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GENETIC ANALYSIS OF YIELD AND ITS CONTRIBUTING ATTRIBUTES IN WHEAT (*Triticum aestivum* L.) UNDER TIMELY SOWN CONDITION

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ABSTRACT

The field experiment was conducted on 94 bread wheat genotypes, including four checks (DBW-222, DBW-187, HD-3086 and NW-5054) using Augmented Block Design to evaluate the genetic variability for 12 morphological and yield-related traits for timely sown condition. The objectives of the study were to assess genetic variation, heritability and the strength and/or direction of correlations between grain yield and its component traits. Harvest index and biological yield per plant were highly significantly and positively correlated with grain yield per plant and 1000 grain weight was significantly positively correlated with grain yield per plant. The path coefficient analysis showed that harvest index, biological yield per plant, 1000-grain weight and peduncle length had the highest positive direct effects on grain yield. The main indirect positive effects on grain yield were due to the biological yield per plant, the harvest index and 1000 grain weight. In all the 12 traits the phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV). The 94 genotypes were classified as nine clusters, with the highest average intra-cluster distance in Cluster VIII, followed by Clusters III, VII and IX while the lowest intra-cluster distance was in Cluster V followed by Clusters I and VI. Genotypes identified as superior could be valuable resources to be used in wheat breeding programmes in the future and for selection of diverse parents.

Key words: Genetic Variability, heritability, Correlation coefficient, Genetic divergence

Introduction

Wheat belongs to the family *Poaceae* (*Gramineae*) and genus *Triticum*, and is one of the most important cereal crops around the world as an energy crop. Bread wheat (*Triticum aestivum* L.), is an allohexaploid species ($2n = 6x = 42$) that includes the A, B and D genomes. Wheat is a key food crop and plays a significant role in meeting the global dietary energy needs. Belderok et al. (2000) reported that the constituents of wheat grain are about 2-3% germ, 13-17% bran (the outer part of the grain) and 80-85% endosperm. The endosperm is rich in proteins (about 13%), lipids (1.5%) and the major gluten forming proteins (gliadins and glutenins) which are

important for dough formation and bread making quality. The global wheat production for 2025–2026 was projected at 844.36 million metric tonnes (USDA, 2025). The population of the world will reach 9.8 billion by 2050, further increasing the demand for food grains by about 70%. India ranks as the second biggest wheat producer in the world with an estimated production of 140.07 million metric tonnes for 2024-2025 (USDA, 2025). Asia experienced the greatest growth in wheat area (47.06%), production (336.86%) and productivity (209.47%) during the period from 1970 to 2020 TE. In 2020 TE, India, China and New Zealand recorded the largest wheat area (30.1 Mha), production (135 Mt) and productivity (9100

Table 1: Analysis of variance for 12 characters in wheat.

S. V	Block	Checks	Error
df.	5	3	15
Days to 50 % flowering	5.296 **	66.471 **	0.163
Days to maturity	5.068 **	31.000 **	0.666
Plant height (cm)	149.796 **	144.647 **	0.013
Spike length (cm)	1.770 **	0.546 **	0.001
Peduncle Length (cm)	243.806 **	4.050 **	0.074
Spikelets/ spike	9.526 **	7.399 **	0.001
No. of grains /Spike	13.969 **	43.383 **	0.039
Tillers /plant	0.282 **	2.588 **	0.002
1000-grain weight (g)	36.303 **	38.175 **	1.462
Biological yield/plant (g)	4.064 **	13.006 **	0.0004
Harvest index (%)	6.439 **	2.627 **	0.009
Grain yield /plant (g)	1.361 **	2.678 **	0.001

kg ha⁻¹), respectively. But wheat production and productivity are increasingly at risk due to changing climatic conditions, which could have significant implications on food security. Thus, technology and genetic improvement are vital to increase wheat productivity and ensure its continuation with increasing environmental stresses.

Material and Methods

The present study was carried out at Main Experiment Station, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during the year 2022-2023 (*Rabi* season). The experimental site is situated between 24°47' N and 26°56' N latitude, and 82°12' E and 83°98' E longitude, at an altitude of 113 m above mean sea level. The area is part of the Sub-Tropical climatic zone and the soil is sandy loam with an average annual rainfall of about 1270 mm where the monsoon is the dominant factor with a maximum strength from July to September from the

South-West region. The experiment consisted of 90 wheat germplasm lines and four checks (viz., DBW-222, DBW-187, HD-3086 and NW-5054) in an Augmented Block Design. The experimental field was split into 6 blocks, containing 15 unreplicated wheat germplasm lines and 4 replicated checks in each block. Therefore, each of the 90 germplasm lines was tested once while the four checks were tested in each of the six blocks. The size of each plot was two rows of 2.5 m long, 5 cm apart inside the row and 20 cm apart between rows. The following 12 morphological and yield traits were considered for evaluation of the genotypes: days to 50% flowering, days to maturity, plant height (cm), spike length (cm), peduncle length (cm), spikelets per spike, grains per spike, effective tillers per plant, 1000-grain weight (g), biological yield per plant (g), harvest index (%), and grain yield per plant (g). All the observations were recorded and analyzed statistically and biometrically. The analysis of variance was done after Panse and Sukhatme (1961) and heritability in the broad sense was estimated after Allard (1960). The correlation coefficients were computed from the data as suggested in Searle (1961) and path coefficient analysis computed as suggested by Dewey and Lu (1959). The wheat genotypes were compared in terms of genetic divergence using non-hierarchical Euclidean cluster analysis. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per Burton and Devane (1953).

Results and Discussion

The analysis of variance (ANOVA) for the 12 traits under the Augmented Block Design is presented in Table 1. The results revealed considerable variability among the wheat genotypes for all the characters studied. The block effects and check effects were significant for all the traits, indicating substantial variation among blocks

Table 2: Estimation of range, mean, coefficient of variation %, and heritability (broad sense) %, genetic advance and genetic advance % mean for 12 characters in wheat genotype under timely sown condition.

Characters	Mean	Range		GCV (%)	PCV (%)	Broad sense heritability % (h ² b)	Genetic advance in % of mean
		Minimum	Maximum				
Days to 50% flowering	81.325	73.757	86.015	2.334	2.386	95.68	4.7035
Days to maturity	125.9151	122.08	130.08	1.098	1.275	74.17	1.9485
Plant height (cm)	88.4258	72.9	104.281	6.247	6.248	99.96	12.866
Spike length (cm)	11.8553	9.59	13.73	6.19	6.195	99.83	12.7407
Peduncle length (cm)	26.6182	18.991	32.836	14.813	14.849	99.52	30.4427
Spikelets/spike	20.0807	16.196	23.406	6.924	6.926	99.95	14.2601
Grains/spike	44.935	35.073	57.503	9.507	9.517	99.79	19.5631
Tillers/plant	4.984	3.9467	6.8767	10.064	10.112	99.06	20.6353
1000-grain weight (g)	39.0446	32.448	45.02	6.274	7	80.33	11.5828
Biological yield/ plant (g)	31.2172	24.668	38.338	7.84	7.84	99.99	16.1495
Harvest index (%)	42.4578	35.053	46.338	7.012	7.015	99.9	14.4376
Grain yield/plant (g)	13.2465	10.221	15.966	10.069	10.071	99.96	20.7374

Table 7: Cluster mean analysis for twelve characters of wheat under timely sown condition.

Characters Clusters	DF	DM	PH	SL	PL	NSS	NGS	TP	GW	BY	HI	GYP
I	83.8	127.762	93.679	10.988	27.178	17.681	42.842	4.556	41.071	29.77	42.263	12.564
II	82	126	96.166	11.703	29.937	19.743	45.321	4.963	40.507	27.724	39.307	10.874
III	82.083	126.417	88.572	12.423	24.502	21.133	41.603	4.805	40.122	32.476	36.334	11.793
IV	81	125.6	89.278	12.244	24.256	20.88	39.136	4.242	39.26	34.25	42.564	14.58
V	78.393	124	86.2	11.856	26.064	20.15	50.116	6.01	39.686	33.163	42.133	13.966
VI	78.714	126.571	95.623	12.5	29.803	21.223	46.87	5.199	40.157	30.969	44.139	13.666
VII	81.692	123.923	87.345	11.183	27.68	18.831	45.958	4.988	38.429	32.452	44.079	14.305
VIII	82.2	127.2	86.108	10.828	30.08	18.4	51.574	5.588	41.62	31.884	42.934	13.646
IX	81.882	126.824	82.617	12.385	21.368	21.071	46.186	5.174	36.824	30.907	44.692	13.814
DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); SL: Spike length (cm); PL: Peduncle length (cm); NSS: No. of Spikelets / spike; NGS: No. of grains /Spike; TP: tillers /plant; GW: 1000-grain weight (g); BY: Biological yield/ plant (g); HI: Harvest index (%); GYP: Grain yield /plant (g)												

days to 50% flowering (0.158), effective tillers per plant (0.086), spikelets per spike (0.077) and spike length (0.015). The positive direct effects of harvest index and biological yield per plant, together with their significant positive correlations with grain yield, indicate their potential importance as selection criteria for improving grain yield. The major positive indirect associations with grain yield were observed through biological yield per plant, harvest index and 1000-grain weight. In contrast, negative associations with grain yield were observed for days to 50% flowering (-0.142), plant height (-0.325) and days to maturity (-0.200). The residual effect was 0.29945, indicating that the traits included in the analysis accounted for a substantial proportion of the variation in grain yield. Path coefficient analysis provides a useful means of understanding the relative contribution of component traits to grain yield and helps in identifying appropriate selection criteria. Similar applications of path analysis for yield improvement in wheat have been reported by Maurya *et al.*, (2020) and Abdulhamed *et al.*, (2021).

Non-hierarchical Euclidean cluster analysis was employed to assess the genetic divergence among the 90 wheat germplasm lines and four checks based on 12 quantitative traits. The pseudo-F test indicated that a nine-cluster arrangement was most appropriate for grouping the 94 genotypes. Accordingly, the genotypes were grouped into nine distinct and non-overlapping clusters. The estimates of intra- and inter-cluster distances are presented in Table 6. The highest average intra-cluster distance was observed in Cluster VIII (21.148), followed by Cluster III (15.696), Cluster VII (15.411), Cluster IX (12.699) and Cluster II (11.777), indicating relatively greater genetic diversity among genotypes within these clusters. The lowest intra-cluster distance was recorded in Cluster V (7.308), followed by Cluster I (7.764) and Cluster VI (8.519). The maximum inter-cluster distance

was observed between Cluster III and Cluster VIII (38.610), followed by Cluster IV and Cluster VIII (37.345), indicating substantial genetic divergence between these clusters. The minimum inter-cluster distance was observed between Cluster V and Cluster VI (16.852), followed by Cluster I and Cluster II (17.317). Therefore, genotypes belonging to clusters with greater inter-cluster distances may provide useful opportunities for selecting genetically diverse parents for hybridization. Similar patterns of genetic divergence and clustering in wheat have been reported by Sapi *et al.*, (2017) and Arain *et al.*, (2018).

Conclusion

Under the timely sown condition, the present investigation showed that there was significant genetic variation among the 94 wheat genotypes for 12 traits. The moderate estimates of GCV and PCV were seen in the peduncle length, effective tillers per plant and grain yield per plant while the rest of the traits showed low estimates of GCV and PCV. The majority of the traits had high heritability and days to maturity had moderate heritability. The traits that showed the highest genetic advance as % of mean were peduncle length, grain yield per plant and effective tillers per plant which suggested that selection would be effective for these traits. Biological yield per plant and harvest index showed highly significant and positive correlations with grain yield per plant, whereas days to maturity showed a significant negative correlation and plant height exhibited a highly significant negative correlation with grain yield per plant. The path coefficient analysis showed that the highest positive direct effect was on harvest index (0.797) followed by biological yield per plant (0.794), 1000 grain weight (0.482) and peduncle length (0.330) which may have importance in the improvement of grain yield. Genetic divergence analysis resulted in nine clusters with the highest inter-

cluster distance found between Clusters III and VIII (38.610) which suggests significant genetic differences between these clusters. Based on the grain yield performance, the following genotypes were considered as promising for timely sown condition; IBWSN 1211, SAWSN 3131, SAWSN 3137, SAWSN 3163 and IBWSN 1190. These genotypes, and especially the ones from genetically divergent clusters, would be valuable sources in breeding for future wheat improvement programmes, as well as for parent selection.

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