



Evaluation of Exogenous Metabolites for Improving Grain Yield and Yield Components of Wheat (*Triticum aestivum* L.) under Drought Stress

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

Drought stress is a major abiotic constraint affecting wheat productivity. The present investigation evaluated the effects of different metabolite treatments on grain yield in four wheat genotypes under drought-stressed and irrigated conditions. The experiment was conducted in a randomised block design with three replications during the Rabi season of 2022–2023 at the Agricultural Research Field, Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi. Four wheat genotypes, namely PBW 343, HUW 468, HUW 510 and RAJ 3567, were evaluated under nine treatments (C, GD1, GD2, LD1, LD2, SD1, SD2, TD1 and TD2). Grain yield data were subjected to analysis of variance to determine the effects of treatments, genotypes and their interaction. The results revealed highly significant effects of treatment, genotype and the treatment × genotype interaction on grain yield under both drought-stressed and irrigated conditions ($p < 0.001$). Under drought stress, the highest grain yield in PBW 343 was recorded with

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SD1 (556.00), whereas HUW 468 showed its highest yield with LD1 (478.00). In HUW 510, the highest yield was recorded with GD2 and SD2 (464.00), whereas RAJ 3567 performed best with TD2 (496.00). Under irrigated conditions, the highest grain yields were observed with GD1 in PBW 343 (622.00), GD2 in HUW 468 (498.00), LD1 in HUW 510 (438.00) and SD1 in RAJ 3567 (512.00). The significant treatment $\times$ genotype interaction indicated differential responses of wheat genotypes to metabolite treatments under contrasting water regimes. These findings identify promising genotype–treatment combinations for further evaluation to improve wheat productivity under drought stress. However, multi-season and multi-environment validation is required before broader recommendations can be made.

Keywords: *Wheat; drought stress; metabolite treatments; grain yield; genotype $\times$ treatment interaction; irrigated conditions.*

1. Introduction

The cultivated species of wheat is *Triticum aestivum* L., commonly known as bread wheat. Bread wheat accounts for approximately 95% of total wheat production worldwide. It belongs to the Poaceae family and is cultivated worldwide, although it originally came from Ethiopia and the Levant region of the East. Wheat is an important cereal crop grown worldwide and has been called the 'King of Cereals' because of its high demand and prominent position in international food-grain trade. Members of the *Triticum* group include bread wheat, which accounts for more than 90% of the nation's total wheat-growing area.

China produces the most wheat worldwide, with an annual production of approximately 126 million metric tonnes from an area of 24 million hectares. According to the United States Department of Agriculture (USDA, 2019), global wheat production during the 2018–19 crop year was 731.35 million tonnes. The USDA projected global wheat production of 765.41 million metric tonnes in 2019/2020. The average productivity of wheat in India during the 2018–19 season was 34.24 q/ha over an area of 29.55 million hectares (IIWBR, 2019). This resulted in a production volume of 101.20 million tonnes in 2018–2019 in Haryana. Wheat is a winter, or Rabi-season, crop. The most favourable growing conditions are cool and moist during the vegetative stage, followed by dry and warm weather during maturation and ripening. Temperatures between 20 and 25 °C are considered ideal for wheat seed germination. By 2050, the world's population is expected to reach approximately 9 billion. Wheat production must increase by 1.6% annually to achieve a 60% net increase by 2050 and feed this population (Giraldo *et al.*, 2019).

Dry and semi-arid regions experience more severe drought stress, which substantially reduces plant productivity. According to Araus *et al.* (2002), the effects of water stress on wheat production depend on the cultivar, duration of stress, crop growth stage and intensity of stress. Physiological characteristics are indicators of yield stability and can be used to evaluate the drought resistance of wheat genotypes. Physiological responses include stomatal closure, reduced photosynthesis, oxidative stress, changes in cell wall integrity and the production of metabolites that are toxic to plants (Bray, 2002). Genotypes that maintain normal growth and yield during water deficits are less affected by stress and can maintain higher leaf water content (Beltrano *et al.*, 2006). Changes in antioxidant enzyme activity and physiological characteristics of wheat under drought stress have also been reported (Sheoran *et al.*, 2015).

A study of plant growth-promoting rhizobacteria in wheat seedlings also reported changes in physiological and biochemical responses under simulated drought stress (Gigaulia *et al.*, 2024).

Drought-tolerant species regulate stomatal function to permit carbon fixation under stress, improve water-use efficiency or reopen stomata rapidly when water deficits are alleviated. Drought affects photosynthetic pigments differently across species and genotypes. Tolerant genotypes typically accumulate soluble sugars, amino acids, proline and chlorophyll and exhibit antioxidant enzymatic and non-enzymatic activities.

Foliar application of glycine betaine in combination with cytokinins has been examined in relation to photosynthetic characteristics and biological yield in drought-stressed wheat (Kaur *et al.*, 2025).

Further research is needed to understand the mechanisms underlying drought tolerance in wheat and the roles of compounds such as GABA, serine, threonine and lysine. This knowledge may facilitate the development of crop varieties that are more resilient to changing environmental conditions. Several important metabolites play roles in plant adaptive responses involving complex metabolic processes. Notable examples include gamma-aminobutyric acid (GABA), serine, threonine and leucine. During drought stress, the non-protein amino acid GABA plays an important signalling role. It helps regulate osmotic balance and reduce oxidative stress by scavenging reactive oxygen species (ROS). The role of GABA in drought-tolerance mechanisms was highlighted by Mekonnen *et al.* (2016). According to Yadav *et al.* (2019), the amino acid serine is associated with drought tolerance. Leucine, another essential amino acid, is important for maintaining cellular integrity and regulating the expression of stress-responsive genes during drought. The role of leucine in improving drought tolerance has been examined in research by Chen *et al.* (2012).

Exogenous application of GABA has been associated with changes in physiological and antioxidant responses in wheat seedlings under drought stress (Zhao *et al.*, 2023). A study of foliar treatments containing serine reported responses in wheat growth and grain yield under drought-induced oxidative stress (Hameed *et al.*, 2023). A separate investigation associated amino acid metabolism during wheat grain filling with responses to post-anthesis drought stress and examined the role of glutamate (Li *et al.*, 2024). Nevertheless, the relative of the selected GABA, serine, threonine and leucine treatments and doses on grain yield and yield-associated traits across the four wheat genotypes under contrasting water regimes require direct evaluation.

Accordingly, the objective of the present study was to compare two doses each of GABA, serine, threonine and leucine with a control for their effects on grain yield and yield-associated traits in PBW 343, HUW 468, HUW 510 and RAJ 3567 under drought-stressed and irrigated conditions.

2. Materials and Methods

Seeds of all four genotypes were sown in a randomised block design (RBD), with three replications under stress and three under control conditions, during the Rabi season of 2022–23 at the Agricultural Research Field, Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi. Each plot comprised paired rows 2 m long, with 20 cm between rows and 5 cm between plants in each replication. Observations were recorded from five randomly selected plants of each genotype for the following characteristics: spikelet number, flag leaf length (cm), NDVI at the heading stage, NDVI at the flowering stage, canopy temperature at the heading stage, canopy temperature at the flowering stage, SPAD at the heading stage, plant height, peduncle length, spike length, biomass (kg), test weight (g) and grain yield (g).

The experimental material comprised four commercially grown wheat genotypes: RAJ 3567, PBW 343, HUW 510 and HUW 468. These genotypes were evaluated to characterise the effects of metabolite doses on drought tolerance at the Agricultural Research Field, Institute of Agricultural Sciences, BHU, Varanasi.

Eight different dose treatments were applied by spraying the following metabolites at the heading and flowering stages of field-grown wheat genotypes under both irrigated and drought-stressed conditions.

Table 1. Various metabolites treatments

Treatments	IC1	IC2	IC3	D1	D2	D3
Control T20 (C)	T20	T20	T20	T20	T20	T20
GABA Dose 1 (GD1)	1mM	1mM	1mM	1mM	1mM	1mM
GABA Dose 2 (GD2)	20mM	20mM	20mM	20mM	20mM	20mM
Serine Dose 1 (SD1)	1mM	1mM	1mM	1mM	1mM	1mM
Serine Dose 2 (SD2)	2mM	2mM	2mM	2mM	2mM	2mM
Threonine Dose 1 (TD1)	1mM	1mM	1mM	1mM	1mM	1mM
Threonine Dose 2 (TD2)	20mM	20mM	20mM	20mM	20mM	20mM
Leucine Dose 1 (LD1)	1mM	1mM	1mM	1mM	1mM	1mM
Leucine Dose 2 (LD2)	20mM	20mM	20mM	20mM	20mM	20mM

2.1 ANOVA (Analysis of Variance)

Variance is a measure of variability. The two main objectives of analysis of variance are:

- To partition variance among different sources.
- To provide a basis for tests of significance.

It is used to test the significance of variation among genotypes using the statistical method described by Panse and Sukhatme (1954).

Two-way ANOVA:

Two-way ANOVA is used to investigate the combined effects of two independent factors (variables) on a measured dependent variable.

Chart 1. ANOVA table

Source of variation	Degree of freedom	Sum of squares	Mean square	F
Factor A	$k - 1$	SSA	$MSA = \frac{SSA}{k-1}$	$F_A = \frac{MSA}{MSE}$
Factor B	$l - 1$	SSB	$MSB = \frac{SSB}{l-1}$	$F_B = \frac{MSB}{MSE}$
Interaction AB	$(k - 1)(l - 1)$	SSAB	$MSAB = \frac{SSAB}{(k-1)(l-1)}$	$F_{AB} = \frac{MSAB}{MSE}$
Error	$kl(m - 1)$	SSE	$MSE = \frac{SSE}{kl(m-1)}$	
Total	$klm - 1$	SST		

Where,

k = number of levels of factor A

l = number of levels of factor B

kl = number of treatments (each one a combination of a factor A level and a factor B level)

m = number of observations on each treatment

SST = Total sum of square

SSA = Factor A main effect sum of square

SSAB = Interaction sum of square

SSE = Error sum of square

2.2 Test of Significance

Mean squares due to genotypes were tested against the error variance using an F-test at the 5% and 1% significance levels. If the calculated F-value is greater than the tabulated F-value, the variation between treatments is considered significant, and vice versa.

2.3 Selection Parameters

Mean: The mean value for each characteristic was calculated by summing all observations and dividing by the corresponding number of observations.

$$\bar{X} = \frac{\sum_{i=1}^N Xi}{N}$$

Where,

$\bar{X}$ = mean

$\sum_{i=1}^N Xi$ = Sum of all observations

N = Number of observations

Range: In statistics, the range of a dataset is the difference between its largest and smallest values. It indicates statistical dispersion and is expressed in the same units as the data. Because it depends on only two observations, it is particularly useful for describing the dispersion of small datasets.

$$\text{Range} = (\text{Highest value of an item in a series}) - (\text{Lowest value of an item in a series})$$

Standard deviation: Standard deviation is a widely used measure of dispersion and is commonly denoted by the symbol 'σ' (sigma). It is defined as the square root of the average of the squared deviations of individual values from the arithmetic mean.

$$\text{Standard deviation } (\sigma) = \sqrt{\frac{\sum (xi - \mu)^2}{N}}$$

Where,

σ = population standard deviation

N = the size of the population

xi = each value from the population

μ = the population mean

Standard error: The standard error (SE) of a statistic is an estimate of the standard deviation of its sampling distribution. It indicates the precision with which a sample statistic estimates the corresponding population parameter.

$$SE = \frac{\sigma}{\sqrt{n}}$$

Where,

SE = standard error of the sample

σ = sample standard deviation

n = number of samples

3. Results and Discussion

3.1 Biomass (BM)

The mean and range of biomass (BM) for different wheat genotypes under drought-stressed and irrigated conditions are presented in Tables 2 and 3.

Under drought-stressed conditions, PBW 343, HUW 468, HUW 510 and RAJ 3567 showed the highest biomass (BM) with the LD1, LD1 and control (TWIN 20) treatments, respectively, with mean values of 1.62 kg, 1.53 kg, 1.49 kg and 1.53 kg. The corresponding ranges were 1.58–1.68 kg, 1.50–1.57 kg, 1.44–1.52 kg and 1.48–1.56 kg. The lowest biomass values were recorded with LD2, LD2, GD2 and SD1, respectively, with means of 0.92 kg, 1.01 kg, 0.15 kg and 1.01 kg. The corresponding ranges were 0.92–0.92 kg, 1.01–1.02 kg, 0.15–0.15 kg and 1.01–1.01 kg per plot, respectively.

Under irrigated conditions, PBW 343, HUW 468, HUW 510 and RAJ 3567 showed the highest biomass (BM) with GD1, SD1, LD1 and SD1, respectively, with mean values of 1.65 kg, 1.51 kg, 1.28 kg and 1.56 kg. The corresponding ranges were 1.63–1.68 kg, 1.46–1.57 kg, 1.28–1.29 kg and 1.55–1.59 kg. The lowest biomass values were obtained with SD2 in all four genotypes, with means of 0.98 kg, 0.70 kg, 1.1 kg and 0.96 kg, respectively. The corresponding ranges were 0.97–0.99 kg, 0.68–0.73 kg, 1.09–1.11 kg and 0.92–0.99 kg per plot, respectively.

Table 2. Mean, Range, SD and SE performance of Wheat genotype under different metabolite concentration of Biomass under drought condition

Sr no	Treatment	Mean	Range		Standard deviation	Standard error
			Min	Max		
PBW 343						
1	C	1.15	1.10	1.19	0.0509	0.0294
2	GD1	1.47	1.47	1.49	0.0106	0.0061
3	GD2	1.48	1.47	1.48	0.0027	0.0015
4	LD1	1.62	1.58	1.68	0.0512	0.0295
5	LD2	0.92	0.92	0.92	0.0025	0.0014
6	SD1	1.23	1.22	1.24	0.0089	0.0051
7	SD2	1.68	1.65	1.73	0.0440	0.0254
8	TD1	1.04	1.04	1.05	0.0028	0.0016
9	TD2	1.53	1.49	1.56	0.0387	0.0223
HUW 468						
10	C	1.46	1.45	1.47	0.0132	0.0076
11	GD1	1.40	1.37	1.44	0.0379	0.0219
12	GD2	1.38	1.36	1.39	0.0149	0.0086
13	LD1	1.53	1.50	1.57	0.0373	0.0215
14	LD2	1.01	1.01	1.02	0.0036	0.0021
15	SD1	1.17	1.12	1.20	0.0452	0.0261
16	SD2	1.47	1.40	1.52	0.0635	0.0367
17	TD1	1.10	1.08	1.13	0.0259	0.0149
18	TD2	1.52	1.47	1.58	0.0575	0.0332
HUW 510						
19	C	0.98	0.95	1.00	0.0248	0.0143
20	GD1	0.92	0.91	0.93	0.0116	0.0067
21	GD2	0.15	0.15	0.15	0.0007	0.0004
22	LD1	1.16	1.13	1.17	0.0208	0.0120
23	LD2	1.12	1.10	1.13	0.0141	0.0082
24	SD1	1.17	1.13	1.20	0.0390	0.0225
25	SD2	1.49	1.44	1.52	0.0388	0.0224
26	TD1	1.21	1.16	1.25	0.0471	0.0272
27	TD2	1.48	1.46	1.49	0.0173	0.0100
RAJ 3567						
28	C	1.53	1.48	1.56	0.0413	0.0238
29	GD1	1.14	1.11	1.17	0.0299	0.0172
30	GD2	1.11	1.09	1.14	0.0300	0.0173
31	LD1	1.29	1.27	1.31	0.0175	0.0101
32	LD2	1.07	1.07	1.07	0.0010	0.0006
33	SD1	1.01	1.01	1.02	0.0018	0.0011
34	SD2	1.38	1.36	1.42	0.0311	0.0180
35	TD1	1.24	1.22	1.27	0.0213	0.0123
36	TD2	1.16	1.14	1.17	0.0125	0.0072

Table 3. Mean, Range, SD and SE performance of Wheat genotype under different metabolite concentration of Biomass under irrigated condition

Sr no	Treatment	Mean	Range		Standard deviation	Standard error
			Min	Max		
PBW 343						
1	C	1.36	1.31	1.39	0.0417	0.0241
2	GD1	1.65	1.63	1.68	0.0253	0.0146
3	GD2	1.65	1.62	1.68	0.0313	0.0181
4	LD1	1.08	1.07	1.09	0.0146	0.0084
5	LD2	1.54	1.50	1.61	0.0557	0.0321
6	SD1	1.36	1.34	1.39	0.0258	0.0149
7	SD2	0.98	0.97	0.99	0.0062	0.0036
8	TD1	1.33	1.29	1.38	0.0454	0.0262
9	TD2	1.47	1.44	1.51	0.0398	0.0230
HUW 468						
10	C	1.25	1.20	1.31	0.0517	0.0299
11	GD1	1.50	1.49	1.51	0.0108	0.0063
12	GD2	1.37	1.36	1.38	0.0074	0.0043
13	LD1	1.13	1.10	1.15	0.0274	0.0158
14	LD2	1.32	1.27	1.37	0.0510	0.0294
15	SD1	1.51	1.46	1.57	0.0570	0.0329
16	SD2	0.70	0.68	0.73	0.0240	0.0138
17	TD1	1.40	1.38	1.41	0.0126	0.0073
18	TD2	1.28	1.25	1.32	0.0392	0.0226
HUW 510						
19	C	1.20	1.16	1.23	0.0378	0.0218
20	GD1	1.25	1.20	1.28	0.0427	0.0247
21	GD2	1.26	1.22	1.30	0.0422	0.0243
22	LD1	1.28	1.28	1.29	0.0069	0.0040
23	LD2	1.18	1.16	1.21	0.0255	0.0147
24	SD1	1.28	1.26	1.31	0.0242	0.0140
25	SD2	1.10	1.09	1.11	0.0089	0.0052
26	TD1	1.22	1.21	1.23	0.0110	0.0063
27	TD2	1.22	1.18	1.28	0.0539	0.0311
RAJ 3567						
28	C	1.28	1.24	1.34	0.0531	0.0306
29	GD1	1.36	1.30	1.40	0.0526	0.0303
30	GD2	1.41	1.40	1.43	0.0115	0.0066
31	LD1	1.11	1.09	1.13	0.0200	0.0116
32	LD2	1.24	1.19	1.30	0.0524	0.0303
33	SD1	1.56	1.55	1.59	0.0211	0.0122
34	SD2	0.96	0.92	0.99	0.0356	0.0206
35	TD1	1.36	1.31	1.43	0.0601	0.0347
36	TD2	1.15	1.14	1.17	0.0156	0.0090

3.2 Grain Yield (GY)

The mean and range of grain yield (GY) for the four wheat genotypes under drought-stressed and irrigated conditions are presented in Tables 4 and 5.

Under drought-stressed conditions, PBW 343, HUW 468, HUW 510 and RAJ 3567 showed the highest grain yield (GY) with SD1, LD1, SD2 and TD2, respectively, with mean values of 556 g, 478 g, 464 g and 496 g. The corresponding ranges were 552.71–561 g, 455.14–495.21 g, 450.08–474.44 g and 487.57–502.32 g. The lowest grain yields were recorded with LD2, LD2, GD1 and LD2, respectively, with mean values of 246 g, 292 g, 252 g and 320.39 g. The corresponding ranges were 237.14–252.64 g, 290.03–294.63 g, 243.31–263.59 g and 319.43–322.29 g per plot, respectively.

Under irrigated conditions, PBW 343, HUW 468, HUW 510 and RAJ 3567 showed the highest grain yield (GY) with GD1, GD2, LD1 and SD1, respectively, with mean values of 622 g, 498 g, 438 g and 512 g. The corresponding ranges were 591.52–644.86 g, 493.14–504.47 g, 417.85–453.11 g and 510.46–513.15 g. The lowest grain yields were recorded with LD1, LD2 and LD1, with mean values of 334 g, 358 g, 290 g and 300 g. The corresponding ranges were 325.73–345.02 g, 348.33–370.89 g, 289.42–290.44 g and 299.40–300.45 g per plot, respectively.

3.3 Test Weight (1000 Seeds)

The mean and range of test weight (1,000 seeds) for the different wheat genotypes under drought-stressed and irrigated conditions are presented in Tables 6 and 7.

Table 4. Mean, Range, SD and SE performance of Wheat genotype under different metabolite concentration of Grain Yield under drought condition

Sr no	Treatment	Mean	Range		Standard deviation	Standard error
			Min	Max		
PBW 343						
1	C	384.00	379.10	390.53	5.8843	3.3973
2	GD1	494.00	475.85	518.21	21.8190	12.5972
3	GD2	547.00	524.03	564.23	20.7085	11.9560
4	LD1	504.00	486.86	516.85	15.4462	8.9179
5	LD2	246.00	237.14	252.64	7.9827	4.6088
6	SD1	556.00	552.25	561.00	4.5105	2.6042
7	SD2	538.00	519.71	551.72	16.4882	9.5195
8	TD1	366.00	363.80	367.65	1.9794	1.1428
9	TD2	534.00	513.17	549.62	18.7723	10.8382
HUW 468						
10	C	468.00	448.34	482.74	17.7177	10.2293
11	GD1	410.00	408.36	411.23	1.4783	0.8535
12	GD2	432.00	422.28	444.96	11.6820	6.7446
13	LD1	478.00	455.06	495.21	20.6814	11.9404
14	LD2	292.00	290.03	294.63	2.3688	1.3677
15	SD1	406.00	395.34	420.21	12.8087	7.3951
16	SD2	508.00	486.16	524.38	19.6899	11.3680
17	TD1	406.00	387.32	420.01	16.8343	9.7193
18	TD2	474.00	461.20	483.60	11.5360	6.6603
HUW 510						
19	C	272.00	270.10	273.43	1.7162	0.9909
20	GD1	252.00	243.31	263.59	10.4489	6.0327
21	GD2	464.00	450.08	474.44	12.5473	7.2442
22	LD1	448.00	427.39	463.46	18.5758	10.7247
23	LD2	364.00	347.26	376.56	15.0928	8.7139
24	SD1	410.00	409.59	410.31	0.3696	0.2134
25	SD2	464.00	459.82	467.13	3.7642	2.1733
26	TD1	424.00	410.43	434.18	12.2300	7.0610
27	TD2	460.00	437.46	476.91	20.3173	11.7302
RAJ 3567						
28	C	472.00	452.65	486.51	17.4437	10.0711
29	GD1	408.00	407.08	409.22	1.1033	0.6370
30	GD2	396.00	390.46	400.16	4.9973	2.8852
31	LD1	420.00	414.54	424.10	4.9216	2.8415
32	LD2	320.39	319.43	322.29	1.6524	0.9540
33	SD1	422.00	418.52	426.64	4.1842	2.4158
34	SD2	470.00	460.60	477.05	8.4730	4.8919
35	TD1	456.00	441.86	466.60	12.7420	7.3566
36	TD2	496.00	487.57	502.32	7.6005	4.3882

Table 5. Mean, Range, SD and SE performance of Wheat genotype under different metabolite concentration of Grain Yield under irrigated condition

Sr no	Treatment	Mean	Range		Standard deviation	Standard error
			Min	Max		
PBW 343						
1	C	540.00	528.12	548.91	10.7085	6.1825
2	GD1	622.00	591.52	644.86	27.4725	15.8613
3	GD2	540.00	524.21	561.06	18.9832	10.9600
4	LD1	334.00	325.73	345.02	9.9351	5.7360
5	LD2	462.00	443.52	475.86	16.6576	9.6173
6	SD1	484.00	472.38	499.49	13.9607	8.0602
7	SD2	338.00	334.96	340.28	2.7420	1.5831
8	TD1	580.00	574.20	584.35	5.2280	3.0184
9	TD2	602.00	600.80	602.90	1.0853	0.6266
HUW 468						
10	C	438.00	437.01	439.31	1.1844	0.6838
11	GD1	456.00	456.00	456.00	0.0000	0.0000
12	GD2	498.00	493.14	504.47	5.8356	3.3692
13	LD1	384.00	373.06	398.59	13.1531	7.5939
14	LD2	358.00	348.33	370.89	11.6171	6.7071
15	SD1	494.00	490.54	496.59	3.1170	1.7996
16	SD2	396.00	385.01	410.65	13.2071	7.6251
17	TD1	448.00	436.91	462.78	13.3261	7.6938
18	TD2	394.00	378.63	405.52	13.8507	7.9967
HUW 510						
19	C	388.00	375.49	404.68	15.0388	8.6826
20	GD1	352.00	350.94	353.41	1.2692	0.7327
21	GD2	368.00	359.72	379.04	9.9513	5.7454
22	LD1	438.00	417.85	453.11	18.1612	10.4854
23	LD2	354.00	349.75	359.66	5.1055	2.9476
24	SD1	306.00	298.35	311.74	6.8956	3.9812
25	SD2	294.00	290.69	298.41	3.9751	2.2950
26	TD1	290.00	289.42	290.44	0.5228	0.3018
27	TD2	348.00	345.91	350.78	2.5095	1.4488
RAJ 3567						
28	C	410.00	407.23	413.69	3.3261	1.9203
29	GD1	400.00	390.10	413.20	11.8983	6.8695
30	GD2	436.00	435.02	437.31	1.1790	0.6807
31	LD1	300.00	299.40	300.45	0.5408	0.3122
32	LD2	356.00	341.05	367.21	13.4776	7.7813
33	SD1	512.00	510.46	513.15	1.3845	0.7994
34	SD2	288.00	276.77	296.42	10.1244	5.8453
35	TD1	510.00	510.00	510.00	0.0000	0.0000
36	TD2	344.00	331.27	353.55	11.4729	6.6239

Table 6. Mean, Range, SD and SE performance of Wheat genotype under different metabolite concentration of Test Weight (1000 Seed) under drought condition

Sr no	Treatment	Mean	Range		Standard deviation	Standard error
			Min	Max		
PBW 343						
1	C	23.57	22.60	24.29	0.8711	0.5029
2	GD1	28.99	27.77	29.90	1.0975	0.6336
3	GD2	31.65	30.61	32.43	0.9415	0.5435
4	LD1	31.70	31.16	32.10	0.4858	0.2805
5	LD2	25.79	25.25	26.51	0.6509	0.3758
6	SD1	35.05	34.68	35.54	0.4423	0.2554
7	SD2	27.25	26.80	27.85	0.5404	0.3120
8	TD1	30.45	29.51	31.16	0.8509	0.4912
9	TD2	29.22	28.52	30.16	0.8428	0.4866
HUW 468						
10	C	29.52	28.99	30.23	0.6386	0.3687
11	GD1	24.13	23.95	24.37	0.2175	0.1256
12	GD2	27.80	27.11	28.32	0.6265	0.3617
13	LD1	26.46	26.14	26.70	0.2862	0.1652
14	LD2	25.19	25.16	25.21	0.0227	0.0131
15	SD1	25.95	25.44	26.62	0.6082	0.3511
16	SD2	26.49	26.12	26.77	0.3343	0.1930
17	TD1	26.94	26.35	27.38	0.5342	0.3084
18	TD2	22.97	22.44	23.37	0.4762	0.2749
HUW 510						
19	C	25.05	24.41	25.90	0.7677	0.4432
20	GD1	31.32	30.76	32.07	0.6776	0.3912
21	GD2	35.71	35.42	35.92	0.2575	0.1487
22	LD1	34.10	32.63	35.20	1.3217	0.7631
23	LD2	32.47	31.84	33.31	0.7610	0.4393
24	SD1	36.23	34.89	37.24	1.2083	0.6976
25	SD2	33.51	32.04	34.62	1.3290	0.7673
26	TD1	31.70	30.58	33.19	1.3430	0.7754
27	TD2	33.59	33.56	33.62	0.0303	0.0175
RAJ 3567						
28	C	27.55	27.12	28.13	0.5215	0.3011
29	GD1	24.66	24.35	25.08	0.3779	0.2182
30	GD2	30.12	29.08	31.51	1.2489	0.7210
31	LD1	27.55	26.81	28.54	0.8940	0.5161
32	LD2	29.67	28.87	30.74	0.9628	0.5559
33	SD1	26.56	26.08	27.20	0.5746	0.3317
34	SD2	28.91	28.63	29.29	0.3388	0.1956
35	TD1	29.43	28.97	30.05	0.5571	0.3216
36	TD2	32.03	30.88	33.57	1.3858	0.8001

Table 7. Mean, Range, SD and SE performance of Wheat genotype under different metabolite concentration of Test Weight (1000 Seed) under irrigated condition

Sr no	Treatment	Mean	Range		Standard deviation	Standard error
			Min	Max		
PBW 343						
1	C	37.44	36.71	38.41	0.8774	0.5066
2	GD1	33.27	32.70	34.04	0.6898	0.3982
3	GD2	29.26	29.11	29.46	0.1846	0.1066
4	LD1	28.73	28.58	28.93	0.1813	0.1047
5	LD2	25.01	24.22	26.06	0.9468	0.5467
6	SD1	32.27	32.17	32.40	0.1164	0.0672
7	SD2	27.84	27.61	28.15	0.2760	0.1594
8	TD1	34.57	33.69	35.75	1.0595	0.6117
9	TD2	41.54	40.73	42.62	0.9735	0.5621
HUW 468						
10	C	28.22	27.56	29.09	0.7886	0.4553
11	GD1	27.98	27.16	29.07	0.9836	0.5679
12	GD2	27.32	26.66	28.19	0.7880	0.4550
13	LD1	36.22	35.51	37.16	0.8489	0.4901
14	LD2	35.44	34.66	36.02	0.7028	0.4058
15	SD1	25.35	25.31	25.40	0.0457	0.0264
16	SD2	22.24	21.49	23.24	0.9021	0.5208
17	TD1	26.52	25.64	27.69	1.0518	0.6073
18	TD2	27.95	27.45	28.62	0.6047	0.3491
HUW 510						
19	C	37.08	36.45	37.55	0.5682	0.3280
20	GD1	32.63	31.68	33.90	1.1471	0.6623
21	GD2	37.74	37.63	37.82	0.1021	0.0589
22	LD1	24.77	24.40	25.05	0.3349	0.1934
23	LD2	28.77	28.45	29.20	0.3890	0.2246
24	SD1	33.55	32.85	34.49	0.8468	0.4889
25	SD2	31.48	30.51	32.77	1.1634	0.6717
26	TD1	29.43	28.64	30.03	0.7163	0.4135
27	TD2	34.01	33.68	34.45	0.3985	0.2301
RAJ 3567						
28	C	30.45	30.18	30.66	0.2470	0.1426
29	GD1	30.37	28.94	31.44	1.2866	0.7428
30	GD2	29.68	29.50	29.81	0.1605	0.0927
31	LD1	32.11	31.31	32.71	0.7236	0.4178
32	LD2	36.81	36.18	37.66	0.7631	0.4406
33	SD1	28.50	28.27	28.67	0.2055	0.1187
34	SD2	29.63	28.85	30.67	0.9348	0.5397
35	TD1	34.18	33.97	34.45	0.2465	0.1423
36	TD2	31.56	30.11	32.65	1.3086	0.7555

Under drought-stressed conditions, PBW 343, HUW 468, HUW 510 and RAJ 3567 showed the highest test weights with SD1, control (TWIN 20), SD1 and TD2, respectively, with mean values of 35.05 g, 29.52 g, 36.23 g and 32.03 g. The corresponding ranges were 34.68–35.54 g, 28.99–30.23 g, 34.89–37.23 g and 30.88–33.57 g. The lowest test weights were recorded with control (TWIN 20), TD2, control (TWIN 20) and GD1, respectively, with means of 23.57 g, 22.97 g, 25.05 g and 24.66 g. The corresponding ranges were 22.60–24.29 g, 22.44–23.37 g, 24.41–25.90 g and 24.35–25.08 g per 1,000 seeds, respectively.

Under irrigated conditions, PBW 343, HUW 468, HUW 510 and RAJ 3567 showed the highest test weights with control (TWIN 20), LD1, GD2 and LD2, respectively, with mean values of 33.44 g, 36.22 g, 37.74 g and 36.81 g. The corresponding ranges were 36.71–38.41 g, 35.51–37.16 g, 37.63–37.82 g and 36.18–36.66 g. The lowest test weights were recorded with LD2, SD2, LD1 and SD1, respectively, with means of 25.01 g, 26.52 g, 27.44 g and 28.50 g. The corresponding ranges were 24.22–26.60 g, 21.49–23.24 g, 24.40–25.05 g and 28.27–287 g per 1,000 seeds, respectively.

4. Conclusion

The findings indicate that wheat genotypes differed in their observed grain yield, biomass and thousand-seed weight responses to the metabolite treatments under contrasting water regimes. Under drought stress, PBW 343 recorded its highest tabulated grain yield with SD1 (556 g), while HUW 468 reached 508 g with SD2. HUW 510 produced the same highest grain yield with GD2 and SD2 (464 g), and RAJ 3567 reached 496 g with TD2. Under irrigated conditions, the highest grain yields were recorded with GD1 in PBW 343 (622 g), GD2 in HUW 468 (498 g), LD1 in HUW 510 (438 g) and SD1 in RAJ 3567 (512 g). These observations demonstrate that the treatment associated with the highest yield varied by genotype and water regime. In addition, some metabolite treatments were associated with lower grain yields than the corresponding controls, indicating that responses cannot be generalised across treatments or genotypes. The identified combinations therefore represent candidates for further testing rather than definitive recommendations. Repeated trials across growing seasons and environments would help establish the consistency of these responses.

5. Limitations

The experiment was conducted during one growing season at a single research site using four wheat genotypes. Consequently, the consistency of the observed treatment responses across seasons, locations and a wider range of germplasm remains uncertain. Although biomass, grain yield and thousand-seed weight were reported, the present results alone do not establish the physiological mechanisms underlying the treatment responses. Additional multi-environment trials would be required before extending the findings to broader production conditions.

Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

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Competing Interests

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

- Araus, J. L., Slafer, G. A., Reynolds, M. P., & Royo, C. (2002). Plant breeding and drought in C_3 cereals: What should we breed for? *Annals of Botany*, 89(7), 925–940. <https://doi.org/10.1093/aob/mcf049>
- Beltrano, J., Ronco, M. G., & Arango, M. C. (2006). Soil drying and rewetting applied at three grain developmental stages affect differentially growth and grain protein deposition in wheat (*Triticum aestivum* L.). *Brazilian Journal of Plant Physiology*, 18(2), 341–350. <https://doi.org/10.1590/S1677-04202006000200011>
- Bray, E. A. (2002). Abscissic acid regulation of gene expression during water-deficit stress in the era of the Arabidopsis genome. *Plant, Cell & Environment*, 25(2), 153–161. <https://doi.org/10.1046/j.1365-3040.2002.00746.x>
- Chen, H., Chen, W., Zhou, J., He, H., Chen, L., Chen, H., & Deng, X. W. (2012). Basic leucine zipper transcription factor OsbZIP16 positively regulates drought resistance in rice. *Plant Science*, 193–194, 8–17. <https://doi.org/10.1016/j.plantsci.2012.05.003>
- Gigaulia, P., Tantwai, K., Sapre, S., Pandey, S., Upadhyay, A. K., & Nema, S. (2024). Efficacy of plant growth promoting rhizobacteria to improve the biochemical properties and development of wheat seedlings under drought stress control. *Journal of Global Agriculture and Ecology*, 16(1), 42–50. <https://doi.org/10.56557/jogae/2024/v16i18528>

- Giraldo, P., Benavente, E., Manzano-Agugliaro, F., & Gimenez, E. (2019). Worldwide research trends on wheat and barley: A bibliometric comparative analysis. *Agronomy*, 9(7), Article 352. <https://doi.org/10.3390/agronomy9070352>
- Hameed, S., Atif, M., & Perveen, S. (2023). Role of gibberellins, neem leaf extract, and serine in improving wheat growth and grain yield under drought-triggered oxidative stress. *Physiology and Molecular Biology of Plants*, 29(11), 1675–1691. <https://doi.org/10.1007/s12298-023-01402-9>
- ICAR–Indian Institute of Wheat and Barley Research. (2019). Director’s report of AICRP on wheat and barley 2018–19 (G. P. Singh, Ed.). ONLINE version not available
- Kaur, A., Thind, S. K., & Singh, G. (2025). Foliar application of glycine betaine and cytokinins regulates photosynthetic attributes and final biological yield in wheat under drought stress. *Journal of Advances in Biology & Biotechnology*, 28(9), 1489–1496. <https://doi.org/10.9734/jabb/2025/v28i92994>
- Li, G., Wei, J., Li, C., Fu, K., Li, C., & Li, C. (2024). Amino acid metabolism response to post-anthesis drought stress during critical periods of elite wheat (*Triticum aestivum* L.) endosperm development. *Environmental and Experimental Botany*, 218, Article 105577. <https://doi.org/10.1016/j.envexpbot.2023.105577>
- Mekonnen, D. W., Flügge, U. I., & Ludewig, F. (2016). Gamma-aminobutyric acid depletion affects stomata closure and drought tolerance of *Arabidopsis thaliana*. *Plant Science*, 245, 25–34. <https://doi.org/10.1016/j.plantsci.2016.01.005>
- Panse, V. G., & Sukhatme, P. V. (1954). Statistical methods for agricultural workers. *Indian Council of Agricultural Research*. <https://agris.fao.org/search/en/providers/122621/records/647761775eb437ddff77fa17>
- Sheoran, S., Thakur, V., Narwal, S., Turan, R., Mamrutha, H. M., Singh, V., Tiwari, V., & Sharma, I. (2015). Differential activity and expression profile of antioxidant enzymes and physiological changes in wheat (*Triticum aestivum* L.) under drought. *Applied Biochemistry and Biotechnology*, 177(6), 1282–1298. <https://doi.org/10.1007/s12010-015-1813-x>
- United States Department of Agriculture. (2019, December). World agricultural production (Circular Series WAP 12-19). Foreign Agricultural Service. <https://apps.fas.usda.gov/PSDOnline/Circulars/2019/12/production.pdf>
- Yadav, A. K., Carroll, A. J., Estavillo, G. M., Rebetzke, G. J., & Pogson, B. J. (2019). Wheat drought tolerance in the field is predicted by amino acid responses to glasshouse-imposed drought. *Journal of Experimental Botany*, 70(18), 4931–4948. <https://doi.org/10.1093/jxb/erz224>
- Zhao, Q., Ma, Y., Huang, X., Song, L., Li, N., Qiao, M., Li, T., Hai, D., & Cheng, Y. (2023). GABA application enhances drought stress tolerance in wheat seedlings (*Triticum aestivum* L.). *Plants*, 12(13), Article 2495. <https://doi.org/10.3390/plants12132495>

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