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**Divya Patel**  
Department of Genetics and  
Plant Breeding, Navsari  
Agricultural University,  
Navsari, Gujarat, India

**BK Davda**  
Main Sorghum Research Station,  
Navsari Agricultural University,  
Athwa Farm, Surat, Gujarat,  
India

**KG Modha**  
Department of Genetics and  
Plant Breeding, Navsari  
Agricultural University, Navsari,  
Gujarat, India

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

Divya Patel, BK Davda and KG Modha

### Abstract

The 'Wani Local' sorghum genotype was exploited to create a mutation by gamma radiation. The experimental material included several gamma radiation dosages viz., 100 Gy, 200 Gy, 300 Gy, 350 Gy, 400 Gy and 500 Gy as well as control seeds. Individual plants were selfed, harvested and recorded for putative mutations that might have been present in the M<sub>1</sub> generations. During *rabi* 2022-23, the M<sub>2</sub> generation, which comprised total of 120 mutant progenies from six different treatments, was assessed using compact family block design with three replications. Among M<sub>2</sub> 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 and panicle length. For the majority of the characters in the segregating M<sub>2</sub> generation, the GCV and PCV values revealed significant variability. High GCV, PCV, heritability and GAM values were found for grain yield per plant, panicle weight, straw yield per plant and harvest index.

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

### 1. Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most significant cereal in the world in terms of area and production. It can be cultivated for its grain (grain sorghum), its sweet sap (sweet sorghum) or as a fodder (forage sorghum). 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 many physical mutagens, including beta radiation, fast neutrons, thermal neutrons and X-rays. It is widely recognised that gamma rays in particular have an impact on plant growth and development by causing cytological, physiological and morphological changes in cells and tissues (Thapa, 2004) [17]. Physical mutagens, like gamma rays, are powerful and effective with shorter wavelength and higher energy per photon as compared to X-rays, which penetrate the surface and cause ionisation. Genetic variability for economic characteristics is required for every successful breeding programme since the degree of responsiveness to selection is proportional to the magnitude of variability.

The Ponk (hurda) sorghum is a new and more remunerative segment of sorghum. The Wani local is mainly cultivated in Gujarat state for the production of tender grain which is also known as "Andhali Wani" due to characteristic of very small opening of flower and grains are mostly covered by glume. The variability present in this segment is very low. Under these circumstances, creating variability through induced mutation will add more scope for improvement in *Ponk* sorghum. The primary focus of the current research on the inducing genetic variability in sorghum (Wani Local) through gamma radiation.

### 2. Materials and Method

The current investigation was conducted at the Main Sorghum Research Station (MSRS), NAU, Athwa farm, Surat, Gujarat during *rabi* 2022-23. Seeds of sorghum genotype *Wani* local were irradiated with gamma rays at BARC, Trombay, Mumbai at dosages of 100 Gy, 200 Gy, 300 Gy, 350 Gy, 400 Gy and 500 Gy and sown as M<sub>1</sub> generation along with control seeds during *rabi* 2021-22.

**Corresponding Author:**  
**Divya Patel**  
Department of Genetics and  
Plant Breeding, Navsari  
Agricultural University,  
Navsari, Gujarat, India

Dominant mutations observed in the  $M_1$  generations were recorded and individual plants were selfed, harvested, and used to raise the  $M_2$  generation during *rabi* 2022-23. A total of 120 mutant progenies from the  $M_2$  generation were assessed in a compact family block design with six treatments and three replications. The observations were recorded on days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), panicle weight (g), 100 grain weight (g), grain and straw yield per plant (g) and harvest index (%). The standard statistical approach for the compact family block design (CFBD) described by Panse and Sukhatame (1978) [11] was used to analyse the variance for differences between and within families. According to the method recommended by Burton (1952) [4] and Allard (1960) [1], the variability parameters, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance were estimated.

### 3. Results and Discussion

In results, for all of the traits under study, the analysis of variance indicated significant differences between the families and progenies, demonstrating the presence of considerable amounts of genetic variability in the experimental materials (Table 1). For all nine 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) [3], Ambli and Mullainathan (2015) [14], Htun *et al.* (2015) [14], Kham *et al.* (2015) [8], Suthakar and Mullainathan (2015) [14] and Takele *et al.* (2021) [15] have all observed such variation for yield and yield attributing traits.

The outcome of the variability parameters is shown in (Table 2). Mean values showed a wide range for the days to 50% flowering (57-74), days to maturity (106-125), plant height (149.45-254.73 cm), panicle length (19.57-38.24 cm), panicle weight (30.57-95.86 g), 100 grain weight (2.80-4.13 g), grain yield per plant (16.83-60.53 g), straw yield per plant (49.19-115.56 g) and harvest index (18.19-51.53%). For each of the nine characters in the  $M_2$  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.

In the present study, phenotypic coefficient of variation (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 Kajjidoni (2014) [3], Kham *et al.* (2015) [8], Shivaprashad *et al.* (2019) [13], Htun *et al.* (2015) [6] and Thange *et al.* (2021) [16] were in agreement with these findings. GCV and PCV values for grain yield per plant were higher (26.34% and 31.69%, respectively), indicating greater variability across progenies for this character and greater possibility for improving this character by selection in the appropriate direction. Additionally, the progeny showed higher GCV and PCV values for the panicle weight (37.93% and 38.79%), straw yield per plant (19.82% and 22.79%) and harvest index (22.33% and 36.36%).

The other variables such as plant height (12.39% and 13.07%), panicle length (12.00% and 13.49%) and 100 grain weight (12.60% and 13.48%) all exhibited moderate GCV and

PCV values respectively. This suggests that the level of variability and the odds of genetic improvement are moderate. The characters days to 50% flowering (3.92% and 4.39%) and days to maturity (2.52% and 2.87%) 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.

Similar results were found for grain yield per plant by Muduli and Misra (2008) [10], Anand and Kajjidoni (2014) [3] and Shivaprashad *et al.* (2019) [13]; for days to flowering and days to maturity by Shivaprashad *et al.* (2019) [13] and Thange *et al.* (2021) [16]; for plant height by Shivaprashad *et al.* (2019) [13]; for panicle length by Raghavendra *et al.* (2023) [12]; for 100 grain weight by Kham *et al.* (2015) [8] and Shivaprashad *et al.* (2019) [13]; for panicle weight, straw yield per plant and harvest index by Raghavendra *et al.* (2023) [12] and Zinzala *et al.* (2018) [18].

High heritability was observed for days to 50% flowering (79.68%), days to maturity (76.94%), plant height (89.97%), panicle length (78.98%), panicle weight (95.63%), 100 grain weight (87.27%), grain yield per plant (69.13%), straw yield per plant (75.60%) and harvest index (71.77%). This suggests that the genotypic effect of phenotypes may be well measured and that selection may be effectively used to enhance these traits. Similar findings for plant height, days to flowering and days to maturity were also noted by Shivaprasad *et al.* (2019) [13] and Thange *et al.* (2021) [16]; for panicle length, Jayaramachandran *et al.* (2010) [7] and Anand and Kajjidoni (2014) [3]; for grain yield per plant by Kham *et al.* (2015) [8], Shivaprasad *et al.* (2019) [13] and Thange *et al.* (2021) [16]; and for 100 grain weight by Jayaramachandran *et al.* (2010) [7], Shivaprasad *et al.* (2019) [13] and Thange *et al.* (2021) [16].

The characters *viz.*, plant height (24.22%), panicle length (21.96%), panicle weight (76.42%), 100 grain weight (24.24%), grain yield per plant (45.12%), straw yield per plant (35.50%) and harvest index (38.97%) all showed high genetic advance as percent of the mean. Supporting results were observed by Muduli and Misra (2008) [10], Anand and Kajjidoni (2014) [3], Shivaprashad *et al.* (2019) [13] and Thange *et al.* (2021) [16]. The traits with low estimates of genetic advance as a percent of mean were days to 50% flowering (7.22%) and days to maturity (4.54%). Shivaprashad *et al.* (2019) [13] and Thange *et al.* (2021) [16] discovered similar results for these traits.

In predicting selection response, heritability combined with genetic advance as percent of mean is more valuable than heritability alone. Plant height, panicle length, panicle weight, 100 grain weight, grain yield per plant, straw yield per plant and harvest index all these traits showed high heritability and high genetic advance as percent of the mean, 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) [10], Anand and Kajjidoni (2014) [3], Shivaprashad *et al.* (2019) [13] and Thange *et al.* (2021) [16] all found comparable results for these traits.

High heritability coupled with low genetic advance was observed for days to 50% flowering and days to maturity indicating non additive gene action. So, these traits cannot be improved through simple selection. Similar results were also observed by Shivaprashad *et al.* (2019) [13] and Thange *et al.* (2021) [16] for days to 50% flowering and days to maturity.

**Table 1:** Analysis of variance for various traits in M<sub>2</sub> generation of sorghum

Source of variance	df	Mean sum of squares								
		DFF	DM	PH (cm)	PL (cm)	PW (g)	100 GW (g)	GYPP (g)	SYPP (g)	HI (%)
Replication (r)	2	1.67	3.41	9.84	10.63	91.66	0.04	46.11	141.01	1.51
Families (f)	5	1134.57*	1347.67*	10078.39*	197.19*	1211.18*	0.24*	565.65*	814.80*	129.32*
Progenies within families (p)	114	7.42*	9.54*	698.16*	14.68*	535.86*	0.18*	114.70*	298.51*	55.76*

Where, d.f = Degrees of freedom, \* = Significant at 5% level

DFF= Days to 50% Flowering DM= Days to Maturity, PH= Plant Height PL= Panicle Length PW= Panicle Weight, 100 GW= 100 Grain Weight, GYPP= Grain Yield Per Plant SYPP= Straw Yield Per Plant, HI= Harvest Index

**Table 2:** Genetic variability parameters for yield and yield contributing traits in M<sub>2</sub> generation of sorghum over all families

Characters	Range		Mean	GV (%)	PV (%)	GCV (%)	PCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GAM (%)
	Min.	Max.							
Days to 50% flowering	57.00	74.00	66.67	6.84	8.58	3.92	4.39	79.68	7.22
Days to maturity	106.00	125.00	117.13	8.67	11.27	2.52	2.87	76.94	4.54
Plant height (cm)	149.45	254.73	209.32	673.16	748.17	12.39	13.07	89.97	24.22
Panicle length (cm)	19.57	38.24	30.61	13.45	17.08	12.00	13.49	78.98	21.96
Panicle weight (g)	30.57	95.86	60.56	527.83	551.90	37.93	38.79	95.63	76.42
100 grain weight (g)	2.80	4.13	3.33	0.18	0.20	12.60	13.48	87.27	24.24
Grain yield/plant (g)	16.83	60.53	37.92	99.83	144.42	26.34	31.69	69.13	45.12
Straw yield/plant (g)	49.19	115.56	82.82	269.52	356.47	19.82	22.79	75.60	35.50
Harvest index (%)	18.29	51.53	31.44	49.29	68.68	22.33	36.35	71.77	38.97

GV = Genotypic variance ( $\sigma^2_g$ ) (%), GCV = Genotypic coefficient of variation (%)

PV = phenotypic variance ( $\sigma^2_p$ ) (%), PCV = Phenotypic coefficient of variation (%)

h<sup>2</sup><sub>bs</sub> = Heritability (Broad sense) (%), GAM = Genetic Advance as per cent of mean (%)

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