Pakistan Academy of Sciences

Research Article

Correlation, heritability and genetic distance analysis in bread wheat (*Triticum aestivum* L.) genotypes

Khushal Khan Bazai[1], Munaiza Baloch[1], Jay Kumar Sootaher[1*], Tarique Ahmed Baloch[2], Muhammad Naeem[2], Tanweer Fatah Abro[1], Muhammad Saleem Chang[3], and Kirshan Kumar Menghwar[1]

[1]Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, Sindh, Pakistan
[2]Directorate of Agriculture Research (Dates), Kech, Turbat, Balochistan, Pakistan
[3]Department of Agronomy, Subcampus Umerkot, Sindh Agriculture University, Tandojam, Sindh, Pakistan

Abstract: The current study was conducted for the estimation of correlation, heritability and genetic distance in eight wheat genotypes in RCBD having three replications at the Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, Sindh, Pakistan during the crop season of 2017-18. The mean squares displayed that majority of the characters exposed highly significant differences in all the tested genotypes, showing that exploited wheat genotypes retain valuable genetic resources, hence may be used in future breeding programs. Considering the mean performance of wheat genotypes, results revealed that the genotype TD^{-1} performed excellently for all the attributes, but other genotypes like AS-2002, Hamal, Abadgar and Moomal performed normally. These genotypes tend to have promising genetic potential, therefore preference should be given in upcoming breeding programs. Correlation exhibited very beneficial results in which plant height, tillers plant^{-1}, grains spike^{-1}, spikelets spike^{-1} and seed index were associated positively and highly significantly with grain yield plant^{-1} with the correlation coefficient of r = 0.6694**, r = 0.7522**, r = 0.7550**, r = 0.6247** and r = 0.6348**), But these yield related traits also manifested good associations with the rest of the characteristics which confirmed a lot of genetic variability present in these genotypes. Heritability displayed the best outcomes in the genotypes in which high heritability estimates were observed for plant height (h^2= 98.70%), tillers plant^{-1} (h^2=99.74%), grains spike^{-1} (h^2=99.54%), spikelets spike^{-1} (h^2 =70.53%), seed index (h^2= 90.68%) and grain yield plant^{-1} (h^2=90.15%). High heritability values for these characteristics manifested that the variation detected was more under genetic control than under environmental control which expressed the influence of additive gene action. The results regarding genetic distance demonstrated that the greater genetic distance of 51.801 was found between Abadgar and Moomal, followed by Abadgar and TD^{-1} (49.496), Moomal and PBG-ST03 (47.804), Moomal and TD^{-1} (43.162), Moomal and KKK (42.855), TD^{-1} and PBG-ST03 (42.230), Moomal and AS-2002 (41.719), Moomal and Hamal (40.181) and Moomal and Imdad (39.701).

Keywords: Correlation, Heritability, Genetic distance, Bread wheat, Genotypes

1. INTRODUCTION

Wheat (*Triticum aestivum* L.), "King of Cereals" plays a pivotal role for large part of global population and is grown in almost all around the world [1]. It comes from the family, Poaceae (Gramineae) with the chromosome number 2n=6x=42 having basic chromosome number x=7 and genomic formula, AABBDD. The genes which regulate the yield components about them a great deal knowledge should be in the mind of a plant breeder as that knowledge is the considered as the first and the most crucial step for a successful breeding approach. [2]. Grains are the most essential food forms which were also cultivated and eaten by the first person of the earth. As this grain is full of different forms

of energy, possessing almost 60-80% carbohydrate, 8.15% protein, 1.5-2% lipid and 2-3% minerals. A wide range of factors are thought to be answerable for low yield, but to select a variety is the most essential among them, because to choose a superior plant with superior seeds is an art which is not occupied by everyone [3].

One-fifth calories from hexaploid wheat is provided to the globe [4]. The global number of persons can almost be more than nine billion till 2050. [5], causing the need of food by 60% in the coming years. This crop is extremely essential than the rest of the crops for the survival of humans, because 20% dietary calories as well as proteins are obtained by males, females and children in the form of golden crop [6].

Grain yield is a complex quantitative parameter which is more affected by the environment and less by the genotype and is also contributed by lots of factors affecting directly and indirectly. Interaction between genotype and environment creates fluctuation in the sustainable production of hexaploid wheat which has been a considerable demand of rising food and herbivores. To complete this gap between production and the speed of utilization, plant breeding needs the breeders who can seed the germplasm for the choice, improvement and development of stable and high yield cultivars [7].

Correlation is a statistical technique that can show where and how strong pairs of variables are related to one another. Among useful breeding characteristics, character association is applied to determine the extent of correlation of certain yield contributing traits with yield (Ali et al., 2008). The relationship between morphological characteristics is of very much importance in selecting appropriate selection criteria. The association between yield traits could be better understood with the assistance of correlation study.

Heritability is known as one of the most genetic analysis, because it notifies about the structure of a population. Its most vital function is that it tells that how much percentage of the attributes transfer from parents to the children or offspring in the form of genes which also assist a plant breeder in foreseeing about the gene interaction in upcoming generations. The highest transmissibility of any trait is estimated from its highest heritability to the progeny [8]. Heritability is found is three ranges like low, moderate and high with the ranges of 1-30%, 31-60% and 61-100%. These amounts of heritability estimates are caused by the interaction between genes and environment. When the contribution of an environment for the expression of a character is always greater than that of genes, low heritability expresses itself. High heritability come into existence when genes performs better than environmental conditions, whereas If both genotypes and environment equally contribute to a trait, moderate heritability is produced. The value of heritability must always be high or moderate which are regarded more effective in selection process.

Genetic distance is very vital for genetic analysis in the field of breeding as it functions as auxiliary equipment and a strong connection between conservation and the utilization of present genetic resources [9]. Being an auxiliary tool, it tells how two organisms of the same species or a different species are different from each other on the basis of genetics. It is also recommended to amplify genetic basis of commercial cultivars for a particular zone. The knowledge of this genetic analysis not only offers biologically oriented choice of crosses and gene introgression from exotic germplasm, but also brings about a better understanding of germplasm organization and higher efficiency during genotypic sampling [10].

Therefore, this investigation was undertaken to find out the genotypes having good estimates of correlation, heritability and genetic distance for yield and yield attributes so that a better selection can be made for the development of new cultivars with desirable attributes.

2. MATERIALS AND METHODS

2.1 Site Description and Experimental Details

MEight elite wheat genotypes were grown in RCBD having three replications at the Botanical Garden, Department of Plant Breeding and Genetics, SAU, Tandojam during the crop season of 2017-18. The genotypes such as TD-1, Hamal, Moomal, KKK, Imdad, PBG-ST03, Abadgar and AS-2002 were tested for the attributes, plant height (cm),

tillers plant[-1], spikelets spike[-1], grains spike[-1], seed index and grain yield plant[-1]. Each row possessed the length of 2.5 meters for each genotype. Seeds were sown by hand dibbling with the plant to plant distance of 15 cm and row to row distance of 30 cm. At the time of maturity for taking data, 10 plants of each genotype from each replication were chosen and tagged. Character were measured during crop growth and development and after harvesting according to the requirements of those characters. Clay loam soil with pH 7.5 was utilized for the experiment. The crop was sown in the month of November, 2017 and harvested in the month of April, 2018. Normal temperature its cultivation was from 25 to 42°C in the whole period with humidity of 40% to 65% in wet and dry weather.

Data of all observations were taken with the help of following methods.

1. Plant height (cm): The height of each tagged plant was measured with a ruler in centimeters from the ground level to the tip of the spike excluding awns at the time of maturity.
2. Tillers plant[-1]: The total number of fertile tillers of each plant was manually counted at the time of maturity.
3. Grains spike[-1]: The total number of seeds from randomly tagged spikes was threshed and grains spike-1 were manually counted.
4. Spikelets spike[-1]: The spikelets of main spikes form each tagged plant were counted and used as average spikelets spike[-1] of each genotype.
5. Seed index (1000 grain weight, g): Thousand seeds from each replication per genotype were counted and weighed in grams on an electric balance in laboratory.
6. Grain yield plant[-1] (g): After harvesting all the spikes from individual tagged plants, the spikes were threshed manually and the separated clean and pure seeds were brought in the laboratory. Next, the brought grains were weighed on an electric balance and grain yield plant[-1] was recorded in grams.

2.2 Statistical analysis

Collected data were analyzed for ANOVA according to the method developed by [11], the means of genotypes for all the traits were compared by using least significant difference (LSD) at 5% probability level according to [12], correlation analysis between different traits was computed according to [13], heritability in broad sense was estimated as suggested by [14] and genetic distance among the genotypes was computed using D2 statistic technique of [15].

3. RESULTS

3.1 Analysis of Variance

The analysis of variance was carried out for six parameters recorded for yield and its related traits (Table 1). Mean squares displayed all of the attributes envisaged highly significant differences ($P \leq 0.01$) among the tested genotypes which informed about the great variation in genotypes.

3.2 Mean performance

Mean performance for various traits of wheat genotypes is given in Table 2. Results revealed that minimum plant height was recorded in TD-1 (64.33 cm), while maximum plant height (112.00 cm) was attained by Abadgar. For tillers plant[-1], maximum tillers were recorded in TD-1 (14.00), followed by AS-2002 (13.00) and minimum tillers were recorded in Moomal (4.93). Regarding grains spike[-1], the maximum grains spike[-1] (59.14) were produced in the genotype TD-1, however minimum grains spike[-1] was set in Abadgar (48.93). Concerning spikelets spike[-1], the maximum spikelets spike[-1] were counted in TD-1 (24.00), while minimum spikelets spike[-1] were noted in AS-2002 (16.10). As far as seed index is concerned, higher seed index was obtained in TD-1 (51.13 g); nonetheless, lower seed index was achieved in KKK (35.50 g). With regard to grain yield plant[-1], TD-1 (20.43 g) produced the greatest seed yield per plant, while minimum was noticed in the genotype Moomal (10.46 g).

3.3 Correlation analysis

Plant height: Plant height had highly significant and negative associations with all the traits such tillers plant[-1] (r = -0.5749**), grains spike[-1] (r = -0.6663**), spikelets spike[-1] (r = -0.4581*), seed index (r = -0.5433**) except grain yield plant[-1] which was associated positively and highly significantly (r = 0.6694**) with the character plant.

Tillers plant^{-1}: The table revealed that tillers plant^{-1} had highly significant and positive associations with all of the attributes like grains spike^{-1} (r = 0.6111**), spikelets spike^{-1} (r = 0.6312**) and grain yield plant^{-1} (r = 0.7522**). While, positive, but significant association tillers plant^{-1} (r = 0.4642*) was also observed with one and only seed index.

Grains spike^{-1}: There was found positive and significant and highly significant correlations of grains spike^{-1} with spikelets spike^{-1} (r = 0.4749*) and grain yield plant^{-1} (r = 0.7550**). On the other hand, seed index showed negative and significant association with grains spike^{-1} (r = -0.5173*).

Spikelets spike^{-1}: Spikelets spike^{-1} expressed not only positive and highly significant relationships with seed index (r = 0.6264**), but also with grain yield plant^{-1} (r = 0.6247**).

Seed index: Interrelationship between seed index and grain yield plant^{-1} was highly significant and positive (r = 0.6348**).

3.4 Heritability estimates

The heritability estimates (h^2) in broad sense, genetic variance (σ^2g) and phenotypic variance (σ^2p) from variance components for various traits studied are depicted in Table 4.

Plant height: For the character plant height, the genetic variance (σ^2g) was 246.858 and phenotypic variance (σ^2p) was 250.088, which reflected high heritability estimates (h^2 = 98.70%) for plant height.

Tillers plant^{-1}: The genetic variance for tillers plant^{-1} was σ^2g = 9.557 and phenotypic variance

was σ^2p = 9.5816, which disclosed high heritability estimates of 99.74% for the character branches plant^{-1}.

Grains spike^{-1}: In case of grains spike, genetic variance (σ^2g = 193.433) was somewhat lower to its phenotypic variance (σ^2p = 194.317), revealed high heritability estimates (h^2 = 99.54%).

Spikelets spike^{-1}: In case of spikelets spike^{-1}, genetic variance (σ^2g = 4.654) was somehow lower to its phenotypic variance (σ^2p = 6.598), revealed highly heritability estimates (h^2 = 70.53%).

Seed index: For the character seed index, the genetic variance (σ^2g) and phenotypic variance (σ^2p) were 21.318 and 23.5074, respectively, which estimated high heritability (h^2 = 90.68%).

Seed yield plant^{-1}: For the character seed yield plant^{-1}, the genetic variance (σ^2g = 10.191) and the phenotypic variance (σ^2p = 11.3041), resulted in high heritability estimates (h^2 = 90.15%).

3.5 Genetic distance

For knowing genetic distance, 45 pairwise comparisons were made. The results demonstrated that the greater genetic distance of 51.801 was found between Abadgar and Moomal, followed by Abadgar and TD^{-1} (49.496), Moomal and PBG-ST03 (47.804), Moomal and TD^{-1} (43.162), Moomal and KKK (42.855), TD^{-1} and PBG-ST03 (42.230), Moomal and AS-2002 (41.719), Moomal and Hamal (40.181) and Moomal and Imdad (39.701). However, the minimum or less genetic distance was observed between AS-2002 and Hamal (4.840), followed by Imdad and Hamal

Table 1. Mean squares for different morphological traits of bread wheat

Source of Variation	D. F.	Plant height (cm)	Tillers plant^{-1}	Grains spike^{-1}	Spikelets spike^{-1}	Seed index (g)	Grain yield plant^{-1} (g)
Replications	2	11.37	0.6579	1.422	0.2721	0.2512	1.9009
Genotypes	7	743.80**	28.69**	581.14**	15.90**	66.14**	31.68**
Errors	14	3.232	2.0246	0.884	1.9440	2.1894	1.1131
Total	23	-	-	-	-	-	-

Table 2. Mean performance of parents for yield and its traits in bread wheat

Genotypes	Plant height (cm)	Tillers plant[-1]	Grains spike[-1]	Spikelets spike[-1]	Seed index (g)	Grain yield plant[-1] (g)
TD-1	64.33	14.00	59.14	24.00	51.13	20.43
Hamal	76.00	11.66	55.90	19.66	44.12	17.97
KKK	82.00	7.00	49.41	18.36	35.50	15.56
Imdad	82.00	12.33	52.17	20.12	46.73	16.43
PBG-ST03	105.00	10.00	54.66	18.00	43.40	18.03
Abadgar	112.00	11.00	48.93	19.43	39.46	19.33
AS-2002	77.33	13.00	50.43	16.10	42.03	17.16
Moomal	80.33	4.93	51.43	20.66	41.20	10.46
LSD (5%)	3.1484	2.4918	1.6462	2.4416	2.5912	1.8476

Table 3. Correlation of coefficient ® among different traits of bread wheat

Traits	Plant height	Tillers plant[-1]	Grains spike[-1]	Spikelets spike[-1]	Seed index
Tillers plant[-1]	-0.5749**				
Grains spike[-1]	-0.6663**	0.6111**			
Spikelets spike[-1]	-0.4581*	0.6312**	0.4749*		
Seed index	-0.5433**	0.4642*	-0.5173*	0.6264**	
Grain yield plant[-1]	0.6694**	0.7522**	0.7550**	0.6247**	0.6344**

Table 4. Estimation of broad sense heritability for different traits of wheat genotypes

Traits	Genotypic variance ($\sigma^2 g$)	Phenotypic variance ($\sigma^2 p$)	Heritability (h^2)
Plant height	246.858	250.088	98.70
Tillers plant[-1]	9.557	9.5816	99.74
Grains spike[-1]	193.433	194.317	99.54
Spikelets spike[-1]	4.654	6.598	70.53
Seed index	21.318	23.5074	90.68
Grain yield plant[-1]	10.191	11.3041	90.15

Table 5. Estimation of genetic distance (mu) among different genotypes of bread wheat

Genotypes	TD-1	Hamal	KKK	Imdad	PBG-ST03	Abadgar	AS-2002	Moomal
TD-1	.000	14.845	26.329	18.718	42.230	49.496	18.418	43.162
Hamal	14.845	.000	12.317	7.151	29.130	36.345	4.840	40.181
KKK	26.329	12.317	.000	14.283	24.733	30.877	10.592	42.855
Imdad	18.718	7.151	14.283	.000	23.708	31.005	8.872	39.701
PBG-ST03	42.230	29.130	24.733	23.708	.000	8.327	27.945	47.804
Abadgar	49.496	36.345	30.877	31.005	8.327	.000	35.052	51.801
AS-2002	18.418	4.840	10.592	8.872	27.945	35.052	.000	41.719
Moomal	43.162	40.181	42.855	39.701	47.804	51.801	41.719	.000

(7.151), Abadgar and PBG-ST03 (8.327) and AS-2002 and Imdad (8.872).

4. DISCUSSION

The ANOVA articulated a large amount differences for all characters in all genotypes, showing valuable genetic resources, hence may be used in future breeding programs. The results were found best owing to better performance under regulation of genes and environmental conditions. There were found interaction between genes and environment, but environment could not lose genes due to strong combination by which the genetic factors succeeded in taking opportunity for expressing themselves in order to function tremendously in the absence of environment. These results were further supported by Khilawat et al. 2014 [16] who found that the genotypes differed highly significantly for all morphological characteristics. Similarly, Farhat et al. 2019 concluded that more number of tillers, grains or spikelets increased the grain yield and proved themselves as superior contributors in the field of breeding for developing wheat genotypes. kachi et al. 2020 [17] finalized that these yield traits performed brilliantly due to more control under genes than surroundings, because genetic variation is more important than the variation of an environment. [18] Results of mean performance revealed that minimum plant height was presented by TD-1. These results about plant height were in conformity with [19]. For tillers plant[-1] and grains spike[-1], maximum values were recorded in TD[-1]. Our findings of two traits were identical to [20]. Concerning parameter spikelets spike[-1] and seed index, the most spikelets spike[-1] and seed index appeared in the same genotype, TD[-1]. [21] also gave the same values for seed index. With regard to grain yield plant[-1], TD[-1] produced the greatest seed yield in a single plant. The previous workers like got the similar results from their research. Asif et al. 2004 and Awan et al. 2005 [22, 23].

The estimates of correlation of coefficients were worked out among six traits (Table 3). There were noticed positive, negative, significant and highly significant correlations among different characters of bread wheat. The results exposed that utilization of these traits would enhance grain yield in wheat genotypes, however, these characters may be set as selection criteria for evolving better performing wheat genotypes. These results had been further confirmed by many research workers. Dutano et al. 2015. Supported this research and reported that almost all traits were positively and significantly correlated with grain yield. Mrad et al. [24] also described positive and significant correlation between yield and its traits. Kaddeme Lal et al. 2014 [25] told that many of the traits were positively and significantly correlated with grain yield. Khabiri et al. 2012 [26]. Our findings were also in agreement with [27]. Zulliffal et al. 2018 revealed a significant and positive relationship of grain yield with a few traits including seed index. [28]

For the character plant height, high heritability estimates were observed. Higher heritability estimates for the character tillers plant[-1] were also found which promoted the genetic variability. In case of grains spike, genotypic and phenotypic revealed high heritability estimates. Spikelets per spike also revealed higher heritability estimates. For seed index, genotypic and phenotypic variances estimated high heritability. Higher heritability estimates were also seen for seed yield per plant. Si et al. 2003; Saifullah et al. 2009 and Mangi et al. 2010 also informed about the highest heritability for the most of the yield traits. Perfection in current yield status can be assimilated by choosing traits showing high heritability [29, 30, 31, 32, 33]. Number of spikelets and grain are very vital for grain yield as they directly contribute to the yield for the economy of an agricultural homeland in which for such vital attributes, [34, 35] also suggested to pay attention to them so as to improve and develop wheat genotypes to raise the yield in upcoming years. These same results for grain yield plant[-1] were also gained by Yousaf et al. 2008 [36].

Genetic distance assessment of plant materials is one of the main pre-breeding activities in breeding field crops [31]. The greater genetic distance was found between Abadgar and Moomal, followed by Abadgar and TD[-1], Moomal and PBG-ST03, Moomal and TD[-1], Moomal and KKK, TD[-1] and PBG-ST03, Moomal and AS-2002, Moomal and Hamal and Moomal and Imdad. However, the minimum or less genetic distance was observed between AS-2002 and Hamal, followed by Imdad and Hamal, Abadgar and PBG-ST03 and AS-2002 and Imdad. Similar results were also contributed by Tabrizi et al. 20018; Arshad et al. 2019 who

also studied genetic distance for yield components and found good outcomes. [37, 38] found the same results and suggested that introduction of new genes into existing breeding materials can broaden their genetic bases. [39] indicated that genetic distance had been a very chief weapon for the betterment of genes to maximize yield, quality, wider adaptability, resistance to pests and disease and tolerance to cold, heat, water and so on [40].

5. CONCLUSIONS

It was concluded that significant differences among all genotypes were noted for all the attributes which articulated the existence of a large amount of genetic variability among them. All genotypes presented good consequences, but the genotype TD^{-1} which performed very well can reliably be exploited under the breeding development programmes to make improvements in the majority of the characteristics in the wheat development in order to fill the gap of food shortage for the day by day increasing population of the globe.

6. ACKNOWLEDGEMENTS

7. REFERENCES

1. G. Hammad, M. Kashif, M. Munawar, U. Ijaz, M. Muzaffar, M.M. Raza, and M. Abdullah. Genetic analysis of quantitative yield related traits in spring wheat (*Triticum aestivum* L.). *American-Eurasian Journal of Agricultural and Environmental Sciences* 13: 1239-1245 (2013).

2. M. Abbas, A.D. Sheikh, M.S. Hazor, and N. Shagufta. Factor responsible for low wheat yield productivity in Punjab. *Pakistan Journal of Agricultural Sciences* 42: 79-82 (2015).

3. K. Jons, and Amos. Environmental effect on the quality of different wheat genotypes quantitative variation of storage proteins. *European Journal of Agriculture* 1: 47-64 (2010).

4. D. Sehgal, P. Vikram, C.P. Sansaloni, C. Ortiz, C.S. Pierre, T. Payne, M. Ellis, A. Amri, C.D. Petroli, P. Wenzl, and S. Singh. Exploring and mobilizing the gene bank biodiversity for wheat improvement. *PLoS ONE* 10: 112-122 (2015).

5. United Nations, Department of Economic and Social Affairs, Population Division. World Population Prospects: The 2015 *Revision, Key Findings and Advance Tables.* Working Paper No. ESA/P/WP.241 (2015).

6. FAO. *FAOSTAT*, FAO, Rome, Italy. 1-2 (2018).

7. M. Zameer, S. Mahmood, Z. Mushtaq, B. Tabasum, and Q. Ali. Detection of bacterial load in drinking water samples by 16s rRNA ribotyping and RAPD analysis. *Advancements in Life Sciences* 2: 135-141 (2015).

8. G.M. Subhani, and M.A. Chowdhry. Correlation and path coefficient analysis in bread wheat under drought stress and normal conditions. *Pakistan Journal of Biological Sciences* 3: 72-77 (2013).

9. S.A. Mohammadi, and B.M. Prasanna. Analyses of genetic diversity in crop plants Salient statistics tools and considerations. *Crop Sciences* 43: 1235-1248 (2003).

10. E.A. Vieira, F.I.F. de Carvalho, I. Bertan, M.M. Kopp, P. D. Zimmer, G. Benin, J.A.G. da Silva, I. Hartwig, G. Malone, and A.C. de Oliveira. Association between genetic distances in wheat (*Triticum aestivum* L.) as estimated by AFLP and morphological markers. *Genetics and Molecular Biology* 30: 392-399 (2007).

11. K.A. Gomez, and A.A. Gomez. *Statistical procedures for agricultural research* (2nd ed.). John Wiley and Sons, New York, p. 680 (1984).

12. R.G.D. Steel, and J.H. Torrie. Principles and Procedures of Statistics: *A Biometrical Approach.* McGraw-Hill Book Company, New York, p. 633 (1980).

13. G.W. Snedecor, and W.G. Cochran. Statistical Methods, 7th edition. Iowa State University Press, Ames, Iowa. 507 pp (1980).

14. E.L. Breese. *Biometrical Genetics and Its Application*. Eucarpia Congress, Cambridge. p. 135–146 (1972).

15. P.C. Mahalanobis. On the Generalized Distance in Statistics. Proceedings of the National Institute of Sciences of India, pp 2: 49-55. (1936)

16. A. Khilwat, Ishaq, I.A. Khalil, I. Shah, Saeed, and N. Ahamd. Genetic potential and variability for morpho-yield traits in durum wheat. *International Journal of Farming and Allied Sciences* 3: 1206-1212 (2014).

17. Y. Farhat, A. Razzaq, N.I. Raja, and H.J. Muhammad. Effect of silver, copper and iron nanoparticles on

wheat germination. *Journal of Agricultural Science* 40: 482-490 (2019).

18. M. Kachi, T.F. Abro, J.K. Sootaher, T.A. Baloch, M.A. Mastoi, T.A. Soomro, K.K. Menghwar, G.M. Jadgal, M.S. Chang, and W.H. Shah. Estimation of heritability and genetic advance in F2 populations of bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Biosciences* 16: 286-295 (2020).

19. M. Malik, F. Anwar, S.I. Awan, and S. Ali. Genetic behavior and analysis of quantitative traits in five wheat genotypes. *Journal of Agriculture and Social Sciences* 1: 313-315 (2005).

20. S. Nazir, A.S. Khan, and Z. Ali. Combining ability analysis for yield and yield contributing traits in bread wheat. *Journal of Agriculture and Social Sciences* 1: 129-132 (2005).

21. M. Akbar, M. Saleem, M.Y. Ashraf, A. Husain, F.M. Azhar, and R. Ahmad. Combining ability studies for physiological and grain yield traits in maize at two temperature regimes. *Pakistan Journal of Botany* 41: 1817-1829 (2009).

22. M. Asif, M.Y. Mujahid, N.S. Kisana, S.Z. Mustafa, and I. Ahmed. Heritability, genetic variability and path coefficient of some traits in spring wheat. *Sarhad Journal of Agriculture* 20: 87-91 (2004).

23. S.I. Awan, M.F.A. Malik, and M. Siddique. Study on seedling traits for drought tolerance in wheat under moisture stress conditions. *SAARC. Journal of Agriculture* 3: 247-254 (2005).

24. D. Dutamo, S. Alamerew, F. Eticha, and E. Assef. Path coefficient and correlation studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) germplasm. *World Applied Sciences Journal* 33(11): 1732-1739 (2015).

25. J. Murad, R. Ahmed, M. Azam, M. Saeed, K. Dost, B. Ahmed, M. Naeem, and S. Khan. Phenotypic association and heritability analysis in bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Biosciences* 14(6): 71-77 (2019).

26. W.K. Kaddem, S. Marker, and G.R. Lavanya. Investigation of genetic variability and correlation analysis of wheat (*Triticum aestivum* L.) genotypes for grain yield and its Component traits. *European Academic Research* 2(5): 6529-6538 (2014).

27. E. Khabiri, A.A. Imani, and H. Shahbazi. Studying the grain yield and yield components in advanced rainfed wheat genotypes. Scholars Research Library. *Annals of Biological Research* 3(12): 5647-5650 (2012).

28. M. Zulkiffal, S. Gulnaz, J. Ahmed, A. Rehman, M. Musa, M. Abdullah, M.M. Javaid and J. Salim. Morphological diversity valuation of exotic and advanced lines of bread wheat (*Triticum Aestivum* L.) via multivariate analysis. *International Journal of Agronomy and Agricultural Research* 13(2): 149-156 (2018).

29. M.A. Sial, M.A. Arain, M.H. Naqvi, A.M. Soomro, S. Laghari, N.A. Nizamani, and A. Ali. Seasonal effects and genotypic responses for grain yield in semi-dwarf wheat. *Asian Journal of Plant Sciences* 2: 1091-1101 (2003).

30. A. Saifullah, N. Zakir, and M.Y. Mujahid. Estimation of genetic parameters and character association in wheat. *Journal of Agricultural and Biological Science* 1: 15-18 (2009).

31. S.A. Mangi, M.A. Sial, B.A. Ansari, M.A. Arain, K.A. Laghari, and A.A. Mirbahar. Heritability studies for grain yield and yield components in F_3 segregating generation of spring wheat. *Pakistan Journal of Botany* 42: 1807-1813 (2010).

32. A.S. Khan, I. Saleem, and Z. Ali. Heritability of various morphological traits in wheat. *International Journal of Agriculture and Biology* 5: 138-140 (2003).

33. N. Ahmed, M.A. Chowdhury, I. Khaliq, and M. Maekawa. The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indonesian Journal of Agricultural Science* 8: 53-59 (2007).

34. R. Riaz, and M.A. Chowdhry. Genetic analysis of some economic traits of wheat under drought conditions. *Asian Journal of Plant Sciences* 2: 790-796 (2003).

35. S.P. Singh, P.B. Jhang, and D.N. Singh. Genetic variability in polygenic traits in late sown wheat genotypes. *Annals of Agricultural Research* 22: 34-36 (2001).

36. A. Yousaf, B. Atta, M. Akhtar, and Z. Lateef. Genetic variability, association and diversity studies in wheat. *Pakistan Journal of Botany* 40: 2087-2097 (2008).

37. H. Zeinalzadeh-Tabrizi, K. Haliloglu, M. Ghaffari, and A. Hosseinpour. Assessment of genetic diversity among sunflower genotypes using microsatellite markers. *Molecular Biology Research Communications* 7: 143-152 (2018).

38. M. Arshad, S. Jan, S. Awan, S. Azam, S. Khalid, and M.A. Khan. Investigation of genetics divergence in newly developed local sunflower (*Helianthus annuus* L.) hybrids. *Pakistan Journal of Agricultural Research* 32: 33-40 (2019).

39. V.K. Baraiya, P.K. Jagtap, D.N. Hadiya, and H.R. Patel. Genetic divergence in sunflower (*Helianthus annus* L.). *International Journal of Chemical Studies* 6: 567-570 (2018).

40. A. Raza, H. Shaukat, Q. Ali, and M. Habib. Assessment of RAPD markers to analyse the genetic diversity among sunflower (*Helianthus annuus* L.) genotypes. *Turkish Journal of Agriculture, Food Science and Technology* 6: 107-111 (2018).