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Unveiling the genetic divergence and phenotypic association in elite Pakistani wheat (*Triticum aestivum* L.) genotypes

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Abstract

The present study was designed to assess genetic divergence between commercial bread wheat genotypes based on yield and its related traits and to carry out phenotypic correlation. Twenty bread hexaploid wheat varieties were assessed for mean performance, correlation analysis and genetic distance. Randomized complete block design was used with three replications during growing season, 2018-2019 at Wheat and Barley Research Institute, Tandojam. The mean squares depicted significant differences (P<0.01) for all the investigated traits among the tested genotypes, proving that used genetic resources possess a great potential for further breeding experiments. Regarding mean performance, the genotypes Sassui and TD-1 displayed desirable performance for a variety of traits, unveiling their importance in wheat breeding programs. The results also showed that tillers plant⁻¹, grains spike⁻¹ and seed index developed significantly positive (P<0.05) interrelationship with grain yield plant⁻¹. This demonstrates that genotypes possessing higher extent of these traits may be chosen in selection for developing high yielding bread wheat genotypes. The larger genetic distance was witnessed between Johar-78 and TD-1, followed by SKD-1 and TJ-83, SKD-1 and Mehran-89, SKD-1 and Johar-78, TD-1 and Khirman, TJ-83 and Imdad-05, Mehran-89 and TD-1 and Johar-78 and TJ-83. These paired showed wide genetic distances, which may also be preferred in wheat hybridization program.

Key words: Genetic distance, hexaploid wheat, morphological traits, trait

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1. INTRODUCTION

Wheat is considered the 2nd essential food crop next to rice in the world¹⁻². About 20% of the calories and protein are provided by wheat for population of the world³. In Pakistan, this crop accounts 8.9% value added in agriculture and 1.6% of GDP. Wheat crop displayed a small increase of 0.5% in production over last year's production but also fell short of the target by 4.9%⁴. Genetic diversity is the principal requisite to start an effective breeding program for the improvement of wheat production⁵. The genetic diversity of crop plant decides their potential and fitness for upcoming breeding and also to increase food production⁶.

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The presence of genetic divergence with useful variability tends to have a critical part in framing a noticeable and effective breeding program. For expanding the target of plant breeding, the genetic diversity is very crucial in context to earliness, increase in yield, improvement in adaptation, advancement in quality, and durability in pest and disease resistance⁷. At several worldwide research organizations, the wheat experts are involved for the improvement of grain yield having better quality along with important morphological characters. Therefore, understanding of genetic diversity within the range of wheat germplasm appears to have a crucial impact on crop production of wheat crop, and such wheat germplasm are strong enough to cope with climate change and diverse environment at the world level. However, taking such large genetic diversity into hybridization and subsequent selection is one of the best approaches for wheat breeding8. The baseline plan in any breeding program relies predominantly on selection criteria and succeeding choice of parental materials to be included in crossing programs. Hybridization among genetically dissimilar parents will results in transgressive segregation, which ultimately can be helpful in developing improved crop cultivars9. The greater genetic divergence between hybridized parents is directly relative to the degree of hybrid vigor observed in progenies¹⁰. Important progress has been made in the production of new high yielding cultivars in recent years, and this work is still ongoing to satisfy the growing demand for wheat. The mechanized wheat production has harmed genetic variation, which must be evaluated and conserved before degradation occurs¹¹. Knowledge regarding germplasm diversity and genetic relatedness among elite breeding material is generally recognized as a critical component in plant breeding¹². Advance bread wheat varieties have been stated to have a small genetic base, so breeding wheat genotypes with a broad genetic base is critical not only for achieving self-sufficiency and sustainability, but also for entering the export market13.

Correlation assists to enumerate and assess the amount of the phenotypic relationship with genetic backgrounds and to examine either the selection for a specific character affects the supplementary traits, and also to observe secondary gains as a result of selection on interrelated character⁸. In wheat breeding, breeders often use basic correlation to know the extent of association between grain yield and other agronomic and morphological traits ¹⁴. Seed yield plant⁻¹ exhibited positive correlations with number of seeds spike⁻¹ ¹⁵. Recently in Pakistan, various researchers found that traits like spike length, grains spike⁻¹, seed index, biological yield and harvest index disclosed positive and significant associations with grain yield¹⁶⁻¹⁸. Thus, keeping in mind the above facts, the current study was planned to detect the extent of genetic dissimilarity in a number of bread wheat genotypes and the phenotypic associations between yield and its components.

2. MATERIALS AND METHODS

Regarding breeding materials, a set of twenty wheat commercial varieties including Benazir, Imdad-05, TD-1, Marvi-2000, Kiran-95, Hamal, Moomal, Khirman, Noori, Mehran-89, Sassui, NIA-Sundar, Anmol-90, Abadgar-91, SKD-1, Johar-78, Soghat, NIA-Sunehri, TJ-83 and Sarsabz. The present research was carried out at Wheat and Barely Research Institute, Tandojam. The experiment was laid-out in a randomized complete block design with three replications during rabi season, 2018-19. For each genotype, the trial consisted of four rows with a length of 320 cm and a width of 20 cm. Dibbling was done as sowing method, holding 20 cm between plants and 30 cm between rows. The recommended dose of fertilizer (134N: 67 P_2O_5 kg ha⁻¹) was given to the trail. In three splits, the N fertilizer was used while before cultivation, the P fertilizer was used. During the whole season, the experiment was irrigated six times. The Loughran weedicide (160 g acre⁻¹) was used to kill weeds. The random selection and labeling of 10 plants were done per replication. Analysis of variance was applied to the data and the means were compared using by using least significant differences test (LSD) at 0.5 level¹⁹ and phenotypic correlations was carried out ²⁰. The computer software SPSS v. 21 was used to estimate the genetic dissimilarity through Euclidean distance.

3. RESULTS AND DISCUSSIONS

The present study was designed to determine the genetic divergence and simple correlation in Pakistani commercial bread wheat genotypes for agronomically important traits (Table 1). The results of each analysis are discussed in their respective headings.

3.1 Mean squares and varietal performance

The mean squares differed significantly among the commercial varieties for all the characters, this appears that the used breeding stocks provide valuable genetic resources for various traits so that they can be widely used for potential breeding programs. Several other researchers have also registered almost identical results^{8, 21-22}. These researchers also found the significant genetic variance for various morphological characters. High variability among genotypes for selection of traits and for grain yield was also observed in newly evaluated hexaploid wheat genotypes¹⁷. Talking about mean performance of different bread wheat genotypes, the varieties TD-1 (plant height of 69.60 cm; tillers plant⁻¹ of 9.00; 1000-grain weight of 65.66 g; grain yield plant⁻¹ of 15.43 g) and Sassui (spike length of 14.96 cm; spikelets spike⁻¹ of 23.66; grains spike⁻¹ of 68.33) remained on top for different characters; therefore, these two varieties may be given priority in upcoming breeding programs to improve bread wheat genotypes.

Table 1. Mean squares of various quantitative traits of bread wheat genotypes

Source of variances	Degree of Freedom	Plant height	Tillers plant ⁻¹	•		Grains spike ⁻¹	Seed index	Grain yield plant ⁻¹	
Replications	2	2.31	0.35	1.31	2.21	63.11	3.94	2.06	
Genotypes	19	191.36**	4.15**	4.02**	12.18**	164.89**	69.22**	15.05**	
Error	38	8.30	0.26	0.24	0.53	16.04	1.16	0.05	

^{** =} Significant at 1% of probability level

3.2 Phenotypic correlations

Correlation coefficient is an essential statistical method that assists wheat breeders in selecting the crop plants for higher yields. Significant and interrelated response between varied and desired morpho-yield and other yield components help as substitution signs and potential characters in the effective selection of genotypes for attaining a conspicuous genetic gain. The prediction of grain yield relies on these component traits, such as days to heading and maturity, spike length, 1000-grain weight, biological yield and yield/ha and other yield attributing traits⁸. In the present study (Table 3), significant and positive correlations were observed between grain yield plant⁻¹ and tillers plant⁻¹ (0.37**), spike length (0.27*), spikelets spike⁻¹ (0.39**), grains spike⁻¹ (0.26*) and seed index (0.32*). This indicates that all the parameters which contribute towards yield play an important role in yield of wheat crop. Moreover, spike length revealed positive and significant association between spikelets spike-1 (0.41**) and grains spike-1 (0.68**), while spikelets spike-1 exhibited significant and positive interrelationship with grains spike-1 (0.53**), referring a comprehensive selection for these traits will eventually improve seed yield in wheat since these three yield contributing traits are interrelated, however, selection in one of these traits will indirectly result in the extension of the other traits. The height of the plant, however, was significantly but negatively correlated with the grain yield grain⁻¹ (0.54**), hence selection for taller plants may be avoided in wheat breeding program. In another study, strong and positive association between grain yield and other related traits including tillers plant⁻¹, spikelets panicle⁻¹, grains panicle⁻¹ and harvest index²³. These outcomes are also in the line of various researchers²⁴⁻³¹. In contrast to our results, other researcher confirmed that the grain yield correlated negatively and high significantly with 1000-grain weight³².

Table 2. Per se performance of various elite wheat genotypes for different traits

Genotypes	Plant height	Tillers plant ⁻¹	Spike length	Spikelets spike ⁻¹	Grains spike ⁻¹	Seed index (g)	Grain yield plant ⁻¹ (g)	
	(cm)	•	(cm)	·	•			
Benazir	101.00	7.66	11.56	20.00	54.667	40.56	8.46	
Imdad-05	99.20	7.33	12.16	21.00	59.00	47.30	12.46	
TD-1	69.60	9.33	13.96	23.00	65.66	50.51	15.43	
Marvi-2000	89.13	6.00	13.76	21.33	64.00	43.45	12.23	
Kiran-95	99.27	7.66	13.23	19.66	65.33	38.91	13.46	
Hamal	100.60	8.00	11.53	22.33	66.66	30.50	12.43	
Moomal	90.48	9.66	12.81	19.33	63.66	37.11	11.36	
Khirman	103.53	6.66	12.13	22.33	67.33	39.01	10.40	
Noori	86.93	8.00	11.83	16.66	54.00	37.31	11.50	
Mehran-89	100.47	6.66	13.86	22.00	65.00	42.98	7.56	
Sassaui	102.87	6.00	14.96	23.66	68.33	39.28	11.40	
Anmol	97.07	7.66	11.50	22.33	55.66	33.70	8.30	
Abadgar-91	102.87	7.66	12.03	21.66	58.33	36.70	7.33	
SKD-1	84.67	8.00	11.06	18.33	46.00	37.51	12.53	
Johar-78	107.53	7.00	13.40	22.33	56.33	43.06	10.46	
Soghat -90	104.40	6.33	11.50	21.66	59.00	35.08	11.40	
NIA-Sundar	104.00	5.33	10.93	17.66	51.33	39.25	9.40	
TJ-83	94.73	9.00	13.16	20.66	66.33	30.58	13.30	
Sarsabz	104.47	5.66	13.60	21.66	66.00	37.53	9.23	
NIA-	98.93	7.33	11.06	21.66	48.00	41.03	7.70	
Sunheri								
LSD (5%)	4.76	0.84	0.82	1.20	3.27	1.78	0.37	

3.3 Genetic distance

With respect to remove the uniformity among various genotypes of wheat, it is extremely necessary for increased genetic diversity and their systematic use to be prevailed for order to generate new gene complexes for better grain yield and tolerance for biotic and abiotic stress. Hence, the efficiency of selection thus depends on the number of genetic divergences that occur for important economic characteristics among the population. The progress of breeding is conditioned, primarily by the magnitude, nature and inter-relationship of genetic variation for various plant characters in such a population³³. Regarding genetic distance, it ranged between 5 and 34, which states that narrow as well as broad genetic dissimilarity is existed in the used genetic materials. Among 190 pairs of comparisons from genetic distance (Table 5), quite a high number of pairs revealed very wide genetic distance, such as Johar-78 and TD-1 (34), followed by SKD-1 and TJ-83 (30), SKD-1 and Mehran-89 (30), SKD-1 and Johar-78 (30), TD-1 and Khirman (29), TJ-83 and Imdad-05 (29), Mehran-89 and TD-1 (29) and Johar-78 and TJ-83 (29). Of the special note, these pairs can better be utilized in heterosis breeding program in wheat since these pairs contain variety of genes for various traits. However, the narrow genetic distance was found between Benazir and NIA-Sundar, Abadgar-91 and Soghat-90 and Noori and Moomal (5), followed by Khirman and Sassui (6), Sarsabz and Khirman (6), Anmol and Abadgar-91 (6), NIA-Sunheri and Benazir (6), Moomal and Kiran-95 (7), Noori and Kiran-95 (7), Mehran-89 and Khirman (7) and Hamal and Anmol (7). Hence, these pairs of genotypes could be proved reliable breeding materials for backcross breeding. From genetic distance of 171 pairs of comparisons, out of those only 10 pairs showed the highest genetic distance; however, only 15 pairs of comparisons revealed narrow genetic²¹. The estimated genetic distance values were ranged from 4.93 to 23.47³⁴.

Table 3. Correlation coefficient (r) between various traits of wheat genotypes

Traits	Plant height	Tillers plant ⁻¹	Spike length	Spikelets spike ⁻¹	Grains spike ⁻¹	Seed index
Tillers plant ⁻¹	- 0.37**					
Spike length	0.22^{NS}	-0.24 NS				
Spikelets spike ⁻¹	0.16 NS	-0.35**	0.41**			
Grains spike ⁻¹	0.09 NS	-0.12 NS	0.68**	0.53**		
Seed index	0.10^{NS}	-0. 2 9*	0.18 NS	0.06 ^{NS}	-0.39 ^{NS}	
Grain yield plant-1	-0.54**	0.37**	0.27^{*}	0.39**	0.26^{*}	0.32^{*}

^{*, ** =} Significant at 5% and 1% of probability level, respectively; NS= Non-Significant

4. CONCLUSIONS

It is concluded that the grain yield plant⁻¹ may be increased by including its related characters such as tillers plant⁻¹, spike length, spikelets spike⁻¹, grains spike⁻¹ and seed index. Several pair of comparisons also showed wide genetic distance, which may also be preferred in wheat hybridization program.

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Conflict of interest

Authors declare no conflict of interest.

Table 4. Genetic distance between different commercial bread wheat genotypes based on yield and its related traits

Genotypes	Kiran	Marvi	Sassui	Khirman	Sundar	Sarsabz	Soghat	TD-1	Imdad	TJ-83	Moomal	Noori	Mehran	Abadgar	Anmol	Benazir	Sunheri	Hamal	SKD-1
Marvi	8	0																	
Sassui	12	14	0																
Khirman	13	16	6	0															
Sunder	13	20	21	18	0														
Sarsabz	10	15	8	6	14	0													
Soghat	10	18	14	11	9	7	0												
TD-1	16	15	27	29	25	26	25	0											
Imdad	13	14	20	19	16	19	18	23	0										
TJ-83	18	18	11	15	28	16	21	27	29	0									
Moomal	7	10	14	16	18	13	14	14	19	15	0								
Noori	7	9	18	19	17	16	16	11	17	19	5	0							
Mehran	15	15	6	7	23	11	17	29	21	13	16	20	0						
Abadgar	11	18	15	12	9	8	5	25	19	22	14	15	17	0					
Anmol	10	16	14	13	14	9	8	21	21	18	10	12	17	6	0				
Benazir	12	18	20	17	5	14	10	23	12	28	16	15	22	9	13	0			
Sunheri	11	15	21	19	10	16	13	18	12	28	15	12	23	12	13	6	0		
Hamal	12	19	11	11	17	8	8	26	24	14	13	17	15	10	7	17	19	0	
SKD-1	16	17	28	28	20	25	22	8	20	30	16	11	30	21	19	18	13	25	0
Johar	18	24	19	14	13	14	12	34	18	29	24	25	21	13	19	13	18	18	30

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