Research Article **ISSN: 0976-7126**
CODEN (USA): IJPLCP **Malik *et al.*, 14(8-9):54-62, 2023**

International Journal of Pharmacy & Life Sciences
Open Access to Researcher

Variability, Correlation & Heritability analysis for Various Quantitative traits in Bread Wheat (*Triticum aestivum* L.)

Parveen Malik[1*], Neeraj Kumar[2], Mohd Nayeem Ali[1], Rajkumar[1] and Anjali Jakhar[1]

Assistant Professor Department of Agriculture[1]
Shri Ram College, Muzaffarnagar (UP) 251001
Department of Genetics & Plant Breeding[2]
C.C.S. University, Meerut

Article info

Received: 16/07/23

Revised: 21/08/2023

Accepted: 20/09/2023

© IJPLS

www.ijplsjournal.com

Abstract

The 25 genotypes of SWRS wheat cultivar were evaluated in simple lattice design with two replications (R1 and R2) and the row to row distance was 0.25 meter. In association analysis based on mean values over environments, significant association ($p<0.01$) of different traits (DOH, DOA, DOH, DOS). Data of heading plants grow 50% hair we collect headings for anthesis in each replication three rows each plot. Data of anthesis at one stage sowing data with 75% of the plants, the numbers reach 75% for physical maturity after maturity.

Key Words: *Triticum aestivum* L, MTA, Agronomic traits, DArT-SNP

Introduction

Wheat is the most important cereal crop for the majority population of the world, several species of wheat combine to form the genus *Triticum*, it consumes about 55% of carbohydrates and 20% of food calories globally (Breman and Groore, *et.al.*, 1995). Wheat is cultivated in a wide range of climatic conditions therefore understanding of genetics is very important for crop improvement. The wheat belongs to the family poaceae *Triticum* one of 15 tribes and tribes with more then 300 species, including wheat. In 1753 linnaeus frist classified wheat. In 1918, (Sakumura *et al.,)* reported a chromosome number set (genome) for each recognized type. They separated wheat into three groups, diploid (2n=14) tetraploids (2n=28) and hexaploids (2n=28). The Centre will soon announce production estimates for rabi crops of 2018-19.wheat output is expected to rise despite fall of around 8 lakh hectare in wheat area to 296 lakh hectare so far this rabi season. The total area under the crop is about 29.8 million hectares in the india country. Russia wheat production for 2019/20 is estimated at 74.2 million metric tons (mmt), down 5 percent from last month but up 4 percent from last year. The estimate includes 55.0 mmt of winter wheat and 19.2 mmt of spring wheat. July 9, 2019. S. K. Malhotra, Agriculture Commissioner stated in The National Conference on Agriculture, Summer Campaign 2019, The India country wheat production might cross 100 MT. An all-time high level, in the current rabi season, helped by good weather conditions during winter.

***Corresponding Author**
Email:parveenmalikccsu@gmail.com

Wheat contain water, 71% carbohydrates and 1.5% fat its 13% protein content is mostly gluten (75-80%) of the protein. wheat cultivation was classified based on their protein on their content, those with more than 12% protein were classified as high protein cultivars (HPCs), where as proteins with less than 10-12% and less than 10% protein were classified as medium protein cultivar (MPC) and low protein cultivation (LPC) .respectively *(*Siroha and A.K, 2017*)*.

The A genomes of tetraploid and hexaploid wheats are clearly related to the A genomes of wild and cultivated einkorn, while the D genome of hexaploid wheat is clearly derived from that of T. tauschii. In fact, the formation of hexaploid wheat occurred so recently that little divergence has occurred between the D genomes present in the hexaploid and diploid species. By contrast, the B genome of tetraploid and hexaploid wheats is probably derived from the S genome present in the Sitopsis section of Aegilops, with Ae. speltoides being the closest extant species. the S genome of Ae. speltoides is also closest to the G genome of T. timopheevi, a tetraploid species with the A and G genomes (Feldman, 2001).

Anthesis in wheat (flowers) retrieved 2019-06-02. Anthesis is the period during which a flower is fully open and functional. It can also refer to the beginning of that period. The optimal growth temperature for wheat is 25 ° C, but satisfactory yield have been achieved at temperatures ranging from 3 to 32°C (Curtis, 2002) the Cultivation of hexaploid wheat in wide environments has become possible mainly due to the selection of optimum time for Flowering. (Gororo *et al*., 2001) In this case of flowering wheat, three pollen-covered stamens are clearly visible. Male reproductive part of the flower, A complete flower has all four limbs, while an incomplete flower is missing at least. A bisexual (or "complete") flower has both stamens and carpel, and a bisexual (or "imperfect") flower either lack a stamen (and is called a carpel) or lacks a carpel. .(And is called stamens). (Craig *et al.,* 1945) All stamens of a flower are collectively called androgens. the female reproductive parts of a flower, see Pistil. Stamens are often numerous, and they occur in drove of four or five. Filaments are usually independent (Petruzello *et al.,* 2013) Both male and female parent plants for hybrid seed production should have been open spikelets to achieve cross-pollination and the following desirable traits The soft lama in the spike have been well leased with long spikes, and will be yellow. (Okada, 2018 and Lewis, 2008)

We developed and evaluated phenotyping methods for flowering and flowering traits with relevance to improved cross-pollination. Heading date was recorded as days after January 1st when 75% of the spikes of an observation plot had emerged to 75% from the flag leaf sheat, Scored as days after January 1st when anther extrusion in an observation plot started, The days after January 1 when 50% of the spikes flower in an observation plot, Observed as the days after January 1 when the flower ended in an observation plot, with the beginning of flowering as the difference between the beginning and end of flowering, Indirectly approach to flowering period. The distance between the tips of the lowest and highest spikes at the beginning of flowering was measured in cm, Spike belts are measured as the distance between the tips of the lowest and highest spikes in cm at the beginning of flowering, but only for spikes above 50 cm in height assuming that only these spikes pollen for hybridization. (Würschum *et al.,* 2014) Avoiding drought through early flowering and / or short growth periods is beneficial Terminal drought stress and where in the atmosphere with physical or chemical barriers Interrupted root development (Turner, 1986 and Blum, 1989) Identified two types of plants in relation to the prevention of dehydration That is, 'water saver' and spend water saver. Important features of these plants are root Symptoms (increase in water content), leaf and stomatal features (decreased) Water loss to reduce osmotic capacity (Blum, 1988) and osmotic adjustment (Acevedo and Ferrous, 1993). It would proceed at levels of water deficit sufficient to inhibit photosynthesis. Heat tolerance; the contribution of heat tolerance to performance under moisture stress needs to be quantified, but it is relatively easy to screen (Reynolds *et al.,* 1998). Currently, increasing grain quality is becoming a widely discussed topic in crop science. The quality of wheat is directly affected by various environmental factors. However, the mechanisms of environmental effects are not completely clear.

which analyzes the effects of very diverse environment condition. Wheat was kept GPC and related processing quality by summarizing by safe the results of several experiments. them us the several possible strategies to enhance GPC and protein-based grain processing quality. (Lingan and Kong, 2013) The haploid DNA content of hexaploid wheat (*Triticum* aestivum L. 2n=42, AABBDD) is approximately 1.7 x 1010 bp, about 100 times larger than the Arabidopsis genome, 40 times that of rice and about 6 times that of maize (Bennett and Smith, 1976; Amuruganathan and Earle, 1991). The large genome of bread wheat has resulted from polyploidy and extensive duplications, such that over 80% of the genome consists of repetitive DNA sequences (Smith and Flavell, 1974). The average wheat chromosome is around 810 MB 25 times that of the average rice chromosome.

They noted the formation of distinct individuals in genotypes, or the presence of genotypically distinct individuals as opposed to environmentally induced differences, which, as a rule, caused only temporary, non-conformational changes of phenotype. The range of possible outcomes of a given situation is known as variability. An inevitable change in the output or outcome of a system (process) because all systems change over time, There are two major types of variations (1) general, inherent in a system, and (2) special, which are caused by changes in conditions or environments. Diversity is, in biology, any difference between cells, individual organisms, or groups of organisms of any species, either due to genetic differences (genotypic variation) or the influence of environmental factors on the expression of genetic factors (phenotypic variation). (Adam Augustyn, 2018).

Materials and Methods

Materials

Seed Material: 25 genotypes of Spring Wheat Reference Set (SWRS) wheat cultivars of bread wheat are obtained from the Department of Genetics and Plant Breeding, Ch. Charan Singh University, Meerut.

List of Wheat Genotype Used For Study

S. No.	Name of Genotypes	S. No.	Name of Genotypes
1.	SWRS 103	**14.**	SWRS 145
2.	SWRS 104	**15.**	SWRS 146
3.	SWRS 105	**16.**	SWRS 147
4.	SWRS 106	**17.**	SWRS 149
5.	SWRS 108	**18.**	SWRS 150
6.	SWRS 109	**19.**	SWRS 151
7.	SWRS 110	**20.**	SWRS 152
8.	SWRS 111	**21.**	SWRS 153
9.	SWRS 121	**22.**	SWRS 154
10.	SWRS 122	**23.**	SWRS 155
11.	SWRS 123	**24.**	SWRS 156
12.	SWRS 124	**25.**	SWRS 157
13.	SWRS 144		

Sowing of 25 genotypes of SWRS wheat diverse lines was done at Research Farm, Department of Genetics and Plant Breeding, Ch. Charan Singh University Meerut on 20 November 2017.

Methods:

The 25 genotypes of SWRS wheat cultivar were evaluated in simple lattice design with two replications (R1 and R2) and the row to row distance was 0.25 meter.

Data Collected:

Data was collected at the following features in each replication three rows in each plot data **Data of Heading:** When plants grow 50% hair we collect headings for anthesis in each replication three rows each plot.

Data of Anthesis: At one stage sowing data with 75% of the plants, the numbers reach 75% for physical maturity after maturity. Plots turn golden yellow. and then record the data.

Data of Tillers: The number of plants per plant was counted in tillers before harvesting time

And the average was recorded for five randomly taken plants between three rows.

Data of Spikes: The total number of spikelets from the three central rows, all five plants was on the main spike count of maturity and the average time was recorded.

Data of Biological Yield: This shows that the total yield above ground at the time of harvesting was cut from the three central rows of each experimental plot. After the gram is harvested with moisture, the moisture in the gram is measured and the seeds are dried to 12.5% using a sensitive balance. Three rows are cut out of the total dry dry three rows of grain because the plot was taken as grain and expressed as grain.

Data of Thousand Grain weight: Randomly distributed according to the sample seed use sensitivity balance, 1000 grams of grain per kilogram is divided into 1000 kernels (grams).

Statistical Analysis

The following statistical analysis was carried out:

(a) Range, Mean Value and Standard Deviation: Range of a set of data is the difference between the largest values and mean value in the average of all the observations. It is sum of all the observation values divided by the total number of observation. Therefore, each character observed in the plant, taken randomly was averaged in accordance with the SPSS. The standard deviations the square root of the mean of squares of the deviations from the arithmetic means's was also calculated using SPSS. SPSS Software is a window based program that can be used to perform data entry and analysis and to create tables and graphs. SPSS is capable of handling large amount.

(b) For histogram preparation, average value of grain size number from two replication of each 25 genotypes was used.

(c) Analysis of Variance (ANOVA): The data collected for studied quantitative trait (grain size) was analyzed for simple lattice design. The analysis of variance was done using SPSS software program.

(d) Genotypic Variance: The genotypic variation (1953) was calculated as following:

= [MS (G) - MSE]/r

Where, MS (G) is the mean square of genotype, MSE is the mean square error and r is the number of replications.

Note: MS (G) is between group Mean square value and MSE is within group Mean square value.

Phenotypic variance: The phenotypic variance (Vp) was estimated using the following formula.

Vp = Vg + MSE

Where, Vp is phenotypic variance, Vg is the genotypic variance and MSE is the mean square error.

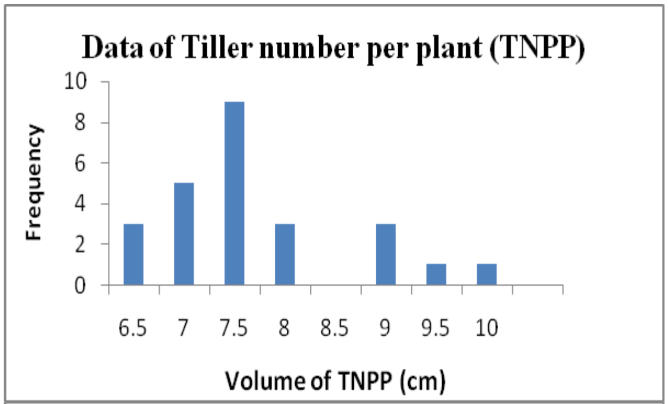
Heritability (H2): Heritability in broad sense was calculated following the method suggested by Singh and Chaudhary (1985).

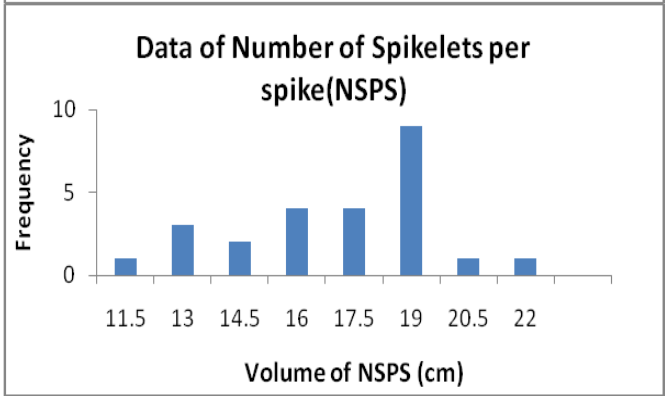
Heritiblity (H2) =Vg /Vp × 100

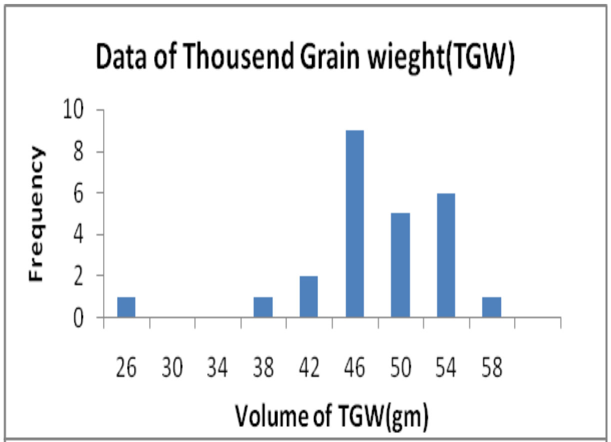
The heritability was categorized 0-30 % as low, 30-60% and above as high as given by Robinson *et al.* (1949).

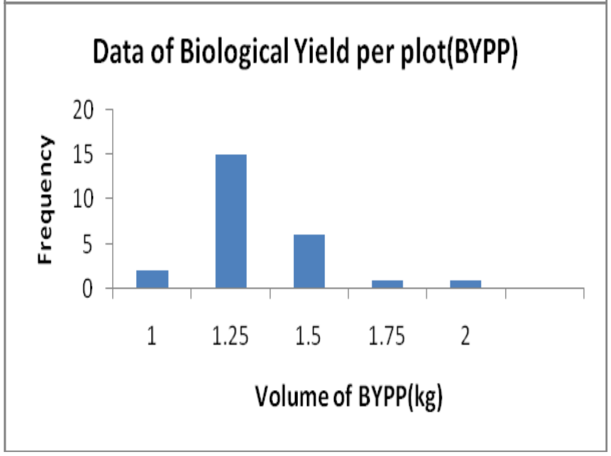
Results and Discussion

Results: Histogram Data









Data of Tiller Number per plant (TNPP):

To measure the Tiller Number per plant (TNPP), 25 genotypes of SWRS wheat cultivar were studied. Out of 25 genotypes, the lowest value of TNPP was observed 6.5 cm. in three genotypes namely as SWRS 122, SWRS 147and SWRS 155. The highest value of TNPP was observed 10 cm. in only one genotype namely as SWRS 151**[Fig. (a)]**.

Data of Number of spikelets per Spike (NSPS):

To measure the Number of spikelets per Spike (NSPS), 25 genotypes of SWRS wheat cultivar were studied. Out of 25 genotypes, the lowest value of NSPS was observed 11.5 cm. in one genotypes namely as SWRS 153. The highest value of NSPS was observed 22 cm. in only one genotype namely as, SWRS 105**[Fig. (b)]**.

Data of Thousand Grain weight (TGW):

To measure the Thousand Grain weight (TGW), 25 genotypes of SWRS wheat cultivar were studied. Out of 25 genotypes, the lowest value of TGW was observed 26 gm. in only one genotypes namely as, SWRS 108, and the highest value of TGW was observed 58 gm. in one genotypes namely as SWRS 154, SWRS **[Fig. (c)]**.

Data of Biological Yield per plot (BYPP):

To measure the Biological Yield per plot (BYPP), 25 genotypes of SWRS wheat cultivar were studied. Out of 25 genotypes, the observed lowest value of BYPP was 1 kg. in only two genotype namely as SWRS 153 and SWRS 147.The observed highest value of BYPP was 2 kg. in one genotype namely as SWRS 145**[Fig. (d)]**.

ANOVA Result:

To study the genetic architecture of the anthesis variability in wheat, we screened 25 accessions of SWRS and have been classified into four different traits on the basis of variability

1. Tiller number per plant
2. Number of spikelets per spike
3. Thousand grain weight
4. Biological yield per plot

Statistical analysis of data was carried out with SPSS v.16.0. (Statistical Package for the Social Science). Wheat Variability has been selected and manipulated even in very agrarian societies and remains a major breeding target. Environmental factors strongly influenced the grain protein content as well as Variability. In this study analysis of variance (ANOVA) showed significant ($P<0.05$) for Anthesis Variability.

The value of genotypic variance of and TNPP, NSPS, TGW and BYPP was observed 1.733, 14.925, 90.606 and 0.077 respectively. The value of phenotypic variance of TNPP, NSPS, TGW and BYPP was observed 1.962, 15.633, 92.884 and 0.094 and value of heritability TNPP, NSPS, TGW and BYPP was observed 88.331, 95.471, 97.547 and 82.010.

Dependent Variable: Tiller No. Per Plant (TNPP):

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Replication	.289	1	.289	1.262	.272
Genotype	44.349	24	1.848	8.076	.000
Error	5.491	24	.229		
Total	2838.680	50			

Dependent Variable: Number of Spikelets Per Spiker (NSPS)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Replication	.039	1	.039	.055	.816
Genotype	366.693	24	15.279	21.595	.000
Error	16.981	24	.708		
Total	13525.160	50			

Dependent Variable Thousend Grain Wieght (TGW)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Replication	16.820	1	16.820	7.383	.012
Genotype	2201.880	24	91.745	40.268	.000
Error	54.680	24	2.278		
Total	105422.200	50			

Dependent Variable: Biological Yield per plant (BYPP)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Replication	.080	1	.080	4.655	.041
Genotype	2.057	24	.086	4.986	.000
Error	.412	24	.017		
Total	81.175	50			

The ANOVA Result of Tiller Number per plant (TNPP), Number of Spikelets per spike (NSPS), Thousend Grain wieght (TGW), Biological Yield per plot (BYPP) is significant at P= <0.05.

The value of genotypic variance of Tiller Number per plant (TNPP), Number of Spikelets per spike (NSPS), Thousend Grain wieght (TGW), Biological Yield per plot (BYPP) was observed 1.733, 14.925, 90.606 and 0.077 and respectively,

The value of phenotypic variance of Tiller Number per plant (TNPP), Number of Spikelets per spike (NSPS), Thousend Grain wieght (TGW), Biological Yield per plot (BYPP) was observed 1.962, 15.633, 92.884, and 0.945and respectively,

The value of heritability of Tiller Number per plant (TNPP), Number of Spikelets per spike (NSPS), Thousend Grain wieght (TGW), Biological Yield per plot (BYPP) was observed 88.331, 95.471, 97.547, and 82.010 and respectively,

Conclusion

Genetic variability in the population is important for biodiversity, because without variability, the population becomes difficult to adapt to environmental changes. The correlation study revealed that plot yield had strong positive association with days to heading, days to anthesis, days to maturity & anther extrusion. It is important to measure the weight of a seed and adjust the sowing rate. Quantitative Characteristic Loci (QTL) Analysis for Grain Weight (GW = 1000 Grain Weight) in Common Wheat One of 100 Recombinant Inbred Lines (RILs) Derived from a Cross' Rye Selection 111 (High WW) × Sugar Spring (Low) The set was done using. (Guinea worm) RIL and their two parent genotypes were evaluated for GW in six different environments (three locations × two years). (Kumar and Gaur, 2006).

Acknowledgement

We would like to acknowledge the Department of Genetics & Plant Breeding (C.C.S. University, Meerut) for providing facilities to conduct the experiment. I am grateful also thankful to Prof. P.K. Gupta & Prof. H.S. Balyan (emeritus professors at CCSU, Meerut) for their constant support.

References

1. Ahmed, N., Chowdhry, M.A., Khaliq, I. and Maekawa, M., 2016. The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indonesian Journal of Agricultural Science*, *8*(2), pp.53-59.
2. Ashfaq, M.U.H.A.M.M.A.D., Khan, A.S. and Ali, Z.U.L.F.I.Q.A.R., 2003. Association of morphological traits with grain yield in wheat (Triticum aestivum L.). *Int. J. Agric. Biol*, *5*(3), pp.262-264.
3. Azhar, F.M. and Ahmad, R., 2000. Variation and heritability of salinity tolerance in upland cotton at early stage of plant development. *Pak. J. Biol. Sci*, *3*, pp.1991-1993.

4. Baloch, M.J., Baloch, E., Jatoi, W.A. and Veesar, N.F., 2013. Correlations and heritability estimates of yield and yield attributing traits in wheat (Triticum aestivum L.). *Pak J Agri*, *29*(2), pp.96-105.
5. Breiman, A. and Graur, D., 1995. Wheat evolution. *Israel Journal of Plant Sciences*, *43*(2), pp.85-98.
6. Brenchley, R., Spannagl, M., Pfeifer, M., Barker, G.L., D'Amore, R., Allen, A.M., McKenzie, N., Kramer, M., Kerhornou, A., Bolser, D. and Kay, S., 2012. Analysis of the bread wheat genome using whole-genome shotgun sequencing. *Nature*, *491*(7426), p.705.
7. Burrell, M.M., 2003. Starch: the need for improved quality or quantity—an overview. *Journal of Experimental Botany*, *54*(382), pp.451-456.
8. Calderini, D.F., Savin, R., Abeledo, L.G., Reynolds, M.P. and Slafer, G.A., 2001. The importance of the period immediately preceding anthesis for grain weight determination in wheat. *Euphytica*, *119*(1-2), pp.199-204.
9. Cartelle, J., Pedró, A., Savin, R. and Slafer, G.A., 2006. Grain weight responses to post-anthesis spikelet-trimming in an old and a modern wheat under Mediterranean conditions. *European Journal of Agronomy*, *25*(4), pp.365-371.
10. Chen Y, Wang RD, Kong J, Zhang W, Nie YB (2005) Studies on wheat quality ecology in Xinjiang. Xinjiang Agr Sci 42:369-376.
11. Dai, J., Bean, B., Brown, B., Bruening, W., Edwards, J., Flowers, M., Karow, R., Lee, C., Morgan, G., Ottman, M. and Ransom, J., 2016. Harvest index and straw yield of five classes of wheat. *Biomass and Bioenergy*, *85*, pp.223-227.
12. Feldman, M. and Kislev, M.E., 2007. Domestication of emmer wheat and evolution of free-threshing tetraploid wheat. *Israel Journal of Plant Sciences*, *55*(3-4), pp.207-221.
13. Fleury, D., Jefferies, S., Kuchel, H. and Langridge, P., 2010. Genetic and genomic tools to improve drought tolerance in wheat. *Journal of experimental botany*, *61*(12), pp.3211-3222.
14. Gororo, N.N., Flood, R.G., Eastwood, R.F. and Eagles, H.A., 2001. Photoperiod and vernalization responses in Triticum turgidum× T. tauschii synthetic hexaploid wheats. *Annals of Botany*, *88*(5), pp.947-952.
15. Gu, R., Chen, F., Liu, B., Wang, X., Liu, J., Li, P., Pan, Q., Pace, J., Soomro, A.A., Lübberstedt, T. and Mi, G., 2015. Comprehensive phenotypic analysis and quantitative trait locus identification for grain mineral concentration, content, and yield in maize (Zea mays L.). *Theoretical and applied genetics*, *128*(9), pp.1777-1789.
16. Kumar, a Gaurav, S.S. and Bahuguna,D.K. Analysis of Variability, Heritability and genetic advance for yield and yield related trait in wheat (triticum Aestivum L.) Genottypes
17. Kumar, N., Kulwal, P.L., Gaur, A., Tyagi, A.K., Khurana, J.P., Khurana, P., Balyan, H.S. and Gupta, P.K., 2006. QTL analysis for grain weight in common wheat. *Euphytica*, *151*(2), pp.135-144.
18. Langer, S.M., Longin, C.F.H. and Würschum, T., 2014. Phenotypic evaluation of floral and flowering traits with relevance for hybrid breeding in wheat (T riticum aestivum L.). *Plant Breeding*, *133*(4), pp.433-441.
19. Li HN, Zhang YL, Wu XQ, Li ZZ (1995) Determination and evaluation on the main quality characters of wheat germplasm resources in China. Sci Agric Sin 28:29-37 (in Chinese with English abstract.
20. Punia, S., Sandhu, K.S. and Siroha, A.K., 2017. Difference in protein content of wheat (Triticum aestivum L.): Effect on functional, pasting, color and antioxidant properties. *Journal of the Saudi Society of Agricultural Sciences*.
21. Ramya, P., Chaubal, A., Kulkarni, K., Gupta, L., Kadoo, N., Dhaliwal, H.S., Chhuneja, P., Lagu, M. and Gupt, V., 2010. QTL mapping of 1000-kernel weight, kernel length, and kernel width in

bread wheat (Triticum aestivum L.). *Journal of applied genetics*, *51*(4), pp.421-429..

22. Richards, R.A., Rebetzke, G.J., Condon, A.G. and Van Herwaarden, A.F., 2002. Breeding opportunities for increasing the efficiency of water use and crop yield in temperate cereals. *Crop science*, *42*(1), pp.111-121.
23. Sadat, M.A. and Choi, J., 2017. Wheat blast: a new fungal inhabitant to Bangladesh threatening world wheat production. *The plant pathology journal*, *33*(2), p.103.
24. Knezevic, D., Zecevic, V., Stamenkovic, S., Atanasijevic, S. and MILOSEVIC, B., 2012. Variability of number of kernels per spike in wheat cultivars (Triticum aestivum L.). *Journal of Central European Agriculture*, *13*(3), pp.0-0.

Cite this article as:
Malik P., Kumar N., Ali Mohd. N., Rajlumar and Jakhar A. (2023). Variability, Correlation & Heritability analysis for Various Quantitative traits in Bread Wheat (*Triticum aestivum* L.) *Int. J. of Pharm. & Life Sci.*, 14(8-9): 54-62.

Source of Support: Nil
Conflict of Interest: Not declared
For reprints contact: ijplsjournal@gmail.com