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## Genetic variability, correlation and path coefficient analysis for yield components and grain minerals in wheat (*Triticum aestivum* L.)

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### Abstract

The present study was undertaken to analyse genetic parameters like variability, heritability, genetic advance and correlation and path coefficient analysis among one hundred wheat genotypes. The field experiment was conducted during Rabi 2021-22 in alpha lattice design with two replications at Wheat section of Bihar Agricultural College, Sabour. The data were recorded on twelve characters namely days to 50% flowering, days to anthesis, days to physiological maturity, flag leaf area, plant height, spike length, peduncle length, number of grains per spike, 1000 grain weight and yield per plot. Analysis of variance revealed highly significant differences among tested 100 genotypes in respect of all the characters studied. High heritability coupled with high genetic advance over percent mean was observed for flag leaf area, peduncle length, grain per spike, 1000 grain weight and grain zinc content, suggesting that characters were governed by additive gene action yield per plot had a significant and positive phenotypic correlation coefficient with number of grains per spike, 1000 grain weight, flag leaf area, peduncle length. Maximum direct effect on yield was exhibited by days to anthesis followed by grains per spike, peduncle length, 1000-grain weight. Selection of wheat genotypes considering these characters would be beneficial to attain higher genetic gain in wheat breeding programme.

**Keywords:** Genetic variability, correlation, genetic advance and path coefficient

### Introduction

Wheat (*Triticum aestivum* L.  $2n=42$ ), the world's most important energy-rich cereal crop, is a self-pollinated crop of the Gramineae family and genus *Triticum*. This cereal occupies around 220 million hectares acreage among all crops with an annual production of around 770 million tonnes with productivity 3491.9 kg/ha (FAOSTAT 2021) [10]. At the global level, India has made amazing growth in wheat production since 1960s, ranking second only to China in terms of wheat production, accounting for around one-tenth of world wheat production. The wheat crop is grown over 31.36 million hectares area with total production of 109.50 million tonnes and productivity 3.46 tonnes ha<sup>-1</sup> in India (FAOSTAT 2021) [10]. Despite the cultivated area of wheat in Bihar, having an agrarian economy, is more than 2 million ha and production is 5-6 million tonnes; yield and productivity are lowest among all wheat producing states of India (Kishore and Vartika 2021) [15]. The leading district in terms of productivity of wheat in the state is Kishanganj, with a CGAR (compound annual growth rate) of 11.46% (Nain 2018) [19]. Grain yield, as a complex trait, is determined by yield component characters like grains per spike, 1000-grain weight, tiller/plant and spike length and their interaction. Estimation of correlation is based on the degree and direction of relationship between two or more factors (Grafius 1960) [13]. Correlation studies improve knowledge of yield components which aids plant breeders in selection (Robinson *et al.* 1951 and Johnson *et al.* 1955) [21, 14]. The path coefficient is essentially a standardized partial regression coefficient that measures the direct influence of one variable on another and allows the correlation coefficient to be divided into components of direct and indirect effects (Wright 1921) [24]. Dewey and Lu (1959) [9] later expanded on the notion of path coefficient analysis. Estimation of heritability and genetic advance is important for breeders in understanding the magnitude, nature and interaction of genotype and environmental variation of the characters (Johnson *et al.* 1955) [14].

### Materials and Methods

The present experiment was conducted to evaluate the one hundred wheat genotypes including two checks namely DBW14 and DBW 187 in an alpha lattice design with two replications

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at Wheat section, Bihar Agricultural College, Sabour during 2021-22. Each genotype was sown in a double row plot of 1.5 m length with 23 cm spacing in the last week of November 2021. All recommended agronomic practices and plant protection measures were applied to raise to healthy crop. The data were recorded on twelve quantitative characters namely days to 50% flowering, days to anthesis, days to physiological maturity, flag leaf area (cm<sup>2</sup>), plant height (cm), spike length (cm), peduncle length (cm), number of grains per spike, 1000 grains weight (g), and grain yield per plot (g). Grain zinc (ppm) and grain iron (ppm) analysed at the Biofortification laboratory, Bihar Agricultural College Sabour using ED-XRF (ED-XRF, S2 PUMA, Bruker, Karlsruhe, Germany). Data from five plants of each genotype were averaged and mean data was used for statistical analysis using package available in R studio version 4.1.2. Mean, range and coefficient of variation (CV) were also estimated. Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were estimated according to Burton (1952) [7]; heritability in broad sense ( $h^2_{bs}$ ) was estimated according to Burton and Devane (1953) [8]; genetic advance (GA) and genetic advance as per cent of mean (GAPM) were calculated according to Johnson *et al.* (1955) [14], correlation coefficient and path coefficient analysis was performed following Robinson *et al.* (1951) [21] and Dewey and Lu (1959) [9], respectively.

## Results and Discussion

Analysis of variance (ANOVA) for all the characters was performed considering genotypes as fixed effects, and replication, block and row coordinates within replication as random effects to differentiate the total variance into genotypes as treatment, replication, block, and other sources of variation. Analysis of variance revealed highly significant differences among tested 100 genotypes in respect of all the characters studied. The mean sum of squares due to genotypes was highest for yield per plot. The highest mean sum of squares due to error was observed for yield per plot followed by grain per spike (Table 1).

The differences between GCV and PCV were high for plant height followed by flag leaf area indicating more environmental influences. PCV was numerically higher than GCV for all characters, showing the presence of environmental effect on expression of character (Table 2) as previously reported by Badole *et al.* (2010) [5] and Ashfaq *et al.* (2014) [4]. Highest phenotypic coefficient of variation was exhibited by yield per plot (19.61%) followed by flag leaf area (18.16%), grain per spike (17.62%), tiller per plant (15.64%), peduncle length (14.55%). The inherent genetic variability is expressed by the genotypic coefficient of variation. Highest values for genotypic coefficient of variation were showed by yield per plot (19.13%), flag leaf area (17.25%), grain per spike (14.92%), peduncle length (14.12%).

Heritability plays a vital role in the transmission of characters from parents to the next generation. The genetic advance is the mean genotypic value over parental population, which is a measure of genetic gain under selection. High heritability coupled with high genetic advance over percent of mean was observed for flag leaf area, peduncle length, grain per spike, 1000 grain weight and grain zinc content. It revealed that the heritability represents additive gene effects and early generations selection may be more desirable for these

characters. A heritability estimate alone is worthless, but when combined with genetic advance, it is more useful in estimating the ultimate effect of selection. These findings are similar to the results recorded by Ali *et al.* (2012) [3], Baranwal *et al.* (2012) [6], Kumar *et al.* (2014) [17] and Kumar *et al.* (2019) [16]. 1000 grain weight (94.37) highest heritability estimates followed by peduncle length (94.16) and flag leaf area (90.30) and others as sown in Table 2. Highest estimates of genetic advance as a per cent of mean was found for yield per plot (38.44), flag leaf area (33.78), peduncle length (28.23), grain per spike (26.04), grain zinc (25.46), flag leaf length (24.34), 1000 grain weight (24.09).

The behaviour of all characters that contribute to the yield may not always be independent but rather may be correlated. Positive correlations can be used simultaneously to improve two or more characters, whereas negative correlations between desirable characters suggest making less stringent target for secondary characters. A significant and positive phenotypic correlation coefficient observed between yield per plot and number of grains per spike (0.463\*\*), 1000 grain weight (0.201\*\*), flag leaf area (0.168\*), peduncle length (0.364\*\*). It showed significant and negative correlation with plant height (-0.336\*\*) and grain zinc (-0.196\*\*) (Table 3 and Figure 1). It implies that by increasing the value of these component characters, seed yield can be drastically increased. These results are in conformity with the findings of Ahmadi *et al.* (2012) [2], Gelalcha and Hanchinal (2013) [12], Garg *et al.* (2014) [11], Abrar *et al.* (2020) [11]. Days to 50% flowering had significant and positive correlation with days to anthesis (0.979 \*\*) and plant height (0.227\*\*) and a negative and significant correlation with peduncle length (-0.208\*\*) and 1000 grain iron content (-0.207\*\*). Days to anthesis had highly significant and positive correlation with plant height (0.213\*\*) and peduncle length and a negative and significant correlation with peduncle length (-0.190\*\*) and grain iron content (-0.227\*\*). Flag leaf area had showed highly positive and significant correlation with plant height (0.270\*\*), peduncle length (0.229\*\*), grain per spike (0.193 \*\*). Flag leaves are the primary photosynthesis organs, accounting for 45-58% of photosynthetic activity during the grain filling stage (Liu *et al.* 2018) [18].

Grain zinc content had showed positive and significant correlation with 1000 grain weight (0.141\*) and a negative and significant correlation with grain per spike (-0.174\*). Grain iron content had showed positive and significant correlation with grain zinc Zn (0.139\*) and a negative and significant correlation with days to 50% flowering (-0.207\*\*) and days to anthesis (-0.227\*\*).

Path analysis divides the correlation coefficient into direct and indirect effects, allows to analyse the cause and effect relationship. Maximum direct effect on yield was exhibited by days to anthesis (0.874) observed via, days to 50% flowering and peduncle length followed by grains per spike (0.502), peduncle length (0.360), 1000-grain weight (0.293) (Table 4). Grains per spike (0.5356) had positive and significant association with grain yield, which exerted maximum direct effect on grain yield, and had relatively high correlation with plant height (0.197) had a positive indirect effect. Thus, grain per spike and 1000 grain weight emerged as one of the major direct yield components. These characters should be considered important for selection in a breeding programme for increasing yield in wheat. These results are similar to Baranwal *et al.* (2012) [6], Phougat *et al.* (2017) [20], Abrar *et*

al. (2020) [1]. The highest positive indirect effect on grain yield was exerted by days to 50% flowering (0.880) via days to anthesis followed by plant height (0.295) via peduncle length. These factors identified as the most important indirect yield contributing characters due to their significant

favourable indirect effect on yield per plot. The remaining indirect impact estimates in this research were relatively low, emphasising the significance of indirect contributions to grain yield.

**Table 1:** Analysis of Variance of twelve studied characters among 100 wheat lines

Source of variation	Treatment	Replication	Block	Row (within replication)	Residuals	
Mean Sum of Square (MSS)	DF*	11.05**	10.12	3.03	2.15	1.76
	DA	10.51**	1.44	2.53	2.45	1.59
	DPM	3.47**	9.24	0.65	1.53	1.25
	FLA	74.93*	0.44	4.98	3.03	4.26
	PH	48.40**	500.8	85.6	6.2	5.3
	SPL	1.42*	0.012	0.24	0.13	0.14
	PDL	62.55**	105.46	2.8	2.13	1.66
	GPS	154.46**	12.5	35.37	25.55	24.6
	TGW	44.23**	2.65	0.67	1.23	1.36
	Zn	22.25**	4.19	0.27	0.32	0.41
	Fe	2.33**	3.2	0.11	0.16	0.13
	YPPT	10850.00**	5112.00**	353	251	279.00

Abbreviation: \*DF= Days to 50% flowering; DA= Days to anthesis; DPM= Days to physiological maturity; FLA= Flag leaf area (cm<sup>2</sup>); PH= Plant height (cm); SPL= Spike length (cm); PDL= Peduncle length (cm); GPS= Number of grains per spike; TGW= 1000 grains weight (g); Zn= Grain zinc (ppm); Fe= Grain iron (ppm); YPPT= Yield per plot (g); \* and \*\* indicates significant at 5% and 1%, respectively.

**Table 2:** Genetic parameters for twelve studied characters among 100 lines of wheat

Character	GM	SEm±	CD (5%)	CV (%)	Range	σ <sup>2</sup> g	σ <sup>2</sup> p	GCV	PCV	h <sup>2</sup> bs	GA	GAPM
								(%)	(%)	(%)	(%)	
DF*	73.77	0.99	2.78	3.46	66.50-79.50	4.55	6.51	2.89	3.46	69.84	3.67	4.97
DA	83.4	0.99	2.78	3.75	76.50-87.50	4.28	6.24	2.48	2.99	68.57	3.53	4.23
DPM	119.24	0.82	2.29	1.31	116.50-122.50	1.07	2.4	0.87	1.3	44.4	1.42	1.19
FLA	34.73	1.38	3.88	18.11	10.44-51.67	35.56	39.38	17.25	18.16	90.3	11.67	33.78
PH	93.14	2.11	5.91	5.98	75.97-102.13	19.76	28.63	4.77	5.74	69.04	7.61	8.17
SPL	10.45	0.27	0.75	8.44	7.98-13.23	0.64	0.78	7.64	8.46	81.68	1.49	14.23
PDL	39	0.97	2.72	14.64	24.30-52.10	30.33	32.22	14.12	14.55	94.16	11.01	28.23
GPS	53.83	3.56	10	17.58	34.67-84.00	64.53	89.93	14.92	17.62	71.75	14.02	26.04
TGW	38.49	0.8	2.25	12.36	27.00-53.50	21.47	22.75	12.04	12.39	94.37	9.27	24.09
Zn	26.32	0.43	1.21	12.76	17.27-33.82	10.94	11.31	12.57	12.78	86.71	6.7	25.46
Fe	36.55	0.26	0.74	3.06	33.80-39.63	1.1	1.24	2.87	3.05	88.76	2.04	5.57
YPPT	380.22	11.61	32.58	19.61	198.44-541.37	5290.33	5559.97	19.13	19.61	78.15	146.16	38.44

Abbreviation: \*DF= Days to 50% flowering; DA= Days to anthesis; DPM= Days to physiological maturity; FLA= Flag leaf area (cm<sup>2</sup>); PH= Plant height (cm); SPL= Spike length (cm); PDL= Peduncle length (cm); GPS= Number of grains per spike; TGW= 1000 grains weight (g); Zn= Grain zinc (ppm); Fe= Grain iron (ppm); YPPT= Yield per plot (g); GM= Grand mean; SEm±= Standard error of mean; CD= critical difference; CV= Coefficient of variation; σ<sup>2</sup>g= Phenotypic variance; σ<sup>2</sup>p= Phenotypic variance; GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation; h<sup>2</sup>bs= Heritability (broad sense); GA= Genetic advance; GAPM= Genetic advance as a percent of mean

**Table 3:** Genotypic (above diagonal) and phenotypic correlation coefficient (below diagonal) for twelve studied characters among 100 wheat lines

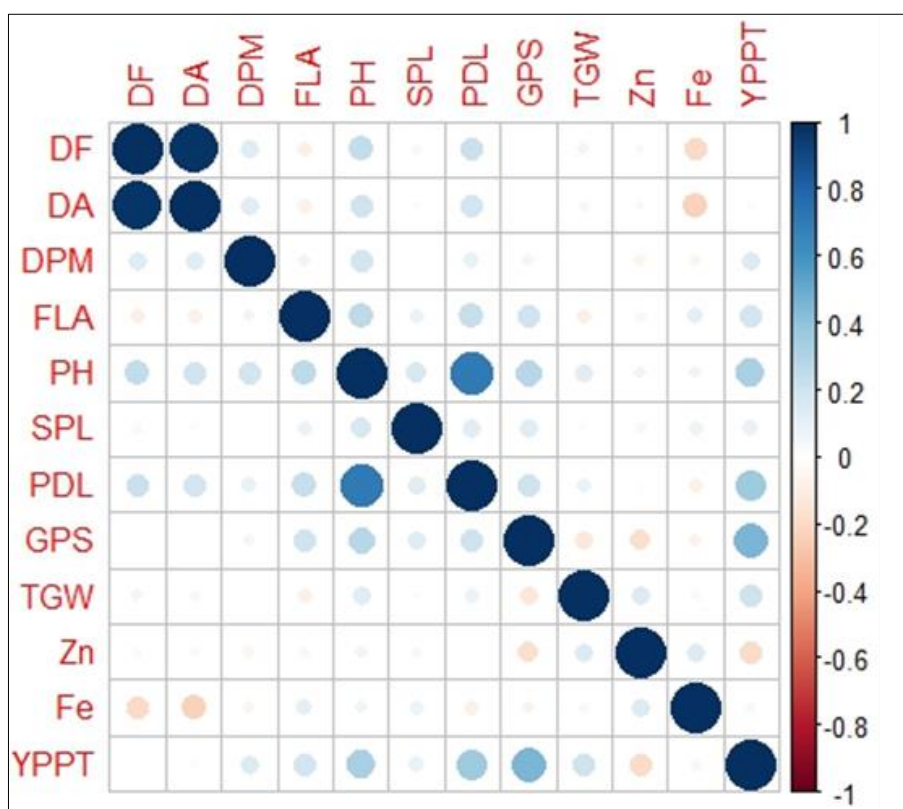
	DF*	DA	DPM	FLA	PH	SPL	PDL	GPS	TGW	Zn	Fe	YPPT
DF	1	0.912 **	0.084	-0.086	0.247 *	0.032	-0.27 *	-0.023	-0.026*	-0.045	-0.271 **	-0.033
DA	0.979 **	1	0.131	-0.064	0.224 *	0.022	-0.248 *	-0.018	0.023	-0.034	-0.280 **	-0.046
DPM	0.126	0.128	1	0.06	0.355 **	0.038	-0.125*	0.138	-0.061*	-0.114	-0.133	-0.155
FLA	-0.08	-0.076	0.063	1	0.361 **	0.108	0.252 *	0.264 **	-0.1	-0.051	0.131	0.195
PH	0.227**	0.213**	0.157 *	0.270**	1	0.184	0.817 **	0.392 **	0.127	0.089	0.074	-0.362 **
SPL	0.035	0.026	-0.007	0.083	0.165*	1	0.147	0.17	-0.002	-0.055	0.109	0.11
PDL	-0.208**	-0.190**	0.079	0.229**	0.706**	0.122	1	0.271 **	0.083*	0.013	-0.079	0.370 **
GPS	0.002	-0.001	0.061	0.193 **	0.290**	0.137	0.215**	1	-0.14	-0.207 *	-0.083	0.549 **
TGW	-0.049	0.042	-0.013*	-0.089	0.123	-0.026	0.078*	-0.124	1	0.143	0.03	0.199**
Zn	-0.036	-0.029	-0.065	-0.046	0.057	-0.048	0.013	-0.174*	0.141*	1	0.151*	-0.191
Fe	-0.207**	-0.227**	-0.07	0.117	0.033	0.078	-0.088	-0.061	0.035	0.139*	1	-0.05
YPPT	-0.009	-0.025	-0.133	0.188**	-0.324**	0.093	0.351**	0.457**	0.206 **	-0.191 **	-0.049	1 **

\* and \*\* indicates significant at p<0.05 and p<0.01%, respectively

Abbreviation: \*DF= Days to 50% flowering; DA= Days to anthesis; DPM= Days to physiological maturity; FLA= Flag leaf area (cm<sup>2</sup>); PH= Plant height (cm); SPL= Spike length (cm); PDL= Peduncle length (cm); GPS= Number of grains per spike; TGW= 1000 grains weight (g); Zn= Grain zinc (ppm); Fe= Grain iron (ppm); YPPT= Yield per plot (g).

**Table 4:** Direct and indirect effect of eleven component characters on yield per plot of wheat as an independent variable at genotypic level

	DF	DA	DPM	FLA	PH	SPL	PDL	GPS	TGW	Zn	Fe	Genotypic correlation with yield/plot
DF	-0.978	0.880	0.005	-0.0007	-0.033	-0.0001	0.097	-0.011	0.008	0.006	-0.005	-0.033
DA	-0.984	0.874	0.008	-0.0005	-0.030	-0.0001	0.089	-0.009	0.007	0.005	-0.005	-0.046
DPM	-0.082	0.115	0.060	0.0005	-0.047	-0.0001	0.045	0.069	-0.018	0.015	-0.002	-0.155
FLA	0.084	-0.056	0.004	0.0077	-0.048	-0.0003	0.091	0.133	-0.029	0.007	0.002	0.195
PH	-0.242	0.196	0.021	0.0028	-0.133	-0.0006	0.295	0.197	0.037	-0.012	0.001	-0.362 **
SPL	-0.031	0.019	0.002	0.0008	-0.025	-0.0031	0.053	0.085	-0.001	0.007	0.002	0.11
PDL	-0.264	0.217	0.007	0.0019	-0.109	-0.0005	0.360	0.136	0.024	-0.002	-0.001	0.370 **
GPS	0.022	-0.016	0.008	0.0020	-0.052	-0.0005	0.098	0.502	-0.041	0.028	-0.002	0.549 **
TGW	-0.025	0.020	-0.004	-0.0008	-0.017	0.0000	0.030	-0.070	0.293	-0.019	0.001	0.199**
Zn	0.044	-0.029	-0.007	-0.0004	-0.012	0.0002	0.005	-0.104	0.042	-0.133	0.003	-0.191
Fe	0.266	-0.245	-0.008	0.0010	-0.010	-0.0003	-0.028	-0.042	0.009	-0.020	0.018	-0.05
Residual		0.5522										



**Fig 1:** Correlation among twelve studies characters in the studied wheat genotypes

**Conclusion**

ANOVA indicated enough variability and significant differences between genotypes for all variables indicating the occurrence of a wide range of genetic variability and the scope of selection for these characters. Based on correlation and path coefficient analysis, the days to anthesis, number of grains per spike, and 1000 grain weight were shown to be the better selection indices for enhancing grain yield because of their significant direct and indirect effects. Several yield-attributing characters influence wheat grain yield and correlate in both positive and negative directions. This centre is located in the North-Eastern Plain Zone (NEPZ), and the major feature of this region is the rice-wheat cropping system. Early-maturing wheat types are very important in this zone. Hence, among 98 genotypes, entry 46, 70, 58, 45 and 60 with days of physiological maturity of ranges 118 days to 121 days are recommended as early genotypes of wheat with high grain

zinc and iron content. 1000-grain weight is one of the most yield contributing characters, entry 30 (53.5 g), 24 (47.0 g) and 10 (46.5 g) showed importance for this trait. Nonetheless, these genotypes will need to be examined further in multilocation experiments for yield, leaf rust and spot blotch disease resistance and other quality parameters for better utilization in future breeding programmes.

**References**

1. Abrar YB, Kumar M, Kumar R. Assessment of cause and effect relationship between different character combinations on yield and quality of bread wheat (*Triticum aestivum* L.). Plant Archives. 2020;20(2):6378-6382.
2. Ahmadi M, Farshadfar E, Veisi S. Evaluation of genetic diversity in land races of bread wheat under irrigated and rainfed conditions. International Journal of Agriculture

- and Crop Sciences. 2012;4(21):1627-1636.
3. Ali IH, EF Shakor. Heritability, Variability, Genetic Correlation and Path Analysis for Quantitative Characters in Durum and Bread Wheat Under Dry Farming Conditions. *Mesopotamia Journal of Agriculture*. 2012;66:37-39.
  4. Ashfaq S, Ahmad HM, Awan SI, Muhammad SA. Estimation of genetic variability, heritability and correlation for some morphological characters in spring wheat. *Journal of Biology, Agriculture and Healthcare*. 2014;4(5):10-16.
  5. Badole SS, Mukharjee S, Pal AK, De DK. Estimation of variability for yield parameters in Bread Wheat (*Triticum aestivum* L.) grown in Genetic, West Bengal. *Electronic Journal of Plant Breeding*. 2010;1(4):764-768.
  6. Baranwal DK, Mishra VK, Vishwakarma MK, Yadav PS, Arun B. Studies on genetic variability, correlation and path analysis for yield and yield contributing characters in wheat (*T. aestivum* L. em Thell.). *Plant archives*. 2012;12(1):99-104.
  7. Burton GW. Quantitative inheritance in grasses. *Proceeding 6<sup>th</sup>. International Grass Land Congress*. 1952;1:227-283.
  8. Burton GW, Dewane EH. Estimating heritability in tall Fescues (*Festuca allamidiaceae*) from replicated clonal material. *Agronomy Journal*. 1953;45:1476-1481.
  9. Dewey DR, Lu KN. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*. 1959;51:515-518.
  10. FAOSTAT. Food and Agriculture Organization of the United Nations statistical database, Rome, FAO, <https://www.fao.org/faostat/en/#data/QCL>. 2021
  11. Garg P, Saharan RP, Chawla V, Gupta M. Correlation and path analysis for yield and its components in wheat (*Triticum aestivum* L em. Thell.) Under normal and drought conditions. *Annals of Biology*. 2014;30(1):71-76.
  12. Gelalcha S, Hanchinal RR. Correlation and path analysis in yield and yield components in spring bread wheat (*Triticum aestivum* L.) genotypes under irrigated condition in Southern India. *African Journal of Agricultural Research*. 2013;8(24):3186-3192.
  13. Grafius JE. Does overdominance exist for yield in corn. *Agronomy Journal*. 1960;52:361.
  14. Johnson HW, Robinson HF, Comstock RE. Genotypic and Phenotypic correlations in soybeans and their implication in selection *Agronomy Journal*. 1955;47:477-483.
  15. Kishore A, Singh V. Seeds, water, and markets to increase wheat productivity in Bihar, India. *CSISA Research Note 19. Cereal Systems Initiative for South Asia (CSISA)*; c2021.
  16. Kumar D. Studies on morpho-physiological characters associated with moisture-stress tolerance in bread wheat (*Triticum aestivum* L.). M.Sc. Thesis, Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya Palampur, India, 2019, 131.
  17. Kumar Y, Lamba RAS, Singh B, Kumar V. Genetic variability, correlation and path analysis in wheat varieties under late sown condition. *Annals of Agri Bio Research*. 2014;19(4):724-727.
  18. Liu K, H Xu, G Liu, P Guan, X Zhou, H Peng *et al*. QTL mapping of flag leaf-related characters in wheat (*Triticum aestivum* L.). *Theoretical and Applied Genetics*. 2018;131:839-849.
  19. Nain G. Bihar Agriculture Scenario Pertaining to the Principal Crops; c2018.
  20. Phougat D, IS Panwar, Saharan RP, Singh V, Godara A. Genetic diversity and association studies for yield attributing characters in bread wheat (*Triticum aestivum* (L.) em. Thell). *Research on Crops*. 2017;18:139-144.
  21. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlation's in wheat and their implications in selection. *Agronomy Journal*. 1951;43:282-287.
  22. Searle SR. Phenotypic, genotypic and environmental correlations. *Biometrics*. 1961;17:474-480.
  23. Shiferaw B, Smale M, Braun HJ, Duveiller E, Reynolds M, Muricho G. Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. *Food Security*. 2013;5(3):291-317.
  24. Wright S. Correlation and causation. *Journal of Agricultural Research*. 1921;20:557-585.