Analysis of Genetic Divergence in Wheat (Triticum aestivum L.) Using Yield Attributes

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Abstract — This study investigates the genetic divergence in wheat (Triticum aestivum L.) using yield-related attributes. Conducted during the Rabi season of 2021-2022, the research involved four wheat genotypes evaluated under a randomized block design. Comprehensive statistical analyses, including phenotypic and genotypic variability, heritability, genetic advance, correlation coefficients, path analysis, and Mahalanobis D^2 statistics, were employed. Results indicated significant variability among genotypes for traits such as plant height, flag leaf area, and harvest index. High heritability and genetic advance values for key traits suggest their potential utility in wheat breeding programs. These findings provide a robust framework for selecting genetically diverse parents to enhance wheat yield, adaptability, and resilience against environmental stresses.

Keywords: Genetic Divergence, Triticum Aestivum, Yield Attributes, Multivariate Analysis, Heritability, Breeding Program, Genetic Variability

I. Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide, serving as a primary source of carbohydrates and proteins for a significant portion of the global population. Wheat cultivation spans diverse agro-climatic regions, owing to its adaptability and significant role in global food security. The rising demand for wheat is attributed to its versatile applications in food products, along with its nutritional value as a source of dietary fiber, vitamins, and minerals.

In India, wheat is a cornerstone of the agricultural economy, contributing substantially to the caloric intake of the population. With increasing pressures from climate change and the growing global population, improving wheat yield and resilience is a priority. Genetic improvement of wheat through breeding programs relies on understanding the genetic variability and associations among yield-contributing traits. Genetic divergence analysis, using methods such as Mahalanobis D^2 statistics, aids in identifying diverse genotypes for use in hybridization programs, paving the way for developing high-yielding and climate-resilient varieties.

Panwar and Singh (2000) evaluated wheat cultivars under varying agro-climatic conditions and reported significant genetic variability in plant height, tillers per plant, and grain yield, highlighting the importance of genotype selection for improved productivity. Kumar and Verma (2004) examined the genetic correlation of yield traits, noting a positive correlation between flag leaf area and 1000-grain weight, while flag leaf area negatively correlated with grain number per spike. Rahman et al. (2012) studied genetic variability and heritability of yield components, finding high heritability for plant height and grain yield per square meter across different sowing conditions. Singh and Upadhyay (2017) conducted divergence analysis in bread wheat, clustering genotypes based on genetic diversity for breeding purposes. Ullah et al. (2011) used path coefficient analysis to identify traits such as grains per spike and spike length that had a direct positive effect on yield. Mahalanobis (1928) introduced a statistical method to measure genetic divergence, which has been widely applied in wheat diversity studies. Dewey and Lu (1959) conducted path-coefficient analysis on crested wheatgrass, laying the foundation for modern yield component studies. Rao (1952) contributed advanced statistical methods for biometric research, aiding genetic evaluations. Ali et al. (2017) and Yadav et al. (2017) provided insights into genetic variability, heritability, and genetic advances in wheat, offering valuable data for selection and breeding programs.

This study aimed to assess the genetic divergence among wheat genotypes and identify traits critical for improving yield and adaptability. Insights from this analysis are intended to guide the selection of parental lines for strategic breeding programs.

II. Methodology

A. Experimental Site

The experiment was conducted at the Agricultural Farm of Baba Farid Institute of Technology, Dehradun, Uttarakhand, India, during the Rabi season of 2021-2022. The farm is situated at 30.3436° N latitude and 77.9367° E longitude, with an elevation of 635 meters above sea level. The region experiences a sub-temperate climate characterized by cool winters, moderate summers, and an average annual rainfall exceeding 1500 mm. The soil type in the experimental field is fertile alluvial, suitable for wheat cultivation.

B. Experimental Design and Genotypes

The study employed a randomized block design (RBD) with three replications to ensure the reliability of results. The experimental material comprised four wheat genotypes: WB02, WB1105, SARTAJ303, and PBW725. Each plot measured 2 m x 1 m, with a row-to-row spacing of 22.5 cm. Standard agronomic practices, including timely irrigation and nutrient management, were followed throughout the crop's growth cycle. Observations were recorded for 13 key yield-related traits, including plant height, spike length, flag leaf area, biological yield, and harvest index.

1) Statistical Analysis

A robust statistical approach was adopted to analyze the data:

- Analysis of Variance (ANOVA): Used to assess the significance of variability among genotypes.
- Phenotypic and Genotypic Coefficients of Variation (PCV, GCV): To quantify the extent of variability.

- Heritability and Genetic Advance: Estimated to evaluate the potential for trait improvement through selection.
- Correlation and Path Analysis: Employed to examine relationships among traits and their direct and indirect contributions to yield.
- Mahalanobis D^2 Statistics: Applied to cluster genotypes and assess genetic divergence. This method helps identify genetically diverse parents for hybridization programs.

III. Results and Discussion

A. Variability Analysis

ANOVA revealed significant differences among the genotypes for all traits studied, indicating substantial genetic variability. Traits such as harvest index, flag leaf area, and biological yield exhibited high PCV and GCV values, underscoring their genetic control and potential for selection-driven improvement. For example, the harvest index demonstrated a GCV of 37.67% and a PCV of 37.99%, suggesting minimal environmental influence on this trait.

High heritability values (e.g., 88% for harvest index and 86% for flag leaf area) combined with high genetic advance (e.g., 76.96% for harvest index) indicate that these traits are governed by additive genetic effects. Such traits are particularly valuable in breeding programs focused on yield enhancement and adaptation to varying environmental conditions.

B. Correlation and Path Analysis

Correlation analysis identified positive and significant relationships between grain yield and traits such as biological yield per plant (r = 0.85), tillers per plant (r = 0.74), and spike length (r = 0.68). These associations suggest that improving these traits can directly enhance grain yield.

Path coefficient analysis provided deeper insights into the direct and indirect effects of these traits. The harvest index exhibited the highest direct positive effect (0.512) on grain yield, followed by biological yield per plant (0.475). Conversely, traits such as days to maturity displayed negligible or negative direct effects, emphasizing the need for balanced trait selection in breeding programs. These findings align with previous studies and highlight the complex interplay among yield-contributing traits.

C. Genetic Divergence

Using Mahalanobis D^2 statistics, the genotypes were grouped into distinct clusters based on their genetic divergence. Genotypes WB1105 and SARTAJ303 emerged as the most genetically diverse, making them ideal candidates for hybridization programs aimed at exploiting heterosis. Such genetic diversity is crucial for developing wheat varieties that combine high yield potential with resilience to biotic and abiotic stresses.

The clustering analysis also revealed that traits such as spike length, flag leaf area, and harvest index contributed significantly to genetic divergence. These findings underscore the importance of these traits in breeding strategies.

ANOVA for Plant height (cm)

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability
Replicate	2	178.485000	89.242520	0.9476	0.4389
Treatments	3	604.477288	201.492429	2.1395	0.1965
Error	6	565.073556	94.178926		
General Mean		86.1067	(5.6029)	95%	99%
S.E.Diff.		7.9238	Critical Diff.	19.3889	29.3766
S.E.Diff from Mean		4.8523	Critical Diff.	11.8732	17.9894
Var Environmental		94.1789	ECV	11.2704 %	
VarGenotypical		35.7712	GCV	6.9459 %	
VarPhenotypical		129.9501	PCV	13.2389 %	
h^2 (Broad Sense)		0.2753	S.E. of h^2	0.5723	
Genetic Advancement		6.4642	8.2842		
Gen.Adv as % of Mean		7.5072 %	9.6208 %(selection intensity at 5% & 1%)		

Table 1: ANOVA for Plant Height (cm)

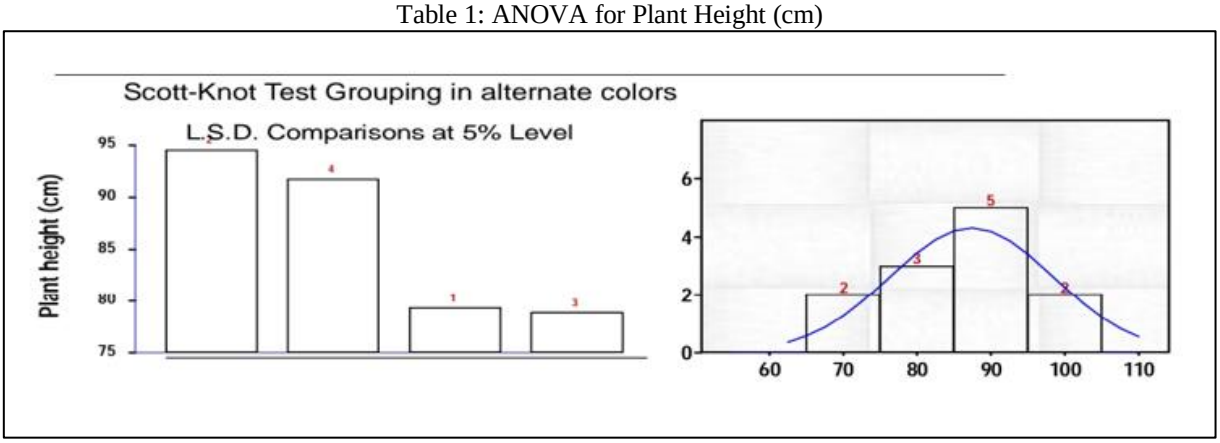

Fig. 1: Plant height (cm) L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability
Replicate	2	0.899317	0.449658	0.6990	0.5335
Treatments	3	8.291264	2.763755	4.2966	0.0611
Error	6	3.859485	0.643248		
General Mean		9.4567	(0.4631)	95%	99%
S.E.Diff.		0.6549	Critical Diff.	1.6024	2.4278
S.E.Diff from Mean		0.4010	Critical Diff.	0.9813	1.4867
Var Environmental		0.6432	ECV	8.4811 %	
VarGenotypical		0.7068	GCV	8.8904 %	
VarPhenotypical		1.3501	PCV	12.2869 %	
h² (Broad Sense)		0.5235	S.E. of h²	0.5936	
Genetic Advancement		1.2532	1.6060		
Gen.Adv as % of Mean		13.2516 %	16.9826 %(selection intensity at 5% & 1%)		

Table 2: ANOVA for Spike Lengh (cm)

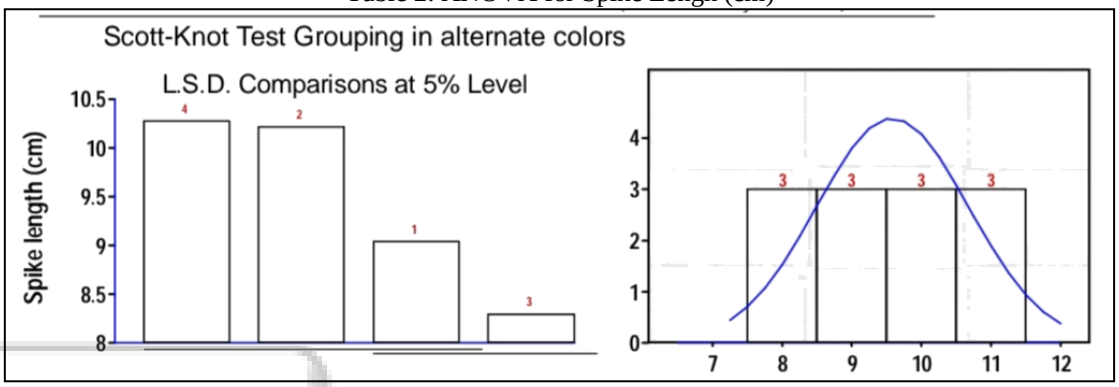

Fig. 2: Spike Length (cm) , L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability	
Replicate	2	2.161818	1.080909	0.0586	0.9436	
Treatments	3	731.470174	243.823391	13.2296	0.0047	**
Error	6	110.581195	18.430199			
General Mean		33.7483	(2.4786)	95%	99%	
S.E.Diff.		3.5053	Critical Diff.	8.5771	12.9954	
S.E.Diff from Mean		2.1465	Critical Diff.	5.2524	7.9580	
Var Environmental		18.4302	ECV	12.7207 %		
VarGenotypical		75.1311	GCV	25.6837 %		
VarPhenotypical		93.5613	PCV	28.6613 %		
h² (Broad Sense)		0.8030	S.E. of h²	0.6167		
Genetic Advancement		16.0007	20.5057			
Gen.Adv as % of Mean		47.4118 %	60.7607 %(selection intensity at 5% & 1%)			

Table 3: ANOVA for Flag Leaf Area

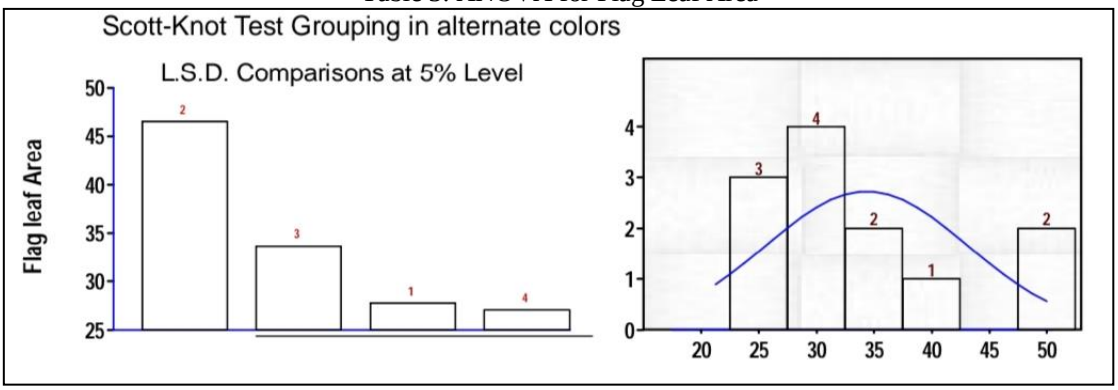

Fig. 3: Flag Leaf Area, L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability
Replicate	2	3.166667	1.583333	0.6404	0.5596
Treatments	3	24.666667	8.222222	3.3258	0.0981
Error	6	14.833333	2.472222		
General Mean		104.6667	(0.9078)	95%	99%
S.E.Diff.		1.2838	Critical Diff.	3.1414	4.7596
S.E.Diff from Mean		0.7862	Critical Diff.	1.9237	2.9146
Var Environmental		2.4722	ECV	1.5022 %	
VarGenotypical		1.9167	GCV	1.3227 %	
VarPhenotypical		4.3889	PCV	2.0016 %	
h^2 (Broad Sense)		0.4367	S.E. of h^2	0.5862	
Genetic Advancement		1.8847	2.4153		
Gen.Adv as % of Mean		1.8006 %	2.3076 %(selection intensity at 5% & 1%)		

Table 4: ANOVA for Days to 50% maturity

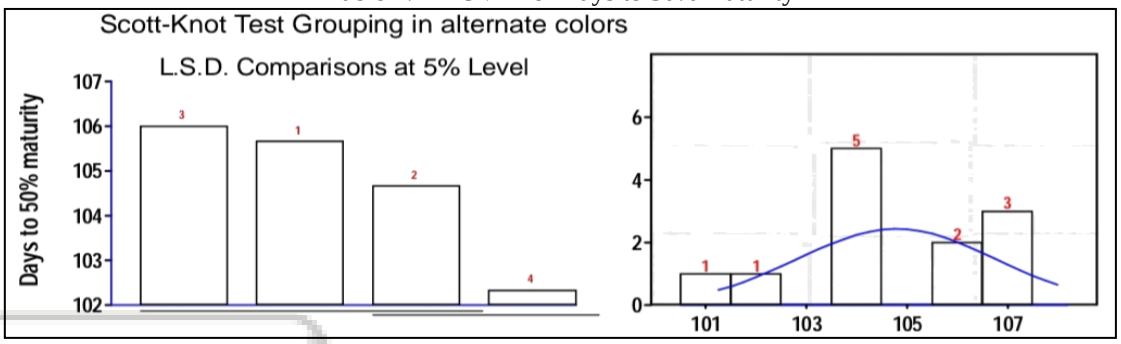

Fig. 4: Days to 50% maturity, L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability
Replicate	2	6.000000	3.000000	1.2273	0.3574
Treatments	3	11.583333	3.861111	1.5795	0.2896
Error	6	14.666667	2.444444		
General Mean		114.2500	(0.9027)	95%	99%
S.E.Diff.		1.2766	Critical Diff.	3.1237	4.7328
S.E.Diff from Mean		0.7817	Critical Diff.	1.9129	2.8982
Var Environmental		2.4444	ECV	1.3685 %	
VarGenotypical		0.4722	GCV	0.6015 %	
VarPhenotypical		2.9167	PCV	1.4948 %	
h^2 (Broad Sense)		0.1619	S.E. of h^2	0.5623	
Genetic Advancement		0.5696	0.7300		
Gen.Adv as % of Mean		0.4986 %	0.6389 %(selection intensity at 5% & 1%)		

Table 5: ANOVA for Days to maturity

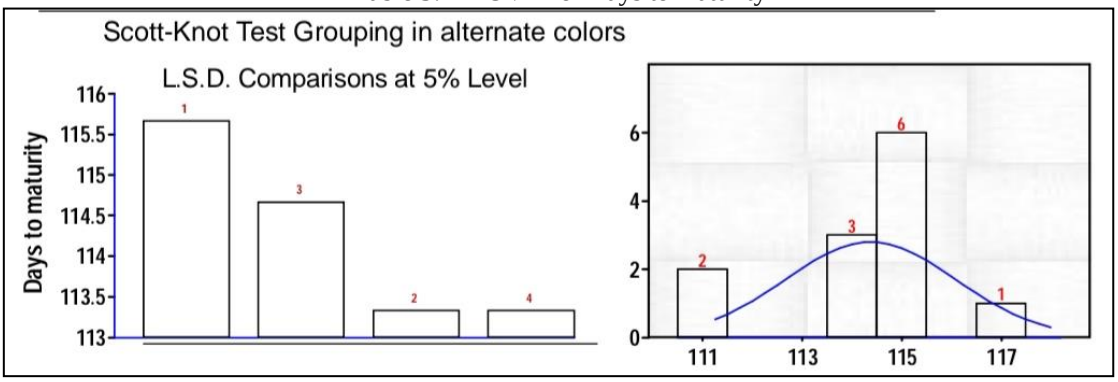

Fig. 5: Days to maturity, L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability
Replicate	2	0.021117	0.010558	0.0664	0.9364
Treatments	3	1.718092	0.572697	3.6023	0.0851
Error	6	0.953883	0.158981		
General Mean		2.3408	(0.2302)	95%	99%
S.E.Diff.		0.3256	Critical Diff.	0.7966	1.2070
S.E.Diff from Mean		0.1994	Critical Diff.	0.4878	0.7391
Var Environmental		0.1590	ECV	17.0334 %	
VarGenotypical		0.1379	GCV	15.8643 %	
VarPhenotypical		0.2969	PCV	23.2769 %	
h^2 (Broad Sense)		0.4645	S.E. of h^2	0.5886	
Genetic Advancement		0.5214	0.6682		
Gen.Adv as % of Mean		22.2732 %	28.5444 %(selection intensity at 5% & 1%)		

Table 6: ANOVA for Biological yield per plant (g)

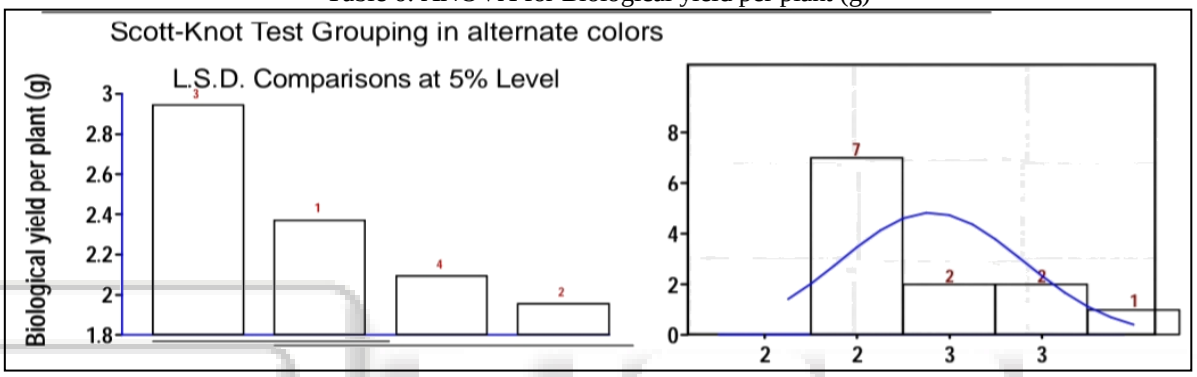

Fig. 6: Biological yield per plant (g), L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability	
Replicate	2	0.000150	0.000075	0.0091	0.9910	
Treatments	3	0.600025	0.200008	24.1702	0.0009	***
Error	6	0.049650	0.008275			
General Mean		0.8075	(0.0525)	95%	99%	
S.E.Diff.		0.0743	Critical Diff.	0.1817	0.2754	
S.E.Diff from Mean		0.0455	Critical Diff.	0.1113	0.1686	
Var Environmental		0.0083	ECV	11.2653 %		
VarGenotypical		0.0639	GCV	31.3073 %		
VarPhenotypical		0.0722	PCV	33.2724 %		
h^2 (Broad Sense)		0.8854	S.E. of h^2	0.6233		
Genetic Advancement		0.4900	0.6280			
Gen.Adv as % of Mean		60.6840 %	77.7698 %(selection intensity at 5% & 1%)			

Table 7: ANOVA for Seed yield per plot (Kg)

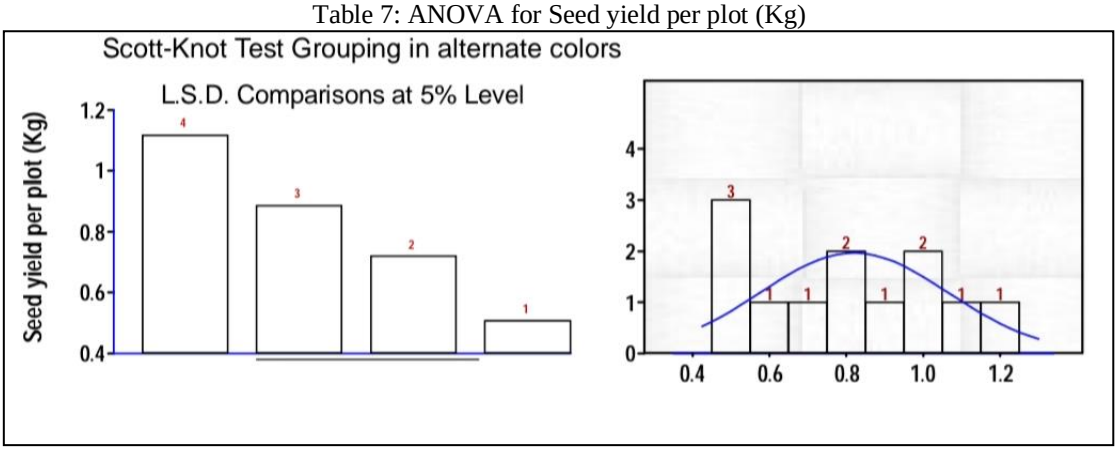

Fig. 7: Seed yield per plot (kg), L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability	
Replicate	2	15.944620	7.972309	2.5977	0.1539	
Treatments	3	1641.903367	547.301122	178.3303	0.0000	***
Error	6	18.414183	3.069030			
General Mean		35.7508	(1.0114)	95%	99%	
S.E.Diff.		1.4304	Critical Diff.	3.5001	5.3031	
S.E.Diff from Mean		0.8759	Critical Diff.	2.1433	3.2474	
Var Environmental		3.0690	ECV	4.9002 %		
Var Genotypical		181.4107	GCV	37.6743 %		
Var Phenotypical		184.4797	PCV	37.9917 %		
h^2 (Broad Sense)		0.9834	S.E. of h^2	0.6311		
Genetic Advancement		27.5141	35.2608			
Gen.Adv as % of Mean		76.9608 %	98.6294 %(selection intensity at 5% & 1%)			

Table 8: ANOVA for Harvest Index (%)

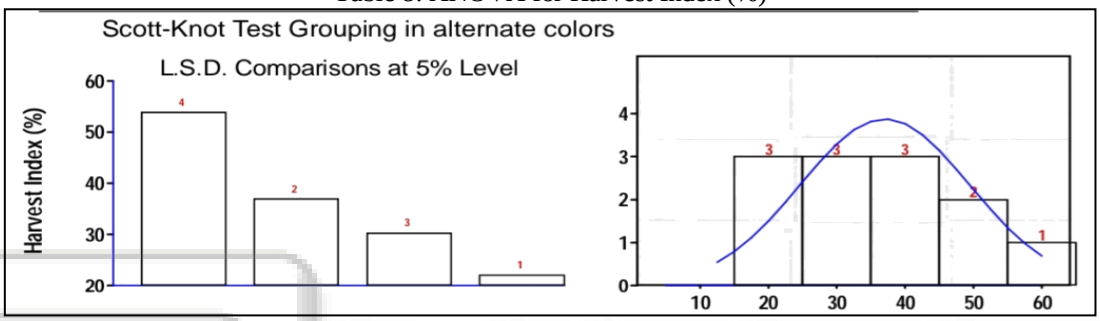

Fig. 8: Harvest Index (%), L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability
Replicate	2	4.918615	2.459308	1.6158	0.2745
Treatments	3	6.336065	2.112022	1.3877	0.3343
Error	6	9.131977	1.521996		
General Mean		32.5933	(0.7123)	95%	99%
S.E.Diff.		1.0073	Critical Diff.	2.4648	3.7345
S.E.Diff from Mean		0.6168	Critical Diff.	1.5094	2.2869
Var Environmental		1.5220	ECV	3.7851 %	
VarGenotypical		0.1967	GCV	1.3606 %	
VarPhenotypical		1.7187	PCV	4.0222 %	
h^2 (Broad Sense)		0.1144	S.E. of h^2	0.5581	
Genetic Advancement		0.3090	0.3961		
Gen.Adv as % of Mean		0.9482 %	1.2151 %(selection intensity at 5% & 1%)		

Table 9: ANOVA for Test weight (g)

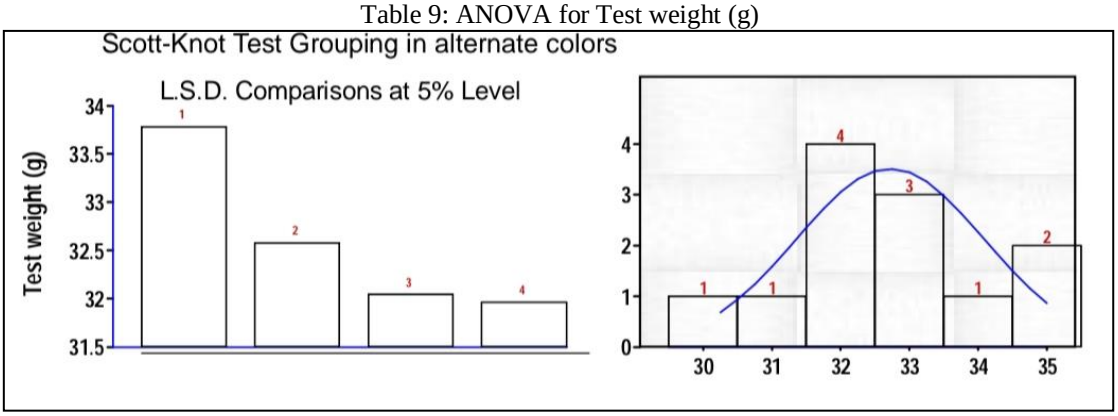

Fig. 9: Test Weight (g), L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability	
Replicate	2	4.352270	2.176135	0.1647	0.8519	
Treatments	3	271.572623	90.524208	6.8495	0.0230	*
Error	6	79.297313	13.216219			
General Mean		31.9367	(2.0989)	95%	99%	
S.E.Diff.		2.9683	Critical Diff.	7.2632	11.0047	
S.E.Diff from Mean		1.8177	Critical Diff.	4.4478	6.7390	
Var Environmental		13.2162	ECV	11.3832 %		
VarGenotypical		25.7693	GCV	15.8951 %		
VarPhenotypical		38.9855	PCV	19.5507 %		
h^2 (Broad Sense)		0.6610	S.E. of h^2	0.6051		
Genetic Advancement		8.5019	10.8957			
Gen.Adv as % of Mean		26.6213 %	34.1166 %(selection intensity at 5% & 1%)			

Table 10: ANOVA for No. of Seeds Per Spike

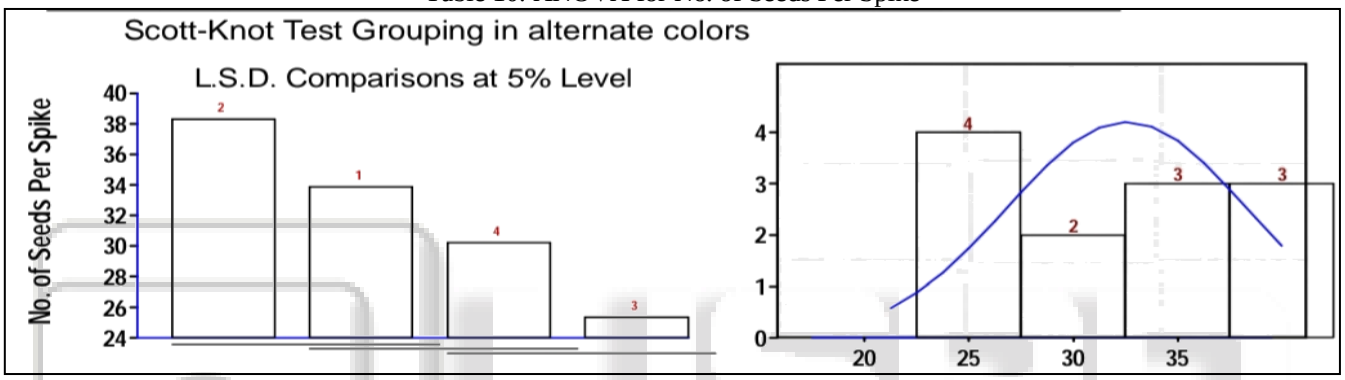

Fig. 10: No. of Seeds Per Spike, L.S.D. Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability	
Replicate	2	1.249318	0.624659	0.4963	0.6317	
Treatments	3	69.863560	23.287853	18.5034	0.0020	**
Error	6	7.551419	1.258570			
General Mean		13.3442	(0.6477)	95%	99%	
S.E.Diff.		0.9160	Critical Diff.	2.2414	3.3960	
S.E.Diff from Mean		0.5609	Critical Diff.	1.3726	2.0796	
Var Environmental		1.2586	ECV	8.4071 %		
VarGenotypical		7.3431	GCV	20.3071 %		
VarPhenotypical		8.6017	PCV	21.9786 %		
h^2 (Broad Sense)		0.8537	S.E. of h^2	0.6208		
Genetic Advancement		5.1577	6.6099			
Gen.Adv as % of Mean		38.6513 %	49.5337 %(selection intensity at 5% & 1%)			

Table 11: ANOVA for Biological yield of Bunch of 5 plants

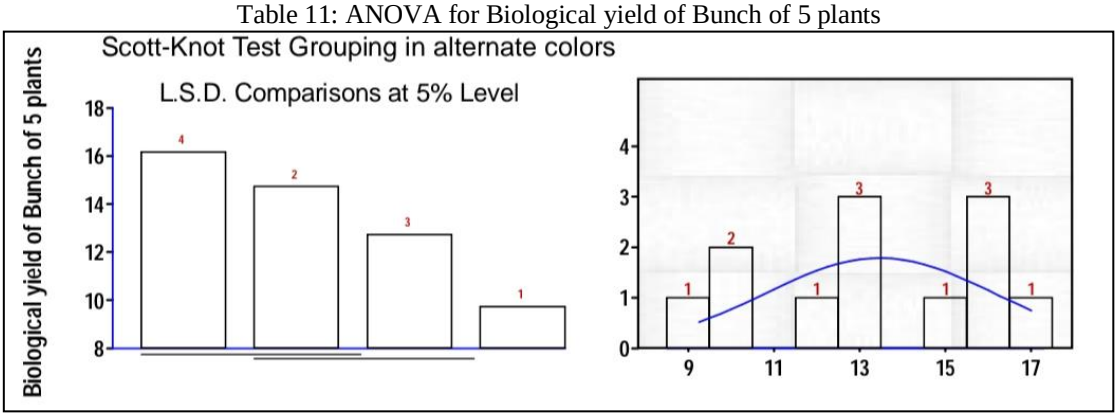

Fig. 11: Biological yield of Bunch of plants, L.S.D Comparisons at 5% Level

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	Probability	
Replicate	2	0.116517	0.058258	0.1579	0.8574	
Treatments	3	12.110299	4.036766	10.9420	0.0076	**
Error	6	2.213550	0.368925			
General Mean		5.4683	(0.3507)	95%	99%	
S.E.Diff.		0.4959	Critical Diff.	1.2135	1.8386	
S.E.Diff from Mean		0.3037	Critical Diff.	0.7431	1.1259	
Var Environmental		0.3689	ECV	11.1074 %		
VarGenotypical		1.2226	GCV	20.2204 %		
VarPhenotypical		1.5915	PCV	23.0703 %		
h^2 (Broad Sense)		0.7682	S.E. of h^2	0.6139		
Genetic Advancement		1.9964	2.5585			
Gen.Adv as % of Mean		36.5084 %	46.7875 %(selection intensity at 5% & 1%)			

Table 12: ANOVA for Economical yield of Bunch of 5 plants

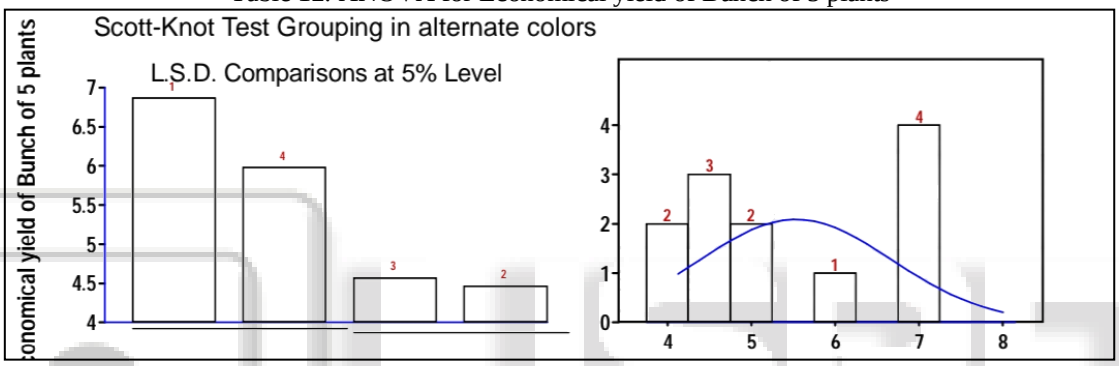

Fig. 12: Economical yield of Bunch of 5 plants, L.S.D. Comparisons at 5% Level

IV. Conclusion and Recommendation:

This study highlights the significant genetic divergence among the wheat genotypes studied. Traits such as harvest index, flag leaf area, and biological yield were identified as key contributors to yield improvement. The high heritability and genetic advance associated with these traits underscore their potential for effective selection in breeding programs.

The findings provide valuable insights for wheat breeding programs, particularly in selecting genetically diverse parental lines for hybridization. By integrating genetic divergence analysis with advanced breeding techniques, this research contributes to the development of high-yielding and resilient wheat varieties, addressing the challenges posed by climate change and increasing food demand.

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