

## Genotype × Environment Interaction and Variability for Grains per Spike and Spike Length in Wheat (*Triticum aestivum* L.) genotypes under Temperate conditions

Shabir H. Wani<sup>1\*</sup>, Mehdi Rahimi<sup>2</sup>, Hanif Khan<sup>3</sup>, Basharat ul Islam<sup>1</sup>, N.R. Sofi<sup>1</sup>, Asif B. Shikari<sup>1</sup>, Ashaq Hussain<sup>1</sup>, F. A. Mohiddin<sup>1</sup>, M. Ashraf Ahanger<sup>1</sup>, I.A. Jehangir<sup>1</sup>, G.H. Khan<sup>1</sup>, Zahoor A. Dar<sup>4</sup>, Aabid H. Lone<sup>1</sup>, J. A. Lone<sup>1</sup>, M. S. Dar<sup>1</sup> and Saba Mir<sup>1</sup>

<sup>1</sup>Mountain Research Centre for Field Crops, Khudwani- 192101, Dryland Agricultural Research Station, Rangreth, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir (J&K), India.

<sup>2</sup>Department of Biotechnology, Institute of Science and High Technology and Environmental Sciences, Graduate University of Advanced Technology, Kerman, Iran.

<sup>3</sup>ICAR- Indian Institute for Wheat and barley Research, Karnal (Haryana), India.

(Corresponding author: Shabir H. Wani\*)

(Received 18 November 2021, Accepted 05 February, 2022)

(Published by Research Trend, Website: [www.researchtrend.net](http://www.researchtrend.net))

**ABSTRACT:** Variability of grains per spike and spike length are one of the important contributors of grain yield in wheat. Also, the experiments measuring the interaction between genotypes and environments measure the spatial (e.g., locations) and temporal (e.g., years) separation and/or combination of these factors. The genotype-by-environment interaction (GEI) is very important in plant breeding programs. It is necessary for researchers that calculate stability indices, and ultimately select the superior genotypes, to dissect their usefulness. The aim of this study was to estimate variability of grains per spike and spike length in 32 genetically divergent wheat accessions and two wheat cultivars evaluated during 2019 and 2020 wheat growing season. The experiment was set up as a randomized block design in three replications. Obtained results indicated differences in average values of grains per spike and spike length among tested lines and cultivars. The results of combined analysis of variance showed that these traits were not affected by the environment and the interaction of genotype with the environment was not significant. The results also showed that there was a significant difference between the lines and cultivars in terms of spike length and number of grains per spike. Accession number 33, 11, 16 and 18 had the highest values for both studied traits (spike length (cm) (13.08, 13.7, 12.9 and 12.3 cm and number of seeds per spike 50.65, 50.77, 49.52 and 57.35) while accessions 4, 13 and 17 had the lowest values. Since increase in these traits contributes in increased yield in wheat and the fact that the interactions of genotype with the environment were not significant, so these four accessions (33, 18, 16 and 11) can be used in breeding programs to increase wheat yield.

**Keywords:** wheat; variability; grains per spike; spike length.

### INTRODUCTION

In recent years due to increasing population growth and food crisis for most countries, especially developing and for high-yield potential (Senapati *et al.*, 2019). Wheat has a tremendous genetic diversity in terms of different quantitative and qualitative traits and compatibility with environmental factors and types of resistance (Adil *et al.*, 2022; Wani *et al.*, 2021). The study of genetic diversity and differentiation of genotypes is possible by examining the degree of similarity and differences in a number of accessions and the condition is to group the samples using the criterion of similarity or dissimilarity and also to use different types of multivariate statistical methods. In addition to utilizing the genetic diversity of native populations and wild species, researchers are also interested in altering certain traits of economic interest within improved cultivars (Balfourier *et al.*, 2019). Heritability, which is

a measure of phenotypic diversity due to genetic reasons, has a predictive role in crop breeding (Songsri *et al.*, 2008). Therefore, traits which are highly heritable can be conveniently used for selections in breeding populations. Cultivars and genotypes that are least affected by different environmental conditions and are stable are suitable for wide cultivation. Spike is the place of wheat grains and is considered as a reservoir for wheat grains and therefore increasing the length of the spike directly increases the number of spikelets per spike, number of grains per spike, and finally wheat grain yield (Singh *et al.*, 2018). Therefore, spike length and number of grains per spike are valuable selection criteria for developing high yielding wheat cultivar. On the other hand, environmental factors cause these traits to be affected and change. Therefore, cultivars and genotypes that are least affected by different environmental conditions and are stable are suitable for

wide cultivation (Roy *et al.*, 2021). The number of seeds per spike depends on the number of primary spikelets produced in the early stages. In addition, climatic conditions and plant nutrition have a great influence on the flowering stage to obtain a maximum number of seeds per spike (Wolde *et al.*, 2019). The selection of adequate genotype of wheat with stable expression of yield component traits for a specific environment paramount importance for maximizing yield (Elhani *et al.*, 2007). Breeding success necessitates a thorough understanding of genotype and environment traits, as well as the genotype/environment interaction (Knezevic *et al.*, 2007). In order to choose superior genotypes, it is necessary to assess the genotype/environment interaction (Dhungana *et al.*, 2007). Wheat has a wide distribution range and grows in a variety of climates. Wheat breeders' primary goal is to create new genotypes with high grain yield potential, improved quality attributes, and high tolerance to biotic and abiotic factors (Akçura, 2009; Gao *et al.*, 2021). The success in breeding wheat for high grain production is dependent on germplasm source for selecting the best parent plants for hybridization and developing progenies with economically important hereditary traits (Labroo *et al.*, 2021). Breeders have devised strategies for producing new high-yielding cultivars based on extensive crossing and testing of early generation progenies to attain a desirable combination of features. Genetic enhancement in grain yield can be achieved by improving the values of yield components such as spike characteristics, photosynthetic efficiency, and fertilizer use efficiency (Elango *et al.*, 2021). In studies by Knezevic *et al.*, (2019). The diversity of different wheat cultivars in terms of spike length and number of grains per spike for two consecutive years was evaluated and the results showed that these cultivars were affected by the environment and good diversity between cultivars were observed. The purpose of this experiment was to investigate the diversity of wheat lines in terms of spike length and number of grains per spike and to investigate the effect of environment on these traits and identify suitable cultivars to increase wheat yield.

## MATERIALS AND METHOD

The plant material consisted of 32 bread wheat accessions from 6<sup>th</sup> WYCYT provided by Director, ICAR Indian Institute of Wheat and Barley Research, Karnal for evaluation under the All India Coordinated Wheat and Barley Research Project functional at

Mountain Research Centre for Field Crops (MRCFC) Khudwani, Sher-e-Kashmir University of Agricultural Sciences and Technology, (SKUAST) Srinagar, Jammu and Kashmir. These accessions are subset of advanced bulks of CIMMYT wheat breeding programme. A total of 34 entries including two released cultivars were used for evaluation in randomized complete block design field experiment with three replications. Four field experiments were conducted in 2019-20 and 2020-21 winter season (wheat growing season) under rainfed (33°70'N latitude, 75°10'E longitude; 1680 m amsl) at MRCFC, Khudwani, Jammu and Kashmir, India. All plots were weed-free and received required doses of NPK fertilizers. Taking into fertilizer recommendation in kg/ha was: 120 N, 60 P, and 40 K kg per hectare was applied for both years of experimentation. These entries were evaluated for spike length and number of seeds per spike in two years (2019 and 2020) and these traits were measured for five plants per entry. These traits were studied in all 34 entries for two years under temperate conditions. The names of the accessions used in this experiment are given in (Table 1). Analyzes were performed using SAS software version 9.4 (SAS-Institute-Inc, 2014) and PAST (Hammer, Harper, & Ryan, 2001).

## RESULTS AND DISCUSSION

Many factors such as abiotic stresses have a significant impact on the yield and quality in wheat (Dar *et al.*, 2020). Therefore, selecting suitable and high-yielding cultivars that have good resistance to stressful conditions is very important (Jeberson *et al.*, 2021; Wani *et al.*, 2018). Spike length and number of grains per spike are important traits of wheat that play a key role in yield potential in wheat. In this study, these traits were studied in advanced wheat lines for two years under temperate conditions. The results of combined analysis of variance of traits are shown in (Table 1).

The results of combined analysis of variance showed that there was a significant difference between genotypes while no significant difference was observed for the effect of year and also the interaction of year × genotype. The results of broad sense heritability are shown in (Table 1). The heritability of the spike length and grains per spike traits were 80.1% and 79.6%, respectively. High heritability of these traits increases the chances of selecting superior genotypes for these traits and can be used in wheat breeding programs.

**Table1: Combined analysis of variance based on randomized complete block design of studied traits in wheat.**

S.o.V	Df	MS of Traits	
		Spike Length (cm)	Grains per Spike
Year	1	0.313 <sup>ns</sup>	7.882 <sup>ns</sup>
R(Year)	4	0.951	10.439
Genotype	33	10.914 <sup>**</sup>	198.482 <sup>**</sup>
year×genotype	33	0.496 <sup>ns</sup>	9.529 <sup>ns</sup>
Error	132	0.398	7.313
CV		5.728	6.278
$h^2_b$		80.1%	79.6%

ns and \*\*: non-significant and significant at 1% probability levels, respectively.

The mean comparison between wheat lines for the studied traits was carried out using Duncan method at the level of one percent (1 %) and the results of comparisons are shown in (Table 2). As can be seen, wheat lines were divided into different groups in terms of these two traits, which indicate presence of diversity and increases the chances of selection for breeders. The results of mean comparison for spike length and number of grains per spike showed that there is a large difference between the lines and this situation increases the chances of selecting the most desirable wheat lines for the breeder.

Lines 33, 18, 16 and 11 had the highest values for both studied traits (spike length and number of seeds per spike) while lines 4, 13 and 17 had the lowest values. Since this increase in these traits increases yield in

wheat and on the other hand due to the fact that the interactions of genotype in the environment were not significant, so these lines (33, 18, 16 and 11) can be selected to increase wheat yield and can be used in breeding programs. The principal component analysis results for these two traits are shown in Fig. 1. The results showed that the cultivars were located in four plot areas. Since the cultivars of region 1 plot are positive in terms of these two traits and increasing them increases the yield, so the cultivars that have the highest value in terms of these two components can be selected and can be used directly in breeding programs. The figures in different areas of the plot can also be used in cross-breeding and hybrid production programs.

**Table 2: Results of comparing the mean of different traits studied for wheat lines in combined analysis.**

Row	Genotype	Mean of Spike Length (cm)	Mean of Grains per Spike
1	KW-6-CYT-18-1	12.0833b-f	42.7d-h
2	KW-6-CYT-18-2	9.9333ij	34.967l-n
3	KW-6-CYT-18-3	11.4667d-h	41f-k
4	KW-6-CYT-18-4	8.7833k-m	31.867n
5	KW-6-CYT-18-5	11.95c-f	47.2b-d
6	KW-6-CYT-18-6	9.0833j-m	36.283l-n
7	KW-6-CYT-18-7	11.5667d-h	46.867b-d
8	KW-6-CYT-18-8	9.7833i-k	39.467g-l
9	KW-6-CYT-18-9	11.8667d-g	37.95i-m
10	KW-6-CYT-18-10	9.1333j-m	39.333g-l
11	KW-6-CYT-18-11	13.7a	50.767b
12	KW-6-CYT-18-12	10.7667g-i	42.767d-h
13	KW-6-CYT-18-13	8.3833m	34.333mn
14	KW-6-CYT-18-14	11.6833d-h	46.9b-d
15	KW-6-CYT-18-15	10.7667g-i	41.9e-i
16	KW-6-CYT-18-16	12.9667a-c	49.517bc
17	KW-6-CYT-18-17	8.6333lm	34.5mn
18	KW-6-CYT-18-18	12.3b-d	57.35a
19	KW-6-CYT-18-19	11.4333d-h	46.317b-e
20	KW-6-CYT-18-20	11.05f-h	44.917c-f
21	KW-6-CYT-18-21	11.5833d-h	41.767e-j
22	KW-6-CYT-18-22	12.2b-e	47.35b-d
23	KW-6-CYT-18-23	11.35d-h	47.167b-d
24	KW-6-CYT-18-24	11.1167e-h	46.65b-d
25	KW-6-CYT-18-25	12.05b-f	48.717bc
26	KW-6-CYT-18-26	9.75i-k	36.917k-m
27	KW-6-CYT-18-27	9.5167j-l	38.4h-m
28	KW-6-CYT-18-28	9.45j-l	37.183j-m
29	KW-6-CYT-18-29	11.0667e-h	39.6g-l
30	KW-6-CYT-18-30	11.7333d-h	46.55b-d
31	KW-6-CYT-18-31	10.6833hi	43.9d-g
32	KW-6-CYT-18-32	11.7667d-h	46.05b-e
33	Shalimar Wheat 1	13.0833ab	50.65b
34	Shalimar Wheat 2	12.0833b-f	46.783b-d

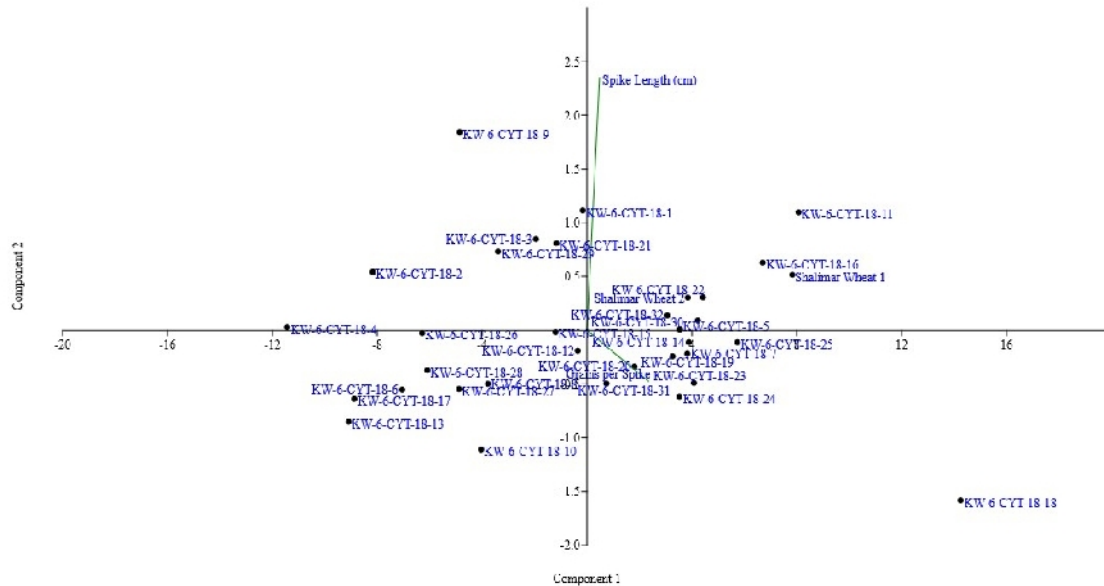
Treatments with similar letters do not differ statistically by one percent.

Differences amongst cultivars in line with cost of spike length are affected greater through genotype than through relationships to the geographic origin (Dotlacil *et al.*, 2003). The sensitivity of duration of spike under environmental variant noticed (Knezevic *et al.*, 2014) and constitute crucial additives of wheat yield. The environmental elements as nicely temperature values, precipitation, nutrients have an impact on growing of ability of spike (Petrovi *et al.*, 2008) and grain yield

(Marijanovi *et al.*, 2010). The investigated trait extraordinarily depended to genetic and environmental factors (Dodig *et al.*, 2008). The spike length is yield additives which extraordinarily undoubtedly correlated to wide variety of spikelets (Akram *et al.*, 2008). The results showed that these traits were not affected by the environment and the interaction of genotype in the environment was not significant. Therefore, selecting the genotypes that have the highest value for these traits

can also play an effective role in wheat breeding for higher yield. The results also showed that there was a significant difference between the lines in terms of spike length and number of grains between the lines. According to these results, it can be concluded that

these lines are different and selection of genotypes for spike length and grain number per spike will be effective for identifying high yielding lines under temperate ecology of Kashmir Valley.



**Fig. 1.** Wheat biplot analysis based on two cultivars.

Application of GT biplot to this investigation on wheat genotypes shows visual interrelationships among the physiological traits. In the study on wheat, cultivars were identified for different environmental conditions. The results of interactions also showed significant differences for different traits (Farshadfar *et al.*, 2015). Also, in other studies, results of combined analysis of variance showed significant differences for site, genotypes and genotype\* site interaction in most of measured traits. The ideal genotypes were G1 and G2 in both irrigation and rainfed condition as compared to the other genotypes (Dabiry *et al.*, 2015). In addition, in the study of Shirinpour *et al.*, (2015), they showed that genotype  $\times$  environment interaction is important in developing and releasing new varieties of crop plants. Also, the results showed that line  $\times$  year interaction was significant for number of grain per spike, number of spike per square meter and 1000 grain weight (Shirinpour *et al.*, 2015).

### CONCLUSION

In this research the variations had been decided amongst wheat genotypes in step with values of grains per spike and spike length. The maximum values of grains per spike and spike length had observed in entries 33, 11, 16 and 18. Increasing of wheat grain yield is viable through enhancing all morphological, physiological tendencies of spike as a significant wheat yield contributing trait. Since increase in these traits contributes in increased yield in wheat and the fact that the interactions of genotype with the environment were not significant, so these four accessions can be used in breeding programs to increase wheat yield.

**Conflict of interest.** The authors declare that they have no conflict of interest.

**Acknowledgment.** Authors acknowledge the financial support for research provided by Director, ICAR IIWBR Karnal under AICRP on Wheat and Barley.

### REFERENCES

Adil, N., Wani, S. H., Rafiqee, S., Mehrajuddin, S., Sofi, N. R., Shikari, A. B., . . . Rahimi, M. (2022). Deciphering Genotype  $\times$  Environment Interaction by AMMI and GGE Biplot Analysis Among Elite Wheat (*Triticum aestivum* L.) Genotypes of Himalayan Region. *Ekin Journal of Crop Breeding and Genetics*, 8(1), 41-52.

Akçura, M. (2009). Genetic variability and interrelationship among grain yield and some quality traits in Turkish winter durum wheat landraces. *Turkish Journal of Agriculture and Forestry*, 33(6), 547-556.

Akram, Z., Ajmal, S. U., & Munir, M. (2008). Estimation of correlation coefficient among some yield parameters of wheat under rainfed conditions. *Pakistan Journal of Botany*, 40(4), 1777-1781.

Balfourier, F., Bouchet, S., Robert, S., De Oliveira, R., Rimbart, H., Kitt, J., . . . Paux, E. (2019). Worldwide phylogeography and history of wheat genetic diversity. *Science advances*, 5(5), Article number, eaav0536.

Dabiry, S., Esmaili, M. A., Haghparast, R., & Ghajarsepanlo, M. (2015). Genetic Variation of Advanced Bread Wheat Genotypes for Remobilization related Traits under irrigated and Rainfed conditions using GGE Biplot Method. *Biological Forum – An International Journal*, 7(1), 254-265.

Dar, S. B., Kanth, R. H., Raja, W., Bangroo, S. A., Rashid, Z., Dar, Z. A., & Wani, S. H. (2020). Performance of wheat variety Shalimar Wheat-2 under rainfed conditions of temperate Kashmir as influenced by sowing dates and nitrogen levels. *Journal of Cereal Research*, 12(2), 129-136.

- Dhungana, P., Eskridge, K. M., Baenziger, P. S., Campbell, B. T., Gill, K. S., & Dweikat, I. (2007). Analysis of genotype-by-environment interaction in wheat using a structural equation model and chromosome substitution lines. *Crop Science*, 47(2), 477-484.
- Dodig, D., Zoric, M., Knezevic, D., King, S. R., & Surlan-Momirovic, G. (2008). Genotype  $\times$  environment interaction for wheat yield in different drought stress conditions and agronomic traits suitable for selection. *Australian Journal of Agricultural Research*, 59(6), 536-545.
- Dotlacil, L., Hermuth, J., & Stehno, Z. (2003). Earliness, spike productivity and protein content in European winter wheat landraces and obsolete cultivars. *Plant Soil and Environment*, 49(2), 67-74.
- Elango, D., Sandoya, G., & Chopra, S. (2021). Techniques and Tools of Modern Plant Breeding. In *Plant Biotechnology* (pp. 17-26): Springer.
- Elhani, S., Martos, V., Rharrabti, Y., Royo, C., & del Moral, L. G. (2007). Contribution of main stem and tillers to durum wheat (*Triticum turgidum* L. var. durum) grain yield and its components grown in Mediterranean environments. *Field Crops Research*, 103(1), 25-35.
- Farshadfar, E., Akbari, L., & Naseri, M. (2015). Evaluation of Genetic Diversity in Bread Wheat using Genotype by Trait Biplot under Different Environmental Conditions. *Biological Forum – An International Journal*, 7(1), 1589-1598.
- Gao, L., Yang, J., Song, S. J., Xu, K., Liu, H. D., Zhang, S.-H., . . . Zhao, Y. (2021). Genome-wide association study of grain morphology in wheat. *Euphytica*, 217(8), 1-12.
- Hammer, Ø., Harper, D., & Ryan, P. (2001). PAST: Paleontological statistics software package for education and data analysis. *Palaeontologia Electronica*, 4, 1–9.
- Jeberson, M. S., Chaudhary, H. K., Chahota, R. K., & Wani, S. H. (2021). Doubled haploid production in advanced back cross generations and molecular cytogenetic characterization of rye chromatin in triticales  $\times$  wheat derived doubled haploid lines. *Biocell*, 45(6), 1651.
- Kashif, M., Wani, S. H., & Shaukat, S. (2021). Wheat Wild Germplasm: A Hidden Treasure. In M. Azhar & S. H. Wani (Eds.), *Wild Germplasm for Genetic Improvement in Crop Plants* (pp. 55-63): Elsevier.
- Knezevic, D., Kondic, D., Markovic, S., Markovic, D., & Atanasijevic, S. (2014). Genetic and phenotypic variability of grain mass and length of spike in wheat (*Triticum aestivum* L.) effected by nitrogen nutrition. *Növénytermelés, suppl*, 63, 47-51.
- Knezevic, D., Micanovic, D., Zecevic, V., Brankovic, G., Kondic, D., Radosavac, A., . . . Urosevic, D. (2019). Variability of length of spike and number of spikelets per spike in wheat (*Triticum aestivum* L.). Paper presented at the X International Agriculture Symposium, Agrosym 2019, Jahorina, Bosnia and Herzegovina, 3-6 October 2019. Proceedings.
- Knezevic, D., Paunovic, A., Madic, M., & Djukic, N. (2007). Genetic analysis of nitrogen accumulation in four wheat cultivars and their hybrids. *Cereal Research Communications*, 35(2), 633-636.
- Labroo, M. R., Studer, A. J., & Rutkoski, J. E. (2021). Heterosis and hybrid crop breeding: a multidisciplinary review. *Frontiers in genetics*, 12, 234.
- Marijanovi, M., Markulj, A., Tkalec, M., Jozi, A., & Kova evi, V. (2010). Impact of precipitation and temperature on wheat (*Triticum aestivum* L.) yields in eastern Croatia. *Acta Agriculturae Serbica*, 15(30), 117-123.
- Petrovi, S., Mari, S., Guberac, V., Drezner, G., & E ed, A. (2008). Influence of environmental conditions and sowing rates on winter wheat yield. *Cereal Research Communications*, 36, 1307-1310.
- Roy, A., Kumar, A., Singh, A., Mandi, A., & Barman, M. (2021). Analysis of genetic diversity and correlation studies on grain yield and its component characters in bread wheat (*Triticum aestivum* L. em Thell) genotypes. *The Pharma Innovation Journal*, 10(5), 341-345.
- SAS-Institute-Inc. (2014). Base SAS 9.4 Procedures Guide: Statistical Procedures, Third Edition. USA: SAS Institute Inc., Cary, NC.
- Senapati, N., Brown, H. E., & Semenov, M. A. (2019). Raising genetic yield potential in high productive countries: designing wheat ideotypes under climate change. *Agricultural and Forest Meteorology*, 271, 33-45.
- Shirinpour, M., Aharizad, S., Vahed, M. M., & Mohammadi, S. A. (2015). Stability of Bread Wheat Recombinant Inbreed Lines Derived from across Zagros and Norstar. *Biological Forum – An International Journal*, 7(1), 684-692.
- Singh, G., Kumar, P., Kumar, R., & Gangwar, L. (2018). Genetic diversity analysis for various morphological and quality traits in bread wheat (*Triticum aestivum* L.). *Journal of Applied and Natural Science*, 10(1), 24-29.
- Songsri, P., Jogloy, S., Kesmala, T., Vorasoot, N., Akkasaeng, C., Patanothai, A., & Holbrook, C. (2008). Heritability of drought resistance traits and correlation of drought resistance and agronomic traits in peanut. *Crop Science*, 48(6), 2245-2253.
- Wani, S. H., Khan, H., Riaz, A., Joshi, D. C., Hussain, W., Rana, M., . . . Kang, M. S. (2021). Genetic diversity for developing climate-resilient wheats to achieve food security goals. *Advances in Agronomy*, 171, 255-303.
- Wani, S. H., Sheikh, F., Najeeb, S., Iqbal, A. M., Kordrostami, M., Parray, G., & Jeberson, M. S. (2018). Genetic variability study in bread wheat (*Triticum aestivum* L.) under temperate conditions. *Current Agriculture Research Journal*, 6(3), 268-277.
- Wolde, G. M., Mascher, M., & Schnurbusch, T. (2019). Genetic modification of spikelet arrangement in wheat increases grain number without significantly affecting grain weight. *Molecular Genetics and Genomics*, 294(2), 457-468.

**How to cite this article:** Shabir H. Wani<sup>\*</sup>, Mehdi Rahimi, Hanif Khan, Basharat ul Islam, N.R. Sofi, Asif B. Shikari, Ashaq Hussain, F. A. Mohiddin, M. Ashraf Ahanger, I.A. Jehangir, G.H. Khan, Zahoor A. Dar, Abid H. Lone, J. A. Lone, M. S. Dar and Saba Mir (2022). Genotype  $\times$  Environment Interaction and Variability for Grains per Spike and Spike Length in Wheat (*Triticum aestivum* L.) genotypes under Temperate conditions. *Biological Forum – An International Journal*, 14(1): 1365-1369.