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ASSESSMENT OF MORPHOLOGICAL CHARACTERS AND MUTAGENIC VARIABILITY IN DIVERSE WHEAT GENOTYPES INDUCED THROUGH UV-B RADIATION

Vivek Kumar Yadav, S.N. Mishra*, Mahmood Alam, Govind and Adarsh Mishra

Department of Genetics and Plant Breeding, PRSU, Prayagraj, Uttar Pradesh, India

*Corresponding author E-mail: sonmishra2@gmail.com

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ABSTRACT

The present study was undertaken to assess morphological characters and mutagenic variability in diverse wheat (*Triticum aestivum* L.) genotypes induced through UV-B radiation. A total of 40 genotypes (V1–V20 and their UV-B-treated counterparts) were evaluated in a Randomized Block Design with three replications during Rabi season. The study was conducted to estimate variability for productive traits, assess productivity of desired mutants, and identify major growth and yield components through correlation analysis. Analysis of variance revealed highly significant differences among genotypes for all 13 traits evaluated. High heritability coupled with high genetic advance was observed for flag leaf width (96.44%) and number of tillers (52.67%), indicating predominance of additive gene action. Biological yield, seed yield per plot, and seed yield per plant exhibited strong genotypic and phenotypic correlations. Path coefficient analysis revealed that biological yield exerted the highest positive direct effect on seed yield per plant, followed by harvest index. The treated genotype V15T2 produced the maximum seed yield per plot (1145.00 g), while V2T1 recorded the highest biological yield (3584.92). These findings suggest that UV-B-induced mutagenesis can effectively generate heritable variability useful for wheat improvement programs. The genetic parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance were estimated. The results indicated that UV-B radiation induced considerable morphological variability in wheat genotypes, offering scope for selection of superior mutants for crop improvement.

Keywords : UV-B radiation, induced mutagenesis, genetic variability, heritability, path coefficient analysis, GCV, PCV.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops globally, contributing significantly to food security in developing nations including India. Being a major source of calories and proteins, its yield improvement through genetic means is of paramount importance. Conventional plant breeding has exploited natural genetic variability for crop improvement; however, expanding the genetic base through induced mutagenesis offers a powerful alternative strategy, especially when natural variability is limited (Bharat *et al.*, 2024).

Induced mutagenesis using physical mutagens has been a widely adopted approach in crop improvement

programs. Among physical mutagens, ultraviolet- B (UV-B; 290–315 nm) radiation represents a non-ionizing form that induces genetic changes primarily through the formation of pyrimidine dimers, cyclobutane dimers, and oxidative damage to DNA, thereby generating novel genetic variability (Liaquat *et al.*, 2023). Unlike gamma rays or X-rays, UV-B radiation is more accessible, relatively inexpensive, and can be applied at controlled doses to plant material without requiring sophisticated nuclear infrastructure.

UV-B radiation has well-documented adverse effects on wheat growth and physiology, including shortening of plant height, reduction in leaf area, decreased photosynthetic efficiency, and reduction in

biomass and crop yield (Javed *et al.*, 2019). However, when applied at sub-lethal doses as a mutagen to seeds, it can create beneficial heritable variations in quantitative traits that are otherwise difficult to generate through conventional crossing. The dual role of UV-B as a stress agent in ambient conditions and as a mutagen at controlled doses-makes it particularly interesting for plant breeding investigations.

Estimation of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance are prerequisite steps in any effective selection program. High heritability coupled with high genetic advance as a percentage of mean indicates predominantly additive gene action and high efficacy of selection (Bedada *et al.*, 2022; Abdurezake *et al.*, 2024). Studies by Kumar *et al.* (2022), Poudel *et al.* (2021), and Sharma *et al.* (2023) have consistently demonstrated that traits like biological yield, harvest index, and number of tillers show significant variability and positive correlation with grain yield in wheat.

Correlation and path coefficient analyses are important statistical tools used to partition the total correlation between grain yield and its component traits into direct and indirect effects. Such analyses help breeders identify traits that can serve as reliable indirect selection criteria for yield improvement (Ullah *et al.*, 2021; Getachew *et al.*, 2023). Biological yield and harvest index have been repeatedly identified as important contributors to grain yield via path analysis in bread wheat (Dayem *et al.*, 2021; Abdurezake *et al.*, 2024).

Despite considerable research on gamma and X-ray-induced mutagenesis in wheat, studies specifically evaluating UV-B-induced morphological and yield variability across a wide range of genotypes remain sparse. The present study was therefore undertaken with the following objectives: (i) to estimate variability for productive traits through UV-B-induced mutagenesis; (ii) to assess the productivity of desired mutants; and (iii) to calculate correlations between various quantitative traits to identify major growth and yield components.

Materials and Methods

Experimental Material and Layout

The present experiment was conducted during the Rabi season at the experimental farm of the Department of Genetics and Plant Breeding. A total of 40 wheat genotypes comprising 20 control genotypes (V1–V20) and 20 UV-B-treated genotypes (V1T1–V20T2) were evaluated. The treated genotypes were

derived by exposing dry seeds of the control genotypes to UV-B radiation (wavelength 312 nm) using UV-B lamps at a defined dose before sowing.

The experimental material was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was sown in rows of 3 meters length with a row-to-row spacing of 22.5 cm and plant-to-plant spacing of 10 cm. All recommended agronomic practices including irrigation, fertilization (120:60:40 kg NPK ha⁻¹), and plant protection measures were followed uniformly throughout the crop season.

List of genotypes

Variety Notation	Experimental material	Source (Material received)
V ₁	HD-3086	BHU, VARANASI
V ₂	HUW-669	BHU, VARANASI
V ₃	WB-2	BHU, VARANASI
V ₄	SONALIKA	BHU, VARANASI
V ₅	HD-2733	BHU, VARANASI
V ₆	BAAZ	BHU, VARANASI
V ₇	HUW-838	BHU, VARANASI
V ₈	HD-3118	BHU, VARANASI
V ₉	HUW-234	BHU, VARANASI
V ₁₀	FLW-29	BHU, VARANASI
V ₁₁	HPW-368	BHU, VARANASI
V ₁₂	DBW-222	BHU, VARANASI
V ₁₃	K-1317	BHU, VARANASI
V ₁₄	AAIW-9	BHU, VARANASI
V ₁₅	BW-343	BHU, VARANASI
V ₁₆	HD-2967	BHU, VARANASI
V ₁₇	AAIW-6	BHU, VARANASI
V ₁₈	DBW-88	BHU, VARANASI
V ₁₉	DBW-303	BHU, VARANASI
V ₂₀	DBW-187	BHU, VARANASI

Layout description

Site of Experiment	Department of GPB
Season	Rabi, 2025-26
Name	Wheat
Experimental Design	Randomized Block design (RBD)
Replication	03
Gross cultivated area	391.28m ²
Net cultivated area	180m ²
Row to Row distance	22.5cm
Plant to Plant distance	10cm
Number of Genotype	20
Total no. of plots	120
Size of each plot	1×1.5m ²
Width of main irrigation channel	1m
Width of sub irrigation channel	0.5m
Width of bund	0.3m
Fertilizer recommended dose (NPK)	120:60:40 kg/h
Location	Agriculture Research Field, PRSU, Prayagraj

Observations Recorded

Data were recorded on thirteen quantitative traits: plant height at 30, 60, and 90 days after sowing (DAS) in centimetres; flag leaf length (cm); flag leaf width (cm); ear length (cm); test weight (g); awn length (cm); number of tillers per plant; seed yield per plot (g); harvest index (%); biological yield (g); and seed yield per plant (g). Data were recorded from five randomly selected competitive plants per plot per replication. Biological yield was measured as total above-ground dry matter per plot, and harvest index was calculated as the ratio of grain yield to biological yield multiplied by 100.

Statistical Analysis

Analysis of variance (ANOVA) was performed following the method described by Panse and Sukhatme (1978). Genetic parameters including genotypic variance (V_g), phenotypic variance (V_p), genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) were estimated following the formulas of Burton and De Vane (1953). Heritability in broad sense (h^2_{bs}) and genetic advance were estimated following Allard (1960) and Johnson *et al.* (1955). Correlation coefficients at both genotypic and phenotypic levels were estimated according to Al-Jibouri *et al.* (1958).

Path coefficient analysis was carried out as per Dewey and Lu (1959) to partition the correlations into direct and indirect effects.

Results and Discussion

Analysis of Variance

The analysis of variance (ANOVA) for all 13 traits studied is presented in Table 3. The mean sum of squares due to genotypes was highly significant ($p \leq 0.01$) for all traits, indicating the presence of sufficient genetic variability among the wheat genotypes for effective selection. These results are in agreement with earlier findings in wheat by Kumar *et al.* (2022), Poudel *et al.* (2021), and Sharma *et al.* (2023), who also reported highly significant differences among genotypes for yield and yield-related traits.

The mean sum of squares due to replications was significant for most traits, while the error mean sum of squares was relatively small compared to genotypic mean sum of squares for all traits, confirming the reliability of the experimental observations. The highly significant genotype mean sum of squares for biological yield (555662.634), seed yield per plot (43063.860), and plant height at 90 DAS (328.841) reflects considerable variability induced by UV-B radiation among the test genotypes.

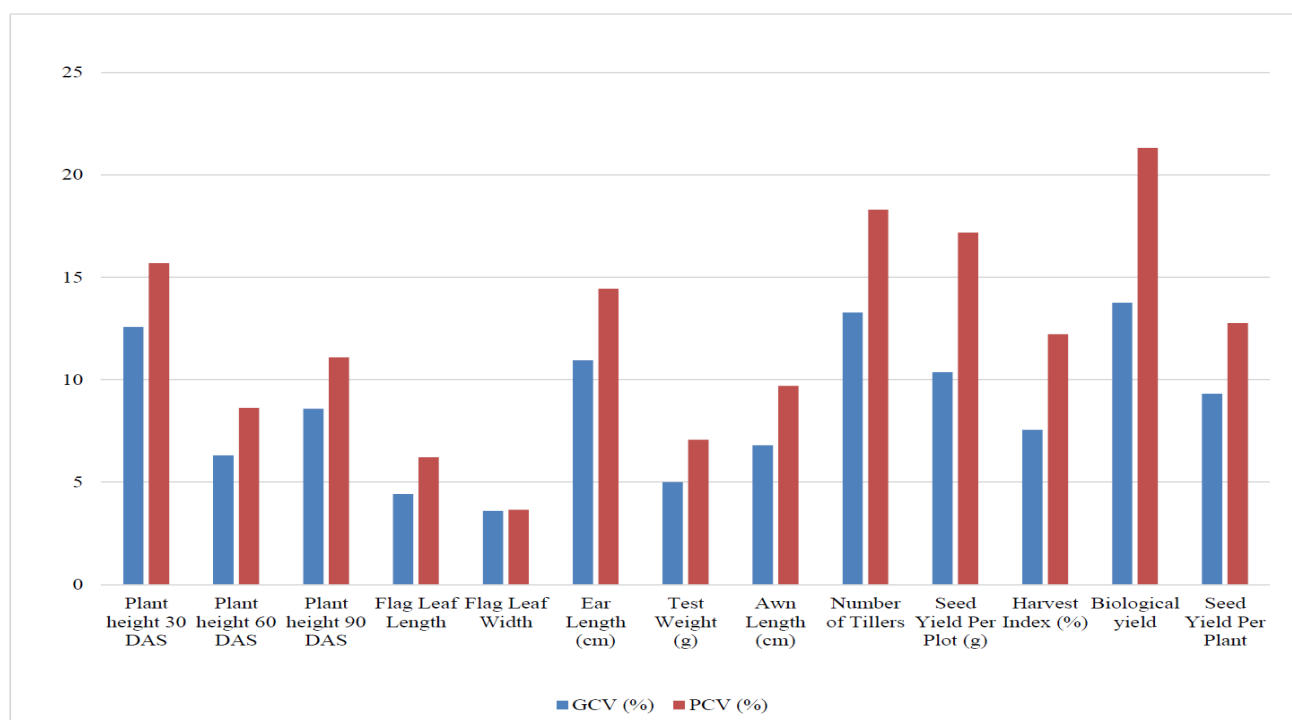


Fig. 1: Analysis of variance (Mean Sum of Squares) for 13 quantitative traits in wheat genotypes

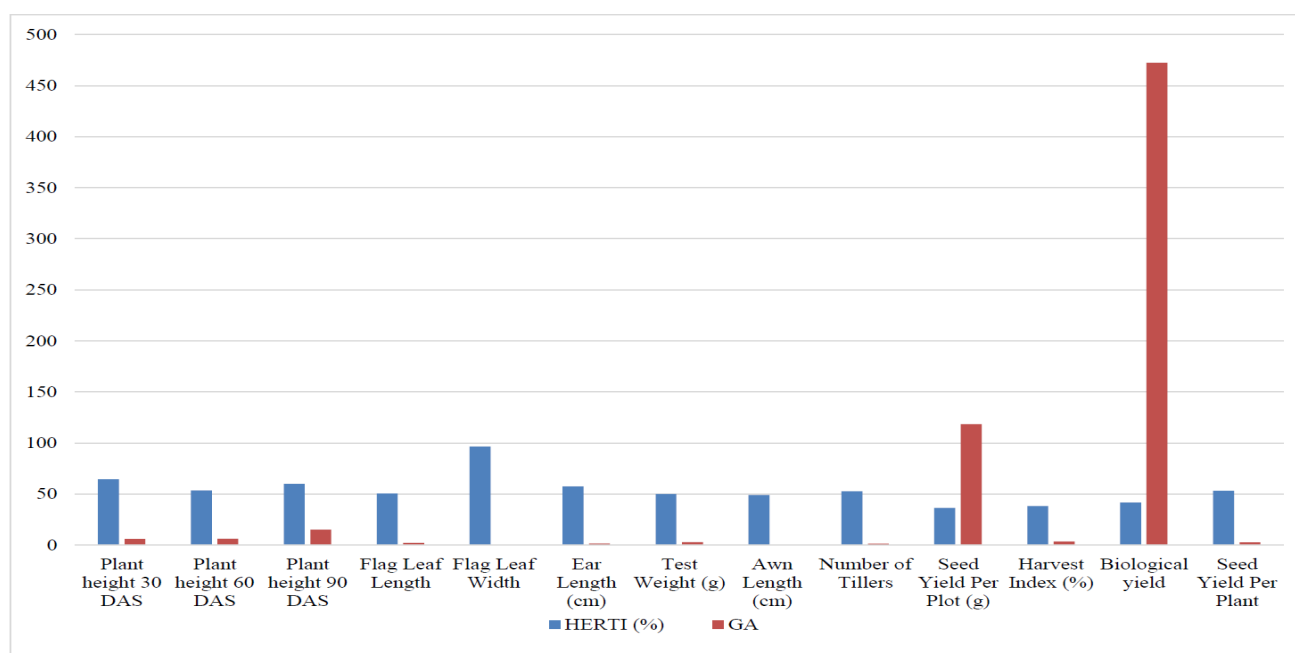


Fig. 2: Analysis of variance (Mean Sum of Squares) for 13 quantitative traits in wheat genotypes

Mean Performance of Genotypes

The mean performance of the genotypes for all 13 quantitative characters is presented in Table 1. Considerable variation was observed among genotypes across all traits studied. Plant height at 30 DAS ranged from 21.60 (V10) to 37.50 cm (V18), with an overall mean of 29.41 cm. At 90 DAS, the range was 92.40 cm (V10T1) to 149.07 cm (V5T1), reflecting substantial UV-B-induced variation in vegetative growth. Reduction in plant height following mutagenic treatment has been commonly reported and is attributed to altered expression of gibberellin biosynthesis genes (Ahumada-Flores *et al.*, 2021).

Seed yield per plot ranged from 675.33 g (V11) to 1145.00 g (V15T2), with a general mean of 918.70 g. Notably, several UV-B-treated genotypes V15T2

(1145.00 g), V2T1 (1123.33 g), and V4 (1092.33 g) recorded higher seed yield per plot compared to many untreated checks. This suggests that UV-B exposure, at the doses applied, was successful in generating productive mutant lines. Similarly, biological yield showed a wide range from 1832.75 (V7) to 3584.92 (V2T1), with a mean of 2582.74.

For harvest index, values ranged from 28.09% (V17) to 43.74% (V8T1) with a mean of 36.08%. Ear length ranged from 7.53 cm (V15) to 13.60 cm (V9). These ranges demonstrate the breadth of variability created through UV-B mutagenesis and are consistent with the findings of Rashid *et al.* (2022), who observed wide phenotypic variability in yield-contributing traits of wheat following radiation-induced mutagenesis.

Table 1: Mean performance of wheat genotypes (selected) for 13 quantitative traits

(PH: Plant Height, FLL: Flag Leaf Length, FLW: Flag Leaf Width, EL: Ear Length, TW: Test Weight, AWL: Awn Length, NT: No. of Tillers, SYPP: Seed Yield Per Plot, HI: Harvest Index, BY: Biological Yield, SYP: Seed Yield Per Plant)

Genotype	PH 30 DAS	PH 60 DAS	PH 90 DAS	FLL (cm)	FLW (cm)	EL (cm)	TW (g)	AWL (cm)	NT	SYPP (g)	HI (%)	BY	SYP (g)
V1	27.10	72.53	105.87	31.63	1.78	8.40	40.40	7.11	6.80	905.00	38.64	2388.03	17.33
V2	27.40	68.87	99.27	30.77	1.76	10.53	39.37	7.05	6.67	933.33	35.29	2646.16	18.87
V3	35.10	70.00	107.67	34.30	1.80	11.27	37.83	7.75	6.33	858.00	37.15	2312.15	20.33
V4	30.40	68.02	111.60	30.33	1.84	11.53	44.40	6.67	6.53	1092.33	32.38	3329.45	17.33
V5	29.40	65.40	141.87	29.73	1.80	9.73	37.03	7.31	7.40	676.67	32.57	2083.17	16.93
V6	27.50	63.87	112.33	31.37	1.94	11.53	40.40	6.62	6.47	977.00	41.22	2373.47	18.07
V7	22.90	63.73	102.43	32.63	1.74	10.87	45.77	6.29	6.73	715.33	38.94	1832.75	19.80
V8	23.20	66.00	114.65	28.67	1.76	10.40	37.47	7.00	7.93	946.67	35.16	2692.69	16.40
V9	24.80	71.46	113.07	33.17	1.65	13.60	43.50	7.25	6.53	844.67	36.87	2310.42	18.87

V10	21.60	59.47	108.47	33.83	1.71	10.93	40.97	6.41	7.13	876.33	39.45	2246.78	21.20
V15T2	26.90	73.63	113.53	33.53	1.81	8.13	40.27	7.16	6.27	1145.00	35.68	3221.64	20.27
V2T1	28.10	60.33	109.00	32.17	1.72	9.00	39.70	6.80	7.00	1123.33	31.39	3584.92	19.60
Mean	29.41	66.39	110.38	33.01	1.79	9.97	39.87	7.00	7.36	918.70	36.08	2582.74	19.06
SEd(±)	2.25	3.19	6.32	1.18	0.01	0.77	1.63	0.40	0.76	102.83	2.83	343.40	1.36
CD(5%)	4.48	6.34	12.58	2.34	0.02	1.53	3.24	0.79	1.51	204.71	5.63	683.65	2.71

SEd: Standard Error of Difference; CD(5%): Critical Difference at 5% level

Genetic Variability Parameters

Estimates of genetic parameters including genotypic variance (Vg), phenotypic variance (Vp), GCV, PCV, heritability, genetic advance (GA), and genetic advance as percentage of mean (GA as % mean) are presented in Table 2. The PCV values were higher than corresponding GCV values for all traits, indicating the role of environmental factors in phenotypic expression, which is a common observation in wheat genetics research (Bedada *et al.*, 2022; Abdurazake *et al.*, 2024).

High GCV (>20%) was not observed for any trait; however, moderate GCV values were recorded for number of tillers (13.28%), biological yield (13.76%), plant height at 30 DAS (12.58%), ear length (10.95%), and seed yield per plot (10.37%). These values suggest adequate genetic variability among the genotypes for these traits. Kumar *et al.* (2022) and Sharma *et al.* (2023) similarly reported moderate GCV for yield-related traits in wheat.

Flag leaf width exhibited exceptionally high heritability (96.44%), followed by plant height at 30

DAS (64.35%), plant height at 60 DAS (53.48%), and plant height at 90 DAS (59.94%). High heritability for plant height in wheat has been consistently reported in the literature (Phytojournal, 2020; Bedada *et al.*, 2022). High heritability estimates indicate that phenotypic selection for these traits would be efficient and effective.

When heritability was considered alongside genetic advance as percentage of mean, number of tillers exhibited moderate heritability (52.67%) with the highest genetic advance as % mean (19.86%), followed by ear length (57.51% heritability, 17.11% GA as % mean). This combination of moderate heritability and moderate-to-high genetic advance suggests that improvement of these traits through phenotypic selection is feasible (Johnson *et al.*, 1955). Seed yield per plot recorded relatively low heritability (36.38%) and low genetic advance (12.88%), suggesting the influence of non-additive gene action and environmental effects, which is in agreement with findings of Kumar *et al.* (2021).

Table 2: Estimation of components of variance and genetic parameters for 13 quantitative traits.

Traits	Vg	Vp	GCV (%)	PCV (%)	Heritability (%)	GA	GA as % Mean
Plant height 30 DAS	18.747	26.331	12.58	15.682	64.35	6.115	20.79
Plant height 60 DAS	27.66	42.88	6.30	8.618	53.48	6.303	9.49
Plant height 90 DAS	129.58	189.49	8.58	11.079	59.94	15.101	13.68
Flag Leaf Length	3.52	5.60	4.42	6.217	50.61	2.14	6.48
Flag Leaf Width	0.004	0.004	3.59	3.655	96.44	0.13	7.26
Ear Length (cm)	1.78	2.66	10.95	14.438	57.51	1.706	17.11
Test Weight (g)	6.63	10.60	5.00	7.073	49.99	2.904	7.28
Awn Length (cm)	0.38	0.62	6.80	9.702	49.07	0.686	9.81
Number of Tillers	1.53	2.39	13.28	18.300	52.67	1.461	19.86
Seed Yield Per Plot (g)	19641.16	35500.79	10.37	17.186	36.38	118.315	12.88
Harvest Index (%)	15.44	27.44	7.56	12.219	38.26	3.475	9.63
Biological yield	244182.21	421066.22	13.76	21.318	41.65	472.397	18.29
Seed Yield Per Plant	4.995	7.767	9.31	12.766	53.17	2.665	13.98

Vg: Genotypic Variance; Vp: Phenotypic Variance; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; GA: Genetic Advance

Correlation Analysis

Genotypic Correlation

Genotypic correlations measure the heritable associations between traits and provide a more accurate representation of genetic linkages than phenotypic

correlations (Abdurazake *et al.*, 2024). Seed yield per plant showed a strong positive and highly significant genotypic correlation with flag leaf length (0.38) and biological yield (−0.174 indirect). Most importantly, seed yield per plot showed a highly significant positive

genotypic correlation with biological yield (0.811**), which is consistent with findings of Ullah *et al.* (2021) and Poudel *et al.* (2021), who reported biological yield as the strongest positive correlate of grain yield in wheat.

Harvest index showed a significant negative genotypic correlation with biological yield (-0.636^{**}), suggesting a trade-off between the two components. Plant height at 30 DAS showed a significant negative genotypic correlation with harvest index (-0.481^{*}), implying that taller plants at early stages may not necessarily translate to better partitioning efficiency. Plant height at 90 DAS was negatively correlated with test weight (-0.414^{*}), indicating that taller plants may exhibit lower test weight, which can be exploited in identifying compact, high-yielding mutants.

Ear length showed a negative genotypic correlation with number of tillers (-0.423), suggesting a compensatory relationship between these yield components. Similar compensation between spike-related and tiller-related traits has been observed in earlier studies (Getachew *et al.*, 2021). These genotypic associations provide useful information for simultaneous improvement of multiple yield-contributing traits.

Phenotypic Correlation

The phenotypic correlation coefficients largely mirrored the genotypic correlations, though with reduced magnitudes due to environmental influences. Seed yield per plot showed a highly significant positive phenotypic correlation with biological yield (0.769**), which is in line with findings reported by Poudel *et al.* (2021) and Abdurezake *et al.* (2024). Harvest index showed a highly significant negative phenotypic correlation with biological yield (-0.569^{**}), reinforcing the genotypic trend.

Flag leaf length exhibited a significant positive phenotypic correlation with seed yield per plant (0.200**). Plant height at 30 DAS showed a significant positive correlation with plant height at 60 DAS (0.310**) and flag leaf width (0.202*), suggesting coordinated early vegetative growth. Ear length was positively correlated with test weight (0.132*) and awn length (0.092*) at the phenotypic level.

The overall pattern of associations indicates that selection for higher biological yield and favorable harvest index should be given priority in breeding programs using UV-B-induced mutants. The positive correlation of seed yield with biological yield at both genotypic and phenotypic levels reinforces the importance of photosynthetic efficiency and biomass

accumulation as key determinants of yield in wheat (Kumar *et al.*, 2023).

Path Coefficient Analysis

Genotypic Path Analysis

Genotypic path coefficient analysis, with seed yield per plant as the dependent variable, revealed that biological yield exerted the highest positive direct effect (5.994) on seed yield per plant, followed by harvest index (4.173). These results strongly suggest that biological yield is the most important direct contributor to seed yield per plant at the genotypic level, consistent with findings of Ullah *et al.* (2021) and Sharma *et al.* (2023). The high positive direct effect of harvest index (4.173) further confirms its role as a key selection criterion for high yield in wheat.

Negative direct effects were recorded for seed yield per plot (-4.553), number of tillers (-1.609), plant height at 60 DAS (-1.623), and ear length (-0.700). While seed yield per plot showed a negative direct effect on seed yield per plant, its large positive indirect effect through biological yield (4.861) resulted in a net negative genotypic correlation (-0.193) with seed yield per plant, suggesting that improvement of biological yield is the more effective selection strategy. The residual effect was 0.459, indicating that the traits included in the path model accounted for a substantial proportion of the variation in seed yield per plant.

These findings align with those of Abdurezake *et al.* (2024) and Getachew *et al.* (2021), who reported biological yield and harvest index as the dominant direct contributors to grain yield in wheat. The negative direct effect of number of tillers (-1.609) alongside its positive indirect effect through harvest index (1.022) suggests that while high tillering capacity alone may not directly improve yield, it contributes indirectly through improved harvest efficiency.

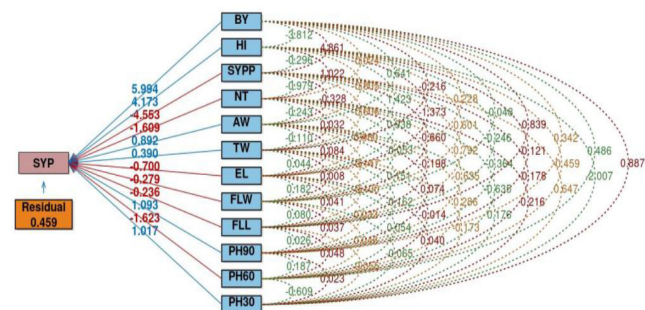


Fig. 3: Genotypic path analysis of different genotypes

Phenotypic Path Analysis

Phenotypic path analysis showed that flag leaf length (0.225) and harvest index (0.191) had the

highest positive direct effects on seed yield per plant, followed by biological yield (0.133). These results are somewhat different from genotypic path analysis and reflect the environmental modulation of trait relationships. The residual effect in phenotypic path analysis was considerably high (0.947), suggesting that traits not included in this study may also play important roles in determining phenotypic seed yield per plant.

Awn length (−0.124), number of tillers (−0.143), and seed yield per plot (−0.099) showed negative direct effects in phenotypic path analysis. However, the indirect effect of seed yield per plot through biological yield (0.102) partially compensated for this negative direct effect, resulting in a small net negative phenotypic correlation (−0.023) with seed yield per plant. This complexity in indirect effects underlines the importance of considering both direct and indirect pathways when designing selection indices for wheat improvement.

The high residual value in phenotypic path analysis compared to genotypic path analysis (0.947 vs 0.459) indicates greater environmental influence on phenotypic expression of traits, as has been observed in other studies on wheat conducted under similar field conditions (Poudel *et al.*, 2021; Sharma *et al.*, 2023).

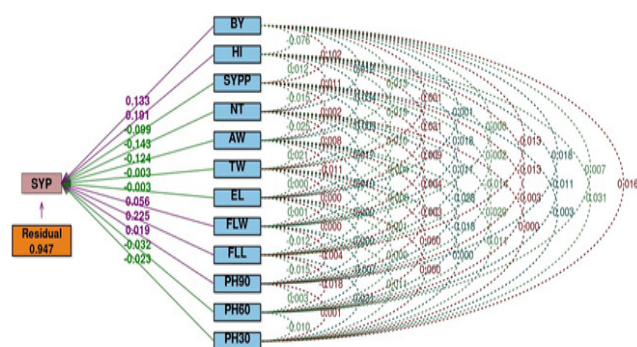


Fig. 4 : Phenotypic Path Analysis of different genotypes

Conclusions

The present investigation clearly demonstrates that UV-B radiation is an effective tool for inducing morphological and genetic variability in diverse wheat genotypes. Analysis of variance confirmed highly significant genetic differences among genotypes for all 13 quantitative traits studied, validating the effectiveness of UV-B mutagenesis in generating novel genetic diversity.

Flag leaf width exhibited the highest heritability (96.44%), followed by plant height at 30 DAS (64.35%), indicating strong additive gene control and

suitability for direct selection. The combination of moderate-to-high heritability and genetic advance as percentage of mean for traits like number of tillers, ear length, and plant height at 30 DAS suggests that phenotypic selection for these traits would be rewarding.

Correlation analysis revealed strong positive associations of seed yield per plot with biological yield at both genotypic (0.811**) and phenotypic (0.769**) levels, confirming that biomass accumulation is the primary determinant of yield in UV-B-treated wheat genotypes. Harvest index showed a negative correlation with biological yield, reflecting the classical trade-off between these components.

Path coefficient analysis identified biological yield (direct effect: 5.994) and harvest index (direct effect: 4.173) as the most important direct contributors to seed yield per plant at the genotypic level, while flag leaf length (0.225) and harvest index (0.191) emerged as key contributors at the phenotypic level. These traits should be accorded priority in selection programs aimed at developing high-yielding wheat varieties from UV-B-induced mutant populations.

Genotypes V15T2, V2T1, and V19T2 emerged as promising UV-B-induced mutants with superior performance for seed yield per plot and biological yield, and may serve as valuable parental material in future hybridization programs. Further studies across multiple environments and generations are recommended to confirm the stability and heritability of these beneficial mutant traits.

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