

GENETIC NATURE OF QUANTITATIVE TRAITS IN DURUM WHEAT

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Abstract

The aim of the study is to determine the genetic nature of quantitative traits associated with productivity in durum wheat and to make recommendations for optimizing the breeding process in the early segregating generations. A diallel cross without reciprocals, was carried out at the Field Crops Institute - Chirpan, with five modern durum wheat varieties. Six quantitative traits were studied. The inheritance of productivity tillering is governed by overdominance, and is possible selection of genotype by phenotype, but in the later segregating generations. For traits such as plant height and thousand kernel weight, inheritance is controlled by incomplete dominance, and genotype selection by phenotype is possible in F_2 . The inheritance of spike length is determined by overdominance, and is possible selection of genotype by phenotype in the later segregating generations. The spikelets number per spike is inherited through overdominance, and selection of genotype by phenotype is possible but should be carried out in the later segregating generations. The grains weight per spike is influenced by overdominance, and genotype selection by phenotype is possible after F_5 .

Key words: additive variance, dominance, narrow sense heritability, broad sense heritability, durum wheat.

INTRODUCTION

Durum wheat is a primary raw material for the production of various semolina-based products. It possesses excellent physical and technological qualities, making it ideal for producing high-quality pasta products. These pasta products have high nutritional value and are also incorporated into various healthy human diets. Breeding and improvement work on durum wheat and the development of new varieties require extensive knowledge in multiple disciplines related to crop science. Understanding the genetic nature and the factors influencing the inheritance of grain yield-related traits is crucial for the effectiveness of the breeding process. The use of diallel crosses by breeders is a systematic method for obtaining information about gene action and genetic nature. Knowledge of the nature and extent of gene action in the expression of quantitative traits is a key component in successfully developing an appropriate strategy for effective breeding programs. Diallel analysis offers an advantage in studying quantitative traits. Although it

requires relatively more work, it provides a highly effective assessment. Detailed information can be obtained from diallel crosses even in a single F_1 generation. Increasing our understanding of the genetic nature of quantitative traits allows for the optimization of the breeding process in durum wheat. This creates an opportunity for properly constructing the breeding strategy and accelerating the breeding process. The variation in gene action largely depends on the parental forms included in the study, the environment, and their interactions. To ensure the success of selection, it is necessary to deepen knowledge about the genetic nature of the most important quantitative traits related to productivity. The relevance of this issue is highlighted by the fact that in recent years, a wide range of new durum wheat varieties has been developed.

Numerous researchers have studied the mechanisms of grain yield inheritance and its components, elucidating the genetic nature of productivity and identifying possible types of gene action responsible for the expression of yield component traits. This indicates that identifying such patterns is extremely

important for determining the strategy in a breeding program. Dagustu (2008) reports that additive variance plays a primary role in the inheritance of the thousand kernel weight trait. On the other hand, Akbar et al. (2009) indicate that dominant parameters have a greater role in the inheritance of this trait. Gami et al. (2010) observe a predominant influence of overdominance on traits such as plant height, thousand kernel weight, productivity tillering and spikelets number per spike. They suggest the action of at least one group of genes showing dominance, responsible for the manifestation of yield components. Ahmad et al. (2011) examined traits including productivity tillering and thousand kernel weight. They found confirmed additive variance and dominant parameters for these traits under early and normal sowing conditions, while only additive variance was significant under late sowing. Vanda and Houshmand (2011) demonstrate a predominance of non-additive (dominant) over additive gene effects for the traits included in their study. Farooq et al. (2011) tracked traits such as spike length, spikelets number per spike, and the number of grains per spike. Additive variance was significant, showing a greater role of additive gene effects for spike length. However, higher dominant parameters were found for the spikelets number per spike, indicating the predominance of non-additive gene effects. Nazeer et al. (2011) reveal the genetic nature of traits including spike length, spikelets number per spike, grains number per spike and grains weight per spike. Additive variance was demonstrated for all traits except grains weight per spike, with higher dominant parameters noted for spike length. Singh and Sharma (2012) conducted experiments to study the genetic components of grain yield-related traits, confirming both additive variance and dominant parameters. Kutlu & Olgun (2015) performed diallel analysis without reciprocal crosses for traits such as plant height, spike length, spikelets number per spike, and grains weight per spike. They found significant values for both additive variance and dominant parameters, suggesting both types are responsible for inheritance. Sadeghzadeh-Ahari et al. (2015) studied a diallel scheme with 6x6 parents of durum wheat, finding that additive

variance played a greater role for spike length and productivity tillering traits. Fellahi et al. (2015) explored inheritance mechanisms using diallel analysis for productivity elements, analyzing traits like thousand kernel weight and spikelets number per spike in F₁ and F₂ generations. They reported that under their study conditions, the inheritance of traits involved 2 to 5 genes showing dominance. Ahmad et al. (2017) suggested that traits like plant height, productivity tillering, spike length and spikelets number per spike are primarily governed by non-additive gene effects (dominant parameters). Heritability coefficients in durum wheat are crucial for determining proper selection. High broad-sense coefficients indicate the possibility of genotype selection based on phenotype, while high narrow-sense heritability suggests that selection can begin in earlier segregating generations. Amin (2013) examined the genetic behavior of certain agronomic traits in durum wheat crosses under normal and heat stress conditions, finding moderate broad and narrow sense heritability coefficients for productivity tillering and thousand kernel weight. In a diallel cross with durum wheat, Hannachi et al. (2013) identified high narrow sense heritability for traits like plant height and thousand kernel weight, a moderate coefficient for the grains number per spike, and a low one for productivity tillering. For broad sense heritability in durum wheat, Basciftci et al. (2013) reported high values for traits including spike length, spikelets number per spike, grains number per spike, grains weight per spike and thousand kernel weight. Hannachi et al. (2017) found high broad and narrow sense heritability coefficients for plant height and moderate coefficients for productivity tillering, grains number per spike and thousand kernel weight. From the reviewed literature, it can be concluded that different assessments of the genetic nature of productivity-related traits in durum wheat are observed depending on the genetic material used and the diverse experimental conditions. Therefore, conducting such an in-depth study under local conditions with modern durum wheat varieties is highly necessary. The aim of this study is to establish the genetic nature of quantitative traits related to productivity and optimize the breeding process

in durum wheat. To create an opportunity for the correct construction of the breeding strategy and acceleration of the breeding process.

MATERIALS AND METHODS

In a diallel cross, five modern durum wheat varieties were used as parents. The varieties Victoria, Predel, Deni, and Progress were selected from the durum wheat breeding program of the Field Crops Institute - Chirpan, along with the foreign variety Superdur. The Victoria and Predel varieties were developed through combining breeding methods, while Deni and Progress were obtained through experimental mutagenesis. The Superdur variety originates from Austria. These varieties are genetically and phenotypically diverse, meeting the requirements for the diallel crossing scheme. The diallel cross was performed by intercrossing the five described varieties without reciprocals. The crossing was carried out under field conditions at the beginning of heading time, with handmade emasculation and pollination. Each year, 30 plants per combination were handmade emasculated and pollinated.

The experiment was set up using a randomized block design with three replications under field conditions. The parents and F_1 hybrids were sown handmade in two rows, while the F_2 hybrids were sown in five row. The length of row was two meters, with a row spacing of 20 cm and 5 cm within the row. At full maturity, twenty plants from each parent, F_1 , and F_2 generations were randomly selected. The experiment was conducted at the breeding experimental field of the Field Crops Institute - Chirpan over three consecutive years (2014-2016). The standard agronomic practices for durum wheat cultivation in the region were applied. The soil type is Eutric Vertisols (according to FAO classification). The preceding crop was green pea. Nitrogen fertilization was performed once in February with a rate of 10 kg/da active substance nitrogen. Weed control included herbicide application with a combination of two herbicides. No pesticides were used to control diseases and pests. During the three years of the study, temperatures were higher than the long-term average. The first and second years had normal precipitation during the growing season, while the third year had

20% less rainfall compared to the long-term average. The following traits were studied: Plant height (cm): Measured from the soil surface to the top of the spike (excluding awns) on the main stem. Productivity tillering (number): Counted the fertile spikes per plant. Spike length (cm): Measured on the main stem from the bottom spike to the top of the uppermost spikelet. Spikelets number per spike (number): Counted the spikelets in the main spike. Grains weight per spike (g): Weighed all grains from the main stem spike after handmade threshing. Thousand kernel weight (g): Weighed the mass of 1000 grains.

Statistical analysis was performed according to Hayman (1954; 1957), Jinks (1954) & Mather (1967) using the statistical software developed by Aksel & Johnson (1962). Heritability coefficients were calculated following the formulas of Mather & Jinks (1982). The parameters and indicators are denoted as follows: D - Component of genetic variance due to additive effect of genes (additive variance), H_1 - Components of genetic variance due to dominance effect, H_2 - Proportion of dominance variance due to the positive and negative effects of the genes in the parents (dominance parameters), h_2 - Dominance effects, as algebraic sum over all the loci in heterozygous phase in all the crosses, F - Covariance of additive and non-additive effects in a single array. It may be positive or negative, $(H_1/D)^{1/2}$ - Mean degree of dominance, $H_2/4H_1$ - Proportion of genes with positive and negative effects in the parents, K_d/K_r - Proportion of dominant and recessive genes in the parents, h_2/H_2 - number of groups of genes with positive and negative effects in the parents.

RESULTS AND DISCUSSIONS

An analysis of the variance (not shown) was conducted, revealing significant differences between the tested genotypes for all traits included in the study. These differences were observed in both F_1 and F_2 generations. The significant differences between genotypes provide a basis for conducting a parametric genetic analysis and determining the parameters and indicators related to the genetic nature and expression of the studied traits. Table 1 presents the genetic parameters and

indicators according to Hayman (1954) & Jinks (1954) from the diallel cross for F₁ and F₂.

The additive variance (D), attributed to the additive action of genes, is significant for productivity tillering and grains weight per spike in F₂ and significant in both F₁ and F₂ generations for all other traits. It is nonsignificant for productivity tillering and grains weight in F₁. This indicates the substantial role of the additive gene action in controlling most productivity-related traits. In the F₂ generation, the traits productivity tillering and grains weight per spike show significant additive variance (D), suggesting that additivity in these traits increases in subsequent generations. Numerous authors report significant additive variance (Zanke et al., 2014; Shehzad et al., 2015; Sadeghzadeh-Ahari et al., 2015; Kutlu & Olgun, 2015).

Table 1 also includes the dominant parameters (H1) and (H2), reflecting the variation due to the dominant gene action. The dominant parameters are significant for all traits in both generations. Our results align with those obtained by Nazeer et al., 2011; Ahmad et al., 2011; Singh & Sharma, 2012. This indicates that dominance plays a major role in determining all traits included in this study. The dominance parameters are higher than the additive variance (D) in both generations for traits such as productivity tillering, spikelets

number per spike, and grains weight per spike, indicating the greater importance of dominance in the expression of these traits. Authors such as Vanda & Houshmand (2011) also report higher dominance parameters than additive variance for these traits. For the remaining traits, the additive variance is greater than the dominance parameters, suggesting a greater role of additivity in trait expression. This corresponds with results obtained by Kutlu & Olgun (2015), Sadeghzadeh-Ahari et al. (2015). For all traits and in both generations, (H1) is greater than (H2). This suggests that the positive and negative alleles at loci showing dominance in the parents are not in equal proportions. The parametric component analysis demonstrates the significance of both additive variance and dominant parameters. This implies that both dominance and additivity are crucial for the inheritance of the studied traits. Breeding programs should include a system that considers both additive variance and dominance parameters to enhance durum wheat productivity.

The parameter (F) is related to the direction of dominance (Table 1). It indicates whether there are more dominant or recessive genes. For traits such as productivity tillering in F₂, plant height, and thousand kernel weight in both generations, and spike length in F₁, (F) is significant and positive.

Table 1. Genetic parameters for 6 quantitative traits from diallel crosses

Traits		D	F	H1	H2	h2
Productivity tillering	F ₁	0.041 ± 0.12	-0.18 ± 0.31	2.46 ± 0.33	1.94 ± 0.30	1.61 ± 0.20
	F ₂	0.129 ± 0.121	0.304 ± 0.303	1.21 ± 0.32	0.81 ± 0.29	0.50 ± 0.20
Plant height	F ₁	87.14 ± 3.04	17.64 ± 7.59	39.16 ± 8.21	25.79 ± 7.44	3.41 ± 5.09
	F ₂	85.09 ± 2.51	28.85 ± 6.29	57.73 ± 6.80	43.57 ± 6.16	70.47 ± 4.16
Spike length	F ₁	0.87 ± 0.0067	0.91 ± 0.016	0.31 ± 0.018	0.29 ± 0.016	0.71 ± 0.011
	F ₂	0.80 ± 0.0078	-0.07 ± 0.019	0.71 ± 0.021	0.068 ± 0.01	0.004 ± 0.01
Spikelets number per spike	F ₁	0.30 ± 0.094	-0.089 ± 0.23	1.56 ± 0.25	0.98 ± 0.23	0.35 ± 0.15
	F ₂	0.35 ± 0.08	0.079 ± 0.20	0.74 ± 0.22	0.46 ± 0.20	0.023 ± 0.13
Grains weight per spike	F ₁	0.083 ± 0.086	0.020 ± 0.021	0.19 ± 0.023	0.18 ± 0.02	0.57 ± 0.014
	F ₂	0.034 ± 0.013	0.025 ± 0.028	0.12 ± 0.03	0.10 ± 0.02	0.18 ± 0.018
Thousand kernel weight	F ₁	41.96 ± 1.48	28.76 ± 3.70	6.96 ± 4.00	3.66 ± 3.63	-1.11 ± 2.45
	F ₂	23.21 ± 1.61	4.05 ± 4.02	16.53 ± 4.35	13.98 ± 3.94	22.2 ± 2.66

* - $P \leq 0.05$; D - Component of genetic variance due to additive effect of genes, H1 - Components of genetic variance due to dominance effect, H2 - Proportion of dominance variance due to the positive and negative effects of the genes in the parents, h2 - Dominance effects, as the algebraic sum over all the loci in the heterozygous phase in all the crosses, F - Covariance of additive and non-additive effects in a single array (can be positive or negative).

This indicates that the positive and negative genes are unevenly distributed. Other traits in the study show variability in significance and changes in direction, likely due to

environmental conditions. The overall measure of dominance is determined by the indicator $(H1/D)^{0.5}$. The degree of dominance $(H1/D)^{0.5}$ (Table 2) reveals that overdominance plays a

primary role in the inheritance of traits such as productivity tillering, spikelets number per spike and grains weight per spike. For traits like plant height and thousand kernel weight, incomplete dominance predominantly influences inheritance. The spike length trait shows incomplete dominance in F_1 but overdominance in F_2 . Our findings are consistent with those of other authors (Menon & Sharma, 1997; Gami et al., 2010; Sadeghzadeh-Ahari et al., 2015).

The parameter F is confirmed by the values of the indicator $H_2/4H_1$, which provides an assessment of the average purity of positive and negative alleles at loci showing dominance (Table 2). The values of the indicator ($H_2/4H_1$) are close to 0.25 for traits such as spike length in F_1 , grains weight per spike in both generations, and thousand kernel weight in F_2 , confirming the presence of symmetry between dominant and recessive alleles. For the remaining traits, there is asymmetry between dominant and recessive alleles.

The ratio of dominant to recessive genes determining the trait (Kd/Kr) (Table 2) indicates varying dominance across generations. For most traits and generations, dominant genes predominate. For productivity tillering and spikelets number per spike in F_1 and spike length in F_2 , values are below one, with recessive genes prevailing. For the other traits, dominant genes are predominant. The indicator (h_2/H_2) suggests the involvement of two major genes determining productivity tillering, one to three genes determining plant height, one - two genes for spike length, two to three genes for spikelets number per spike, one gene for grains weight per spike, and one to two genes for thousand kernel weight. These genes are often grouped according to the polygenic nature of the studied traits. The control of the traits mainly involves one to three major genes or gene groups showing dominance under environmental conditions.

Table 2. Genetic indicators for 6 quantitative traits from diallel crosses

Traits		$(H_1/D)^{1/2}$	$H_2/4H_1$	Kd/Kr	h_2/H_2
Productivity tillering	F_1	7.74	0.19	0.55	1.20
	F_2	3.06	0.16	2.24	1.62
Plant height	F_1	0.66	0.16	1.35	2.56
	F_2	0.81	0.18	1.51	0.61
Spike length	F_1	0.59	0.23	1.19	0.40
	F_2	2.73	0.002	0.72	1.7
Spikelets number per spike	F_1	2.28	0.15	0.87	2.8
	F_2	1.45	0.15	1.16	2.0
Grains weight per spike	F_1	1.5	0.23	1.66	0.31
	F_2	1.87	0.20	1.47	0.55
Thousand kernel weight	F_1	0.4	0.09	11.6	2.39
	F_2	0.84	0.21	1.23	0.62

* - $P \leq 0.05$; $(H_1/D)^{1/2}$ - Mean degree of dominance, $H_2/4H_1$ - Proportion of genes with positive and negative effects in the parents, Kd/Kr - Proportion of dominant and recessive genes in the parents, h_2/H_2 - number of groups of genes with positive and negative effects in the parents, H_2 - broad sense heritability coefficient and h_2 - narrow sense heritability coefficient.

Heritability coefficients are directly related to selection effects and breeding efficiency. The broad sense heritability coefficients H_2 are high for all traits included in this study in both generations (Table 3). This suggests that genotype selection by phenotype is feasible. The narrow-sense heritability coefficients provide the most accurate estimate of additive (breeding-useful) variance. For traits like plant

height and thousand kernel weight, effective selection is possible in early segregating generations, while for all other traits, selection should start in later segregating generations (F_5 - F_6). The results for heritability coefficients match those obtained by a number of authors (Gami et al., 2010; Yao et al., 2011; Khodadadi et al., 2012; Fellahi et al., 2015; Hannachi et al., 2017).

Table 3. Broad and narrow sense heritability coefficients in F₁ and F₂ for 6 quantitative traits from diallel crosses

Traits	Heritability coefficients F ₁		Heritability coefficients F ₂	
	H2 (broad sense)	h2 (narrow sense)	H2 (broad sense)	h2 (narrow sense)
Productivity tillering	0.95	0.41	0.92	0.32
Plant height	0.97	0.84	0.97	0.74
Spike length	0.76	0.12	0.99	0.98
Spikelets number per spike	0.86	0.57	0.80	0.56
Grains weight per spike	0.89	0.39	0.90	0.33
Thousand kernel weight	0.66	0.61	0.94	0.71

The obtained results indicate that the traits are suitable for individual selection by classical breeding methods. Therefore, in most cases, breeders can count on faster and higher results in improving these traits, with the exception of grain weight per spike and productivity tillering. The results of the diallel analysis presented in this way clarify the possibilities for increasing grain productivity by improving the individual traits related to it. Hannachi et al. (2017) reach such a conclusion. The unification and differentiation of traits with high heritability and genetic independence is most often associated with increasing productivity. Selection by a single trait can increase yield, but a more significant increase would be obtained by simultaneously improving its elements.

CONCLUSIONS

Additive variance and dominant parameters are important for all studied traits. A system incorporating both variances is needed to achieve maximum results. Overdominance plays a key role in the inheritance of traits such as productivity tillering, spike length, spikelets number per spike and grains weight per spike. For traits like plant height and thousand kernel weight, incomplete dominance is more significant. Broad sense heritability coefficients are high for all traits, enabling genotype selection by phenotype. Effective selection for plant height and thousand kernel weight is possible in early generations, while for other traits, selection should begin in later segregating generations (F₅-F₆). Individual selection is recommended for improving all studied traits.

REFERENCES

- Ahmad, E., Akhtar, M., Badoni, S., & Jaiswal, J. P. (2017). Combining ability studies for seed yield related attributes and quality parameters in bread wheat (*Triticum aestivum* L.). *Journal of Genetics, Genomics & Plant Breeding*, 1(1), 21–27.
- Ahmad, F., Khan, S., Ahmad, S. Q., Khan, H., Khan, A., & Muhammad, F. (2011). Genetic analysis of some quantitative traits in bread wheat across environments. *African Journal of Agricultural Research*, 6(3), 686–692.
- Akbar, M., Anwar, J., Hussain, M., Qureshi, M. H., & Khan, S. (2009). Line x tester analysis in bread wheat (*Triticum aestivum* L.). *Journal of Agricultural Research*, 47(1), 21–30.
- Aksel, R., & Johnson, L. P. V. (1962). Analysis Of a dialled cross. A Worked out example. *Adv.Front.Plant.Sci.*, 2, 37–64.
- Amin, L. A. (2013). Genetic Behaviour of Some Agronomic Traits in Two Durum Wheat Crosses under Heat Stress. *Alexandria Journal of Agricultural Research*, 58(1), 53–66.
- Başçıftçi, Z. B., Kinaci, G., & Kinaci, E. (2013). Genetic variability and heritability association with spike yield and related characters in durum wheat (*Triticum durum* Desf.). *Journal of Food, Agriculture & Environment*, 11(3 & 4), 781–784.
- Dagustu, N. (2008). Genetic analysis of grain yield per spike and some agronomic traits in diallel crosses of bread wheat (*Triticum aestivum* L.). *Turkish Journal of Agriculture and Forestry*, 32, 249–258.
- Farooq, J., Khaliq, I., Ali, M. A., Kashif, M., Rehman, A., Naveed, M., Ali, Q., Nazeer, W., & Farooq, A. (2011). Inheritance pattern of yield attributes in spring wheat at grain filling stage under different temperature regimes. *Australian Journal of Crop Science*, 5(13), 1745–1753.
- Fellahi, Z. E. A., Hannachi, A., Bouzerzour, H., & Benbelkacem, A. (2015). Inheritance pattern of metric characters affecting grain yield in two bread wheat (*Triticum aestivum* L.) crosses under rainfed conditions. *Jordan Journal of Biological Sciences*, 8 (5), 175–181.

- Gami, R. A., Tank, C. J., Thakor, D. M., Burungale, S. V., & Patel, C. G. (2010). Estimation of components of genetic variance and graphical analysis in durumwheat (*Triticum durum* Desf.) under timely and late sown conditions. *International Journal of Plant Sciences*, 5(2), 642–646.
- Hannachi, A., Fellahi, Z., Rabti, A., Guendouz, A., & Bouzerzour, H. (2017). Combining ability and gene action estimates for some yield attributes in durum wheat (*Triticum turgidum* L. var. *durum*). *Journal of Fundamental and Applied Sciences*, 9(3), 1519–1534.
- Hannachi, A., Fellahi, Z. E. A., Bouzerzour, H., & Boutakrabi, A. (2013). Diallel-cross analysis of grain yield and stress tolerance-related traits under semi-arid conditions in Durum wheat (*Triticum durum* Desf.). *Electronic Journal of Plant Breeding*, 4(1), 1027–1033.
- Hayman, B. I. (1954). The theory and analysis of diallel crosses. *Genetics*, 39, 789–809.
- Hayman, B. I. (1957). Inheritance, heterosis and diallel crosses. *Genetics*, 42, 330–355.
- Jinks, J. L. (1954). The analysis of continuous variation in diallel cross of *Nicotiana rustica* varieties. *Genetics*, 39, 767–788.
- Khodadadi, E., Aharizad, S., Sabzi, M., Shahbazi, H., & Khodadadi, E. (2012). Combining ability analysis of bread quality in wheat. *Annals of Biological Research*, 3(5), 2464–2468.
- Kutlu, I., & Olgun, M. (2015). Determination of genetic parameters for yield components in bread wheat. *International Journal of Biosciences*, 6(12), 61–70.
- Mather, K. (1967). Complementary and duplicate gene interactions in biometrical genetics. *Heredity*, 22, 97–103.
- Mather, K., & Jinks, J. L. (1982). Biometrical genetics, study of continuous variation, third ed., *Chapman and Hall, London, New York*. 396-403.
- Menon, U., & Sharma, S. N. (1997). Genetics of yield determining factors in spring wheat over environments. *Indian Journal of Genetics and Plant Breeding*, 57(3), 301–306.
- Nazeer, W., Farooq, J., Tauseef, M., Ahmed, S., Khan, M. A., Mahmood, K., Hussain, A., Iqbal, M., & Nasrullah, H. M. (2011). Diallel analysis to study the genetic makeup of spike and yield contributing traits in wheat (*Triticum aestivum* L.). *African Journal of Biotechnology*, 10(63), 13735–13743.
- Sadeghzadeh-Ahari, D., Sharifi, P., Karimizadeh, R., & Mohammadi, M. (2015). Estimation of genetic parameters of morphological traits in rainfed Durum wheat (*Triticum turgidum* L.) using Diallel method. *Plant Genetic Researches*, 2(1), 45–62.
- Shehzad, M., Hussain, S. B., Qureshi, M. K., Akbar, M., Javed, M., Imran, H. M., & Manzoor, S. A. (2015). Diallel cross analysis of plesiomorphic traits in *Triticum aestivum* L. genotypes. *Genetics and Molecular Research*, 14(4), 13485–13495.
- Singh, M. K., & Sharma, P. K. (2012). Genetic components analysis for heat tolerance and yield component traits in bread wheat. *Crop Improv.*, 39(2), 189–195.
- Vanda, M., & Houshmand, S. (2011). Estimation of genetic structure of grain yield and related traits in durum wheat using diallel crossing. *Iranian Journal of Crop Sciences*, 13(1), 206–218. (In Persian).
- Yao, J. B., Ma, H. X., Ren, L. J., Zhang, P. P., Yang, X. M., Yao, G. C., Zhang, P., & Zhou, M. P. (2011). Genetic analysis of plant height and its components in diallel crosses of bread wheat (*Triticum aestivum* L.). *Australian Journal of Crop Science*, 5(11), 1408–1418.
- Zanke, C. D., Ling, J., & Plieske, J. (2014). Whole Genome Association Mapping of Plant Height in Winter Wheat (*Triticum aestivum* L.). *PLOS One*, 11, 1–16.