

ASSOCIATION AMONG QUANTITATIVE ATTRIBUTES IN HEXAPLOIDY WHEAT GENOTYPES FOR SUSTAINABLE FOOD SECURITY

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ABSTRACT

In the present research, thirty-three wheat genotypes were studied to check association among the quantitative traits of hexaploid wheat. The wheat genotypes were grown using complete randomized design with three replications to study the attributes like number of grains per spike (NGS), plant height (PH), peduncle length (PL), spike weight (SW), spike length (SL), spikelet per spike (SPS), and grain yield per plant (GYP). The analysis of variance (ANOVA) for the attributes used in the experiment was executed. ANOVA revealed that a significant difference present in plant performance. The correlation analysis showed that there was a positive and significant association among different traits. Peduncle length is positively correlated with plant height (0.97). The attributes like number of grains and spikelet per spike were associated positively with spike length (0.83 and 0.69, respectively). The peduncle length, grain weight, and spikelet per spike, which were positively correlated with grain yield and exhibited direct effects on grain yield and can be used as major selection criteria in breeding studies. On the basis of current findings, the genotypes that performed well are suggested for widespread use as commercial cultivars in breeding programs which can be helpful in the future.

Key-words: Spring Wheat; Morphological traits; Genotypes; Pakistan; Correlation

INTRODUCTION

Wheat (*Triticum aestivum* L., $2n = 6x = 42$) is ranked third important cereal staple food around the world. The demand of wheat crop is increasing day by day and it is expected that it will be achieved nearly about 40% in next decade (Dixon, 2009). In agriculture, wheat grants 13.8 percent of value, and it accounts for 3.4 percent of GDP. As food supplement, wheat is one of the few crops which grown widely, Bread wheat is from a few species which is grown widely as a food source, and it was most likely central to the beginnings of agriculture. The composition of the wheat comprises up of essential amino acids, vitamins and minerals along with the some phytochemicals and dietary fibre which are beneficial for the living organisms (Shewry, 2009).

Demand of the wheat is also rising as the world's population grows. Thus, efficient resource management, which also includes a good seed source for higher yield output which is the result of breeders efforts to develop varieties of the wheat with high production even under drought environment, is required. Wheat is primarily a crop which is self-pollinated, and due to auto-gamous behavior of reproduction, wheat populations attain homozygosity after hybridization only in a single cropping season. The selection of suitable genotypes in a breeding program for crop improvement could benefit from the evaluation of genotypes based on morphological and quantitative attributes, specifically those of economic importance (Xhulaj and Koto, 2022).

Quantitative characteristics are frequently used to evaluate the attributes of wheat because of their significance in estimating genetic diversity and differentiating between closely related types of the species

(Xhulaj and Koto, 2022). There is an urgent need to create genotypes especially with increased yield potential to produce in a specific unit area. This could be accomplished by maximizing the potential of the genetic material from available wheat germplasm (Sadiq *et al.*, 1994). The most essential aspect in any breeding plan is yield. A breeder's primary goal is to improve yield. It is, however, a considerably more challenging aspect.

To create high-yielding and adaptable wheat varieties to fulfil the growing demand from consumers, an efficient and innovative wheat breeding program is necessary. It is essential to enhance the development of this crop by producing cultivars that are tolerant of the diverse environmental conditions in the region and have a high yield potential. Existing resources must be used more efficiently for this purpose. As a result, rather than keeping hundreds of crosses, wheat breeders need to work on a limited number of crosses resulting from parents with strong genetic potential. Any yield improvement program must begin with the selection of superior hybridization parents (Hasnain *et al.*, 2006). Increasing the spike length and the number of spikelet per spike will increase crop production. When a plant has the greater number of spikelets per spike and the length of the spikes is increased, the number of grains per spike is also maximized. Because spike length and grain production are indirectly related through fertile spikelet, breeders must prioritize these attributes of wheat. In current study 33 wheat genotypes was studied to check relationship between quantitative traits of wheat. The analysis of variance was done which showed that highly significant difference was present among the genotypes for studied traits. The analysis of the correlation was also executed which showed association among different quantitative traits. The correlation analysis is useful technique to identify the character that are positively correlated with yield (Maqbool *et al.*, 2010). In this experiment the plant height was positively correlated with peduncle length. The grain yield also positively correlated with spike weight. There was significant and positive association among spikelet per spike and spike length. The main objective of this study was to determine the association between quantitative traits.

MATERIALS AND METHODS

The experiment was carried out at field conditions. In this experiment, 33 genotypes of wheat with three replications were evaluated using randomized complete block design (RCBD). The wheat genotypes studied are presented in Table 1. The seeds of these 33 genotypes were provided from the regional agriculture research institute (RARI). Each genotype was sown in a 5m length with plant to plant and row to row spacing of 15cm and 30cm respectively. In order to remove the edge effects, the non-experimental lines were additionally planted at the start and end of each replication. All genotypes were subjected to the same cultural and management practices. The plant height (PH), peduncle length (PL) and spike length (SL) were measured by measuring tape. Spikelets per spike (SPS) and number of grain per spike (NGS) were counted. For grain yield per plant (GYP) all grain from a plant was weighted on weight balance.

Statistical Analysis

The given data was analyzed by analysis of variance (ANOVA) (Steel and Torrie, 1960) to check the significance level using software Statistics 8.1. The significance level (α) was 0.01 and 0.05 for highly significant and significant effects, respectively. Highly significant characters were further analyzed through correlation analysis to check the linkage between these traits. The correlation was calculated by Pearson correlation formula (Benesty *et al.*, 2009).

RESULTS

The analysis of variance displayed in Table 2 showed that all the six traits were highly significant. The highest values exhibited for the mean square were shown by the variable plant height (129.995) and lowest value was revealed in the grain yield per plant (0.02918) in the hexaploid 33 wheat genotypes. The highly significant results mentioned that genetic variability in the experimental genotypes.

Mean Variability

The best performance genotypes in plant height variables were G10 followed by G19 and G32 expressing the mean variability as 99.9cm, 98.5cm and 96cm, respectively (Table 3 and 4). The mean performance of genotypes is displayed in Fig. 1 and 2. The highest mean variability exhibited for the peduncle length was observed in G8 (28.7cm) followed by G10 (32.5cm) and G 19 (31.5cm) in this study.

The genotypes had high mean variability for spikelet per spike were G23 (19.8) followed by G31 (20.4) and G32 (21) as exhibited in Table 3 & 4. The genotypes G18 (11.8cm) followed by G24 (11.4cm) and G32 (12.5cm) showed the highest mean variability in Table 3 and 4 for spike length. The mean performance of genotypes is also displayed in Fig. 1 and 2. The genotypes expressed the highest mean variability G10 (58) followed by G19 (55) and G32 (53.2) for the trait number of grain per spike as presented in Table 3 & 4. The grain yield per plant has the highest mean variability value in the genotypes G10 (24g) followed by G32 (22g) and G 28 (21.5g) as showed in Table 3 and 4. The mean performance of genotypes also displayed in Fig. 1 and 2. The genotypes that showed the lowest performance for plant height trait were G3 (78cm), G15 (77cm) and G33 (78.4cm). The genotypes G3 (18.5cm), G15 (17) and G33 (16cm) were the lowest performing genotypes for the peduncle length. The spikelet per spike exhibited the minimum values for the genotypes were G3 (13), G15 (11) and G33 (13) as shown in Table 3. The mean performance of genotypes is displayed in Fig- 1 and 2. The genotypes that have lower performance for the spike length in Table 3 were G3 (8.5cm), G15 (9cm) and G33 (7.5cm). Table 3 and 4 revealed the genotypes G3 (47), G15 (46) and G33 (45) expressed the lowest values for the number of the grain per spike. The trait grain yield per spike have the lowest values for the genotypes were G3 (18g), G15 (17.5g) and G33 (17g) as given in the Table 3 and 4. The mean performance of genotypes is also displayed in Fig. 1 and 2.

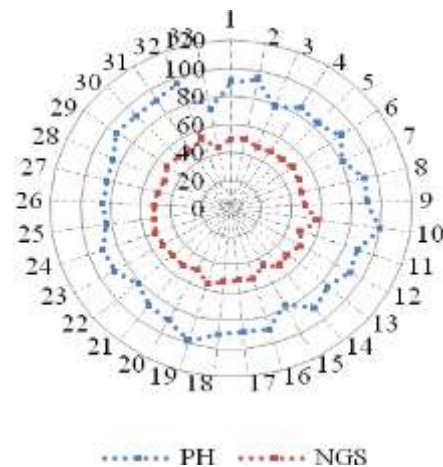


Fig. 1. Radar graph for plant height (PH) and number of grain per spike (NGS).

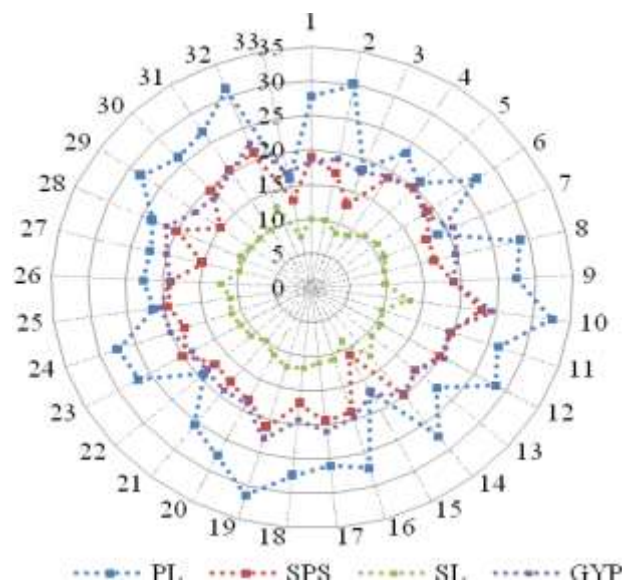


Fig. 2. Radar graph for spikelets per spike (SPS), spike length (SL) and peduncle length (PL), grain yield per plant (GYP).

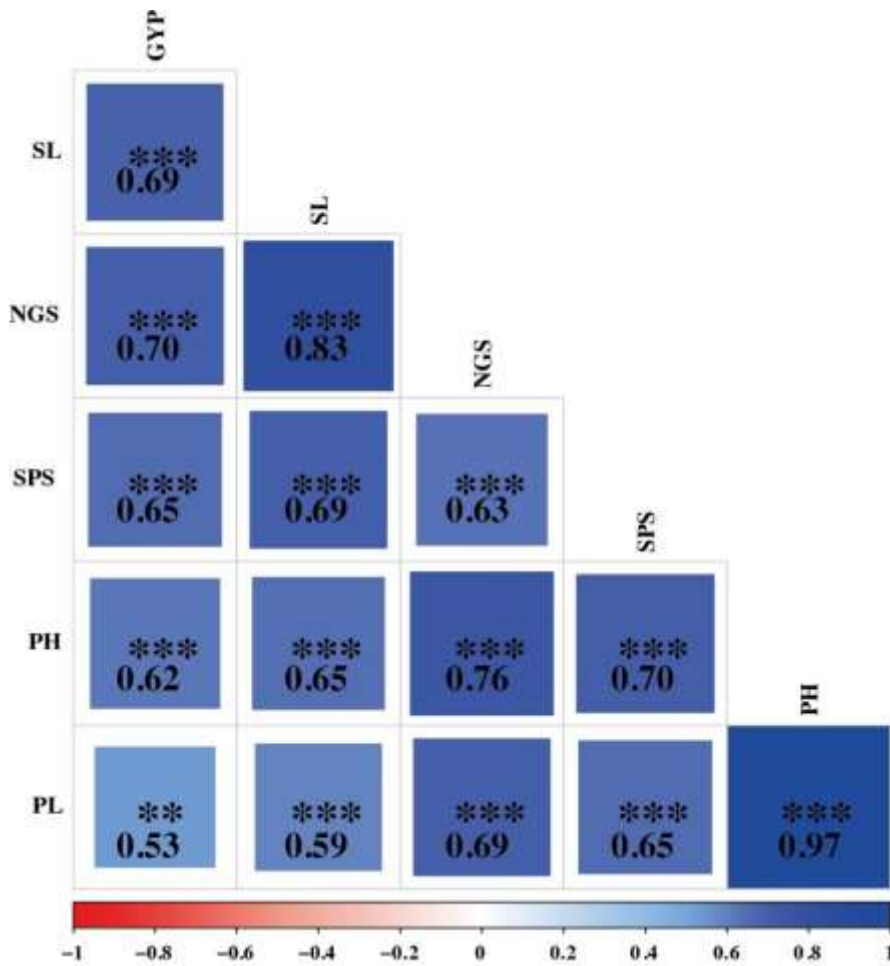


Fig. 3. Association among quantitative attributes in hexaploidy wheat.

Table 1. List of 33 hexaploid wheat genotypes used in this experiment.

S. No.	Genotypes	S. No.	Genotypes
1	G133	18	G116
2	G132	19	G115
3	G131	20	G114
4	G130	21	G113
5	G129	22	G112
6	G128	23	G111
7	G127	24	G110
8	G126	25	G109
9	G125	26	G108
10	G124	27	G107
11	G123	28	G106
12	G122	29	G105
13	G121	30	G104
14	G120	31	G103
15	G119	32	G102
16	G118	33	G101
17	G117		

Table 2. Analysis of Variance for studied traits.

Source	DF	PH	PL	SPS	SL	NGS	GYP
Replication	2	5.616	0.7980	0.76768	4.21212	0.02336	0.42636
Genotype	32	129.995**	34.4059**	4.75253**	2.90530**	0.87595**	0.18023**
Error	64	47.241	7.6521	1.14268	1.34754	0.28368	0.02918
Total	98						

PH=Plant Height, PL= Peduncle Length, SPS= Spikelets per Spike, SL= Spike Length, NGS= Number of grains per Spike, GYP= Grain Yield per Plant,

Table 3. Mean values of 33 hexaploid wheat genotypes for quantitative attributes.

Genotypes	PH	PL	SPS	SL	NGS	GYP
G1	90.3	27.8	19	10	50	18.5
G2	93.7	30	17	10	51	19
G3	78	18.5	13	8.5	47	18
G4	85.8	23.3	19	9	48	19.2
G5	83.5	21	19.8	10.4	49	20
G6	89.6	27.1	19.2	10.9	50	18.4
G7	81.2	18.7	17	10.8	49.5	21
G8	91.2	28.7	17	10	48	20
G9	90	27.5	19	10	49.2	19
G10	99.9	32.5	23	13.3	58	24.5
G11	88.9	26.4	19.8	10	49	19.4
G12	91	28.5	19.8	10.7	53	20.6
G13	84.7	22.2	18.4	10.7	50	18.5
G14	90	27.5	20	12.6	52	19.7
G15	77	17	11	9	46	17.5
G16	89.9	27.4	18.8	10.9	52	19.8
G17	88.5	26	19.6	11	51	21
G18	90	27.5	17	11.8	53	19.4
G19	98.5	31.5	21.2	12	55.5	23
G20	90	27.5	18.4	11.1	49	19
G21	87.9	25.4	17.6	9.9	51.5	19
G22	81.6	19.1	17	10.7	51	18.5
G23	89.3	26.8	19.8	11	52	18.5
G24	89.9	27.4	18	11.4	53	20
G25	83.8	21.3	19.4	11	52	20.4
G26	85.1	22.6	19	12	51	19
G27	84.8	22.3	15	10	50	20
G28	85.9	23.4	19.8	10.5	48.7	21.4
G29	93.4	28	15	10	52	19
G30	91.2	26	19.4	10	51	18.5
G31	92	27	20.4	10	49	20
G32	96	31	21	12.5	53.2	22.5
G33	72.4	16	13	7.5	45	17

PH=Plant Height, PL= Peduncle Length, SPS= Spikelets per Spike, SL= Spike Length, NGS= Number of grains per Spike, GYP= Grain Yield per Plant,

Table 4. Best and Poor performer wheat genotypes with their mean values.

Traits	minimum mean	maximum mean	Grand mean	Genotype number and their higher mean values	Genotype number and their lower mean values
Plant Height	72.4	99.9	88.030	G10(99.9),G19(98.5),G32(96.0)	G33(72.4), G15(77),G3(78)
Peduncle length	16	32.5	25.239	G10(32.5), G19(31.5),G8(28.7)	G33(16),G15(17),G3(18.5)
Spikelet per spike	11	23	18.224	G32(21),G21(20.4),G23(19.8)	G33(13),G15(11),G3(13)
Spike length	7.5	13.3	10.581	G32(12.5),G18(11.8),G24(11.4)	G33(7.5),G15(9),G3(8.5)
Number of grains per spike	45	58	50.593	G10(58),G19(55),G32(53.2)	G33(45),G15(46),G3(47)
Grain yield per plant	17	24.5	19.675	G10(24),G32(22),G28(21.5)	G33(17),G15(17.5),G3(18)

Table 5. Association among quantitative attributes in hexaploidy wheat.

	PH	PL	SPS	SL	NGS
PL	0.97**	1			
SPS	0.70**	0.65**	1		
SL	0.65**	0.59**	0.69**	1	
NGS	0.76**	0.69**	0.63**	0.83**	1
GYP	0.62**	0.53**	0.65**	0.69**	0.70**

PH=Plant Height, PL= Peduncle Length, SPS= Spikelets per Spike, SL= Spike Length, NGS= Number of grains per Spike, GYP= Grain Yield per Plant, *** = highly significant ** = significant

CORRELATION STUDY

Plant Height

The plant height had highly significant and positive association with peduncle length having value (0.97). The plant height was positively and highly significant correlated with the spikelets per spike (0.70) as shown in Table 5 and expressed in Fig-3. The correlation between plant height and spike length observed was (0.65) highly significant and positive. The plant height exhibited a positive and highly significant correlation with the numbers of grain per spike (0.76) and grain yield per plant (0.62).

Peduncle Length

The observed findings mentioned that the peduncle length had positive and highly significant association with spikelets per spike (0.65). The association of peduncle length with spike length (0.65) was positive and highly significant. The positive and highly significant association was present in peduncle length and grain per spike with the value (0.69). The result revealed in this study that peduncle length exhibited positive association with grain yield per plant and was highly significant as mentioned in Table 5 and displayed in Fig. 3.

Spikelets per spike

The spikelets per spike exhibited the highly significant and positive correlation with peduncle length (0.65). The correlation observed between SPS and SL was (0.69) positive and highly significant. The SPS showed the highly significant and positive correlation with the trait number of grain per spike having value (0.63) as shown in Table 5 and expressed in Fig-3. The spikelets per spike associated positively and highly significant with grain yield per plant (0.65).

Spike Length

The association exhibited in the present study between spike length and peduncle length (0.59) was highly significant and positive. The spike length also had positive and highly significant association with spikelets per spike (0.69) and number of grain per spike (0.83). In this study, the spike length observed positive correlation with grain yield per plant and was highly significant as exhibited in Table 5 and expressed in Fig-3.

Number of grains per spike

The number of grains per spike mentioned the positive and highly significant association with peduncle length (0.69), spikelets per spike (0.63) and spike length (0.83) as showed in Table 5 and expressed in Fig-3. The number of grain per spike was highly significant and positively correlated with the grain yield per plant (0.70).

DISCUSSION

ANOVA

Analysis of variance revealed that all the traits like peduncle length, plant height, spike length, spikelet per spike, number of grains per spike and grain yield per plant had highly significant differences that showed variation among the studied attributes. According to analysis of variance, the plant height showed the highest value and grain yield per plant showed the lowest value in 33 genotypes. These results are in agreement with Nukasani *et al.*, (2013)

Mean Variability

The 3 genotypes performed best in plant height variables expressing the mean variability. As plant height increases, grain yield of wheat is also increased. Maximum plant height was attained by G10, G19 and G32 and minimum height was attained by the G3 and G15. Similar results were observed by Khan *et al.* (2010). Maximum mean variability for the peduncle length showed by the genotype G8, G10 and G19. The direct positive effect exhibited by peduncle length on grain yield (Ahmadizadeh *et al.*, 2011). There were also other traits like spikelet per spike, grain per spike and grain yield observed the best performing genotypes had high value of mean variability. In breeding program of wheat, the trait number of grains per spike was considered selection trait and contribute as an important yield component. High mean variability was directly associated with grain yield. Aycicek and Yildirim (2006) also reported the similar results.

Correlation study

In current study, plant height mentioned highly significant and positive association with peduncle length. When the plant height has positive correlation with peduncle length, the grains yield increases. Similar result was also observed by the researcher (Amiri *et al.*, 2013) which stated that plant height showed positive association with peduncle length. Spikelet per spike, spike length and number of grains per spike also exhibited positive and highly significant relation with plant height. Abinasa *et al.* (2011) also discussed the same results that PH had positively and highly significant with these traits that results in yield increases. In our study, grain yield showed positive correlation and highly significant with plant height. The plant height had direct association with grain yield of a plant. Due to increase in peduncle length, the increase in plant height occurred which direct increase the grain yield. Aydin *et al.* (2010) also stated in his report that PH had greatest direct linkage with GYP and plant height was the first priority.

Peduncle length was positively and highly significant correlated with spikelet per spike. These traits had positive direct effect on each other. There was a positive association present between the peduncle length and spike length, grain per spike and grain yield. All these traits were interlinked and positively correlated. Similar results were collaborated with the researcher (Khan *et al.*, 2010; Ali *et al.*, 2015). If the peduncle length increases, the grain yield per plant also increases.

Spikelets per spike had a positive and highly significant relation with peduncle length. SPS also had strong correlation with spike length (Mwadzingeni *et al.*, 2016). The trait spikelets per spike was also highly correlated and highly significant with other traits like NGS and GYP. Similar results were mentioned by the researchers (Ajmal *et al.*, 2013; Baloch *et al.*, 2021). High number of SPS increases the grains number per spike and grain yield as previously reported (Mecha *et al.*, 2017). SPS revealed positive highly significant association with SL and also had highly significant correlation with NGS (Mecha *et al.*, 2017).

Spike length exhibited the positive and highly significant association with the peduncle length, spikelets per spike, number of grains per spike and also had positive correlation with grain yield of plant. When the spike length of plant extended, the other traits like peduncle length, spikelets per spike, number of grains and grain yield per plant also increases with spike length. The current findings were also in agreement with (Slafer and Andrade, 1993; Ahmadizadeh *et al.*, 2011).

Positive correlation found between the number of grain per spike and peduncle length. NGS also positively correlated with other attributes like SPS, SL and with GYP. (Mollasadeghi *et al.* 2011) also stated that number of grains expressed positive direct effect on grain yield. Increases in number of grains per spike causes the increase in grain yield. Because both were positively correlated and highly significant. There was also a positive correlation present between the number of grains and spike length. The results were in agreement with those of Bano *et al.* (2012). Grain yield per plant mentioned positive relationship with spike length and grains per spike as reported by wheat breeders (Munir *et al.*, 2007).

REFERENCE

- Abinasa, M., A. Ayana and G. Bultosa (2011). Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. durum) genotypes. *African Journal of Agricultural Research*, 6: 3972-3979.
- Ahmadizadeh, M., A. Nori, H. Shahbazi, and S. Aharizad (2011). Correlated response of morpho-physiological traits of grain yield in durum wheat under normal irrigation and drought stress conditions in greenhouse. *African Journal of Biotechnology*, 10: 19771-19779.
- Ajmal, S. U., N. M. Minhas, A. Hamdani, A. Shakir, M. Zubair and Z. Ahmad (2013). Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*) germplasm. *Pak. J. Bot.*, 45: 1643-1648.
- Ali, M., M. Zulkiffal, J. Anwar, M. Hussain, J. Farooq and S. Khan (2015). Morpho-physiological diversity in advanced lines of bread wheat under drought conditions at post-anthesis stage. *Journal of Animal & Plant Sciences*, 25: 431-441.
- Amiri, R., S. Bahraminejad and S. Jalali-Honarmand (2013). Effect of terminal drought stress on grain yield and some morphological traits in 80 bread wheat genotypes. *International Journal of Agriculture and Crop Sciences*, 5:1145-1153.
- Aycicek, M. and T. Yildirim (2006). Path coefficient analysis of yield and yield components in bread wheat (*Triticum aestivum* L.) genotypes. *Pakistan Journal of Botany*, 38: 417-424.
- Aydin, N., C. Sermet, Z. Mut, H. O. Bayramoglu and H. Özcan (2010). Path analyses of yield and some agronomic and quality traits of bread wheat (*Triticum aestivum* L.) under different environments. *African Journal of Biotechnology*, 9: 5131-5134.
- Baloch, A. W., M. Baloch and I. Ahmed (2021). Association and path analysis in advance Pakistani bread wheat genotypes. *Pure and Applied Biology*, 3: 115-120.
- Bano, A., F. Ullah and A. Nosheen (2012). Role of abscisic acid and drought stress on the activities of antioxidant enzymes in wheat. *Plant, Soil and Environment*, 58: 181-185.
- Benesty, J., J. Chen, Y. Huang and I. Cohen (2009). *Pearson correlation coefficient. Pages 1-4 Noise reduction in speech processing*. Springer.
- Dixon, J. (2009). What causes civil wars? Integrating quantitative research findings. *International Studies Review*, 11: 707-735.
- Hasnain, Z., G. Abbas, A. Saeed, A. Shakeel, A. Muhammad and M. A. Rahim (2006). Combining ability for plant height and yield related traits in Wheat. *J. Agric. Res.*, 44: 167-173.
- Khan, A., F. Azam and A. Ali (2010). Relationship of morphological traits and grain yield in recombinant inbred wheat lines grown under drought conditions. *Pak. J. Bot.*, 42: 259-267.
- Maqbool, R., M. Sajjad, I. Khaliq, A. Rehman, A. Khan and S. Khan (2010). Morphological diversity and traits association in bread wheat (*Triticum aestivum* L.). *American-Eurasian J. Agric. & Environ. Sci.*, 8: 216-224.
- Mecha, B., S. Alamerew, A. Assefa, D. Dutamo and E. Assefa (2017). Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) genotypes. *Adv Plants Agric Res.*, 6: 128-136.
- Mollasadeghi, V., A. A. Imani, R. Shahryari and M. Khayatnezhad (2011). Correlation and path analysis of morphological traits in different wheat genotypes under end drought stress condition. *Middle-East journal of scientific research*, 7: 221-224.

- Munir, M., M. Chowdhry and T. Malik (2007). Correlation studies among yield and its components in bread wheat under drought conditions. *International Journal of Agriculture and Biology* (Pakistan), 9: 287-290.
- Mwadzingeni, L., H. Shimelis, S. Tesfay and T. J. Tsilo (2016). Screening of bread wheat genotypes for drought tolerance using phenotypic and proline analyses. *Frontiers in plant science*, 7: 1276. doi: 10.3389/fpls.2016.01276.
- Nukasani, V., N. R. Potdukhe, S. Bharad, S. Deshmukh and S. M. Shinde (2013). Genetic variability, correlation and path analysis in wheat. *Journal of Cereal Research*, 5: 48-51.
- Sadiq, M., K. A. Siddique, C. R. Arain and A. R. Azmi (1994). Wheat Breeding in a Water-stressed Environment, delineation of Drought Tolerance and Susceptibility. *Plant Breed*, 113: 36-46.
- Shewry, P. R. (2009). Wheat. *Journal of Experimental Botany*, 60: 1537-1557.
- Slafer, G. A. and F. H. Andrade (1993). Physiological attributes related to the generation of grain yield in bread wheat cultivars released at different eras. *Field Crops Research*, 31: 351-367.
- Steel, R. G. D. and J. H. Torrie (1960). *Principles and procedures of statistics*.
- Xhulaj, D. B. and R. Koto (2022). Estimation of genetic variability of autochthonous wheat (triticum aestivum l.) Genotypes using multivariate analysis. *Poljoprivreda i Sumarstvo*, 68: 131-143.

(Accepted for publication March 2023)