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GENETIC VARIABILITY ANALYSIS FOR YIELD AND RELATED TRAITS IN WHEAT (*TRITICUM AESTIVUM* L.) MUTANT GENOTYPES

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ABSTRACT

In order to estimate the genetic component of variability, including PCV, GCV, heritability, and genetic advance among various traits of wheat mutant genotypes, the current study was conducted on 34 stable mutant genotypes along with two checks, namely HD 2967 and GW 322, which were evaluated for 17 traits in a randomized block design at the agricultural research farm of RVSKVV, Gwalior (M.P.) during the rabi season of 2023–2024. Analysis of variance revealed highly significant differences ($p < 0.01$) among the mutant genotypes for all the traits studied, indicating the presence of substantial genetic variability. For all characters, phenotypic coefficient of variation (PCV) values was higher than the corresponding genotypic coefficient of variation (GCV) values, suggesting the influence of environmental factors on trait expression. Notably, biological yield per plot and grain yield per plot exhibited high PCV and GCV estimates, reflecting wide genetic variation and considerable potential for genetic improvement through selection. These traits also showed high heritability coupled with high genetic advance as a percentage of the mean, indicating the predominance of additive gene action in their inheritance. The substantial genetic variability observed for economically important traits suggests that effective improvement in yield components and overall grain productivity can be achieved through direct phenotypic selection in advanced generations.
***Keywords*: Genotype, mutants, heritability, genetic advance and genetic variability.**

Introduction

Hexaploid wheat (*Triticum aestivum* L.), commonly known as bread wheat, is one of the most important cereal crops in the world. It possesses a chromosome number of $2n = 6x = 42$ and belongs to the tribe Triticeae (Hordeae) of the family Poaceae (Gramineae). Owing to its wide adaptability, wheat is cultivated across diverse agro-climatic regions and plays a vital role in national and global food security. In India, it occupies nearly 14% of the wheat-growing area and contributes about one-third of the total cereal production, ranking second only to rice (Mahajan and Gupta, 2009). During 2023–2024, India produced 112.92 million tonnes of wheat from 31.23 million hectares, making it the world's second-largest producer (Anonymous, 2024).

Wheat productivity is however limited in many areas despite its economic and nutritional significance because of smallholder farming practices, a lack of irrigation facilities, and frequent exposure to biotic and abiotic stressors. Genetic improvement through the creation of stress-resistant and high-yielding cultivars is crucial in such circumstances. Induced mutagenesis has emerged as an effective approach for generating novel genetic variability, and wheat mutant genotypes serve as valuable genetic resources for broadening the genetic base and enhancing adaptive potential.

Precise knowledge of genetic variability and the proportional contributions of genetic and environmental factors to significant traits is necessary for effective crop improvement programs. Understanding the nature of gene action and the efficiency of selection can be gained by estimating genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advancement. Therefore, the present study was undertaken to assess these genetic parameters in wheat mutant genotypes for yield and related traits, with the objective of identifying superior lines for use in future breeding programmes.

Materials and Methods

Thirty-four advanced-generation (M_7) wheat mutant genotypes, designated as Trombay Gwalior Wheat (TGW) followed by numeric codes (Table 1), along with two check varieties, HD 2967 (BARC, Trombay, Mumbai) and GW 322 (RVSKVV, Gwalior, M.P.), were used for the evaluation of genetic variability, heritability, and genetic advance. The mutant populations were developed at the Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai (NABTD, BARC, India), through gamma ray irradiation at a dose of 300 Gy with a dose rate of 58.6 Gy min^{-1}.

The field experiment was conducted during the Rabi season of 2023–2024 at the Agricultural Research Farm, Department of Genetics and Plant Breeding, College of Agriculture, RVSKVV, Gwalior, M.P., using a randomized block design with three replications. Each genotype was sown in unit plots consisting of three rows, each 3 m long and spaced 30 cm apart. Standard agronomic practices were followed throughout the cropping season to ensure uniform crop growth and minimize environmental variation.

Observations were recorded on days to 50% heading, days to 50% flowering, days to maturity, plant height, flag leaf area, number of tillers per plant, peduncle length, grain filling duration, spike length, number of spikelets per spike, spikelet density, grain weight per spike, thousand-grain weight, number of grains per spike, biological yield per plot, and harvest index at appropriate phenological stages. Data were collected from five randomly selected plants per genotype in each replication, selected on the basis of uniform growth and adaptability. The mean values of these observations were subjected to analysis of variance (ANOVA). Genetic parameters, including genotypic and phenotypic coefficients of variation, heritability, and genetic advance, were estimated using R software (version 3.4.1).

Table 1 : List of wheat mutant genotypes used in the investigation

S. No.	Genotypes	S. No.	Genotypes
1	TGW 1	19	TGW 85
2	TGW 8	20	TGW 88
3	TGW 10	21	TGW 90
4	TGW 16	22	TGW 91
5	TGW 20	23	TGW 92
6	TGW 25	24	TGW 93
7	TGW 27	25	TGW 101
8	TGW 48	26	TGW 102
9	TGW 55	27	TGW 103
10	TGW 60	28	TGW 105
11	TGW 62	29	TGW 109
12	TGW 64	30	TGW 110
13	TGW 68	31	TGW 114
14	TGW 69	32	TGW 120
15	TGW 72	33	TGW 125
16	TGW 74	34	TGW 134
17	TGW 78	35	HD 2967 (C)
18	TGW 84	36	GW 322 (C)

Results and Discussion

In the present study, seventeen yield and yield-related traits were evaluated in thirty-four advanced-generation wheat mutant genotypes along with two check varieties. Analysis of variance revealed significant differences among the genotypes for all the studied traits (Table 2), indicating the presence of substantial genetic variability within the mutant population. This observed variability justifies the use of these genotypes for the estimation of genetic parameters. Similar findings have been reported earlier in wheat by Arya *et al*. (2018) and Thapa *et al*. (2019); however, the present investigation is distinct in its focus on mutant derivatives of the variety Borlaug 100. The results demonstrate that a single mutant population developed through exposure to 300 Gy gamma rays was sufficient to generate considerable genetic divergence among genotypes, thereby providing a valuable base material for selection based on induced genetic variability.

Table 2: Analysis of variance (ANOVA) for yield and yield attributing traits in thirty-four mutant genotypes including two checks of wheat

Mean sum of Square (MSS)			
Source	**Replication (DF =2)**	**Treatment (DF=35)**	**Error (DF=70)**
DTH	5.0093NS	66.5426**	2.4854
DTA	0.7315NS	36.9616**	3.9601
DTM	2.1111NS	19.6286**	6.6349
PH	5.25NS	73.9881**	3.3167
FLA	0.0206NS	34.8516**	5.1932
NT/P	1.6759NS	12.5362**	1.1712
PL	1.0833NS	8.7690**	1.0262
GFD	0.4537NS	47.6029**	2.4632
SL	0.8356NS	8.3656**	1.1856
NS/S	0.7037NS	7.9608**	1.9989
SD	0.0027NS	0.0077*	0.0041
GW/S	0.0328NS	1.1612**	0.0284
1000 GW	58.8548*	349.5494**	14.6621
GN/S	443.3981**	388.3101**	45.3029
BY/P	477.5278NS	1463331.8357**	11343.3373
GY/P	1048.9537NS	126499.9354**	1095.0299
HI	0.7314NS	285.2369**	32.1440

Note: DTH: days to 50% heading; DTA: days to 50% anthesis; DTM: days to maturity; PH: plant height; FLA: flag leaf area; NT/P: numbers of tillers per plant; PL: peduncle length; GFD: grain filling duration; SL: spike length; NS/S: number of spikelet per spike; SD: spikelet density; GW/S: Grain weight per spike; 1000 GW: 1000 grain weight; GN/S: grain number per spike; BY/P: biological yield per plot; GY/P: grain yield per plot; HI: harvest index

Table 3 : Range, mean, phenotypic and genotypic variance, PCV, GCV, heritability, genetic advance and genetic advance as percentage of mean for all the yield related traits in wheat

Source	**Range**		**Mean**	**Phenotypic variance**	**Genotypic variance**	**PCV**	**GCV**	**Heritability**	**Genetic advance**
	Max	**Min**							
DTH	88	61	73.49	23.83	21.35	6.64	6.28	89.57	9.00
DTA	89	72	80.15	14.96	11.00	4.82	4.13	73.53	5.85
DTM	116	104	109.27	10.96	4.33	3.03	1.90	39.50	2.69
PH	86	64	74.25	26.87	23.55	6.98	6.53	87.66	9.36
FLA	43.26	27.12	35.35	15.07	9.88	10.98	8.89	65.56	5.24
NT/P	16	6	11.21	4.95	3.78	19.86	17.35	76.39	3.50
PL	16	8	11.86	3.60	2.58	16.01	13.54	71.55	2.79
GFD	59	42	52.62	17.50	15.04	7.95	7.37	85.93	7.40
SL	16	9	11.98	3.57	2.39	15.78	12.91	66.87	2.60
NS/S	25	17	20.98	3.98	1.98	9.51	6.71	49.85	2.05
SD	0.82	0.43	0.57	0.005	0.001	12.74	6.12	23.07	0.03
GW/S	4.92	2.03	3.52	0.40	0.37	18.07	17.43	93.00	1.22
1000GW	80.23	35.12	62.14	126.29	111.62	18.08	17.00	88.39	20.46
GN/S	99	50	71.46	159.63	114.33	17.68	14.96	71.62	18.64

BY/P	3300	500	1539.97	495339.50	483996.16	45.70	45.17	97.71	1416.63
GY/P	1277	325	819.24	42896.66	41801.63	25.28	24.95	97.45	415.76
HI	83.33	30.83	57.01	116.50	84.36	18.93	16.11	72.41	16.10

Note: DTH: days to 50% heading; DTA: days to 50% anthesis; DTM: days to maturity; PH: plant height; FLA: flag leaf area; NT/P: numbers of tillers per plant; PL: peduncle length; GFD: grain filling duration; SL: spike length; NS/S: number of spikelet per spike; SD: spikelet density; GW/S: Grain weight per spike; 1000 GW: 1000 grain weight; GN/S: grain number per spike; BY/P: biological yield per plot; GY/P: grain yield per plot; HI: harvest index

The mean and range performance for seventeen yield and yield-related traits among the wheat mutant genotypes are shown in Table 3. Gamma-ray-induced mutagenesis exerted a positive influence on the expression of most traits, resulting in considerable variation in mean values across the mutant population. The evaluated genotypes exhibited wide ranges for days to 50% heading (61–88), days to 50% anthesis (72–89), days to maturity (104–116), plant height (64–86 cm), flag leaf area (27.12–43.26 cm²), number of tillers per plant (6–16), peduncle length (8–16 cm), grain filling duration (42–59 days), spike length (9–16 cm), number of spikelets per spike (17–25), spikelet density (0.43–0.82), grain weight per spike (2.03–4.92 g), thousand-grain weight (35.12–80.23 g), number of grains per spike (50–99), biological yield per plot (500–3300 g), grain yield per plot (325–1277 g), and harvest index (30.83–83.33%).

The mutant phenotypes were initially isolated from the M_2 generation and subsequently subjected to continuous selection and stabilization up to the M_8 generation. This systematic selection process resulted in the improvement of mean trait values and expansion of trait ranges compared with the parental genotype (Borlaug 100) and the check varieties HD 2967 and GW 322. These findings demonstrate the effectiveness of gamma-ray-induced mutagenesis in generating useful variability and enhancing agronomic performance in wheat.

The estimates of range, mean, phenotypic variance, genotypic variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), genetic advance, and genetic advance as a percentage of mean are shown in Table 3. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 3.03% to 45.70% and 1.90% to 45.17% respectively. The coefficient of variation is classified into low (<10%), moderate (10–20%), and high (>20%) based on measured values (Sivasubramanian and Menon, 1973). The traits biological yield per plot (45.70% and 45.17%) and grain yield per plot (25.28% and 24.95%) showed high values of PCV and GCV (Table 3). Medium PCV and low GCV were observed for flag leaf area (10.98% and 8.89%) and spikelet density (12.74% and 6.12%) while medium PCV with medium GCV has been reported for number of tillers per plant (19.86% and 17.35%), peduncle length (16.01% and 13.54%), spike length (15.78% and 12.91%), grain weight per spike (18.07% and 17.43%), 1000 grain weight (18.08% and 17%), grain number per spike (17.68% and 14.96%) and harvest index (18.93% and 16.11%). The Medium values of PCV and GCV for the traits imply that genetic differences among genotypes exist but are not extremely large and the trait is influenced by both genetics and environment, but genetics still plays a notable role. The present finding lined with high PCV and GCV reported for grain yield and biological yield reported by Dutamo *et al*., 2015 and Tilahun *et al*., 2020. Similarly, Fikre *et al*. (2015) reported moderate PCV and GCV for thousand Kernel Weight, number of kernels per spikes, number of productive tiller and Rajput *et al*. (2019) reported low PCV and GCV for number of tillers per plants. In Contrast to the current result, Dutamo *et al*. (2015) observed high PCV and GCV for thousand Kernel Weight, number of kernels per spike, number of fertile tillers and Atinafu *et al*. (2020) observed high PCV and GCV for peduncle length.

The phenotypic and genotypic coefficients of variation were found to be low (<10%) for days to 50% heading (6.64% and 6.28%), days to 50% anthesis (4.82% and 4.13%), days to maturity (3.03% and 1.90%), plant height (6.98% and 6.53%), grain filling duration (7.95% and 7.37%) and number of spikelets per spike (9.51% and 6.71%) respectively. The current outcome is in accordance with Tilahun *et al*. (2020) and Kabir *et al*. (2017). Similarly, Obsa *et al*. (2017) reported low PCV and GCV for number of spikelets per spike. In this study the narrow difference between PCV and GCV estimates indicates that environmental influence on trait expression was minimal, and that genetic factors contributed predominantly to the observed variation. Therefore, traits with a high GCV should be considered during selection.

Table 3 displays the estimated heritability and genetic advance values. Broad sense heritability estimates can be divided as low (<40%), moderate (40-60%) and high (>60%). The heritability ranged from 23.07% to 97.71%. High heritability estimates have been observed for the traits., days to 50% heading (89.57%), days to 50% anthesis (73.53%), plant height

(87.66%), flag leaf area (65.56%), number of tiller per plant (76.39%), peduncle length (71.55%), Grain filling duration (85.93%), spike length (66.87%), grain weight per spike (93%), 1000 grain weight (88.39%), grain number per spike (71.62%), biological yield per plot (97.71%), grain yield per plot (97.45%) and harvest index (72.41%). Moderate value of heritability for number of spikelets per spike (49.85%) and low value of heritability for days to maturity (39.50%) and spikelets density (23.07%) were observed. Similar results have also been reported by Yadav *et al.* (2011), Bhushan *et al.* (2012), Kumar *et al.* (2014), Arya *et al.* (2018), Thapa *et al.* (2019), Singh *et al.* (2020) and Porte *et al.* (2020).

The estimates for genetic advance as a percent of means were observed ranging from 2.46% for days to maturity to 91.99% for biological yield per plot. Genetic advance as a percent of mean can be divided into 3 groups *viz.*, low (<10%), moderate (10-20%) and high (>20%). Number of tillers per plant (31.25%), peduncle length (23.60%), spike length (21.75%), grain weight per spike (34.62%), 1000 grain weight (32.92%), grain number per spike (26.08%), biological yield per plot (91.99%), grain yield per plot (50.75%) and harvest index (28.24%) showed highest estimate of genetic advance as a percentage of mean. Traits such as., days to 50% heading (12.25%), plant height (12.60%), flag leaf area (14.83%) and grain filling duration (14.07%) showed moderate advance, while days to 50% anthesis (7.30%), days to maturity (2.65%), spikelet density (6.05%) and number of spikelets per spike (9.77%) showed less genetic advance. Similar results were also found by Arya *et al.* (2018) for grain yield per plant and Thapa *et al.*, (2019) for number of productive tillers per plant.

In addition to high heritability coupled with high genetic advance as percent of mean was observed for the traits like biological yield per plot (45.70% and 91.99%) and grain yield per plot (25.95% and 50.75%) signifying the effectiveness of selection in enhancing major yield components and yield itself. Similar results for wheat genotypes having higher heritability with the higher genetic advance were reported by Yadav *et al.*, 2011, Kumar *et al.* 2014, Arya *et al.* 2018 and Dwivedi *et al.* 2025.

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