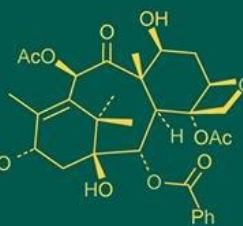
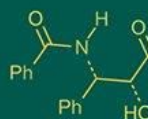


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Anuradha Singh

M.Sc. Scholar, Department of Genetics and Plant Breeding, Indira Gandhi Krishi, Vishwavidyalaya, BTC CARS Bilaspur, Chhattisgarh, India

Roshan Parihar

Scientist, Department of Genetics and Plant Breeding, Indira Gandhi Krishi, Vishwavidyalaya, ZARS, Jagdalpur, Chhattisgarh, India

DJ Sharma

Assistant Professor, Department of Genetics and Plant Breeding, Indira Gandhi Krishi, Vishwavidyalaya, BTC CARS, Bilaspur, Chhattisgarh, India

Geet Sharma

Scientist, Department of Agronomy, Indira Gandhi Krishi Vishwavidyalaya, BTC, CARS, Bilaspur, Chhattisgarh, India

NK Chaure

Professor, Department of Agri statistics, Indira Gandhi Krishi Vishwavidyalaya, BTC, College of Agriculture and Research Station, Bilaspur, Chhattisgarh, India

Pritul Joshi

M.Sc. Scholar, Department of Genetics and Plant Breeding, Indira Gandhi Krishi, Vishwavidyalaya, BTC CARS Bilaspur, Chhattisgarh, India

Corresponding Author:**Anuradha Singh**

M.Sc. Scholar, Department of Genetics and Plant Breeding, Indira Gandhi Krishi, Vishwavidyalaya, BTC CARS Bilaspur, Chhattisgarh, India

Genetic analysis for yield and yield attributing characters on advanced lines of wheat (*Triticum aestivum* L.) under restricted irrigation condition

Anuradha Singh, Roshan Parihar, DJ Sharma, Geet Sharma, NK Chaure and Pritul Joshi

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Abstract

An experiment entitled “Genetic analysis for yield and yield attributing characters on advanced lines of Wheat (*Triticum aestivum* L.) under restricted irrigation condition” was conducted during Rabi 2024-25 at BTC College of Agriculture and Research Station Bilaspur (IGKV, Raipur), using twenty two wheat (*Triticum aestivum* L.) genotypes evaluated in a randomized block design with four replication. Analysis of variance revealed highly significant difference among genotypes for all yield contributing characters. High genotypic and phenotypic coefficient of variation were recorded for grain yield per plot(kg), moderate GCV and high PCV were recorded for spike length(cm). Moderate PCV and GCV were recorded for grain filling period, no. of effective tillers per plants, flag leaf length(cm), test weight(g). High heritability for all contributing characters and genetic advance were moderate and low for yield contributing characters. Correlation analysis showed significant positive associations of grain yield per plot(kg) with no. of effective tillers, spike length, spikelets per main spike, no. of grain per main spike and harvest index (%). Path coefficient analysis revealed grain filling period, no. of effective tiller/plant, spike length(cm), spikelets per main spike, and harvest index (%) as the most important direct contributors to yield. Overall, genotypes HI1700 and CG1052 were superior in yield performance over all checks, indicating their promise for future improvement to restricted irrigated condition.

Keywords: Bread wheat, genetic variability, heritability, genetic advance, correlation coefficient and path analysis

Introduction

Wheat (*Triticum aestivum* L.) is a major global staple crop belonging to the family Gramineae. As a C3 plant primarily cultivated in temperate climates, it also thrives in tropical regions during the winter season. Hexaploid bread wheat (*T. aestivum*, $2n = 6x = 42$) originated through two natural hybridization events involving *T. urartu* (A-genome donor) and *T. speltoides* (B-genome donor), leading to the formation of *T. turgidum*.

Water scarcity, erratic rainfall, and frequent drought stress conditions increasingly intensified by climate change significantly affect wheat growth, physiological processes, and final grain yield. Restricted or deficit irrigation, which supplies water below full crop requirements, has emerged as an important water-saving strategy. When properly scheduled, deficit irrigation can enhance water productivity while maintaining or minimally reducing yield by balancing vegetative and reproductive growth. Wheat productivity suffers greatly under moisture and heat stress, necessitating the development of varieties tolerant to drought and uneven water availability. Since grain yield is a complex, polygenically controlled trait, indirect selection through yield-contributing characters is often more effective than direct selection.

In Chhattisgarh, wheat is cultivated under restricted irrigation using water-efficient varieties. The variety CG 1023 (Chhattisgarh Hansa) released by IGKV, Bilaspur is notable for its high yield, superior chapati quality, and elevated zinc content, making it suitable for timely sowing under limited water conditions. Globally, wheat production in 2024–25 was estimated at 785 million metric tons, a slight decrease from the previous year. India contributed 113.55 million metric tons, accounting for about 17% of global output, with wheat area expanding to 341.57 lakh hectares during the 2024 season.

Materials and Methods

The present investigation was conducted during *Rabi* 2024-25 at the Research Farm of Barrister Thakur Chhedilal College of Agriculture and Research Station, Bilaspur, under Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The experiment comprised twenty-two bread wheat genotypes along with four standard checks, namely DBW110, HI8627, CG1040, HI8823. Each genotype was grown in plot size 1.60 m X 5.00 m = 8 m² per entry per replication. The crop was managed with the recommended package of practices, including fertilizer application and intellectual operations to ensure uniform growth. Observations were recorded to thirteen quantitative traits using five competitive plants selected from each replication and average data were subjected to statistical analysis.

The variability among genotypes was assessed through analysis of variance. Phenotypic and genotypic coefficient of variation (PCV and GCV) were computed as Falconer (1964). Heritability (broad sense) was estimated using the method of Allard (1960), and from these estimates, genetic advance (GA) was calculated following Burton (1958). Genetic advance percentage as mean was further classified into categories as suggests by Johnson *et al.*, (1955). Correlation coefficients were estimated according to the proposed by Miller *et al.*, (1958), while path coefficient analysis was carried out based on the method suggested by Wright (1921) and later elaborated by Dewey and Lu (1959) [10].

Results and Discussion

Analysis of variance

The Analysis of variance results revealed that the mean sum of squares attributed to genotypes were highly significant for the traits *viz.*, days to maturity, grain filling period, days to maturity, plant height(cm), number of tillers per plant, spike length (cm), spikelets per main spike, flag leaf length (cm), peduncle length (cm), number of grains per main spike, test weight(g), harvest index (%), grain yield per plot (kg).

Genetic parameters of variation

Estimates of variability components (GCV, PCV, heritability, and genetic advance) are presented in Table 5. In all traits PCV values were slightly higher than GCV, indicating minimal environmental influence and that phenotypic expression closely reflects underlying genotypic differences.

The high GCV and PCV for grain yield per plot(kg) and moderate GCV and high PCV for spike length(cm).

Moderate GCV and PCV were recorded for Grain filling period, no. of effective tillers per plant, flag leaf length(cm), test weight (g), harvest index (%), no. of grain per spike respectively indicating that these traits were under the major influence of genetic control and less variable due to environmental factors.

In the present experimental set, high heritability coupled with high genetic advance percentage as mean were recorded for grain filling period, no. of effective tillers per plant, spike length(cm), flag leaf length(cm), test weight(g), grain yield per plot(kg).

The above results indicated that these characters had additive gene effect indicating effectiveness of selection for the improvement of these traits under restricted irrigated condition in bread wheat.

Correlation coefficient

Correlation analysis showed significant positive associations of grain yield per plot(kg) with no. of effective tillers, spike length, spikelets per main spike, no. of grain per main spike and harvest index, similar findings recorded by Gaddam *et al.*, (2025) [13], Tolwani *et al.*, (2025) [29], Yadav *et al.*, (2025) [33], Mishra *et al.* (2024) [23], Tiwari *et al.*, (2024) [28], Pandaey *et al.*, (2021) for no. of effective tillers per plant, spikelets per main spike; Dagade *et al.*, (2020) [8], Baye *et al.*, (2020) [6], Hadi *et al.*, (2016), no. of grain per main spike; Gaur *et al.*, (2024) [14], Ayer *et al.*, (2017), harvest index(%); Shiferaw *et al.*, (2022) [27], Mandal *et al.*, (2022) [22], Upadhyay *et al.*, (2020) [30], Tolwani *et al.*, (2025) [29], Yadav *et al.*, (2025) [33].

Path analysis

Path coefficient analysis revealed grain filling period, no. of effective tiller/plant, spike length, spikelets per main spike, no. of grain per main spikes and harvest index (%) were recorded highly significant and direct effect on grain yield. Similarly, findings recorded by Abdulrazak *et al.*, (2023) for grain filling period, Gaddam *et al.*, (2025) [13], Yadav *et al.*, (2025) [33], Gaur *et al.*, (2024) [14], Khare *et al.*, (2022) [18] for no. of effective tillers per plant, spike length; Gaddam *et al.*, (2025) [13], Pandey *et al.*, (2021) [24], Dasheva *et al.*, (2021), spikelets per main spike; Tolwani *et al.*, (2025) [29], Dagade *et al.*, (2020) [8], Ibrahim *et al.*, (2019) [15].

Overall results highlight spike length, no. of effective tillers, spikelets per main spike, no. of grain per main spike, harvest index key yield enhanced traits in bread wheat suggesting that these characters should receive emphasis in selection and breeding strategies aimed at yield improvement.

Table 1: Analysis of variance (ANOVA) for different character of wheat genotypes/accessions.

S. No.	Trait	Mean sum of square		
		Replication	Treatment	Error
	Degree of freedom	3	21	63
1	Days to heading	5.40	147.61**	12.33
2	Grain filling period	20.19	163.98**	8.54
3	Days to maturity	0.28	45.77**	13.92
4	Plant height	3.23	199.89**	13.51
5	Number of effective tillers per plant	0.27	2.53**	0.23
6	Spike length	1.04	9.15**	0.40
7	Spikelets per main spike	0.28	10.39**	2.25
8	Flag length	0.73	31.08**	0.84
9	Peduncle	2.37	44.66**	9.56
10	No. of grain per main spike	1.73	86.28**	23.16
11	Test weight	3.16	117.60**	2.52
12	Harvest index	3.09	72.49**	11.45
13	Grain yield (kg/ha.)	0.16	1.28**	0.10

** significant at 1% probability level, * significant at 5% probability level

F table value - Replication (3,63) = 6.13 at 1% and 2.75 at 5%

Genotypes (21, 63) = 2.11 at 1% and 1.72 at 5%

Table 2: Genetic parameters of variation for grain yield and its components in 22 wheat genotypes

S. N.	Characters	Mean	Range		Variance		CV (%)		h ² (bs)	G.A.	GAM
			Min	Max	GV	PV	PCV	GCV			
1.	Days to heading	67.70	56.50	80.00	33.82	46.15	8.59	10.03	73.28	10.25	15.14
2.	Grain filling period	47.08	37.00	57.50	38.86	47.40	13.24	14.62	81.98	11.62	24.69
3.	Days to maturity	116.39	110.50	120.50	7.96	21.89	2.42	4.02	36.37	3.50	3.01
4.	Plant height	73.74	63.12	85.72	46.59	60.11	9.25	10.51	77.51	12.38	16.78
5.	No. of effective tiller per plant	4.90	3.50	6.75	0.57	0.80	15.45	18.32	71.18	1.31	26.86
6.	Spike length	7.52	4.92	10.12	2.18	2.59	19.56	21.39	84.45	2.80	37.21
7.	No. of spikelets per spike	15.39	13.00	18.75	2.03	4.28	9.26	13.44	47.47	2.02	13.15
8.	No. of grain per main spike	17.96	14.38	25.54	15.77	38.94	8.62	13.55	90.00	5.37	29.91
9.	Flag leaf length	34.51	30.69	42.43	7.56	8.4	15.30	16.13	47.86	4.22	12.23
10.	Peduncle length	46.05	39.00	56.25	8.77	18.33	8.58	12.40	40.51	5.20	11.30
11.	Grain yield	2.60	1.66	4.29	0.29	0.39	20.84	24.17	74.34	0.96	37.02
12.	Test weight	42.23	34.00	51.25	28.77	31.22	12.69	13.24	91.94	10.59	25.08
13.	Harvest index	46.52	40.91	58.77	15.26	11.45	8.39	11.10	57.12	6.08	13.07

Where, GCV (%) and PCV (%) genotypic and phenotypic coefficient of variance, h²(bs) (%) = heritability (broad sense), GA= genetic advance,

GAM = genetic advance expressed as percentage of mean respectively

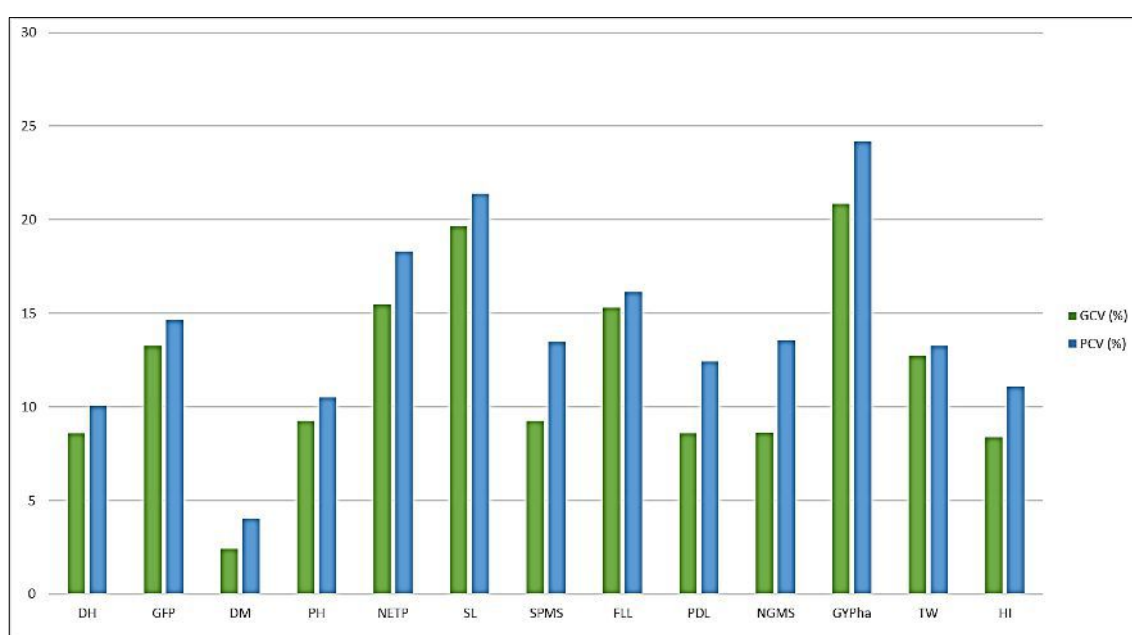
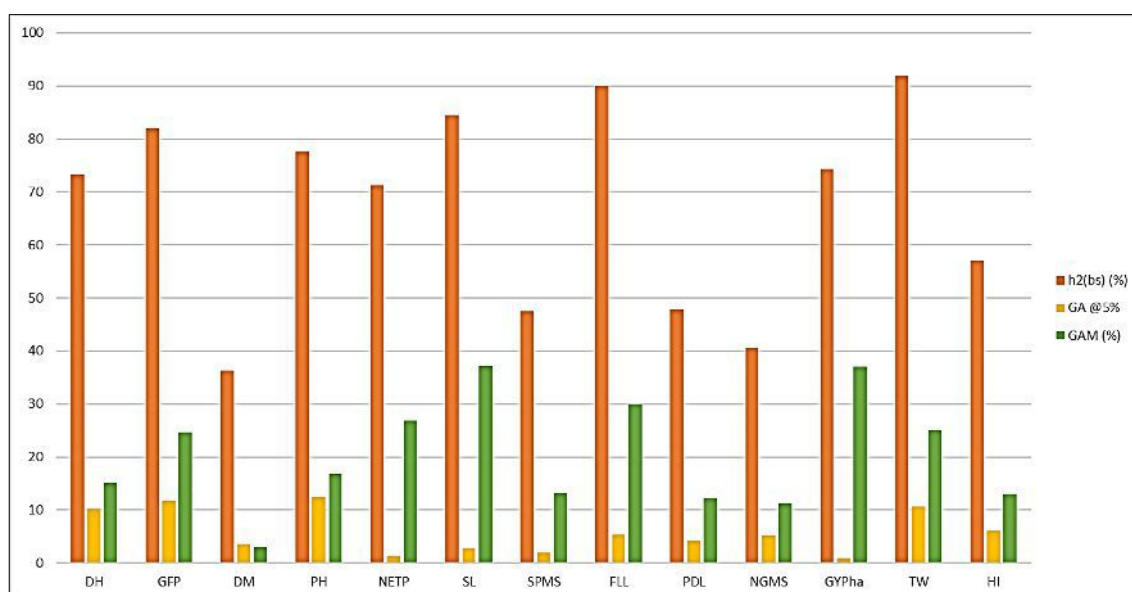
**Fig 1:** Graphical representation of genotypic, phenotypic and environmental coefficient of variation for thirteen characters in wheat.**Fig 2:** Graphical representation of heritability (b.s) and genetic advance expressed as percent of mean for thirteen characters in wheat.

Table 3: Genotypic and phenotypic correlation matrix. (Above diagonal Phenotypic and below diagonal Genotypic)

Trait	DH	GFP	DM	PH	NETP	SL	SPMS	FLL	PDL	NGMS	TW	HI	GYPha
DH	1	-0.749**	0.056	-0.252*	0.001	-0.181	-0.178	0.156	-0.275**	-0.198	0.112	-0.116	-0.286**
GFP	-0.739**	1	0.302**	0.510**	-0.209	0.324**	0.203	-0.271*	0.231*	0.244*	-0.144	0.088	0.141
DM	0.055	0.298**	1	0.196	-0.176	0.108	0.009	-0.356**	-0.231*	0.118	-0.023	-0.045	-0.092
PH	-0.250*	0.502**	0.196	1	-0.177	0.466**	0.331**	0.045	0.081	0.338**	-0.274**	0.016	0.05
NETP	0.001	-0.204	-0.174	-0.175	1	0.029	0.341**	-0.122	-0.007	0.329**	-0.004	0.059	0.739**
SL	-0.183	0.322**	0.107	0.459**	0.018	1	0.344**	0.159	0.202	0.336**	-0.247*	0.221*	0.264*
SPMS	-0.179	0.199	0.009	0.330**	0.343**	0.338**	1	-0.102	-0.003	0.967**	-0.153	0.037	0.513**
FLL	0.154	-0.273*	-0.354**	0.046	-0.118	0.153	-0.100	1	0.164	-0.140	-0.142	-0.135	-0.166
PDL	-0.274**	0.231*	-0.230*	0.081	-0.062	0.194	0.001	0.165	1	0.014	-0.135	0.06	0.021
NGMS	-0.198	0.238*	0.118	0.271*	-0.008	-0.245*	-0.154	-0.141	-0.138	1	-0.144	0.083	0.494**
TW	0.113	-0.146	-0.023	-0.271*	-0.008	-0.245*	-0.154	-0.141	-0.138	-0.144	1	-0.144	-0.213*
HI	-0.112	0.091	-0.046	0.016	0.056	0.221*	0.034	-0.137	0.057	0.081	-0.142	1	0.317**
GYPha	-0.280**	0.134	-0.009	0.054	0.739**	0.246*	0.512**	-0.159	0.026	0.493**	-0.211*	0.312**	1

** significant at 1% probability level, * significant at 5% probability level

DH = Days to heading, GFP =Grain filling period, DM= Days to maturity, PH=Plant height(cm), NETP = Number of effective tillers per plant, SL = Spike length(cm), SPMS = Spikelets per main spike, FLL= Flag leaf length(cm), PDL= Peduncle length (cm), NGMS= No. of grain per main spike, GYPP = Grain yield per plot (kg), TW = Test weight (g), HI= Harvest index (%).

Table 4: Direct and indirect effects of yield component on grain yield in bread wheat (genotypic path matrix)

Trait	DH	GFP	DM	PH	NETP	SL	SPMS	FLL	PDL	NGMS	TW	HI	GYPP
DH	-0.132	0.097	-0.007	0.033	-0.002	0.024	0.023	-0.020	0.036	0.026	-0.015	0.014	-0.280**
GFP	-0.086	0.116	0.034	0.058	-0.023	0.037	0.023	-0.031	0.026	0.027	-0.017	0.010	0.134
DM	-0.000	-0.003	-0.011	-0.002	0.002	-0.001	-0.001	0.004	0.002	-0.001	0.000	0.000	-0.090
PH	0.008	-0.017	-0.007	-0.035	0.006	-0.016	-0.011	-0.001	-0.002	-0.012	0.009	-0.000	0.053
NETP	0.008	-0.136	-0.115	-0.116	0.666	0.012	0.228	-0.078	-0.041	0.219	-0.005	0.037	0.739**
SL	-0.009	0.016	0.005	0.023	0.000	0.050	0.016	0.007	0.009	0.016	-0.012	0.011	0.245*
SPMS	-0.088	0.098	0.044	0.163	0.169	0.167	0.495	-0.049	-0.001	0.479	-0.076	0.016	0.512**
FLL	-0.001	0.002	0.003	-0.000	0.001	-0.001	0.009	-0.009	-0.001	0.001	0.001	0.001	-0.159
PDL	0.007	-0.006	0.006	-0.002	0.001	-0.005	0.000	-0.004	-0.028	-0.000	0.003	-0.001	0.025
NGMS	0.059	-0.071	-0.035	-0.108	-0.098	-0.098	-0.288	0.041	-0.004	-0.298	0.043	-0.024	0.493**
TW	-0.012	0.016	0.002	0.029	0.000	0.026	0.016	0.015	0.015	0.015	-0.109	0.015	-0.210*
HI	-0.025	0.021	-0.010	0.003	0.012	0.050	0.007	-0.031	0.013	0.018	-0.032	0.230	0.312**

Residual effect =0.291

** significant at 1% probability level, * significant at 5% probability level

DH = Days to heading, GFP =Grain filling period, DM= Days to maturity, PH=Plant height(cm), NETP = Number of effective tillers per plant, SL = Spike length(cm), SPMS = Spikelets per main spike, FLL= Flag leaf length(cm), PDL= Peduncle length (cm), NGMS= No. of grain per main spike, GYPP= Grain yield per plot (kg), TW = Test weight (g), HI= Harvest index (%).

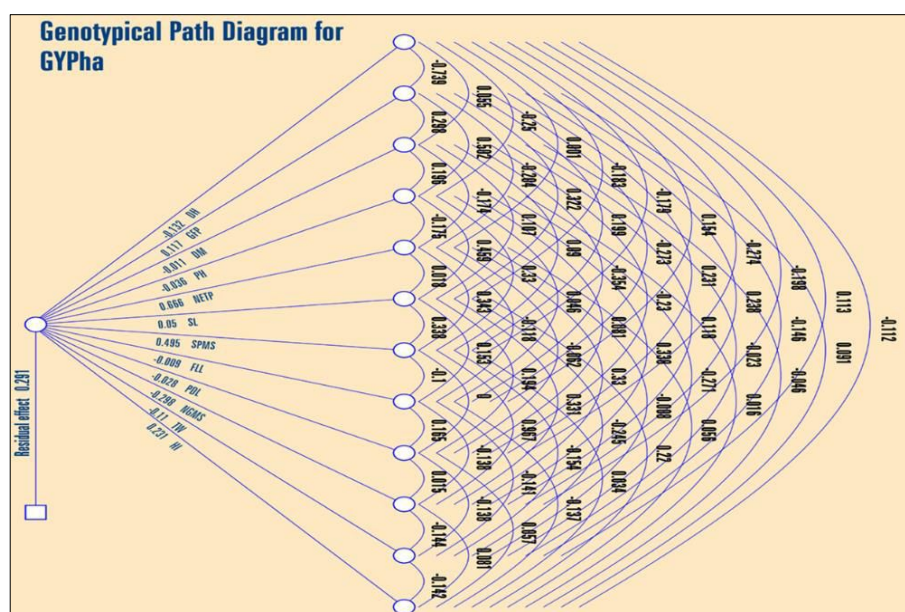
**Fig 3:** Genotypic path diagram for grain yield per plot(kg)

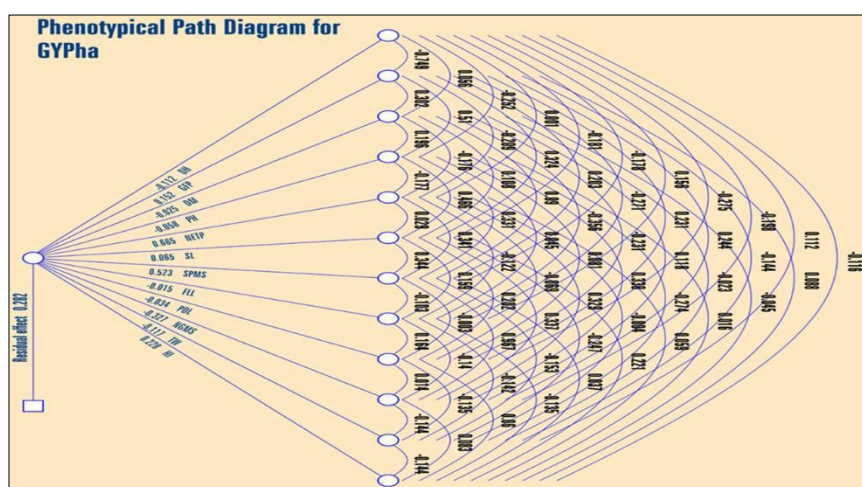
Table 5: Direct and indirect effects of yield component on grain yield in bread wheat (phenotypic path matrix)

Trait	DH	GFP	DM	PH	NETP	SL	SPMS	FLL	PDL	NGMS	TW	HI	GYPP
DH	-0.112	0.084	-0.006	0.028	-0.001	0.020	0.020	-0.017	0.030	0.022	-0.012	0.013	-0.285**
GFP	-0.114	0.152	0.046	0.077	-0.0318	0.049	0.030	-0.041	0.035	0.037	-0.022	0.013	0.140
DM	-0.001	-0.007	-0.024	-0.004	0.004	-0.002	-0.002	0.008	0.005	-0.002	0.006	0.001	-0.092
PH	0.014	-0.029	-0.011	-0.058	0.010	-0.027	-0.019	-0.002	-0.004	-0.019	0.015	-0.000	0.050
NETP	0.004	-0.138	-0.117	-0.117	0.665	0.019	0.226	-0.081	-0.046	0.219	-0.002	0.039	0.738**
SL	-0.011	0.020	0.007	0.030	0.001	0.064	0.022	0.010	0.013	0.021	-0.015	0.014	0.264*
SPMS	-0.093	0.106	0.047	0.173	0.178	0.179	0.523	-0.053	-0.001	0.506	-0.079	0.019	0.513**
FLL	-0.002	0.004	0.005	-0.007	0.001	-0.002	0.001	-0.014	-0.002	0.002	0.002	0.002	-0.166
PDL	0.009	-0.007	0.007	-0.002	0.002	-0.006	0.000	-0.005	-0.033	-0.005	0.004	-0.002	0.021
NGMS	0.064	-0.079	-0.038	-0.110	-0.107	-0.110	-0.316	0.045	-0.004	-0.327	0.047	-0.027	0.494**
TW	-0.013	0.016	0.002	0.032	0.005	0.028	0.017	0.016	0.015	0.016	-0.116	0.016	-0.212*
HI	-0.026	0.020	-0.010	0.003	0.013	0.050	0.008	-0.030	0.013	0.019	-0.032	0.228	0.317**

Residual effect = 0.282

** significant at 1% probability level, * significant at 5% probability level

DH = Days to heading, GFP = Grain filling period, DM= Days to maturity, PH=Plant height(cm), NETP = Number of effective tillers per plant, SL = Spike length(cm), SPMS = Spikelets per main spike, FLL= Flag leaf length(cm), PDL= Peduncle length (cm), NGMS= No. of grain per main spike, GYPP = Grain yield per plot (kg), TW = Test weight (g), HI= Harvest index (%).

**Fig 4:** Phenotypic path Diagram for grain yield per plot(kg)

Conclusion

The study of variability parameters revealed that high to moderate estimates of GCV and PCV were observed for grain filling period and test weight and high to low estimates of GCV and PCV were observed for grain yield. Traits like number of grains per spike (NGMS), spikelets per spike (SPMS), and number of effective tillers per plant (NETP) showed strong positive genotypic correlations with grain yield and exhibited high direct effects, making them crucial for yield improvement under moisture stress.

Multiple studies show negative correlations between yield and days to heading (DH) and days to maturity (DM) under water stress. This reflects a drought escape strategy where early maturity helps avoid terminal drought damage. For example, in trials across stress environments, yield remained positively associated with early flowering and short duration, confirming that early heading/maturity is beneficial for breeding drought-tolerant genotypes. Likewise, Lemma *et al.* (2021) and others reported that early phenology is a key criterion in breeding for drought resilience, while prolonged maturity often reduces yield.

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Conflict of study

The authors declare that there is no conflict of interest regarding the publication of this research work.

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