (3.24% and 3.86%), days to maturity (0.47% and 1.11%), number of primaries per panicle (2.15% and 3.23%), number of grains per primary (2.00% and 2.49%), panicle length (cm) (1.66% and 2.63%), panicle width (g) (2.62% and 3.96%), fodder yield per plant (g) (6.15% and 9.17%), Relative water content (%) (2.53% and 4.96%), Chlorophyll content (SPAD values) (7.40% and 9.11%) and Leaf area (cm2) (3.60% and 5.13%). This characters and had low GCV and PCV levels. Low PCV values with marginally low GCV values in these traits suggested a limited level of variability in the materials and a low likelihood of genetic improvement. This suggests that the level of variability and the odds of genetic improvement are moderate. Similar results were found for grain yield per plant by Patel et al., (1980b), Kumar and Singh (1986), Cheralu and Rao (1989), Biradar et al. (1996); for days to flowering and days to maturity by Nimbalkar et al. (1988), Nguyen et al. (1998), Narkhede et al, (2001); for plant height by Patel et al. (1980a), Patel et al., (1980b), Singh et al., (1980), Amrithadevarathinam et al. (1994), Nguyen et al. (1998); for panicle length and chlorophyll content (spad values) by Narkhede et al, (2001); for 100 grain weight by Nguyen et al. (1998), Negash et al., (2005); for relative water content by Pawar (2007); for leaf area by Amanullah et al. (2007), Ali et al. (2009a) and flag leaf area by Ali et al. (2009a).

High heritability was observed for grain yield per plant (77.05%), plant height (70.53%), number of grains per primary (64.49%), and chlorophyll content (SPAD values) (66.00%). Additionally, the progeny showed moderate heritability for days to 50% flowering (44.12%), number of primaries per panicle (44.38%), panicle length (39.67%), panicle weight (43.62%), 100 grain weight (39.84%), fodder yield per plant (44.98%), leaf area (49.15%) and flag leaf area (34.28%). This suggests that the genotypic effect of phenotypes may be well measured and that selection may be effectively used to enhance these traits. These results are conformity with the results reported by Khaing Wah Htum et al., (2015). Anand and Kajidoni (2014). Nang Htwe Kham et al., (2015) in sorghum, Kole et al. (2008) in rice.

The characters viz., plant height (9.99%), leaf area (28.83%), flag leaf area (21.08%), and grain yield per plant (15.73%)all showed moderate genetic advance. Supporting results were observed by Khaing Wah Htum et al., (2015). Anand and Kajidoni (2014). Nang Htwe Kham et al., (2015) in sorghum, Kole et al. (2008) in rice. The traits with low estimates of genetic advance were days to 50% flowering (1.16%), days to maturity (0.48%), number of primaries per panicle (1.54%), number of grains per primary (3.47%), panicle length (cm) (0.48%), panicle width (g) (0.26%), 100 grain weight (g) (0.25%), fodder yield per plant (g) (3.92%), Relative water content (%) (1.26%) and Chlorophyll content (SPAD values) (6.28%). Shivaprashad et al. (2019) and Thange et al. (2021) discovered similar results for these traits.

In predicting selection response, heritability combined with genetic advance is more valuable than heritability alone. Plant height, grain yield per plant, number of grains per primary and leaf area all these traits showed high heritability and moderate genetic advance, which indicates the role of additive gene effects and least effects of environmental factors on the expression of the traits. Thus, simple phenotypic selection offers a greater potential for improving these traits**.** Muduli and Misra (2008), Anand and Kajjidoni (2014), Shivaprashad et al. (2019) and Thange et al. (2021) all found comparable results for these traits.

High heritability coupled with low genetic advance was observed for number of grains per primary and chlorophyll content (SPAD values) indicating non additive gene action. So, these traits cannot be improved through simple selection. Similar results were also observed by Shivaprashad et al. (2019) and Thange et al. (2021).

**Table 1**: Analysis of variance for yield and yield contributing characters in *rabi* sorghum

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **df** | **DFF** | **PH (cm**) | **DM** | **NPPP** | **NGPP** | **PL (cm)** | **PW (cm)** |
| **Treatments** | **6** | 3.05\* | 114.07\*\* | 2.19\* | 5.33\* | 15.56\*\* | 0.62\* | 0.16\* |
| **Replication** | **2** | 0.90 | 9.22 | 0.14 | 3.57 | 8.19 | 0.24 | 0.17 |
| **Error** | **12** | 0.90 | 13.95 | 1.31 | 1.57 | 2.41 | 0.21 | 0.05 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **df** | **100 SW (g)** | **FYPP (g)** | **RWC (%)** | **CC (spad values)** | **LA (cm2)** | **FLA (cm2)** | **GYPP (g)** |
| **Treatments** | **6** | 0.16\* | 33.99\* | 8.38\* | 49.50\*\* | 1668.02\*\* | 1501.3\*\* | 249.54\*\* |
| **Replication** | **2** | 0.14 | 30.46 | 2.27 | 24.99 | 668.9 | 286.2 | 27.98 |
| **Error** | **12** | 0.05 | 9.84 | 4.08 | 7.25 | 412.3 | 585.3 | 22.54 |

 \* and \*\* Significant at 5 % and 1% level of significance, respectively.

DFF= Days to 50% Flowering, PH= Plant Hight, DM= Days to Maturity, NPPP= Number of Primaries Per Panicle, NGPP= Number of Grains Per Primary, PL= Panicle Length PW= Panicle Width, 100 SW= 100 Seed Weight, FYPP= Fodder Yield Per Plant, RWC= Relative Water Content, CC= Chlorophyll Content, LA= Leaf Area, FLA= Flag Leaf Area , and GYPP= Grain Yield Per Plant.

**Table 2:** Genetic variability parameters for yield and yield contributing characters in M2 generation of *rabi* sorghum.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sr. No.** | **Characters** | **Mean** | **G V (%)** | **P V (%)** | **GCV (%)** | **PCV (%)** | **H2bs****(%)** | **GA (%)** | **GAM (%)** |
| 1 | **Days to 50% Flowering** | 64 | 0.71 | 1.62 | 1.32 | 1.99 | 44.12 | 1.16 | 1.81 |
| 2 | **plant height (cm)** | 178.3 | 33.37 | 47.32 | 3.24 | 3.86 | 70.53 | 9.99 | 5.61 |
| 3 | **Days to maturity** | 114 | 0.29 | 1.60 | 0.47 | 1.11 | 18.32 | 0.48 | 0.42 |
| 4 | **No. of primaries per panicle** | 52 | 1.25 | 2.83 | 2.15 | 3.23 | 44.38 | 1.54 | 2.96 |
| 5 | **No. of grain per primaries** | 105 | 4.38 | 6.79 | 2.00 | 2.49 | 64.49 | 3.47 | 3.31 |
| 6 | **Panicle length [cm]** | 22.3 | 0.14 | 0.34 | 1.66 | 2.63 | 39.67 | 0.48 | 2.15 |
| 7 | **Panicle width [cm]** | 7.3 | 0.04 | 0.08 | 2.62 | 3.96 | 43.62 | 0.26 | 3.56 |
| 8 | **100 seed wight[g]** | 2.3 | 0.04 | 0.09 | 8.36 | 13.25 | 39.84 | 0.25 | 10.87 |
| 9 | **Fodder yield per plant[g]** | 46.1 | 8.05 | 17.89 | 6.15 | 9.17 | 44.98 | 3.92 | 8.50 |
| 10 | **Relative water content [%]** | 47.4 | 1.43 | 5.51 | 2.53 | 4.96 | 26.02 | 1.26 | 2.66 |
| 11 | **Chlorophyll content [spad values]** | 50.7 | 14.08 | 21.34 | 7.40 | 9.11 | 66.00 | 6.28 | 12.39 |
| 12 | **Leaf area [cm2]** | 555.3 | 398.61 | 810.93 | 3.60 | 5.13 | 49.15 | 28.83 | 5.19 |
| 13 | **Flag leaf area[cm2]** | 287.6 | 305.34 | 890.64 | 6.08 | 10.38 | 34.28 | 21.08 | 7.33 |
| 14 | **Grain yield per plant[g]** | 54.5 | 75.67 | 98.21 | 15.97 | 18.19 | 77.05 | 15.73 | 28.87 |

GV = Genotypic variance (σ2 g) (%), GCV = Genotypic coefficient of variation (%) PV = phenotypic variance (σ2 p) (%), PCV = Phenotypic coefficient of variation (%) h2 bs = Heritability (Broad sense) (%), GAM = Genetic Advance as per cent of mean (%)

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