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Original paper

Response of durum wheat (*Triticum durum*) genotypes to cadmium stress: Growth and oxidative stress indicators at seedling stage

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Abstract: In this study, the response of 17 durum wheat genotypes to cadmium stress was assessed using an aeroponic growth system at the seedling stage. The following parameters were evaluated: glutathione peroxidase (GPX), root dry weight (RDW), malondialdehyde (MDA), cadmium of root (CR), leaf dry weight (LDW), catalase (CAT), cadmium of leaf (CL), ascorbate peroxidase (APX), chlorophyll (Chl) based on SPAD index, seedling dry weight (SDW), electrical conductivity (EC), and glutathione S-transferase (GST). Biplot analysis revealed that the first two principal components explained 64% of the observed variabilities. The pentagon plot highlighted that genotype G15 under cadmium stress exhibited the highest values for GST, GPX, MDA, and CAT; while under non-cadmium stress, it showed high APX activity and superior RDW, LDW, Chl, SDW, and EC values. G2 under cadmium stress was notable for its high CR and CL levels. Regarding seedling dry weight performance, G2 and G15 under non-cadmium stress, followed by G14 and G16, demonstrated the highest results. APX emerged as the most discriminative trait, followed by GST, GPX, CAT, and EC, as determined by the treatment-by-trait biplot. Under cadmium-stress , genotypes G6, G8, G9, G11, and G12 were identified as superior for seedling dry weight.

Keywords: Antioxidant enzymes, biplot, genotype-trait interaction, seedling dry weight.

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Introduction

Heavy metal contamination in soil poses a critical challenge to ecosystems and living organisms, as rapid industrialization and urbanization have led to a dramatic increase in soil heavy metal concentrations (Li et al., 2019) .Also, they adversely affecting plant growth, mineral balance, metabolic functions, and agricultural productivity. Among heavy metals, cadmium is particularly concerning, ranked among the top ten most toxic heavy metals, is commonly found in the Earth's crust alongside zinc, lead, and copper (Irfan et al., 2021). Key sources of cadmium contamination include excessive use of fertilizers and pesticides, mining, metallurgy, and electroplating activities (Genchi et al., 2020). When crops grow in cadmium-contaminated soils, the metal's high mobility facilitates its absorption and accumulation in various plant organs.

Cadmium poses serious risks to both plants and animals and is considered a significant environmental pollutant.Once inside the plant, cadmium inhibits growth, disrupts mineral nutrition, and impairs photosynthesis. Seed germination, a vital phase in a plant's life cycle, is particularly vulnerable to cadmium toxicity while high soil cadmium levels decrease germination rates and impede seedling growth (Shankar, 2020). Cadmium-induced toxicity triggers a cascade of physiological, biochemical, morphological, and molecular disruptions in plants (Vijiyakumar and Prince, 2024).

Cadmium, a non-essential element without any biological effects in plants, is highly mobile in soil. This mobility allows it to be readily obtained by roots and transported to aerial parts of the plant (Cai et al., 2023). Cadmium's interference in intracellular processes leads to an increase in reactive oxygen species within plant cells (Adil et al., 2020). These molecules are vital for cellular integrity; for instance, lipids play a central role in membrane structure and metabolic regulation (Li et al., 2020). Oxidation of membrane lipids compromises membrane permeability and generates toxic byproducts (Wang et al., 2017). Even at low concentrations, triggering metabolic pathways that further damage cellular components, such as increased endonuclease activity and cytochrome c-oxidase release (Alshehri, 2024). A prominent effect of cadmium toxicity is the generation of oxidative stress resulting in the production of reactive oxygen species in various species, which prompts the induction of defense systems. This system works collectively to neutralize reactive oxygen species and mitigate damage (Dumanović et al., 2021). Non-enzymatic metabolites also contribute by regulating osmotic balance and enhancing reactive oxygen species scavenging (Zandi and Schnug, 2022). Previous researches highlight the role of antioxidant enzyme activity in plant resistance to cadmium stress (Gutiérrez-Martínez et al., 2020; Pan et al., 2021). However, most investigations on mustard plants have focused on later seedling stages, with limited research addressing germination and early seedling growth stages.

Cadmium is naturally released into the environment through volcanic eruptions, weathering, erosion, and river transport. However, human activities contribute significantly to its release. Mining, non-ferrous metal smelting and refining, fossil fuel combustion, municipal waste incineration, production of orthophosphates, and recycling process of cadmium-contained materials are major sources (Singh et al., 2024). Drainage from historic mining activities further contributes to contamination. While high soil cadmium levels are typically localized to areas near mining sites, lower to moderate magnitudes of cadmium are widespread in agricultural soils. This is largely due to the use of cadmium-contaminated fertilizers, poor-quality biowaste, and peri-urban atmospheric deposition. Although cadmium levels in these soils may not directly affect plant growth or soil fertility, the risk lies in its potential transfer to humans via food and water. Recognizing cadmium's toxicity and prevalence, some researchers identify it as the one of critical pollutant martials in farming soils, emphasizing its implications for food safety and human health (Suhani et al., 2021). Addressing cadmium pollution is essential to ensure sustainable agricultural practices and protect food security. This investigation provides comprehensive grasp into the morphological, and biochemical changes induced by cadmium toxicity during germination and early seedling development across some durum wheat genotypes.

Materials and Methods

Trial and traits

Sterile seeds from 17 durum wheat cultivars (from ICARDA, Table 1) using 0.1% SDS, stirred for 20 min, and thoroughly rinsed with deionized water were obtained and their germination was done on filter papers in darkness at 25°C for two days in the laboratory of University of Maragheh. Seedlings were then transferred to an aeroponic system and cultivated as a factorial arangment in a completely randomized design with three replicates Growth conditions in the chamber included 16:8 hours light: darkness, temperature of 25°C, 65% relative humidity, and a light intensity of 6000 lux provided by yellow and white fluorescent light sources. Seven days post-germination, plants were grown with half-strength Hoagland's protocol, which was replaced with a full-strength solution after 14 days. At the 4- to 5-leaf stage, cadmium was induced by treating the seedlings with 250 mM cadmium chloride. The seedlings were maintained under stress circumstances for 14 days. Samples were collected to evaluate several parameters including biomass measurements, leaf dry weight (LDW), root dry weight (RDW), and seedling dry weight (SDW), were taken, along with chlorophyll content (Chl) and electrical conductivity (EC). Chlorophyll was measured via Minolta SPAD-502-PLUS digital chlorophyll meter (Minolta Co., Jeapan). Cadmium concentrations in roots (CR) and leaves (CL) were determined using atomic absorption spectrometry following the procedure of (Prkić et al., 2013). Additional samples were gathered from mature, well-developed leaves, then frozen in liquid nitrogen for measuring of the next physiologic indices. These included malondialdehyde (MDA), glutathione peroxidase (GPX), catalase (CAT), glutathione S-transferase (GST) and ascorbate peroxidase (APX), which were analyzed using protocols described by (Hossain et al., 2013).

Statistical analysis

The data for all measured traits were first subjected to a normality test using the Anderson-Darling method in Minitab 22.0 (Minitab, Pennsylvania, USA). This approach evaluates the strength of alignment between the dataset and a normal distribution. Subsequently, Pearson's correlations were analyzed by calculating simple correlation coefficients with IBM-SPSS 25.0 (IBM-SPSS, Chicago, USA).

Table 1. The code and pedigree of durum wheat genotypes used.

Code	Pedigree
G1	Saji
G2	45558
G3	2Gdr
G4	Green-14
G5	1-Mna/3Marb
G6	45632
G7	75MEXICALI
G8	8081A-Mar۱۴
G9	Bisu-1//Chen
G10	Gromtel-1
G11	45667
G12	Ajaia-12/F3
G13	45704
G14	45868
G15	Mrf1/Stj2//Bcrch1
G16	Rascon-37/2*Tarro-
G17	Hydranassa30/Silver-

To further explore the relationships among traits and identification of those most significantly influencing yield performance, a genotype × trait interaction analysis was conducted. This analysis utilized a biplot model within a principal component analysis framework, based on the formula via GGEbiplot software:

$$\frac{g_{ij} - t_j}{SD_j} = \sum_{n=1}^{2} \lambda_n \alpha_{in} \beta_{jn} + \theta_{ij}$$

In the model, g_{ij} represents the observed performance of genotype i for trait j, t_j is the average performance across all g_{ij} for trait j, and SD_j is the square root of variance g_{ij} for every j. The eigenvalue corresponding to the principal component n which is denoted as lambda n, while alpha in and beta jn signify the contributions of genotype i and trait j to the principal component n, respectively. The residual variance is captured by theta ij, representing unexplained variation in the model. To ensure symmetric scaling of genotypes and traits, the eigenvalues were normalized by adjusting vector magnitudes. This allowed for a standard presentation format and facilitated the visual interpretation of relationships between genotypes, traits, and their interactions. The dataset was transformed using a scaling factor of 1, while centering was performed with a setting of 2 to standardize the values. Singular value decomposition with a value of 2 was used to calculate singular values. The singular value partitioning parameter was set to 1, providing an optimal graphical representation of the genotype.

associations through the perfect genotype display. The abiotic tolerance index Mousavi et al. (2008) as one effective index of tolerance evaluation was calculated via formula:

$$ATI = [(Xp - Xs)/[(\bar{X}p/\bar{Y}Xs)][\sqrt{(XpXs)}]$$

where, Xp is the performance of non-stress circumstance; Xp is the performance of stress circumstance; $\bar{X}p$, is the mean of Xp; and $\bar{X}s$, is the mean of Xs. This index is identified as one of the effective stress tolerance indices for detection of the most tolerant genotypes in durum wheat based on Afrooz et al. (2021) and (Sedghiyeh et al., 2025)

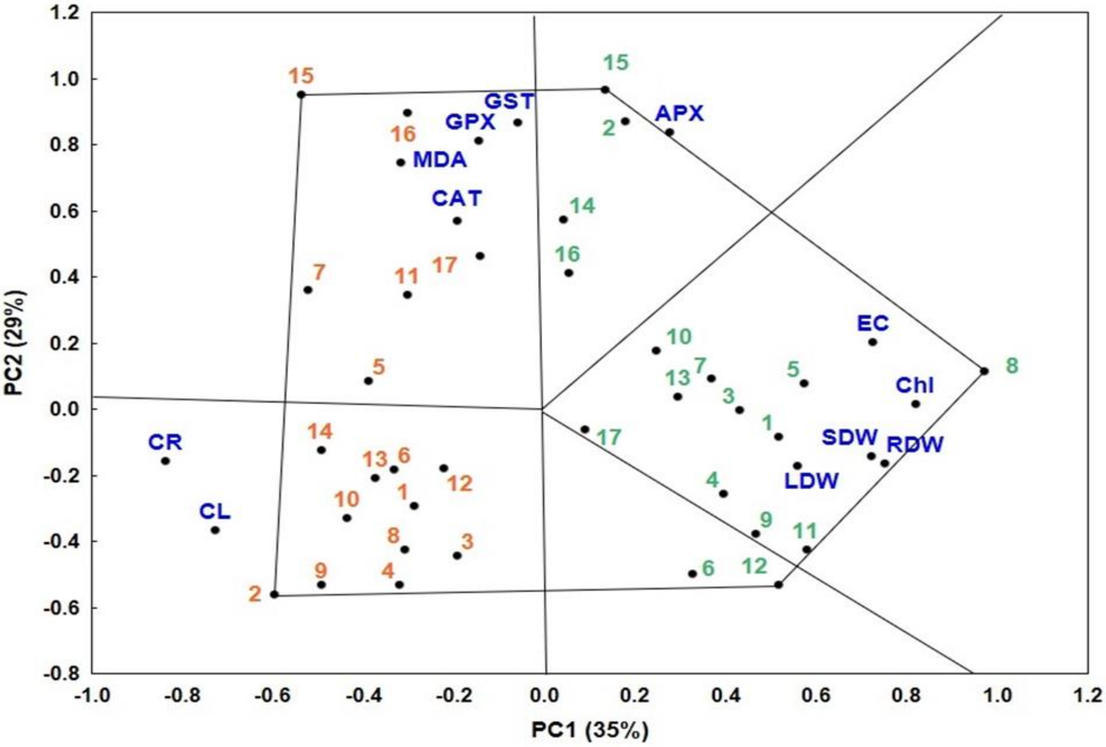


Figure 1. The pentagon of fitted model which indicated the situation of measured traits across two conditions: non-cadmium stress (green color genotypes) versus cadmium stress (orange color genotypes). Traits are: root dry weight (RDW), leaf dry weight (LDW), cadmium of root (CR), cadmium of leaf (CL), catalase (CAT), ascorbate peroxidase (APX), glutathione peroxidase (GPX), glutathione S-transferase (GST), malondialdehyde (MDA), chlorophyll (Chl), seedling dry weight (SDW), and electrical conductivity (EC).

otypes. Four of these genotypes exhibited superior performance in specific traits: G15 under cadmium stress showed elevated levels of glutathione peroxidase (GPX), malondialdehyde (MDA), glutathione S-transferase (GST), and catalase (CAT); G15 under non-cadmium stress excelled in ascorbate peroxidase (APX) activity; genotype 15 under non-cadmium stress also demonstrated high values for root and leaf dry weight (RDW and LDW), chlorophyll (Chl), seedling dry weight (SDW), and electrical conductivity (EC); and G2 under cadmium stress had the highest levels of cadmium accumulation in roots (CR) and leaves (CL). In contrast, G12 under non-cadmium stress did not show notable performance in any of the evaluated traits.

Results

The first two principal components of the biplot model accounted for 35% and 29% of the observed variation, respectively, capturing a combined 64% of the total variance in the wheat datasets. This proportion indicates a robust representation of the relationships among traits. Figure 1 demonstrates the utility of the biplot model in visualizing genotype performance across traits, identifying superior genotypes for specific characteristics. These insights are valuable for selecting candidates for breeding programs or commercial cultivation. A pentagon-shaped plot was observed, with perpendicular lines drawn to its edges to facilitate comparisons among the vertex genotypes. Four of these genotypes exhibited superior performance in specific traits: G15 under cadmium stress showed elevated levels of glutathione peroxidase (GPX), malondialdehyde (MDA), glutathione S-transferase (GST), and catalase (CAT); G15 under non-cadmium stress excelled in ascorbate peroxidase (APX) activity; genotype 15 under non-cadmium stress also demonstrated high values for root and leaf dry weight (RDW and LDW), chlorophyll (Chl), seedling dry weight (SDW), and electrical conductivity (EC); and G2 under cadmium stress had the highest levels of cadmium accumulation in roots (CR) and leaves (CL). In contrast, G12 under non-cadmium stress did not show notable performance in any of the evaluated traits.Also, from Fig. 1, it can be grasped that the genotypes of section G15 under non-cadmium stress (2, 14, and 16) had high amounts of APX while the genotypes of section G15 under cadmium stress (5, 7, 11, 16, and 17) had high magnitudes of some biochemical components related to antioxidants like GST, GPX, MDA, and CAT. Thus, the rection of these genotypes especially G15 and G16 was higher under stress conditions, so these genotypes are relatively tolerant genotypes to cadmium stress. For selecting of the most tolerant genotypes, the abiotic tolerance index (ATI), was used for RDW, LDW, and SDW based on Mousavi et al. (2008), and ranking of genotypes regarding this index indicated that G14 and G17 following to G4, G10, G15, and G16 were detected as the most tolerant genotypes to cadmium stress (Table 2).

Table 2. The amount and rank of the abiotic tolerance index (ATI) for some traits.

Genotypes	ATI values			Ranks			Mean
	RDW	LDW	SDW	RDW	LDW	SDW	Rank
G1	0.02189	0.00149	0.00473	8	12	2	7.3
G2	0.01112	0.00643	0.00047	13	5	9	9.0
G3	0.06477	0.00547	0.00010	2	6	16	8.0
G4	0.06190	-0.00443	0.00022	4	17	15	12.0
G5	0.06332	0.00731	0.00101	3	3	6	4.0
G6	0.02078	0.00531	0.00023	10	7	14	10.3
G7	0.01545	0.00690	0.00155	12	4	5	7.0
G8	0.07745	0.06573	0.00582	1	1	1	1.0
G9	0.04408	0.00272	0.00042	6	10	11	9.0
G10	0.01592	-0.00311	0.00061	11	16	8	11.7
G11	0.03490	0.01919	0.00267	7	2	3	4.0
G12	0.02109	0.00014	0.00201	9	13	4	8.7
G13	0.05689	-0.00242	0.00067	5	15	7	9.0
G14	-0.00025	-0.00185	0.00044	15	14	10	13.0
G15	0.00463	0.00223	0.00033	14	11	13	12.7
G16	-0.01541	0.00350	0.00037	16	9	12	12.3
G17	-0.02210	0.00516	0.00004	17	8	17	14.0

Traits are: root dry weight (RDW), leaf dry weight (LDW), and seedling dry weight (SDW).

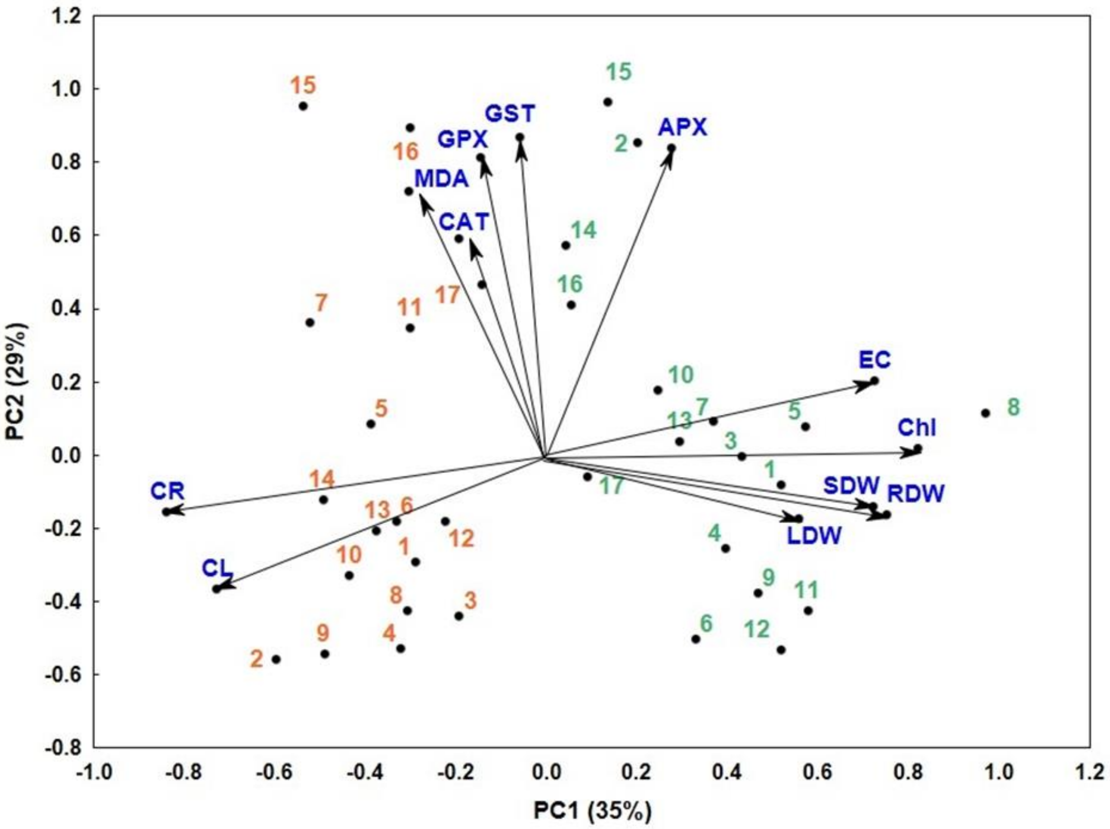


Figure 2. The vector display of fitted model which indicated the association among of measured traits across two conditions: non-cadmium stress (green color genotypes) versus cadmium stress (orange color genotypes).Traits are: root dry weight (RDW), leaf dry weight (LDW), cadmium of root (CR), cadmium of leaf (CL), catalase (CAT), ascorbate peroxidase (APX), glutathione peroxidase (GPX), glutathione S-transferase (GST), malondialdehyde (MDA), chlorophyll (Chl), seedling dry weight (SDW), and electrical conductivity (EC).

Comparison these results with pentagon of biplot verified the potential of G15 and G16 as the tolerant genotypes with acceptable dry yield of roots, leaves and seedlings followed by G14 and G17. Thus, these genotypes could be advised for cultivation in cadmium contaminated soils and used in future breeding projects.

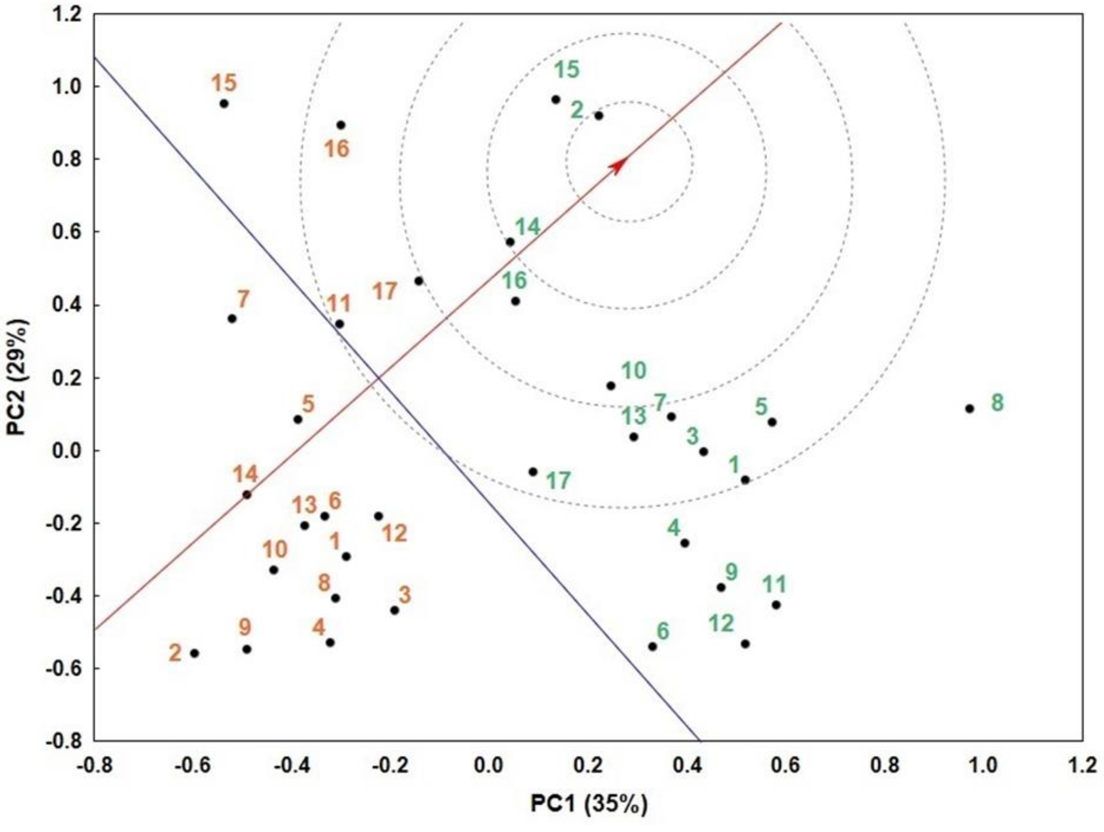
In this study, the fitted model effectively captured and predicted genotype-by-trait associations. The biplot model accounted for a substantial proportion of variation, with trait correlations revealed by the cosine of the vectors. Figure 2 illustrates significant relationships, including: (i) positive correlations between GST, GPX, MDA, and CAT, as indicated by a cosine of 0° (+1); (ii) positive correlations between RDW, LDW, Chl, SDW, and EC, suggested by close angles; (iii) a positive correlation between CR and CL, with a cosine of 0° (+1); (iv) near-zero correlations between GST, GPX, MDA, and CAT with RDW, LDW, Chl, SDW, and EC, as well as with CR and CL, indicated. by a cosine of 90° (0); and (v) Negative correlations between RDW, LDW, Chl, SDW, and EC with CR and CL, demonstrated by a cosine of 180° (-1). Finally, the predictions of the fitted model align well with the numerical associations (Table 3), while there are some inconsistencies, related to the issue that the model explains for 64% of the variation rather than total. Figure 3 shows the position of the ideal genotype, with the genotypes closest to this position considered the best performers. G2 and G15 under non-cadmium stress, followed by G14 and G16 under the same conditions, were positioned nearest to the ideal genotype, indicating their superior performance.

Table 3. Pearson's correlation coefficients among measured traits of durum wheat based on 17 data.

	RDW	LDW	CR	CL	CAT	APX	GPX	GST	MDA	Chl	SDW
LDW	0.48†										
CR	-0.48	-0.22									
CL	-0.41	-0.22	0.67								
CAT	-0.01	-0.03	-0.02	-0.10							
APX	0.11	-0.05	-0.38	-0.49	0.52						
GPX	-0.29	-0.18	-0.20	-0.27	0.44	0.66					
GST	-0.06	-0.10	-0.06	-0.35	0.48	0.77	0.75				
MDA	-0.16	0.01	0.14	-0.10	0.46	0.53	0.59	0.86			
Chl	0.57	0.22	-0.73	-0.61	0.03	0.26	-0.03	0.02	-0.20		
SDW	0.55	0.63	-0.41	-0.31	0.03	0.09	-0.24	-0.05	-0.07	0.50	
EC	0.35	0.34	-0.71	-0.59	0.02	0.25	0.19	0.14	0.10	0.47	0.37

The significant levels are 0.48 and 0.60 in 5 and 1 % level, respectively. Traits are: root dry weight (RDW), leaf dry weight (LDW), cadmium of root (CR), cadmium of leaf (CL), catalase (CAT), ascorbate peroxidase (APX), glutathione peroxidase (GPX), glutathione S-transferase (GST), malondialdehyde (MDA), chlorophyll (Chl), seedling dry weight (SDW), and electrical conductivity (EC).

Figure 3. The position of perfect genotype across two conditions: non-cadmium stress (green color genotypes) versus cadmium stress (orange color genotypes).



In contrast, G2 and G9 under cadmium stress were positioned farthest from the ideal genotype, making them less desirable. Most of the wheat genotypes under cadmium stress were located below the average axis, indicating less desirable performance, while a few genotypes (G11, G15, G16, and G17) were positioned above the average axis. However, it appears that the perfect genotype's ability to distinguish traits is limited under stress conditions. Therefore, it is recommended to evaluate genotypes under normal conditions to fully reveal their potential for agronomic traits. Identifying these "ideal" genotypes is essential for wheat genetic improvement programs, especially considering that leaf yield performance and yield components often show low correlations in many field crops.

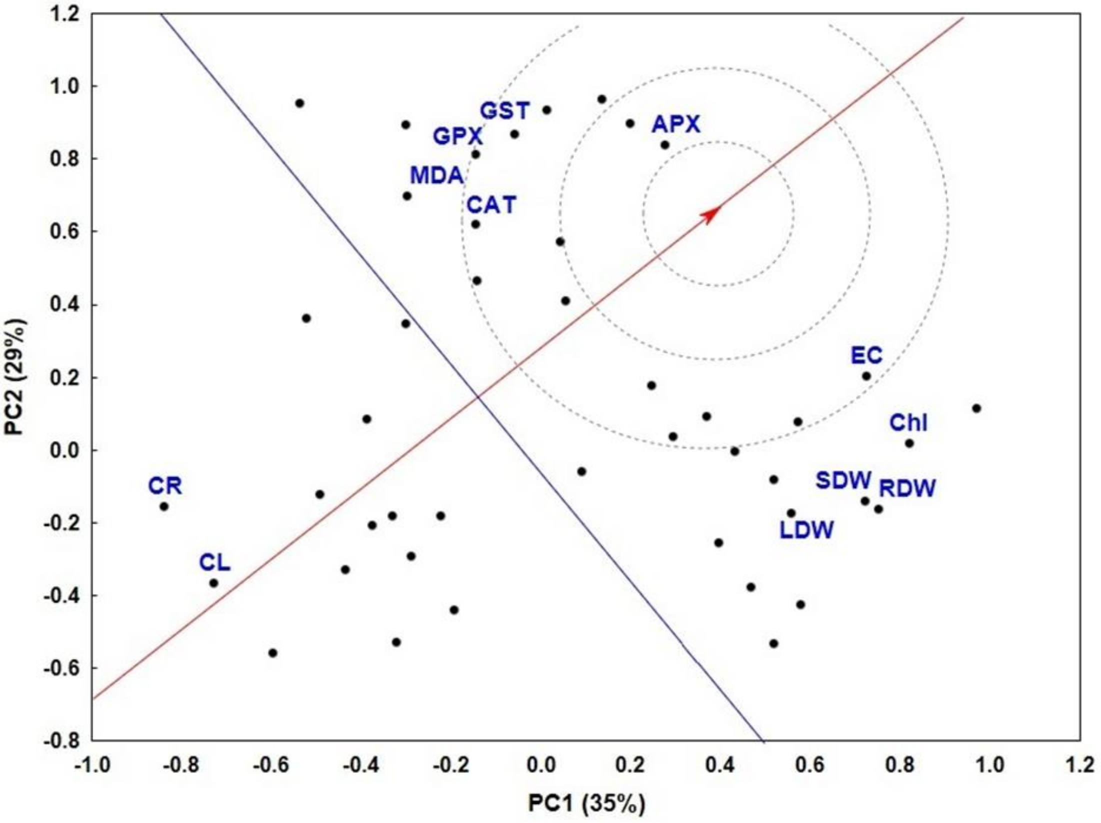


Figure 4. The position of perfect trait across two conditions: non-cadmium stress (green color genotypes) versus cadmium stress (orange color genotypes). Traits are: root dry weight (RDW), leaf dry weight (LDW), cadmium of root (CR), cadmium of leaf (CL), catalase (CAT), ascorbate peroxidase (APX), glutathione peroxidase (GPX), glutathione S-transferase (GST), malondialdehyde (MDA), chlorophyll (Chl), seedling dry weight (SDW), and electrical conductivity (EC).

Genotypes that performed above average for SDW are located above the average axis. The distance of each genotype from the horizontal axis represents the standard deviation, with smaller distances indicating lower variability, which makes them more desirable for selection. Consequently, G8, G9, and G11 under non-cadmium stress were recommended due to their relatively low variability compared to G6 and G12. In contrast, genotypes such as 2 and 9 under cadmium stress, which are farther from the horizontal axis, exhibit higher variability and are considered less desirable (Fig. 5). Evaluating wheat genotypes is essential for breeding under stress conditions and effectively managing genetic improvement tasks.

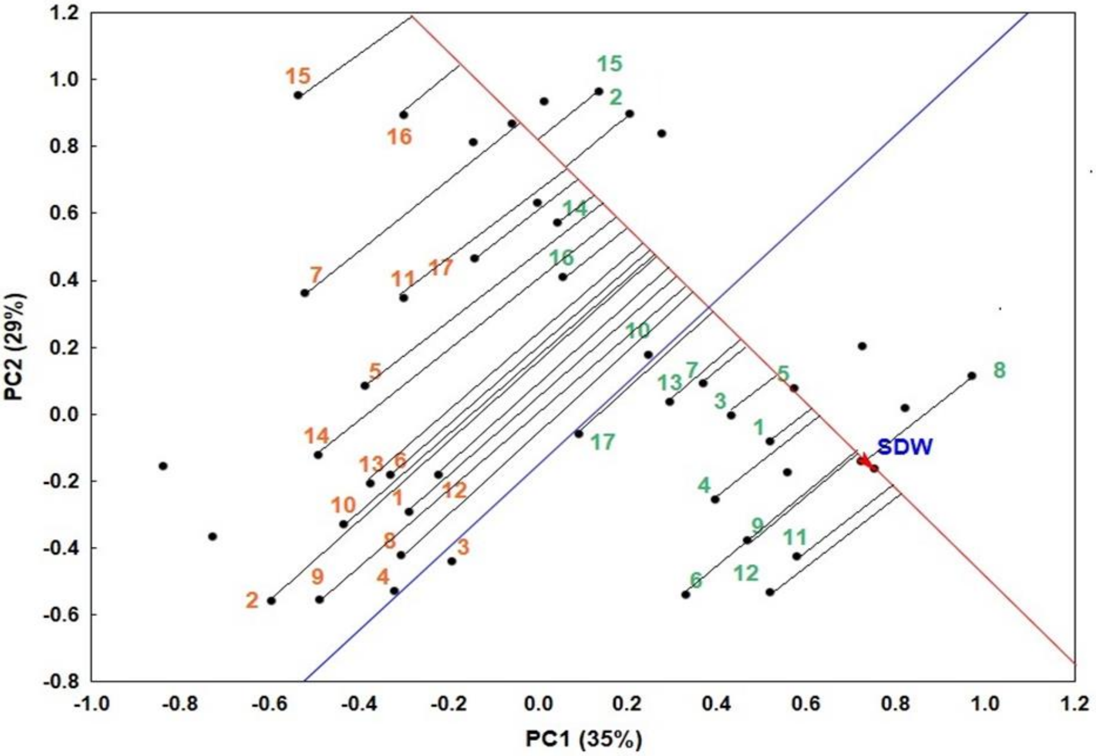


Figure 5. The examining of seeding dry weight (SDW) across two conditions: non-cadmium stress (green color genotypes) versus cadmium stress (orange color genotypes).

Discussion

The fitted biplot model accounted for 64% of the observed variation, which indicates a robust representation of the relationships among traits. The benefits of the fitted biplot model observed in this study align with findings in other crops, such as corn Santana et al. (2021) and safflower Ebrahimi et al. (2023), supporting its effectiveness in generating actionable insights for crop improvement. Cadmium stress impacts plants by accumulating in leaves, which reduces stomatal conductance and impedes carbon dioxide uptake in photosynthetic cells. This deficiency limits the production of critical metabolites required for cellular growth.

The reaction of genotypes G15 and G16 was higher under stress conditions, so these genotypes are relatively tolerant genotypes to cadmium stress. Cadmium disrupts respiration, decreasing energy production and carbon skeleton availability for essential biomolecules. It also inhibits the stabilization of nitrogen and its decrease in cells, restricting the changes of α-ketoglutarate into amino acids (Xue et al., 2023). These disruptions result in delayed and insufficient production of vital cellular components, ultimately leading to reduced the dry weight of shoots in even the more tolerant genotypes under insufficient production of vital cellular components, leading to reduced dry weight of shoots in even the more tolerant genotypes under stress. The results of the abiotic tolerance index (ATI), relatively verified the above-mentioned results whereas comparing them with the pentagon of the biplot verified the potential of genotypes G15 and G16 as the tolerant genotypes with an acceptable dry yield of roots, leaves, and seedlings. Thus, these genotypes could be advised for cultivation in cadmium-contaminated soils as well as using in future breeding projects.

To investigate the relationships among traits, vectors were drawn from the origin to each trait, which helped to clarify the interactions between them. The model revealed both additive and crossover interactions, suggesting that the ranking of genotypes based on the measured traits could change. This finding aligns with Sabaghnia et al. (2015), who highlighted the complexity of selecting genotypes without considering genotype-by-trait interactions.. These results are consistent with Li et al. (2022), which reported a positive association between root, shoot, and leaf dry weights in wheat, and a negative association between cadmium content in roots and seedlings with yield traits. In general, the biplot model provided a clear visual representation of trait relationships in wheat, in line with findings by Chen et al. (2021), who observed positive correlations between leaf and root dry weights with seedling weight in some wheat genotypes. Although, the biplot method prepares a visual overview of trait associations based on the overall structure of the dataset, the correlation coefficients assess direct interrelationships among traits and may not always match the biplot outcomes. Cadmium disrupts the plant's water balance, leading to dry weight loss and a reduction in calcium absorption, which impairs growth and decreases biomass. The cadmium accumulation in the leaves remarkably increased under cadmium stress, which agrees with the findings of (Sabella et al., 2022). Cadmium is highly mobile in soil, making it easily absorbed by wheat roots, and its accumulation in the roots can be transferred to the leaves. This study showed that cadmium levels were significantly elevated in both the roots and shoots. Genotypes G8, G9, and G11 under non-cadmium stress were recommended due to their relatively low variability compared to genotypes G6 and G12. The effectiveness of this approach for identifying favorable genotypes for target traits has been demonstrated in studies on sweet corn Stansluos et al. (2023) and safflower (Ebrahimi et al., 2023). This study identified substantial variation among wheat genotypes, which is consistent with previous research reporting significant diversity in wheat (Qu et al., 2020; Saleh et al., 2020). The genotype × trait interaction biplot model revealed a relatively high level of variation and confirmed the presence of both simple and complex interactions among the genotypes and traits. Similar patterns of interaction have been observed in other crops, such as durum wheat Kendal (2019) and barley (Karahan and Akgün, 2020). These interactions resulted in varying rankings of genotypes across traits, making it challenging to identify the most superior genotypes. Ignoring these interaction effects complicates the selection process due to the genotype × trait interaction's influence on genetic factors. Despite reduced Calvin cycle activity and decreased dry matter production, durum wheat genotypes exhibited a unique ability to isolate and store cadmium in vacuoles. The high generation of reactive oxygen species did not necessarily cause to a corresponding increase in antioxidant enzyme activity. Bouchama et al. (2023) found that the addition of cadmium to the environment increased guaiacol peroxidase activity in the leaves of Phragmites australis. This enzyme plays a crucial role in managing oxidative stresses due to high cadmium amounts. The enhanced activity of oxidative enzymes helped mitigate the negative effects of cadmium, reducing lipid peroxidation, and allowing cells to maintain their metabolic activity.

Conclusion

The genotype × trait interaction biplot model explained 64% of the variation and confirmed that cadmium stress negatively impacts agronomic traits, inducing oxidative stress in wheat. G8, G9, and G11, followed by G6 and G12, exhibited the most desirable seedling dry weight performance under stress. The current investigation provided a valuable grasp for genetic improvement projects for enhancing wheat performance under cadmium stress conditions. Breeders can use these findings to prioritize effective traits in their genetic improvement programs, with the ultimate goal of increasing wheat yield.

Supplementary Materials

No supplementary material is available for this article.

Author Contributions

Conceptualization, A.P.; methodology, S.M.; software, N.SX.; validation, A.P., and N.S.; formal analysis, A.P.; investigation, S.M.; resources, A.P.; data curation, N.S.; writing—original draft preparation, N.S.; writing—review and editing, A.P.; visualization, N.S.; supervision, A.P.; project administration, A.P. All authors have read and agreed to the published version of the manuscript.

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Conflict of Interest Statement

The author declares no conflict of interest.

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مقاله پژوهشی

اثرات تنش کادمیوم بر رشد و شاخص‌های تنش اکسیداتیو در گیاهچه‌های برخی از ژنوتیپ‌های گندم دوروم

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چکیده: در این مطالعه با استفاده از سامانه رشد هواکشت، پاسخ گیاهچه‌های ۱۷ ژنوتیپ گندم دوروم به تنش کادمیوم ارزیابی گردید. پارامترهای گلوتاتیون پراکسیداز (GPX)، وزن خشک ریشه (RDW)، مالون دی آلدئید (MDA)، کادمیوم ریشه (CR)، وزن خشک برگ (LDW)، کاتالاز (CAT)، کادمیوم برگ (CL)، آسکوربات پراکسیداز (APX)، کلروفیل (Chl) بر اساس شاخص SPAD، وزن خشک گیاهچه (SDW)، هدایت الکتریکی (EC) و گلوتاتیون S-transferase (GST) مورد ارزیابی قرار گرفتند. تجزیه و تحلیل بای پلات نشان داد که دو مؤلفه اصلی اول ۶۴ درصد از متغیرهای شناسایی شده را به خود اختصاص دادند. از نمودار پنج ضلعی می توان استنباط نمود ژنوتیپ G15 تحت تنش کادمیوم دارای بالاترین مقادیر GST، GPX، MDA و CAT بود در حالیکه این ژنوتیپ تحت تنش غیر کادمیوم، فعالیت بالای APX و مقادیر بالای RDW، LDW، Chl، SDW و EC را بخود اختصاص داد. G2 تحت تنش کادمیوم به دلیل سطوح بالای CR و CL قابل توجه بود. از نظر عملکرد وزن خشک گیاهچه، ژنوتیپ‌های G2 و G15 تحت تنش غیرکادمیمی و پس از آن ژنوتیپ‌های G14 و G16 بهترین نتایج را نشان دادند. APX به عنوان مهمترین صفت متمایزکننده شناسایی شد و پس از آن صفات GST، GPX، CAT و EC دارای این ویژگی بودند که توسط بای‌پلات ژنوتیپ در صفت تعیین شدند. در بین ژنوتیپ‌های بدون تنش کادمیوم، ژنوتیپ‌های G6، G8، G9، G11 و G12 به عنوان بهترین ژنوتیپ برای وزن خشک گیاهچه شناخته شدند.

کلمات کلیدی: آنزیم‌های آنتی‌اکسیدانی، تجزیه بای‌پلات، برهمکنش ژنوتیپ و صفت، وزن خشک گیاهچه.

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