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Research Article

EVALUATION OF AGRO-MORPHOGICAL CHARACTERISTICS IN BREAD WHEAT GENOTYPES AND FULL DIALLEL HYBRIDS IN THE EARLY SEEDLING STAGE

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ABSTRACT. In bread wheat (*Triticum aestivum* L.), optimal agronomic practices and variety performance are crucial for achieving high grain yields. Furthermore, the interaction between physiological and morphological traits in successive phenological periods in wheat determines grain yield per unit area. Several statistical analysis techniques provide the opportunity to identify promising genotypes among the genotypes examined and to evaluate the correlation between the traits together. This contributes to breeders and, therefore, to the sustainability of food production and food security. Present research was conducted to identify important breeding traits in winter bread wheat and to demonstrate the performance of genotypes obtained from hybridization using different statistical and analysis methods (Biplot and scatter plot analysis, PCA). In this study, a total of 12 [4x(4-1)] hybrid combinations obtained from full diallel crosses of four winter bread wheat genotypes (Bayraktar 2000, Sönmez 2001, KRL-213, and KRL-210) were grown under field conditions according to a randomized plot design by three replications. The experiment was terminated when the plants reached the 3-leaf stage (initiation of tillering) to examine some important selection parameters in the early seedling stage. According to the results of the variance analyses, the differences between the genotypes in shoot length, tiller plant^{-1}, leaf plant^{-1}, and shoot dry weight were determined to be statistically significant. According to the findings of the present study, it may be concluded that the main parameters related to biomass are decisive in revealing genetic variation. Additionally, results presented that a wide range of genetic variation was observed between F_1 hybrids and their parents, and it was determined that leaf number, shoot length, and dry weight parameters were the key factors in genotype selection. It has been concluded that the genotypes highlighted in the research findings can be used in various hybridization studies to improve the desired characteristics in terms of sustainability, can be recommended to increase the yield and quality-related parameters that are prominent for bread wheat, and can be evaluated in breeding studies to develop new varieties.

Keywords: *agronomic variables, breeding, genetic diversity, seedling traits, sustainable agriculture*

INTRODUCTION

Wheat, one of the three main cereals worldwide, is a vital crop, with a total annual production quantity of 730 million tons. It's quite high, and a consistent yield makes it crucial for the sustainability of food security and food supply, and the demand for wheat continues to increase annually. Wheat ranks first among cool-season cereals globally in terms of both cultivation and production. Assuming that the global population and food consumption continue to grow, it is anticipated that wheat will continue to be a strategic crop in the coming years. When evaluating the global wheat consumption, it is noted that 95.8% of the wheat used for human food is bread wheat, while the remaining 4.2% is durum wheat [1]. Wheat is used to produce products such as bread, pasta, bulgur, noodles, and more. These wheat-derived products constitute a significant portion of the human diet. An ever-growing population will increase demand for wheat, with yields increasing by a ratio of 60% by 2050, representing a mean annual increase of 2% ratio [2]. In order to increase yield for the field on a plant breeding basis, considering heterosis and heterobeltiosis rates together greatly increases the ability of breeders to make the right choices [3]. The superiority of hybrids over their parents in yield and resistance is attributed to the heterotic effects observed in the F1 generation. It was stated [4] that intermediate parental and superior parental heterosis values are critical in determining superior hybrid varieties. The main reasons for yield losses in plant production include climate change, drought, floods, inadequate rainfall (lack of soil moisture), inappropriate seed sowing time, and ineffective use of fertilizer and irrigation [5,6,7]. Among these factors, drought stress is a main abiotic-based stress factor that limits seed yield per unit area of wheat, and it is generally produced in dry agricultural lands, causing various serious problems in many regions of the world [8,9]. Some studies on the environmental impacts caused by crop production have reported that irrigation is the most energy-consuming activity in agricultural arid regions and therefore causes significant greenhouse gas emissions [10,11]. However, when the interactive effects of the factors affecting stability in agricultural production are taken into account, as well as their individual effects, the importance of sustainability becomes clear.

Statistical analyses, such as diallel analysis and principal component analysis, are performed using data on seed yield and other agricultural characteristics. The relationship between the examined components is then visualized using the GGE biplot technique. Whether caused by abiotic stress factors like drought or any biotic stress factors, intensive plant breeding efforts are essential. Furthermore, while some regions worldwide have a high number of registered varieties, mitigating the effects of changing yield-limiting factors through breeding is crucial for sustainability. Identifying different combinations of genotypes frequently preferred by farmers, revealing components related to quality as well as grain yield with high adaptability, is crucial for the foundations of agricultural sustainability [4,11]. This study was purposed to demonstrate the various performances of commonly preferred wheat genotypes by crossbreeding them and to determine their potential for future research. For this purpose, some yield-related parameters were examined in winter bread wheat genotypes obtained through full diallel crossbreeding, and the results were interpreted using various statistical analysis programs.

MATERIALS AND METHODS

Present research is based on the first author's PhD thesis and was carried out in the trial field of the Field Crops Department - Faculty of Agriculture - Selcuk University for two vegetation years between 2023-2024 and 2024-2025 growing seasons. In the first year of the experiment, four bread wheat genotypes, namely Bayraktar 2000, Sönmez 2001, KRL-213, and KRL-210, were used for hybridization. Table 1 presents the characteristics of the bread wheat genotypes that are subjected to diallel combination in the research. The field experiment was carried out using a total of 12 [4x (4-1)] hybrid combinations derived from full diallel crosses among the 4 mentioned genotypes and 4 parent genotypes, using a randomized plot design with 3 replications. Pots were selected with a volume of 3 liters, and the soil mixture consisted of 65% peat, 25% perlite, and 10% sand. Because the soil material was dry, the field capacity of the mixture in the pots was calculated before planting, and water was applied accordingly to ensure that the entire soil mixture reached field capacity. Sowing of 3 healthy seeds was done by hand at a depth of approximately 3 cm per pot. For fertilizing, the DAP (Content: 18% N and 46% P2O5) fertilizer was applied at a rate of 150 kg ha-1 along with the seed planting. The experiment was terminated when the plants had three leaves (the beginning of tillering) to examine certain parameters during the early seedling period.

***Table 1.** Combinations obtained by diallel hybridization in bread wheat genotypes.*

Genotypes	**Bayraktar 2000**	**Sönmez 2001**	**KRL 210**	**KRL 213**
Bayraktar 2000	-	X	X	X
Sönmez 2001	X	-	X	X
KRL 210	X	X	-	X
KRL 213	X	X	X	-

In the research, traits such as shoot length, tiller number, leaf number, weight of fresh shoot, and dry weight of shoot were studied in order to determine the agro-morphological characteristics of fully diallel hybrid genotypes and parents in the early seedling period. Variance analysis of the values obtained from the study was performed in the JMP-17 package program, and Biplot, scatter plot, and PCA (Principal Component Analysis) analyses were performed in RStudio.

RESULTS AND DISCUSSION

According to the scope of the study, variance analysis (Table 2) was conducted for F_1 hybrids and parent genotypes for shoot length, tiller count, leaf count, fresh weight, and dry weight traits. The results of the variance analysis revealed statistically significant differences among genotypes for shoot length, tiller count, leaf count, and dry weight traits. However, no significant differences were found for fresh weight. These results suggest that there is a wide variation among genotypes for the traits studied, and that biomass-related parameters, in particular, are more decisive in reflecting genetic differences.

Table 2 presents the mean values and grouping tests for genotypes determined to have statistically significant differences in variance analysis. It is observed that the variation between genotypes in terms of shoot length is statistically significant at the 1% level. The highest value for the shoot length was obtained from the genotype Sönmez 2001 x KRL 210 hybrid combination (15.33). Among the parent genotypes, KRL-210 (14.5) had the highest shoot length. This result indicates that there is significant variation among genotypes in shoot length and that some hybrids stand out. This situation revealed that some F_1 hybrids can exhibit superior performance by exceeding the mean of their parents.

***Table 2.** Mean values of the measured traits during the early seedling stage and grouping of genotypes based on Student's t-test results.*

	Genotypes	**Shoot length (cm)**	**Number of tillers (piece)**	**Number of leaves (piece)**	**Fresh shoot weight (g)**	**Dry shoot weight (g)**
Parents	**KRL 213**	11.0 b-d**	2.33 a-c**	12.00 ab**	0.94	0.18 ab**
	KRL 210	14.5 ab	2.33 a-c	10.00 bc	1.08	0.22 a
	Bayraktar 2000	10.23 cd	3.33 a	14.00 a	0.77	0.17 ab
	Sönmez 2001	12.23a-c	2.00 b-d	9.00 bc	0.70	0.08 c-e
	Mean of Parents	*11.99*	*2.50*	*11.25*	*0.87*	*0.16*
Hybrids	**KRL 213 x KRL 210**	14.50 ab	2.00 b-d	7.00 cd	0.65	0.16 a-c
	KRL 213 x Bayraktar 2000	9.73 cd	2.67 ab	6.67 cd	0.37	0.06 de
	KRL 213 x Sönmez 2001	7.67 d	0.67 e	6.67 cd	0.26	0.03 e

	KRL 210 x KRL 213	14.40 ab	2.00 b-d	7.67 cd	0.67	0.16 a-c
	KRL 210 x Bayraktar 2000	9.23 cd	1.33 c-e	6.33 cd	0.47	0.08 c-e
	KRL 210 x Sönmez 2001	11.67 a-c	2.00 b-d	7.00 cd	0.49	0.10 b-e
	Bayraktar 2000 x KRL 213	9.73 cd	2.00 b-d	8.00 cd	0.29	0.03 e
	Bayraktar 2000 x KRL 210	10.17 cd	2.00 b-d	8.33 b-d	0.53	0.08 c-e
	Bayraktar 2000 x Sönmez 2001	10.17 cd	1.33 c-e	6.00 cd	0.46	0.08 c-e
	Sönmez 2001 x KRL 213	11.83 a-c	2.00 b-d	7.67 cd	0.66	0.10 b-e
	Sönmez 2001 x KRL 210	15.33 a	1.00 de	6.00 cd	0.58	0.14 a-d
	Sönmez 2001 x Bayraktar 2000	12.50 a-c	2.00 b-d	7.33 cd	0.51	0.14 a-d
	Mean of Hybrids	*11.41*	*1.75*	*7.06*	*0.50*	*0.10*
LSD	**(% 1)****	4.49	1.48	4.58	0.61	0.10
	(% 5)*	3.34	1.10	3.40	0.45	0.07

**: 1% statistically significance level, *: 5% statistically significance level

It is reported in the literature that shoot length is an important parameter closely related to morphological development and yield, and is used as a reliable criterion, especially for young plant development [12, 13]. Given this knowledge, the genotypes highlighted in the study can be used in selections for shoot development and biomass increase in breeding programs. Related research has shown that shoot length in winter wheat ranged from 38.00 to 85.62 cm2, depending on plant density [14], which is a wide range. As is well known, cultural practices have significant effects on yield and yield components and have been reported to consistently increase many traits, including straw yield and root-shoot biomass, as well as root length [15]. On the other hand, abiotic stress factors elicit significant plant responses. For example, in one study, salt-based stress markedly decreased shoot length in wheat genotypes. Foliar applications did not significantly affect this parameter under saline conditions. A similar response was observed for genotype differences [16].

Table 2 shows that there are statistically significant differences at the 1% level between genotypes in terms of the number of tillers. The highest tiller number was found in the Bayraktar-2000 genotype among the parent genotypes, and among the hybrid genotypes, the KRL 213 x Bayraktar 2000 (2.67) hybrid combination had the highest tiller number. Although there were differences between genotypes in terms of tiller numbers, the genotypes with the highest values stood out clearly. When the literature on the subject was reviewed, it was emphasized that the effective qualified tiller number in wheat plants is a 1/3 basic component of the unit area yield of wheat plants, and that having the optimum tiller number is essential for obtaining higher seed yields from wheat plants [17]. In a uniform growing environment, the growth characteristics of wheat plants show lower variability, and no statistically significant differences occur in traits such as tiller number, plant height, pigment, and biomass [18]. It has been stated that the interaction between sulfuric acid levels and salinity levels has complex effects on tillering in wheat plants [19]. Additionally, tillering status is an important agronomic characteristic in winter wheat plants and enables the development of extra shoots that contribute significantly to the seed yield of plants [20].

The difference in leaf number among genotypes was found to be statistically significant at the 1% level (Table 2). The Bayraktar 2000 genotype had the highest leaf number, followed by KRL-213, one of the parent genotypes. Hybrid genotypes had lower leaf numbers than all parent genotypes. Some genotypes showed significant superiority in leaf number. This trait, particularly because of its link to biomass, can be used as a selection criterion. Leaf number plays a critical role in plant development because it is directly related to photosynthetic capacity. Indeed, a related report [21] found that genotypes with higher leaf numbers generally exhibit higher photosynthetic efficiency and increased yield potential. In wheat treated [22] with LED light, leaves developed mostly in the first 30 days, reaching a daily leaf count of 0.24. On the other hand, although differences in leaf growth rate and duration occurred between treatments, the total number of leaves per plant remained constant during the flowering period, reaching a value of eight leaves per main stem. Wheat plants had leaf numbers per plant between 7.667 and 13.170 under several irrigation levels [23]. Another study [24] reported a positive correlation (r = 0.56) between the number of leaves and the number of median roots in wheat. According to another report [25], the number of leaves ranged between 2.60 and 4.70, depending on chemical and chemical + biological management techniques.

In the present research, the fresh weight parameter was found to be statistically insignificant, as indicated in Table 2. In other words, there were no statistically significant differences in fresh weight among genotypes. This suggests that environmental factors or measurement variations may have been influential. Therefore, fresh weight is more strongly influenced by environmental factors than by genetic differences. In this study, fresh weight is not a decisive criterion for distinguishing between genotypes, but it can be significant when evaluated in conjunction with other biomass measures. In a study [26] investigating the relationship between genetic variation and stem morphology in wheat, significant differences were reported among wheat genotypes in plant height, fresh and dry weights per plant, and mechanical characteristics of the stem. A similar report [27] revealed that shoot fresh weight in wheat ranged from 1.58 g pot-1 to 6.67 g pot-1 owing to the effects of salt, zinc, and phosphorus. According to the findings of a study [28] on arsenic stress in wheat, chlorophyll content in wheat seedlings, as well as some growth factors such as shoot and root length, decreased significantly due to increased oxidative stress in plants subjected to 75 mg/L and 150 mg/L amounts of the “As” element. A decrease in shoot fresh weight was observed in plants treated with 75 mg/L and 150 mg/L, with ratios of 17.6% and 46.1%, respectively, and fresh weight of plant roots also decreased with ratios of 28.5% and 60.1%, respectively, compared with the control group.

Statistically significant differences were identified between genotypes for dry weight at the 1% level. An examination of Table 2 revealed that the highest dry weight value was found in the hybrid genotype KRL-210, while among the hybrid genotypes, KRL-213 x KRL-210 had the highest value. Dry weight is considered one of the parameters that best reflects the true biomass potential of a plant. Indeed, the study concluded that genotypes with outstanding dry weight could be strong candidates for advanced breeding programs targeting biomass and yield increases. In a study [29] on biochar application, which is important for sustainability, it was determined that the amount of proline, a stress indicator, decreased in wheat shoots, and the dry weight values of roots and shoots, which are closely related to plant growth and unit area productivity, increased. In another study [30], the effects of combined applications of plant growth-inducing rhizobacteria (Pantoea conspicua) and biochar obtained from rice straw to reduce Cr stress (control + 2-dose application) in wheat plants grown under controlled conditions were investigated. At the end of the study, shoot dry weight was 0.095 g, while with Cr applied at 75 and 150 ppm, this value decreased by 0.074 g and 0.055 g, respectively. Following rhizobacteria inoculation, shoot dry weight was determined as 0.097 g and 0.083 g, while with biochar application, these values were determined as 0.093 g and 0.077 g. Depending on the results of the combined implementation, the highest shoot dry weights were determined as 0.105 g and 0.096 g under both applied stress treatments, respectively. An overall evaluation of that research showed that shoot dry weight ranged from 0.055 g to 0.132 g depending on several application factors.

According to the results of the SCAR plot analysis (Fig. 1), a wide variation was observed among the genotypes and F_1 combinations examined for all traits. Shoot length was concentrated in the range of 10–15 cm, with some genotypes exceeding these values. For tiller count, most genotypes varied between 1 and 3, with some combinations exhibiting higher tillering values. Leaf count varied between 5 and 12 among genotypes, with certain combinations exhibiting significantly higher leaf counts than others. Fresh weight values were concentrated between 0.2 and 0.8 g, and dry weight values varied between 0.05 and 0.2 g, respectively. It was stated that [31] that in principal components biplot analyses, relationships between genotypes and the examined traits can be visually seen.

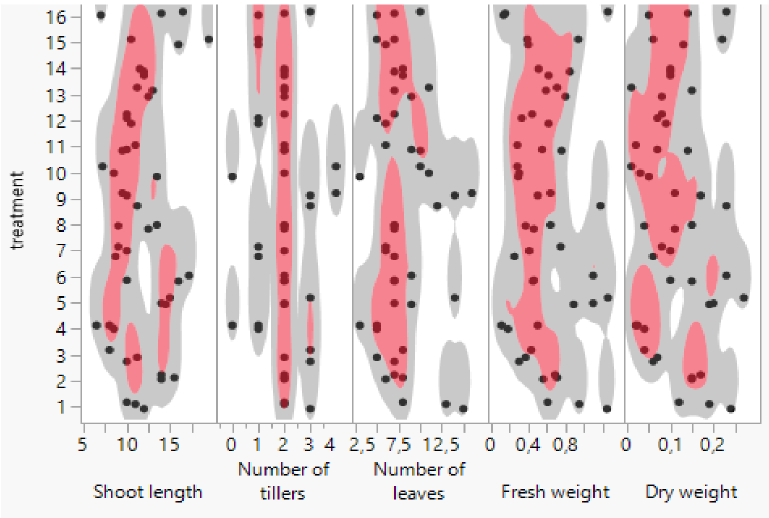

Fig. 1. *Biplot and scatter plot analysis showing genotype–trait relationships at the early seedling stage.*

Figure 1 shows that all traits examined exhibited distinct distributions among genotypes, with some F_1 combinations exhibiting superior performance beyond parental values. Furthermore, this diversity in trait distribution demonstrates the power of genetic variation and its potential for use in breeding programs. Biplot analysis is known as a two-way design table that graphically images the column and row factors. This qualified analysis process visualizes both the relationships amongst individual rows and also the column factors in addition to their pairwise interactions. Biplot analysis allows two-way data analysis of genotypes across multiple traits and environments [32].

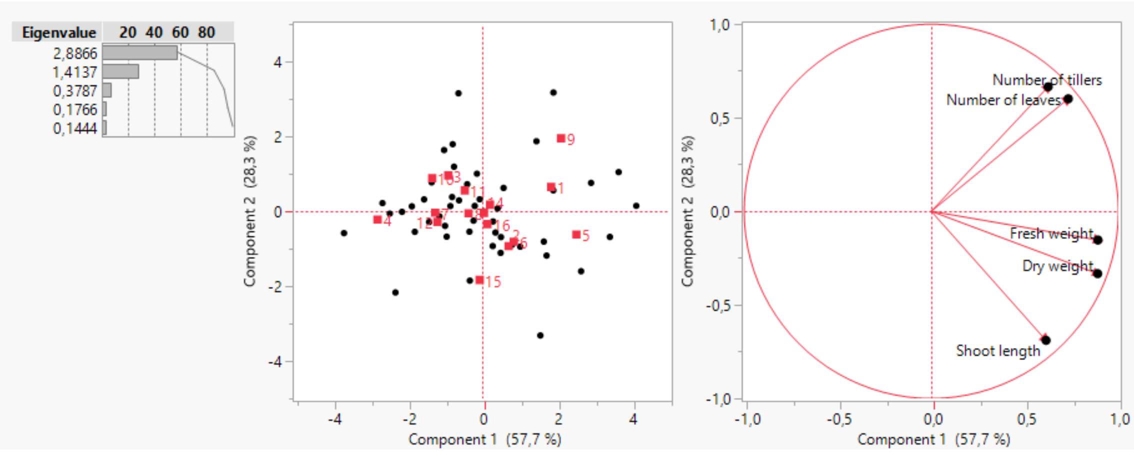

Fig. 2. *Principal Component Analysis (PCA) showing genotype–trait relationships at the early seedling stage.*

PCA analysis implied that a 57.7% ratio for total variance was elucidated over the first (PC1) and 28.3% by the second (PC2). The first two quantities together represent 86% of the total, which is a relatively high percentage. Trait inheritance systems, tiller counts, and leaf spacing clustered in the same direction, demonstrating high contribution rates on PC1. Fresh and dry weight traits also loaded highly on PC1, indicating that the biomass parameter analyses were complete. Shoot length differed from other traits. This indicates that leaf count and tiller determined the genotypes examined in some methods, and by biomass (fresh/dry weight) in others.

The graphical representation shows that the parental values of some genotypes are positioned differently, and this genetic disease diversity was successfully demonstrated by PCA (Figure 2). PCA and biplot approaches are frequently used and quite successful approaches by researchers, providing the opportunity to visually evaluate the examined traits and genotypes simultaneously based on the principle of visually presenting and evaluating the relationships between the examined parameters, thus having the ability to determine the positive and negative correlations of the examined traits and the relationship of genotypes with these traits [33], while it has been stated that PCA has been used successfully in highlighting important parameters in combined analyses of bread wheat [34]. It is fair that PCA analysis provides fundamental information regarding which characteristics can be evaluated together to select genotypes within populations in breeding studies. Indeed, it has also provided a clearer interpretation of the present research findings.

CONCLUSION

As a conclusion of the present research, parental genotypes and F_1 hybrids were evaluated for shoot length, tiller count, leaf count, fresh weight of shoot, dry weight of shoot, and the resulting data were analyzed using various statistical methods. Analysis of variance results highlighted statistically important differences amongst the wheat genotypes for shoot length, tiller count, leaf count, and dry weight. However, fresh weight did not show statistically significant differences among genotypes. This suggests that biomass-related parameters are more decisive in reflecting genetic variation. PCA analysis showed that first two components described 86% of total difference. Tiller number, leaf number, and fresh and dry weight were particularly significant contributors to the variation, while shoot length represented a slightly different dimension in distinguishing genotypes. SCAR plot analysis also revealed a wide distribution across genotypes for all traits, with some F_1 hybrids exhibiting superior performance, exceeding their parental means. Overall, this study revealed a wide genetic variation between F_1 hybrids and their parents, with shoot length, leaf number, and dry weight emerging as key determinants for genotype selection. These findings provide a solid foundation for developing effective selection strategies aimed at improving biomass accumulation and yield potential in bread wheat breeding programs. From a future perspective, the primary goal of this research is to identify genetically diverse parental lines with superior combining ability and to exploit heterotic cross combinations for enhancing early vigor and biomass-related traits. The integration of these results into breeding programs will facilitate the rational selection of parents and the design of targeted crossbreeding strategies, ultimately contributing to the development of high-yielding and stress-resilient wheat genotypes.

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REFERENCES

[1] Anonymous. (2020): TMO. Toprak Mahsulleri Ofisi Genel Müdürlüğü 2020 yılı hububat sektör raporu Ankara (in Turkish), http://www.tmo.gov.tr/Upload/Document/sek torraporlari/

[2] Li, L., Wang, J., Li, C., Mao, X., Zhang, X., Sun, J., Jing, R. (2023): Insights into progress of wheat breeding in arid and infertile areas of China. Elsevier 109-220. https://doi.org/10.1016/j.fcr.2023.109220

[3] Yıldırım, C., Okumuş, O., Uzun, S., Turkay, Ş. N., Say, A., Bakır, M. (2022): Genetic characterization of some species of vetch (*Vicia* L.) grown in Turkey with SSR markers. Journal of Agricultural Sciences 28(3): 518-524. https://doi.org/10.15832/ankutbd.934655

[4] Singh, S., Sharma, S. K., Sharma, R. P. (2004): Heterosis and inbreeding depression in bread wheat (*Triticum aestivum* L.). Indian Journal of Agricultural Research 38(2): 77-81.

[5] Şimşek, Ö., Isak, M. A., Dönmez, D., Dalda Şekerci, A., İzgü, T., Kaçar, Y. A. (2024): Advanced biotechnological interventions in mitigating drought stress in plants. Plants 13(5): 717. https://doi.org/10.3390/plants13050717

[6] Coban, F., Özer, H. (2025): Agronomic performance of fenugreek genotypes grown under various sowing and nitrogen rates in a highland environment. Turkish Journal of Agriculture and Forestry 49(1): 51-62. https://doi.org/10.55730/1300-011X.3248

[7] Dinç, A., Toğay, Y. (2025): The impact of climate change and agricultural drought on Turkish agriculture. Euroasia Journal of Mathematics, Engineering, Natural & Medical Science 12(2): 387-396. https://doi.org/10.5281/zenodo.17226713

[8] Shavrukov, Y., Kurishbayev, A., Jatayev, S., Shvidchenko, V., Zotova, L., Koekemoer, F., Groot, S., Soole, K., Langridge, P. (2017): Early flowering as a drought escape mechanism in plants: How can it aid wheat production? Frontiers in Plant Science 8(Article 1950): 1-8. https://doi.org/10.3389/fpls.2017.01950

[9] Kodaz, S., Haliloğlu, K., Öztürk, A. (2025): Trait-based characterization of barley genotypes under simulated early drought stress conditions. Turkish Journal of Field Crops 30(1): 206-222. https://doi.org/10.17557/tjfc.1664378

[10] Mohammadi, A., Rafiee, S., Jafari, A., Dalgaard, T., Knudsen M. T., Keyhani, A., Mousavi-Avval, S. H., Hermansen, E. (2013): Potential greenhouse gas emission reductions in soybean farming: a combined use of life cycle assessment and data envelopment analysis. Journal of Cleaner Production 54: 89-100. https://doi.org/10.1016/j.jclepro.2013.05.019

[11] Wang, Z., Zhang, H., Lu, X., Wang, M., Chu, Q., Wen, X., Chen, F. (2016): Lowering carbon footprint of winter wheat by improving management practices in North China Plain. Journal of Cleaner Production 112(1): 149–157. https://doi.org/10.1016/j.jclepro.2015.06.084

[12] Hu, J., Cai, J., Xu, T., Kang, H. (2022): Epitranscriptomic mRNA modifications governing plant stress responses: underlying mechanism and potential application. Plant Biotechnology Journal 20(12): 2245-2257.

[13] Ali, S., Tyagi, A., Mir, R. A., Rather, I. A., Anwar, Y., Mahmoudi, H. (2023): Plant beneficial microbiome a boon for improving multiple stress tolerance in plants. Frontiers in Plant Science 14: 1266182.

[14] Manntschke, A., Hempel, L., Temme, A., Reumann, M., Chen, T. W. (2025): Breeding in winter wheat (*Triticum aestivum* L.) can be further progressed by targeting previously neglected competitive traits. Frontiers in Plant Science 16: 1490483.

[15] Lopez, G., Hadir, S., Mouratidis, S. D., Shuva, M. A., Hüging, H., Bauke, S. L., ... & Seidel, S. J. (2025): Winter wheat shoot and root phenotypic plasticity under fertilized and nutrient-deficient field conditions. European Journal of Agronomy 168: 127634.

[16] Nadeem, M., Shahbaz, M., Ahmad, F., Waraich, E. A. (2025): Enhancing wheat resistance to salinity: The role of gibberellic acid and β-Carotene in morphological, yielding and ionic adaptations. Journal of Ecological Engineering 26(6): 76-94.

[17] Feng, Z., Cai, J., Wu, K., Li, Y., Yuan, X., Duan, J., ... & Feng, W. (2025): Enhancing the accuracy of monitoring effective tiller counts of wheat using multi-source data and machine learning derived from consumer drones. Computers and Electronics in Agriculture 232: 110120.

[18] Chen, P., Wang, F. (2022): Effect of crop spectra purification on plant nitrogen concentration estimations performed using high-spatial-resolution images obtained with unmanned aerial vehicles. Field Crop Res. 288: 108708. https://doi.org/ 10.1016/j.fcr.2022.108708.

[19] Saddozai, U. K., Ullah, A., Khan, R., Farooq, M., Li, X., Baloch, M. S., Khan, H. (2025): Evalutaion of the interactive effect of different salinity levels and amendments on wheat productivity. Annual Methodological Archive Research Review 3(6): 381-404.

[20] Shang, Q., Wang, Y., Tang, H., Sui, N., Zhang, X., Wang, F. (2021): Genetic, hormonal, and environmental control of tillering in wheat. The Crop Journal 9(5): 986–991. https:// doi. org/ 10. 1016/j. cj. 2021. 03. 002

[21] Zhang, Y., Cai, C., Gu, Y., Shi, Y., Gao, X. (2022): Microplastics in plant-soil ecosystems: a meta-analysis. Environmental Pollution 308: 119718.

[22] Guo, X., Wang, Z., Li, M., Zhang, Z., Xue, X., Zhang, Y., Gu, L. (2025): Faster and more wheat production governed by LED light in controlled environment agriculture. Journal of Integrative Agriculture (Advanced Publication).

[23] Al-Aisaee, M. M., Velazhahan, R., Nawaz, A., & Farooq, M. (2025): Morphological, physiological, and biochemical impacts of drought on wheat–pest–pathogen interactions. Physiologia Plantarum 177(4): e70364.

[24] Govta, N., Govta, L., Sela, H., Peleg, G., Distelfeld, A., Fahima, T., ... & Krugman, T. (2025): Plasticity of root system architecture and whole transcriptome responses underlying nitrogen deficiency tolerance conferred by a wild emmer wheat qtl. Plant, Cell & Environment 48(4): 2835-2855.

[25] Bellinaso, F., Bonini, G., Bagolin, J. V., Seifert, S. K., Silva, T. B., Carvalho, I. R., ... & Foguesatto, F. R. (2025): Yielding performance of wheat cultivars subjected to different management techniques. Agronomy Science and Biotechnology 11: 1-24.

[26] Shah, F., Li, Z., Fu, M., Li, C., Wu, W. (2025): Mitigating wheat lodging through varietal selection and nitrogen management. Food and Energy Security 14(2): e70071.

[27] Abbas, M., Murtaza, G., Owens, G., Khursheed, M. M., Hussain, T. (2025): Interactive effects of zinc oxide nanoparticles and phosphorus on wheat (*Triticum aestivum* L.) grown under salt-affected soil conditions. Journal of Plant Nutrition and Soil Science 188(1): 139-150.

[28] Karimi, N., Pakdel, H., Souri, Z., Norouzi, L., Rizwan, M., Yong, J. W. H. (2025): Effects of phytostabilized zinc sulfide nanocomposites on growth and arsenic accumulation in wheat (*Triticum aestivum* L.) under arsenic stress. Plant stress 16(2025): 100886.

[29] Farid, Y., Ali, I., Abdelhafez, A., Abbas, M. H. (2025): Enhancing wheat productivity in salt-affected soils using traditional and acidified biochars: A sustainable solution. Egyptian Journal of Soil Science 65(1): 121-134.

[30] Jalal, F., Ahmad, A., Iqbal, A., Khan, Z. H., Fahad, S., … & Nawaz, T. (2025): Biochar and plant growth-promoting rhizobacteria: a promising combination enhancing wheat (*Triticum aestivum* L.) growth under Chromium stress. Rhizosphere 36(2025): 101167.

[31] El-Harty, E.H., Alghamdi, S. S., Khan, M. A., Migdadi, H. M., Farooq, M. (2018): Adaptability and stability analysis of different soybean genotypes using biplot model. International Journal of Agriculture and Biology 20(10): 2196-2202.

[32] Yan, W., Tinker, N. A. (2006): Biplot analysis of multi-environment trial data: Principles and applications. Canadian Journal of Plant Science 86(3): 623–645.

[33] Yau, S. K. (1995): Regression and ammi analyses of genotype x environment interactions: an empirical comparison. Agronomy Journal 87(1): 121-126. https://doi.org/10.2134/agronj1995.00021962008700010021x

[34] Khan, S., Ali, N., Khan, F. U., Din, I. U., Amjad, M., Ahmad, I. (2025): Genetic diversity in wheat landraces for agronomic traits and yellow rust resistance. Genetic Resources and Crop Evolution (72): 6165-6179. https://doi.org/10.1007/s00122-006-0365-4