GENETIC VARIATION IN ENZYMES AND PHYSIOLOGICAL RESPONSES OF WHEAT CULTIVARS UNDER DROUGHT CONDITIONS

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SUMMARY

Crop production decreases because of water deficit stress conditions worldwide. Understanding genetic variation in enzymes and physiological responses of wheat genotypes under drought conditions is necessary to select tolerant genotypes for cultivation under drought conditions. These goals set 15 wheat genotypes for cultivation in the fall of 2022 with two irrigation interval regimes to evaluate their growth and yield-related traits for drought tolerance. The experiment had a randomized complete block design with three replications. Results showed highly significant differences among studied genotypes for all assessed traits. Genotype G11 gave the highest values in aldehyde dehydrogenase activity, spike per meter, grain yield, and biological yield (9.620 milliunits/mL, 975.8 spikes m^{-1}, 10.725 t ha^{-1}, and 29.568 t ha^{-1}, respectively). Genotype G1 emerges with the utmost value for glutamate dehydrogenase activity (9.62 milliunits/mL), G2 for tillers per meter (1030.0 tillers m^{-1}), G4 for spike length (11.17 cm), G6 for 1000-grain weight (40.8 g), G12 for grains per spike (40.9 grain $spike^{-1}$), and G14 for plant height (117.2 cm). Likewise, water level treatments exhibited a significant impact on the studied traits. However, genotype G11 was leading in grain and biological yields. The five-day irrigation interval treatment gave the highest values in all studied traits except for glutamate dehydrogenase activity. Therefore, the study concluded that wheat genotypes responded differently to water level treatments and water stress at 14-day irrigation intervals, which can benefit screening the wheat genotypes for water deficit stress.

Keywords: Wheat (*Triticum aestivum* L.), genotypes, genetic variation, irrigation intervals, drought conditions, growth and yield traits, aldehyde dehydrogenases

Key findings: Genotype G11 had the highest aldehyde dehydrogenase activity, spike count, grain, and biological yields (9.620 milliunits/mL, 975.8 spike m^{-1}, 10.725 t ha^{-1}, and 29.568 t ha^{-1}, respectively). Genotype G1 had the utmost glutamate dehydrogenase activity (9.62 milliunits Ml^{-1}), G2 for tillers per meter (1030.0), G4 for lengthiest spikes (11.17 cm), G6 for heaviest grains (40.8 g), G12 for grains per spike (40.9 grains spike^{-1}), and G14 the tallest plants. Furthermore, the 5-day water level treatment significantly affected the growth and yield-attributing traits.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most crucial food crops. The area of land harvested with wheat worldwide during 2021 was more than 220 million hectares, which produced around 770 million metric tons, with a grain yield of 3.491 t ha^{-1} (FAO, 2023). The expected rise in world population to more than 10 billion by 2050 requires more demand for food resources. Water is a critical factor that limits wheat cultivation in Iraq, especially after climate change, notably decreasing the rainfall and increasing temperature, raising competition for water resources.

The area harvested with wheat in Iraq in 1981 was more than 1,832,000 hectares, but in 2021, it declined to 1,591,000 hectares (FAO, 2023). In the meantime, Iraq's population increased threefold. The wheat-cultivated area declined as massive wheat farms exited from agricultural investment, whether irrigated or rainfed. It might be due to the low and irregular distribution of rains in the growing season in proportion to the water needs of wheat crops, exposing crop plants to short and long periods of drought, which negatively affected crop growth and development. Global warming also led to higher temperatures and increased water loss rates by evapotranspiration, exposing the crop plant to water stress conditions adversely affecting plant growth and production. Therefore, it was necessary to improve the wheat tolerance to water stress conditions to maintain stability in grain yield.

Proposed various ways to overcome the water stress conditions have emerged, and selecting drought-tolerant genotypes is one of the highly effective and economical means to maintain grain yield stability in arid and semi-arid regions (Ashraf *et al*., 1994; Hadi *et al*., 2023). For drought tolerance, tolerant genotypes have several mechanisms to cope with such unfavorable conditions. Water stress causes many modifications in the plant structure and various plant processes in a way that improves the ability of plants to withstand unsuitable environmental conditions. These adaptations arise from increasing the sensitivity of closing pores to reduce water losses by evapotranspiration, maintaining the turgor potential within plant cells, and boosting the ability to osmotic adjustment, reducing the leaf surface area (Westgate and Boyer, 1985). Also considered one of the most relevant adaptive traits associated with water stress tolerance is the formation of waxy deposits on the surfaces of leaves and stems and the increase in root-to-shoot ratio. It develops a deep and branched root system to help reach the deep, moist soil layers, allowing sufficient water absorption to replace water loss by evapotranspiration (Gharsallah *et al*., 2013).

Studying durum wheat genotypes to investigate the effect of water stress during the stages revealed the maximum decrease in grain yield traits occurred with the plants' exposure to water stress throughout the growing season (Ismail *et al*., 1999; Jessup *et al*., 2020). A study of the physiological mechanisms and enzymes that benefit plants under drought tolerance can benefit plant-breeding programs (Zaharieva *et al*., 2001; Alogaidi *et al*., 2019). Physiologists and plant breeders stressed the need for crop models with morphological traits that help the plant withstand drought and resist lack of water (Bazzaz *et al*., 2000).

The search for genotypes with high photosynthetic efficiency is vital to use them as genetic sources for developing high-yielding genotypes. Variation among water stress-tolerant genotypes is mainly critical to selecting water stress-tolerant genotypes. Severe water stress during the flowering stage

causes a decline in the number of spikes, grains, and grain weight (Aspinall, 1984; Al-jawaheri and Alogaidi, 2020). Studies conducted by Nachit (1992) have indicated that drought in the Mediterranean Basin showed that the number of spikes was the most crucial indicator of grain yield for durum wheat, and the positive correlation manifested between the number of spikes and grain yield (Alshugeairy *et al.*, 2023).

Drought is one of the chief abiotic stresses that impede wheat production. Aldehydes accumulated in cells caused by reactive oxygen species (ROS) materialized due to abiotic and biotic stresses. Toxic aldehyde elimination via aldehyde homeostasis made by aldehyde dehydrogenases (ALDH) belongs to a family of enzymes. In wheat, osmotic stress caused stimulation of three homologs of the *ALDH7B4* gene. The over-expression of the TraeALDH7B1-5A gene helped enhance drought tolerance in transgenic *Arabidopsis* thaliana (Chen *et al.*, 2015). Functional studies indicated that plant's tolerance to drought gains enrichment by the ectopic expression of the ALDH21 gene in cotton and tobacco crops (Yang *et al.*, 2015). Glutamate (Glu) is a known protein amino acid that signals the growth and development of crop plants, which also takes part in root architecture (Forde, 2014; López-Bucio *et al.*, 2018). It also participates in abiotic stress adaptation (Philippe *et al.*, 2019), salt (Abed *et al.*, 2018; Cheng *et al.*, 2018), heat (Li *et al.*, 2019), and nitrogen (Okab and Abed, 2023) in addition to other physiological processes. The presented research aims to evaluate the performance of wheat genotypes for water stress tolerance under drought conditions.

MATERIALS AND METHODS

The pertinent experiment commenced during the winter of 2022–2023 in the field of the College of Agricultural Engineering Sciences, Al-Jadriya, University of Baghdad, Baghdad, Iraq (with an altitude of 34 masl at a latitude of 33.28 ° North and a longitude of 44.39 ° East). Fifteen wheat genotypes (17-drought, AL-Baraka, 2C, AL-Rasheed, 18B-drought, 18A-drought, 41-drought, 31-drought, 249S2, 7RS1, 19RS1, 3C, Babel, 1C, and 6PRS1) received labeling as G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, and G15, and acquired two irrigation interval treatments (Water levels) after their cultivation. The first irrigation had five-day intervals (well-watered), and the second had 14-day irrigation intervals (water stress) throughout the growing season. Applying two free irrigations uniformly to both treatments transpired before starting the irrigation intervals to evaluate the wheat genotypes' growth and yield-related traits and drought stress tolerance.

The experiment proceeded in a randomized complete block design (RCBD) with a split-plot arrangement and three replications. Irrigation intervals progressed on main plots, with the wheat genotypes placed randomly in the subplots. The experimental land underwent two plowing perpendicularly, then smoothed and leveled. Phosphorus broadcasting as superphosphate (46% P_2O_5) occurred before sowing at a rate of 200 kg ha^{-1} (Saleh and Salman, 2005). The wheat genotype sowing in rows on November 15, 2022, had a distance of 30 cm between the rows at a seed rate of 100 kg ha^{-1}. Nitrogen fertilizer application as side dressing had the rate of 200 kg N ha^{-1} in the form of urea (46% N), underwent dividing into two equal doses for the first fertilization after 21 days of sowing and the second dose during heading. Manual weeding also ensued whenever required. Harvesting wheat genotypes happened on May 21, 2023.

Data recorded

The recording of data included the traits, i.e., plant height, tiller per square meter, spikes per square meter, spike length, grains per spike, 1000-grain weight, grain yield, biological yield, aldehyde dehydrogenase activity (ALDH), and glutamate dehydrogenase activity (GDH).
The ALDH activity determination of the wheat genotypes used the following equation (according to sigma-aldrich.com):

$$ALDH\ Activity == \frac{B \times Sample\ Dilution\ Factor}{Reaction\ Time\ X\ V}$$

B = Amount (nmole) of NADH generated between T_{inital} and T_{final}

Reaction Time = T_{final} - $T_{initial}$ (minutes)

V = Sample volume (mL) added to well

ALDH activity is reported as nmole/min/mL = milliunit/mL

One unit of ALDH is the amount of enzyme that will generate 1.0 µmole of NADH per minute at pH 8.0 at room temperature.

The GDH activity detection of wheat genotypes employed the following equation (according to sigma-aldrich.com):

$$GDH\ Activity = = \frac{B \times Sample\ Dilution\ Factor}{Reaction\ Time \times V}$$

B = Amount (nmole) of NADH generated between T_{inital} and T_{final}

Reaction Time = T_{final} - $T_{initial}$ (minutes)

V = Sample volume (mL) added to well

GDH activity is reported as nmole/min/mL = milliunit/mL

One unit of GDH is the amount of enzyme that will generate 1.0 µmole of NADH per minute at pH 7.6 at 37 °C.

The procedure used for determining the ALDH and GDH activities was according to sigma-aldrich.com. The normality of the data verification ensured that there were no outliers and that the data followed a normal distribution. Data analysis also proceeded statistically for the studied traits according to the design used.

RESULTS AND DISCUSSION

Plant height

The results revealed that the wheat genotypes' different genetic constitutions significantly affected the plant height (Table 1). Genotype G14 showed the highest mean plant height (117.2 cm), with an increase rate of 46.46%, compared with the genotype G5 recorded with the lowest plant height (80 cm). A reason might be due to the genetic difference of these genotypes for the said trait, as it is one of the characteristics linked to the genetic composition and growth factors for length and the number of internodes, which manifested in the plant height. Ali and Al-Shugeairy (2023) and Hussein and Al-Shugeairy (2023) also found significant differences in genotypes for the plant stature. Moreover, the results indicated that irrigation intervals substantially affected the plant height, which revealed notable variations among the wheat genotypes' plant height. The wheat genotypes grown with an irrigation interval of five days showed an

Table 1. Effect of wheat genotypes, irrigation intervals, and their interaction on the plant height.

Genotypes	Irrigation Intervals		Means (cm)
	14 days	5 days	
G1	81.3	80.0	80.7
G2	78.0	85.3	81.7
G3	90.3	91.0	90.7
G4	95.3	91.7	93.5
G5	70.7	89.3	80.0
G6	84.3	85.0	84.7
G7	88.0	86.0	87.0
G8	89.0	88.0	88.5
G9	87.7	78.0	82.8
G10	98.3	110.3	104.3
G11	79.0	95.7	87.3
G12	83.3	84.7	84.0
G13	90.0	82.3	86.2
G14	118.3	116.0	117.2
G15	91.7	93.3	92.5
Means (cm)	88.4	90.4	

$LSD_{0.05}$ Genotypes: 4.538**, Irrigation Intervals: 0.817*, C × I Interaction: 6.211**

increased plant height relative to genotypes irrigated with 14-day intervals, and an study factors on the plant height, and genotype G14, with an irrigation interval of 14 days, showed the highest plant height (118.3 cm) (Table 1).

Tillers per m^2

The wheat genotypes revealed significant differences for tillers per meter square (Table 2). Genotype G2 enunciated the utmost mean (1030 tiller m^{-2}); however, the said genotype did not differ significantly from the genotype G11 (1010 tiller m^{-2}), with an observed increase rate of 128.89% and 124.44%, respectively, compared with the genotype G14, recording the lowest mean (450 tiller m^{-2}). The differences in genotypes for the said trait might be due to the dissimilarity in their genetic structure for their ability to provide more tillers. The nature of the shoot system and the growth length period are apparent in the increased size of the shoot, its efficiency in intercepting light, and its investment in raising the rates of assimilation of nutrients and their distribution to the shoots that grow (Wuhaib *et al.*, 2018). These results were also analogous to the findings of Ziara (2014), who also reported significant differences among the wheat genotypes for tillers per plant.

The results further revealed significant differences between the irrigation durations for the number of tillers (Table 2). The irrigation duration of five days showed the highest mean for the said trait (780.7 tiller m^{-2}) with an increase of 20.44% compared with the irrigation interval of 14 days, recording the lowest mean (648.2 tiller m^{-2}). These results were consistent with the findings of Endris and Mohammed (2007), who also reported a notable decrease in the number of tillers in wheat genotypes from exposure to water stress conditions. The outcomes further indicated a relevant effect of the interaction between genotypes and irrigation duration on the trait. The interaction of wheat genotypes and irrigation intervals resulted in the differences for tillers per meter square (Table 2). The genotype G2, with an irrigation interval of five days, showed the maximum mean (1165 tiller m^{-2}); however, it did not differ

remarkably from the genotype G11 with the same irrigation duration (1160 tiller m^{-2}).

Spikes per m^2

The results exhibited meaningful differences among the genotypes, irrigation durations, and their interactions for spikes m^2 (Table 3). The genotype G11 showed the highest mean number of spikes per square meter (975.8 spikes m^{-2}) but did not differ significantly from the genotype G2 (962.5 spikes m^{-2}). Both genotypes showed an increased number of spikes per meter (135.13% and 131.93%, respectively) compared with the genotype G14, with a recorded lowest mean (415 spikes m^{-2}). Perhaps it might be due to the difference between the genotypes for their ability to produce more or less tillers per plant. It is because wheat genotypes with a high ability to produce metabolic materials that support shoot's natural growth and development ably produced the highest number of spikes per unit area compared to genotypes with a limited ability to produce tillers (Table 2). These results agreed with the findings of Rabiei *et al.* (2012), who concluded that the variation in the number of spikes came as a result of the variation of genetic composition to produce shoots and metabolic materials that extend the growth of shoots until they turn into fertile shoots (Carr *et al.*, 2003). In cereal crops, the stage of shoot production is one of the most crucial physiological processes during the vegetative growth period (Mitchell *et al.*, 2013; Jessup *et al*, 2020).

The results showed significant differences between irrigation durations for the number of spikes (Table 3). The irrigation duration of five days gave the highest mean number of spikes (729.8 spikes m^{-2}), with an increased rate of 21.80% compared with the irrigation interval of 14 days, with the lowest mean number of spikes (599.2 spike m^{-2}). The decrease in spikes with a 14-day irrigation interval might be due to unavailable nutrients in the stages of emergence and seedling development, causing higher competition for metabolic materials and lowering the number of tillers bearing spikes (Gonzalez *et al.*, 2007). A significant effect of the interaction between

Table 2. Effect of wheat genotypes, irrigation intervals, and their interaction on the number of tillers per square meter.

Genotypes	Irrigation Intervals		Means (tiller m^{-2})
	14 days	5 days	
G1	553.3	825.0	689.2
G2	895.0	1165.0	1030.0
G3	498.3	601.7	550.0
G4	385.0	625.0	505.0
G5	755.0	888.3	821.7
G6	488.3	545.0	516.7
G7	660.0	756.7	708.3
G8	793.3	765.0	779.2
G9	480.0	583.3	531.7
G10	605.0	683.3	644.2
G11	861.7	1160.0	1010.8
G12	680.0	913.3	796.7
G13	746.7	746.7	746.7
G14	371.7	528.3	450.0
G15	950.0	923.3	936.7
Means (tiller m^{-2})	648.2	780.7	
LSD$_{0.05}$ Genotypes: 74.61**, Irrigation Intervals: 50.40*, C × I Interaction: 104.54**			

Table 3. Effect of wheat genotypes, irrigation intervals, and their interaction on the number of spikes per square meter.

Genotypes	Irrigation Intervals		Means (spikes m^{-2})
	14 days	5 days	
G1	480.0	783.3	631.7
G2	825.0	1100.0	962.5
G3	460.0	570.0	515.0
G4	360.0	585.0	472.5
G5	683.3	840.0	761.7
G6	461.7	503.3	482.5
G7	625.0	691.7	658.3
G8	706.7	711.7	709.2
G9	446.7	518.3	482.5
G10	545.0	613.3	579.2
G11	818.3	1133.3	975.8
G12	635.0	848.3	741.7
G13	695.0	696.7	695.8
G14	343.3	486.7	415.0
G15	903.3	865.0	884.2
Means (spikes m^{-2})	599.2	729.8	
LSD$_{0.05}$ Genotypes: 79.58**, Irrigation Intervals: 32.96*, C × I Interaction: 109.74**			

the studied factors on the said trait also occurred (Table 3). It indicates that the genotypes behaved differently due to the influence of irrigation durations, with the wheat genotype G11 recorded with the highest mean for an irrigation duration of five days (1133.3 spikes m^{-2}). However, it did not differ significantly from the genotype G2 with the irrigation regime (1100 spikes m^{-2}).

Spike length

The wheat genotypes enunciated a marked impact on the spike length trait (Table 4). The

Table 4. Effect of wheat genotypes, irrigation intervals, and their interaction on the spike length.

Genotypes	Irrigation Intervals		Means (cm)
	14 days	5 days	
G1	7.00	7.67	7.33
G2	8.17	8.17	8.17
G3	7.33	9.00	8.17
G4	10.67	11.67	11.17
G5	6.83	8.17	7.50
G6	5.83	7.00	6.42
G7	7.50	7.50	7.50
G8	6.83	10.33	8.58
G9	9.00	7.67	8.33
G10	7.83	9.00	8.42
G11	9.00	8.17	8.58
G12	9.00	10.00	9.50
G13	9.17	10.17	9.67
G14	8.83	9.83	9.33
G15	8.00	7.83	7.92
Means (cm)	8.07	8.81	

LSD$_{0.05}$ Genotypes: 1.677**, Irrigation Intervals: N.S, C × I Interaction: N.S.

genotype G4 proved superior by giving the highest mean of spike length (11.17 cm), with an increased rate of 73.99% compared with the genotype G6, providing the lowest mean of 6.42 cm. The difference among the genotypes could be because of the influence of the genetic factor, as also mentioned in past studies on wheat genotypes (Sharma *et al*., 2003; Al-Anbari, 2004; Al-Falahi *et al.,* 2021). However, there were nonsignificant outcomes of the irrigation intervals and their interaction with wheat genotypes on the spike length.

Grains per spike

The results attained considerable variations among the wheat genotypes for grains per spike (Table 5). The wheat genotype G12 showed the utmost mean of 40.9 grains spike^{-1}; however, it did not differ significantly from the genotype G11 (39.8 grain spike^{-1}). The above-promising genotypes showed an increased rate of 75.54% and 70.82%, respectively, compared with genotype G5, giving the lowest number of grains per spike (23.3). Among the wheat genotypes, the differences may refer to the genetic disparities among the genotypes for the trait. The superiority of some genotypes may be due to the genetic structure, as the grains per spike quantitative trait is one determined genetically

(Al-Majidy *et al.,* 2017; Al-Kafaei, 2018). Al-Mehemdi and Abed (2016) also reported the maximum and minimum number of grains per spike in barley (50.01 and 45.99, respectively). The irrigation intervals showed nonsignificant differences for the grains per spike. The results indicated a notable influence of the interaction between the studied factors on this trait, as the increase in the number of grains was relevant (Table 5), with the genotype G11 recorded with the highest mean with an irrigation duration of 14 days (51.7 grain spike^{-1}).

A thousand-grain weight

The data revealed a significant effect of wheat genotypes on the 1000-grain weight (Table 6). The genotype G6 showed the highest mean for the said trait (40.8 g), with an increase of 65.18% compared with two other genotypes, G3 and G4, which gave the lowest mean (24.7 g). The superiority of genotype G6 may refer to the genetic structure leading to a shorter spike length (Table 4) and a decrease in the number of grains per spike (Table 5), enhancing grain size and weight. These results aligned with the findings of Valerio *et al*. (2009), Wuhaib *et al*. (2017), and Mahdi and Omran (2021), who also reported that it might be due to the compensation mechanism that

Table 5. Effect of wheat genotypes, irrigation intervals, and their interaction on the number of grains per spike.

Genotypes	Irrigation Intervals		Means (grains spike^{-1})
	14 days	5 days	
G1	21.2	30.3	25.8
G2	23.5	37.0	30.3
G3	21.7	49.0	35.3
G4	37.0	29.7	33.3
G5	21.0	25.7	23.3
G6	17.7	30.3	24.0
G7	28.7	30.0	29.3
G8	22.7	44.7	33.7
G9	37.7	29.7	33.7
G10	30.3	29.0	29.7
G11	51.7	28.0	39.8
G12	39.2	42.7	40.9
G13	41.5	36.0	38.8
G14	35.3	39.3	37.3
G15	21.0	42.8	31.9
Means (grains spike^{-1})	30.0	34.9	
LSD$_{0.05}$ Genotypes: 5.724**, Irrigation Intervals: N.S., C × I Interaction: 8.360**			

Table 6. Effect of wheat genotypes, irrigation intervals, and their interaction on the 1000-grain weight.

Genotypes	Irrigation Intervals		Means (g)
	14 days	5 days	
G1	34.3	27.7	31.0
G2	30.4	26.5	28.5
G3	24.0	25.5	24.7
G4	24.0	25.3	24.7
G5	28.7	34.8	31.7
G6	38.8	42.8	40.8
G7	31.2	35.0	33.1
G8	26.4	28.3	27.3
G9	42.0	32.9	37.5
G10	27.5	29.1	28.3
G11	34.5	29.3	31.9
G12	29.0	33.3	31.2
G13	33.0	30.1	31.5
G14	25.7	29.1	27.4
G15	32.2	32.6	32.4
Means (g)	30.8	30.8	
LSD$_{0.05}$ Genotypes: 5.58*, Irrigation Intervals: N.S., C × I Interaction: N.S.			

worked to enhance the grain yield. The results further revealed the nonsignificant effect of irrigation durations and their interaction with wheat genotypes on the 1000-grain weight.

Grain yield

Remarkable differences were visible among the wheat genotypes for grain yield (Table 7).

Table 7. Effect of wheat genotypes, irrigation intervals, and their interaction on the grain yield.

Genotypes	Irrigation Intervals		Means (t ha^{-1})
	14 days	5 days	
G1	3.166	7.579	5.372
G2	6.013	9.055	7.534
G3	2.787	4.122	3.455
G4	2.783	4.350	3.567
G5	3.741	10.629	7.185
G6	2.630	4.950	3.790
G7	5.142	8.209	6.675
G8	4.336	9.323	6.830
G9	6.027	6.016	6.022
G10	4.796	7.327	6.062
G11	9.594	11.855	10.725
G12	8.116	11.193	9.655
G13	6.891	8.714	7.803
G14	4.351	4.840	4.596
G15	8.834	9.389	9.111
Means (t ha^{-1})	5.281	7.837	
LSD$_{0.05}$ Genotypes: 0.860**, Irrigation Intervals: 0.433*, C × I Interaction: 1.191**			

Genotype G11 provided the maximum grain yield (10.725 t ha^{-1}), with an increase of 210.42% compared with genotype G3, providing the minimum mean grain yield (3.455 t ha^{-1}). The G11's superiority in the grain yield was due to its dominance in the characteristics, i.e., the number of tillers, spikes, and grains per spike (Tables 2, 3, and 5, respectively). These results were in contest with past findings, which showed a notable difference between the studied genotypes in the grain yield per unit area (Ahmed and Al-Amiri, 2012; Al-Rijabo *et al.*, 2014; Al-Temimi and Abed, 2016; Khurshid, 2022).

The results signified substantial differences between irrigation durations for total grain yield (Table 7). The irrigation duration of five days provided the highest mean grain yield (7.837 t ha^{-1}), with an increase of 48.4% versus the irrigation interval of 14 days (5.281 t ha^{-1}). The outcomes further revealed a significant influence of the genotypes by irrigation regimes' interaction on the grain yield. Genotype G11 appeared with the maximum mean with an irrigation duration of five days (11.855 t ha^{-1}); however, it did not differ significantly from genotype G12 with the same irrigation interval (11.193 t ha^{-1}).

Biological yield

The data showed remarkable variations among the wheat genotypes for the biological yield (Table 8). Genotype G11 proved superior for the said trait, giving the highest biological yield (29.568 t ha^{-1}), with an increase of 129.58% compared with genotype G6, recording the lowest biological yield (12.879 t ha^{-1}). The superiority of the genotype G11 in biological yield was due to its supremacy in the number of tillers, spikes, grains per spike, and grain yield (Tables 2, 4, 5, and 7, respectively). These results were in higher analogy with the findings of Al-Kafaei (2018), Jessup *et al.* (2020), and Sun *et al.* (2013), as they also reported that the high-yielding genotypes have a distinction for better dry matter accumulation by increasing the effectiveness of carbon metabolism.

The results revealed noteworthy variances between irrigation durations for the biological yield (Table 8). The irrigation duration of a five-day interval provided the utmost mean biological yield (22.323 t ha^{-1}), with an increase of 28.92% compared with the irrigation duration of 14 days (17.315 t ha^{-1}). The biological yield from the irrigation duration

of a five-day interval appeared for plant height and tillers per square meter (Tables 1 and 2). A significant effect of the interaction between the studied factors on the said trait emerged, and wheat genotype G11 with an irrigation interval of five days recorded the highest mean of biological yield (32.876 t ha^{-1}).

Aldehyde dehydrogenase (ALDH) activity

The outcomes showed significant differences among the wheat genotypes for aldehyde dehydrogenase activity (Table 9). Genotype G11 provided the maximum mean for the said trait (9.620 milliunit/mL) compared with genotype G5, recording the minimum mean (1.308 milliunit/mL). However, the genotypes did not differ significantly from the wheat genotype G13. The irrigation regimes indicated nonsignificant differences in aldehyde dehydrogenase activity. On interaction effects, most wheat genotypes gave more aldehyde dehydrogenase activity with an irrigation interval of 14 days than the five-day interval, except for wheat genotypes G7 and G15. A notable influence arose on the interaction between the studied factors on aldehyde dehydrogenase activity, with genotype G11 recording the highest mean with an irrigation duration of 14 days (10 milliunit/mL).

Glutamate dehydrogenase (GDH) activity

Wheat genotypes revealed remarkable differences in glutamate dehydrogenase activity (Table 10). Wheat genotype G1 exhibited the highest mean (9.62 milliunits/mL) compared with genotype G8, which showed the lowest mean (2.91 milliunits/mL). The irrigation durations indicated substantial variations in glutamate dehydrogenase activity. The irrigation duration of 14 days gave the higher mean of glutamate dehydrogenase activity (6.94 milliunit/Ml), with an increase of 64.07% than the irrigation duration of five days, contributing a lower mean of glutamate dehydrogenase activity (4.23 milliunit/mL). Additionally, a considerable impact surfaced in the interaction between the wheat genotypes and irrigation regimes on the glutamate dehydrogenase activity, and the wheat genotype G1 was superior with the maximum mean at irrigation duration of 14 days (11.79 milliunit/mL).

Table 8. Effect of wheat genotypes, irrigation intervals, and their interaction on the biological yield.

Genotypes	Irrigation Interval		Means (t ha^{-1})
	14 days	5 days	
G1	10.232	19.273	14.753
G2	15.992	24.857	20.424
G3	13.345	16.478	14.912
G4	14.067	21.098	17.582
G5	15.542	24.165	19.854
G6	12.262	13.495	12.879
G7	16.420	19.930	18.175
G8	19.517	23.381	21.449
G9	14.078	17.581	15.830
G10	20.718	22.671	21.694
G11	26.260	32.876	29.568
G12	21.418	29.034	25.226
G13	19.031	23.129	21.080
G14	18.357	22.372	20.365
G15	22.478	24.507	23.493
Means (t ha^{-1})	17.315	22.323	

LSD$_{0.05}$ Genotypes: 2.876**, Irrigation Intervals: 1.804*, C × I Interaction: N.S.

Table 9. Effect of wheat genotypes, irrigation intervals, and their interaction on the aldehyde dehydrogenases (ALDH) activity.

Genotypes	Irrigation Intervals		Means (milliunit/mL)
	14 days	5 days	
G1	4.565	3.095	3.830
G2	3.620	2.280	2.950
G3	3.335	1.475	2.405
G4	4.995	3.055	4.025
G5	1.690	0.925	1.308
G6	4.170	3.950	4.060
G7	4.830	7.685	6.258
G8	1.740	1.355	1.548
G9	3.035	1.615	2.325
G10	7.575	5.405	6.490
G11	10.000	9.240	9.620
G12	6.410	5.035	5.723
G13	1.830	0.905	1.368
G14	3.895	2.385	3.140
G15	2.400	2.460	2.430
Means (milliunit/mL)	4.273	3.391	

LSD$_{0.05}$ Genotypes: 1.0535**, Irrigation Intervals: N.S., C × I Interaction: 1.6876**

Table 10. Effect of wheat genotypes, irrigation intervals, and their interaction on the glutamate dehydrogenases (GDH) activity.

Genotypes	Irrigation Intervals		Means (milliunit/mL)
	14 days	5 days	
G1	11.79	7.44	9.62
G2	8.52	5.41	6.97
G3	5.57	2.93	4.25
G4	3.36	3.68	3.52
G5	5.34	2.78	4.06
G6	4.00	2.63	3.32
G7	8.42	7.97	8.20
G8	4.33	1.49	2.91
G9	7.32	5.83	6.58
G10	9.54	2.85	6.19
G11	6.05	2.28	4.17
G12	3.72	2.67	3.19
G13	5.45	4.47	4.96
G14	11.57	8.44	10.01
G15	9.14	2.49	5.82
Means (milliunit/mL)	6.94	4.23	

LSD$_{0.05}$ Genotypes: 1.618**, Irrigation Intervals: 0.860**, C × I Interaction: 2.245**

CONCLUSIONS

Water stress caused a significant decrease in almost all the studied traits compared with the irrigated treatments. Genotypes also varied in their response to water stress, as Genotype G11 showed the highest values in aldehyde dehydrogenase activity, spike per meter, grain yield, and biological yield, and Genotype G2 was successful with the maximum value in tillers per meter, G6 in 1000-grain weight, and G12 in grains per spike. Therefore, these genotypes can be advantageous in breeding and genetic improvement programs.

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