__Original Research Article__

Identification the superior wheat genotypes under low irrigation conditions using agro-physiological traits and grain quality in North Delta of Egypt

Abstract

Water scarcity in Egypt and globally makes producing new varieties having high grain yield using less water requirements is an important goal for wheat breeders. The present research was conducted to assess the response of sixteen bread wheat genotypes under normal irrigation (five irrigations) and low irrigation (one irrigation,25 days, after sowing irrigation.) during 2018/19 and 2020/21 seasonsat the Experimental Farm of Sakha Agricultural Research Station, Egypt. A randomized complete block design with three replicates was used for each irrigation treatment separately. Results showed that the normal irrigation treatment had considerably higher mean values for all studied traits except, proline, malondialdehyde, activity of peroxidase and catalase enzymes,1000-kernel~~s~~ weight, protein content, wet and dry gluten which had significantly higher mean values under low irrigation treatment. Under low irrigation conditions, the four genotypes Sakha 95, Line 4, Line 8 and Misr 3 superior other genotypes in grain yield with insignificant difference among them. Sakha 95 and Line 8 had the highest chlorophyll a and b, proline content, chlorophyll florescence, activity of both catalase and peroxidase enzymes. While, Line 4 had the highest activity of catalase and peroxidase, heaviest 1000-kernel~~s~~ weight and high content of crude protein. In addition to Misr 3 recorded the best values of both wet and dry gluten. It could be recommended with cultivation Sakha 95 or Misr 3 to achieve high grain yield with less irrigation water. While Line 8 and Line 4 need more evaluation to use it in the regions which suffering from water shortage also it will be benefit for breeder to use these genotypes in wheat breeding program.

Keywords:*wheat, water shortage, physiology, yield, protein, gluten*.

1. Introduction

Wheat (*Triticum aestivum* L.) is a critical strategic crop not only in Egypt but also globally. In 2020, the Egyptian cultivated area was 1.37 million hectares, producing 9 million metric tons with a median of 6.56~~-~~tons ha^{-1}**.** Egypt imported 9.04 million metric ton as the second-largest wheat importer**[1].**

In Egypt, irrigation water is a limiting factor for crop production. Water scarcity reached less than 1000 m^{3}capita^{-1}year^{-1}, and according to population projections for 2025, Egypt will be at an absolute scarcity level of 500 m^3 per capita per year**[2].**Water shortage affects growth and yield of wheat. Losses in yield might be due to its injurious effects on physiological characteristics and many researchers investigated how photosynthesis and yield are affected by soil water content and relative water content of leaves**[3]**, chlorophyll content significantly decreased by water shortage**[4],**~~while,~~while proline accumulated as an osmo-regulator and genotypes that accumulated more proline showed more tolerance against stress by maintaining plant water potential**[5]**. Also, antioxidant enzymes response is a beneficial tool for water shortage tolerance in different wheat genotypes, where catalase and peroxidase enzymes play an important role in determining response of genotypes**[6].**The tolerance of studied cultivar might be due its high activity of antioxidants enzymes and low lipids peroxidation (MDA) under water shortage conditions **[7].**

Wheat is considered as a vital source of protein and carbohydrates for humans around the world **[8].**It is well known that the reduction in grain yield that occurs under water stress conditions is related to an increment in protein content **[9]; [10];[11]; [12]and [13].** Improving the stability of the quality and quantity of the grains is an important breeding object under water stress conditions **[14].**

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Therefore, the present work aimed to study the effect of low irrigation on agronomical, physiological and quality traits in sixteen bread wheat genotypes, and also selecting the most superior genotypes which had the best traits under low water conditions using simplified rank summation index.

MATERIALS AND METHODS

The current study was carried out ~~on~~ atSakha Agricultural Research Station Experimental Farm (31^{o} 06 N, 30^{o} 56 E) and the Laboratory of Seed Technology, Kafr El-Sheikh, Egypt. Nine high yielding promising lines from the ~~national~~ National ~~breeding~~ Breeding ~~program~~Program, as well as seven bread wheat cultivars were used and grown on 30th and 25th of November during 2018/19 and 2020/21 winter seasons, respectively. Table 1 shows the names and pedigrees of the studied genotypes.

Two separate irrigation experiments using the flood irrigation method were conducted during each season. The first experiment was irrigated four times after planting irrigation (normal irrigation treatment, N), whereas the second experiment received only one surface-irrigation after 28 days from planting irrigation (low irrigation treatment, L).

To reduce water infiltration, every experiment was encircled by a 10 m wide border and to avoid the high-water table effect, the experimental site was selected close to the main drainage. Except the irrigation treatments, all other agricultural practices were followed as recommended for wheat cultivation in old land at the convenient times. In both seasons, maize was the preceding crop. The experimental design was a randomized complete block design (RCBD) with three replicates for each irrigation treatment. Plot size was 4.2 m^{2} (six rows with 3.5 m long and 20 cm apart).

Table 1: Names and pedigree of the studied wheat genotypes

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Ser	Name	Abbrev.	Pedigree and selection history
1	Misr 1	G 1	OASIS / SKAUZ // 4*BCN /3/ 2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S
2	Msr 2	G 2	SKAUZ / BAV92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S
3	Misr 3	G 3	ATTILA*2/PBW65*2/KACHU CMSS06Y00582T-099TOPM-099Y-099ZTM-099Y-099M-10WGY-0B-0EGY
4	Sakha 95	G 4	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1. CMSA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
5	Gemmiza 12	G 5	OTUS /3/ SARA / THB // VEE CMSS97Y00227S-5Y-010M-010Y-010M-2Y-1M-0Y-0GM
6	Sids 14	G 6	BOW "S" /VEE "S"//BOW "S"/TSI/3/BANI SEWEF 1 SD293-1SD-2SD-4SD-0SD
7	Shandweel 1	G 7	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH
8	Line 1	G 8	SIDS1/ ATTILA // GOUMRIA-17 S. 16498-042S-013S-21S -0S
9	Line 2	G 9	MINO /6/ SAKHA 12 /5/ KVZ // CNO 67 / PJ 62 /3/ YD "S" / BLO "S" /4/ K 134 (60) / VEE S. 16869 -010S -07S-1S-2S -0S
10	Line 3	G 10	SIDS 12 // WBLL1*2/BRAMBLING S. 16965 -018S -011S-1S -0S
11	Line 4	G 11	NS-732/HER/3/PRL/SARA//TSI/VEE # 5/4/FRET2/5/ WHEAR/SOKOLL CMSA09Y00712S-050Y-050ZTM-0NJ-099NJ-4WGY-0B-0EG
12	Line 5	G 12	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA//TSI/VEE#5/4/CROC_1/ AE.SQUARROSA(224)//2*OPATA*2/6/HUW234+LR34/ PRINIA//UP2338*2/VIVITSI CMSS10B01047T-099 TOPY-099M-099NJ-099NJ-13WGY-0B
13	Line 6	G 13	SAKHA 94 // WBLL1 *2/BRAMBLING S.16945 -013S -016S-5S -0S
14	Line 7	G 14	SERI/RAYON*2//PFAU/WEAVER /3/ MISR 2 S.2011-40-033S-013S-1S-0S
15	Line 8	G 15	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/6/2*OASIS/5*BORL95/5/CNDO/ R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI CMSA10M00162T-050Y-099ZTM-099NJ-099NJ-18WGY-0B
16	Line 9	G 16	BAVIS #1*2/4/PASTOR// HXL7573/2*BAU /3/SOKOLL/WBLL1 CMSA10M00223T-050Y-099ZTM-099NJ-099NJ-9WGY-0B

Table 2: Amount of irrigation water and total rainfall in m^{3}f~~a~~ed^{-1} in the two irrigation treatments during 2018-2019 and 2020-2021 seasons.

Treatments	Season	Total irrigation m^{3}fed^{-1}	Rainfall m^{3}f~~a~~ed^{-1}	Total water m^{3}f~~a~~ed^{-1}
Normal irrigation	2018/19	2008	307.02	2315.02
	2020/21	2041	348.33	2389.33
Low irrigation	2018/19	830	307.02	1137.02
	2020/19	821	348.33	1169.33

Soil samples were randomly taken at various depths up to 60 cm from the two sites of the experiment, in the two seasons of the study to determine chemical and mechanical analysis of the soil and the mean values were shown in Table 3. The meteorological data were illustrated for the two winter growing seasons as shown in Table 4.

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Table 3: Chemical and mechanical analysis of experimental sites during 2018-2019 and 2020-2021 seasons

Season	Chemical analysis					Soil texture class
	EC dS m^{-1}	pH	N (ppm)	P (ppm)	K (ppm)	
2018-2019	3.20	8.60	50.1	5.85	376	clayey
2020-2021	3.70	8.71	54.2	6.02	382	clayey

Data analyzed at laboratory of Water and Soil Research Dept. (Water, Soil and Environment Research Institute, ARC, Egypt), at Sakha Agricultural Research Station.

Table 4: ~~the metrological~~ Metrological data during the ~~two winter~~two-winter growing 2018/2019 and 2020/2021 seasons.

Month	AT ^{O}C 2018/19		AT ^{O}C 2020/21		RH%		Rainfall (mm)	
	Max.	Min.	Max.	Min.	2018/19	2020/21	2018/19	2020/21
December	20.55	14.42	22.04	14.11	75.58	64.30	21.70	18.78
January	18.87	12.38	21.08	13.57	68.15	74.73	14.90	19.65
February	19.71	14.90	20.99	12.56	73.29	75.25	15.30	15.74
March	21.98	17.68	22.46	14.60	71.65	65.28	17.30	28.18
April	25.15	20.56	26.95	18.96	68.78	61.79	3.90	0.69
May	31.97	25.52	32.72	24.70	56.83	57.68	0.00	0.00

Air temperature = AT ^{O}C, Max = maximum temperature, Min = minimum temperature, relative humidity = RH %, rainfall (mm/month)

Studied traits:

Physiological traits

- At heading stage ten flag leaves of the main stem of ten plants were randomly taken from each plot to estimate. Relative water content (RWC %), which measured according to **[53]** and using the equation RWC % = FW – DW / SW-DW x100. Leaf chlorophyll fluorescence (Fv/Fm)~~,~~ was measured using chlorophyll fluorometer (OS-30, ~~OPti sciences~~Opti sciences, inc.USA) and using the equation as follow: Fv/Fm= (Fm-Fo) / Fm as shown by **[15],**where: Fv/Fm is the maximal quantum efficiency of PSll (MQE), Fm is the maximal chlorophyll fluorescence and Fo minimum chlorophyll fluorescence (in the dark). Chlorophyll content (chlorophyll a and b) (chl.a and b µg ml^{-1}) using N-N-Dimethyl~~e~~-formamide and UV-VIS Spectro-photometer according to **[16].**Proline content of leaves (mg g^{-1}FW) was determined according to the method of **[17].**Malondialdehyde (MDA µmols g^{-1} FW.) was measured

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according to the methods of **[18].**Enzymatic antioxidants (Catalase activity CAT µmol min^{-1} g protein^{-1}) and (Peroxidase activity POD µmol min^{-1} g protein^{-1}) was determined as shown by **[19].**

Agronomic traits

Days to heading (DH, day), days to maturity (DM, day) and plant height (PH, cm), number of spikes m^{-2} (SM^{-2}, spike), number of kernels spike^{-1} (KS^{-1}, kernel), 1000-kernel weight (1000KW, g) and grain yield (GY, Kg plot^{-1}) were measured according to the standard method.

Grain quality traits:

Crude protein content (protein, %): was measured according to **[20].**Wet and dry gluten percentage (Wet Gl., Dry Gl. %): were measured by hand washing 25 g flour, according to standard method **[21].**

Statistical analyses

Collected data in the two seasons were subjected to individual analysis of variance (ANOVA) of randomized complete block design for each season. Data were performed to the homogeneity test of individual error before combined analysis **[22].**Then, combined analysis over the two seasons and two irrigation treatments was done according to **[23]**. The least significant differences (LSD) at the level of 0.05 of probability were used to compare the differences among the means of the treatments according to **[24]**.

Simplified ranks summation index **[25]**was used to realize the estimates of genetic gains for each trait in order to select superior genotypes under the low irrigation condition. Genotypes were classified according to the traits always adopting the criterion of classifying the best genotype for each trait with value 1, and so on. The individuals classified as 1 were those with the highest averages for all traits and with the lowest average for the traits days to heading, days to maturity and MDA, according to the nature of these traits. After obtaining the classification values for each genotype, its indices were calculated as follows: $I_j = \sum n_{ij}$

With I_j being the index for genotype j, and n_{ij} the classification number of the trait i for the genotype j. Genotype with the lowest I_j was considered better.

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RESULTS

The water table level after 60 and 63 days of planting was deeper than 195 cm in low irrigation treatment in the two seasons, respectively.While, reached the same level after 153 and 154 days under normal irrigation in the two seasons, respectively. Table 4 depicts air temperature (^{o}C), relative humidity (RH %), and rain fall (mm) values during the two growing seasons. In comparison, 2020/2021 season had the highest max., and lowest min. air temperatures in the two growing seasons and the lowest relative humidity from March to May. The second season was considered dry due to high temperatures and low relative humidity values overall, which affected all studied traits.

Analyses of Variance

The results of **[22]** proved homogeneity of the separate error variances for all studied traits that permits to apply combined analysis across the two conditions (normal irrigation and low irrigation) in each growing season. All studied factors (genotypes and irrigation) were fixed except seasons that considered random factors.

Tables 5 and 6 show the analysis of variance for the studied traits across seasons and water treatments. Mean squares due to seasons, water treatments and genotypes were significant for all traits, exceptseasons for POD and CAT (Table 5). The interaction of seasons x water treatments was significant for RWC, proline, MDA, Fv/Fm and protein. While, season x genotypes interaction was significant for all traits except POD and CAT; interaction of water treatments x genotypes was significant for all traits except DH, DM and MDA. Season x water treatments x genotypes interaction was significant for all traits except CAT, DH, DM, SM, KW and GY

RWC, Proline, MDA, Fv/Fm, CAT, DH, DM, PH, Wet Gl. % and Dry Gl. % were significantly higher in the first season than in the second one. While, the remaining examined traits were significantly higher in the second season (Tables 7 and 8).

Irrigation treatments effect

All evaluated attributes were strongly affected by irrigation treatments. The normal irrigation treatment recorded considerably higher mean values for all studied traits except, Proline, MDA, POD, CAT, 1000KW, Protein, Wet Gl. %, and Dry. Gl. %, which gave significantly higher mean values under low irrigation treatment. (Tables 7 and 8)

Genotype effect

Highly significant differences among genotypes were observed in all studied traits when the data were combined across seasons and irrigation treatments. Therefore, the comparisons among genotypic means are valid.

Table 5.Mean squares of physiological and biochemical traits of wheat genotypes combined over the two seasons of 2018/2019 and 2020/2021.

SOV	df	RWC	Chl. a	Chl. b	proline	MDA	Fv/Fm	POD	CAT
Seasons (S)	1	105.53**	712.52**	22.22**	0.003*	66640.6**	0.002**	0.30	0.013
Irrigation treatments (I)	1	1295.89**	309.19**	95.51**	0.752**	709897.2**	0.034**	16.49**	0.105**
S x I	1	69.25**	6.49	0.27	0.010**	15714.6**	0.001**	0.68	0.0001
Error a	8	5.92	3.94	1.32	0.001	170.8	0.000	1.01	0.005
Genotypes (G)	15	10.58**	5.21**	0.54**	0.004**	2104.3**	0.001**	0.59**	0.009**
S x G	15	12.69**	3.91**	0.46**	0.004**	700.3**	0.0001**	0.02	0.0001
I x G	15	15.84**	0.71**	0.38**	0.004**	170.1	0.0002**	0.043**	0.001**
S x I x G	15	15.28**	0.69**	0.18**	0.003**	314.9**	0.0001**	0.02*	0.0002
Pooled Error	120	2.69	0.26	0.07	0.001	120.5	0.0000	0.012	0.0002
Total	191								

RWC (relative water content), chl. a (chlorophyll a), chl. b (chlorophyllb), MDA (~~malondealdehyde~~malondialdehyde), POD (peroxidase enzyme), CAT (catalase enzyme).*, ** = significant at 0.05 and 0.01, probability levels, respectively.

Table 6.**Mean squares of agronomic and quality traits of wheat genotypes combined over the two seasons of 2018/2019 and 2020/2021.**

SOV	df	DH	DM	PH	SM^{-2}	KS^{-1}	1000KW	GY	Protein %	Wet Gl. %	Dry Gl. %
Seasons (S)	1	11463.6**	2187.7**	393.88**	467.1	406.0**	55.38**	4.58*	106.66**	172.03**	573.67**
Irrigation treatments	1	445.4**	299.8**	940.76**	81519.6**	2121.35**	536.32**	16.91**	59.59**	498.07**	104.99**
S x I	1	0.478	5.9	0.13	330.5	0.20	2.34	0.16	3.98**	2.65	4.31
Error a	8	2.025	8.9	30.4	2250.7	0.89	0.77	0.41	0.17	3.43	1.12
Genotypes (G)	15	561.2**	143.2**	772.84**	14831.7**	383.06**	193.19**	1.94**	11.32**	144.01**	27.82**
S x G	15	23.3**	16.1**	52.77**	2392.3**	9.68**	3.09**	0.17**	8.77**	35.06**	8.59**
I x G	15	2.1	1.6	14.09**	3542.7**	13.19**	3.05**	0.24**	0.78**	6.53**	4.09**
S x I x G	15	1.9	2.0	5.69*	605.8	4.758**	0.88	0.03	0.66**	7.07**	4.011**
Pooled Error (Eb)	120	1.3	1.4	3.14	714.5	1.306	0.93	0.04	0.065	1.11	0.19
Total	191										

DH = Days to heading, DM = Days to maturity, PH = Plant height, SM^{-2}= no. of spikes m^{-2}, KS^{-1} = no. of kernels $spike^{-1}$, 1000 KW = 1000 kernel weight, GY = Grain yield $plot^{-1}$,Protein % = Crude protein, Wet Gl. = Wet gluten and Dry Gl. % = dry gluten.*, ** = significant at 0.05 and 0.01, probability levels, respectively.

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Physiological characteristics

Concerning physiological traits data presented in Table 7 show that the highest percent of RWC of flag leaves (86.37, 85.81 and 85.76%) were obtained from line 2 (G 9), line 3 (G10) and line 8 (G15), respectively. The same three genotypes recorded the highest concentrations of chl.a (11.72, 11.11 and10.79 µg ml^{-1}) for line 8(G15), line 2 (G9) and line 3 (G10), respectively. On the other hand, Sakha 95(G4), line 8(G15) and Misr 1 (G1) gave the highest concentration of chl.b (4.10, 4.09 and 4.01 µg ml^{-1}), respectively. Concerning flag leaf contents of proline, data showed that line 8 (G15), line 2 (G10) and line 6 (G13) had the highest contents of proline (0.25, 0.25 and 0.23 mg g^{-1}FW) respectively. The lowest and favorable contents of MDA (197.87, 204.69, 215.47 and 217.29 µmols g^{-1} FW.) were recorded by Sakha 95 (G4), line 8 (G15), line 3(G10) and line2 (G9), respectively. Sakha 95 (G4) and line 8 (G15) gave the highest values of Fv/ Fm (0.85 and 0.84), the maximum activity of POD enzyme (3.22 and 3.23 µmol min^{-1} g protein^{-1}) and activity of CAT (0.33 and 0.36 µmol min^{-1} g protein^{-1}) respectively.

Agronomic characteristics

Data of agronomic traits in Table 8 showed that Line 2 (G9) was the earliest genotype regarding to DH and DM (76 and 139, respectively). Also, it had the heaviest 1000-KW (56.78 g). Meanwhile, Sids 14 (G6) had the tallest PH (131 cm). The largest number of SM^{-2} was recorded by Misr 2 (G2) being 447 spikes m^{-2}. The greatest KS^{-1} was recorded by Line 7 (G14) being 72 kernels. The highest GY was obtained by Line 4 (G11) followed by Sakha 95 (G4) and Line 8 (G15) which recorded 5.43, 5.38 and 5.34 kg plot^{-1}, respectively.

Table 7: Mean performance of all studied genotypes for physiological and biochemical traits combined over the two irrigation treatments and the two seasons

	RWC %	Chl. a µg ml^{-1}	Chl. b µg ml^{-1}	proline mg g^{-1}FW	MDA µmols g^{-1} FW	Fv/Fm	POD µmol min^{-1} g $protein^{-1}$	CAT µmol min^{-1} g $protein^{-1}$
1st Season	85.12	8.27	3.37	0.22	244.92	0.83	2.82	0.309
2nd Season	83.63	12.12	4.05	0.21	207.66	0.82	2.90	0.292
F-test	**	**	**	*	**	**	N.S	N.S
N Irr.	86.97	11.46	4.41	0.15	165.48	0.84	2.57	0.28
L Irr.	81.78	8.93	3.00	0.27	287.10	0.81	3.15	0.32
F-test	**	**	**	**	**	**	**	**
Genotypes								
G 1	83.52	9.92	4.01	0.20	235.64	0.82	2.59	0.28
G 2	84.21	9.35	3.55	0.21	227.61	0.82	2.48	0.27
G 3	83.19	9.38	3.68	0.21	225.83	0.83	2.78	0.31
G 4	84.28	10.75	4.10	0.20	197.87	0.85	3.22	0.33
G 5	84.38	10.06	3.78	0.21	225.03	0.83	2.95	0.28
G 6	84.68	9.47	3.38	0.20	245.83	0.82	2.65	0.26
G 7	83.55	10.11	3.62	0.20	232.60	0.82	2.59	0.27
G 8	83.16	10.05	3.63	0.22	243.39	0.82	2.77	0.26
G 9	86.37	11.11	3.71	0.22	217.29	0.83	3.02	0.30
G 10	85.81	10.79	3.60	0.25	215.47	0.83	2.91	0.32
G 11	84.07	9.94	3.41	0.22	223.49	0.83	3.12	0.32
G 12	83.57	9.56	3.73	0.22	226.41	0.82	2.82	0.30
G 13	84.31	10.38	3.58	0.23	225.40	0.83	2.93	0.33
G 14	84.43	10.03	3.66	0.19	244.56	0.82	2.74	0.30
G 15	85.76	11.72	4.09	0.25	204.69	0.84	3.23	0.36
G 16	84.71	10.51	3.77	0.18	229.53	0.82	2.97	0.32
Mean	84.38	10.20	3.71	0.21	226.29	0.83	2.86	0.30
LSD G $_{(0.05)}$	1.33	0.41	0.22	0.02	8.87	0.006	0.09	0.014
G X I	**	**	**	**	NS	*	**	**

N Irr (Normal irrigation), L Irr (Low irrigation), RWC (relative water content),chl. a(chlorophyll a), chl. b (chlorophyll b), MDA (~~malondealdehyde~~malondialdehyde),POD (peroxidase enzyme activity) , CAT (catalase enzyme activity). *, ** and NS = significant at 0.05 and 0.01, probability levels, and not significant respectively.

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Grain quality characteristics

Concerning grain quality traits, data in Table 8 indicated that Line 4 (G11) recorded the highest contain of crude protein (14.85%). While, Line 2 (G9) was the highest genotype in both wet and dry gluten (34.39% and 15.84%, respectively).

Table 8: Mean performance of all studied genotypes for agronomic and quality traits combined over the two irrigation treatments and the two seasons.

	DH	DM	PH	SM^{-2}	KS^{-1}	1000KW	GY	Protein %	Wet Gl. %	Dry Gl. %
1st Season	99.25	149.75	119.13	359.31	62.5	50.52	4.57	12.14	28.30	13.84
2nd Season	83.94	143.06	116.31	362.50	65.4	51.59	4.88	13.63	26.40	10.39
F-test	**	**	**	N.S	**	**	*	**	**	**
N Irr	93.07	147.59	119.81	381.56	67.3	49.38	5.02	12.33	25.74	11.38
L Irr	90.03	145.09	115.50	340.44	60.6	52.72	4.43	13.44	28.96	12.85
F-test	**	**	**	**	**	**	**	**	**	**
Genotypes (G)										
G 1	95	148	117	406	54	51.98	4.66	12.55	26.20	11.49
G 2	98	150	127	447	57	43.83	4.52	12.01	25.67	11.15
G 3	94	149	117	375	66	51.58	5.17	13.04	31.73	13.35
G 4	95	147	122	396	64	52.24	5.38	11.70	28.66	12.87
G 5	93	145	115	361	59	49.99	4.32	12.95	25.58	10.98
G 6	97	148	131	365	64	52.70	4.89	11.97	28.83	12.71
G 7	94	148	119	378	67	43.05	4.39	11.45	22.87	10.06
G 8	78	140	102	345	59	52.97	4.36	11.78	30.32	13.87
G 9	76	139	107	334	56	56.78	4.26	13.59	34.39	15.84
G 10	82	142	102	339	61	52.93	4.42	13.85	29.91	13.33
G 11	96	150	118	349	70	54.88	5.43	14.85	26.86	11.38
G 12	90	145	119	299	71	51.28	4.40	14.06	29.73	12.46
G 13	92	145	120	328	70	48.84	4.59	13.01	25.58	11.66
G 14	98	150	124	359	72	45.05	4.71	13.37	22.59	10.12
G 15	92	148	120	363	67	53.61	5.34	12.35	27.06	11.97
G 16	94	147	121	331	65	55.13	4.74	13.60	21.63	10.63
Mean	91.50	146.31	117.56	360.94	64	51.05	4.72	12.88	27.35	12.12
LSD G $_{(0.05)}$	**0.91**	**0.95**	**1.43**	**21.61**	**0.92**	**0.78**	**0.15**	**0.21**	**0.85**	**0.36**
G X I	NS	NS	**	**	**	**	**	**	**	**

N Irr. (Normal irrigation), L Irr. (Low irrigation), DH = Days to heading, DM = Days to maturity, PH = Plant height, SM^{-2}= no. of spikes m^{-2}, KS^{-1} = no. of kernels spike^{-1}, 1000KW = 1000 kernels weight,GY = Grain yield plot^{-1}. Protein % = Crude protein, Wet Gl. = Wet gluten and Dry Gl. % = dry gluten.*, ** and NS = significant at 0.05 and 0.01 probability levels, and not significant, respectively.

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Interaction effects

The genotypes × irrigation interaction was the most interesting objective in this study. Therefore, it was only diagrammatically presented and discussed. Scatterplot graph was used to interpret the genotypes × irrigation interaction and to select the superior wheat genotypes in both normal and low irrigations simultaneously as well as in each type of irrigation separately, as shown in Figures 1, 2, 3, 4 and 5).

The designed scatterplot graph was divided into four main groups (four quarters coded as A, B, C and D). The bold horizontal axe represents the grand mean for the sixteen genotypes under the low irrigation, while the bold vertical axe reflected the mean performance under the normal irrigation. The region located between the horizontal and vertical dotted line (based on LSD values 0.05) contains the elite genotypes that is significantly surpassed the others under both normal and low irrigation treatments.

Interestingly, the scatterplots revealed that the genotypes contributors' quarter A were the elite genotypes under the two treatments (normal and low irrigation). While the genotypes of quarter B recorded the highest mean for each trait under normal irrigation only. Likewise, quarter D recorded the highest mean for each trait at low irrigation only. Contrarily, genotypes of quarter C contributed the lowest mean under the two treatments, (normal and low irrigation) (susceptible genotypes).

Physiological characteristics

Data in Table 9 and Fig. 1 showed that the highest percentage of RWC were obtained by Misr 2 (G2), Sids 14 (G6), and Shandaweel 1 (G7) under normal treatment where they located at quarter B, while under low irrigation treatment Line 2 (G9), Sakha 95 (G4), Line 9 (G16) and Gemmiza 12 (G5) gave the highest percentage of RWC (quarter D). On the contrary, the lowest values were obtained by Misr 3 (G3), Line 1 (G8), Misr 1 (G1) and Line 5 (G12) under low irrigation treatment. While, Line 3 (G10) and Line 8 (G15) had the highest RWC % under both normal and low treatments (quarter A).

With regard to chl.a, data showed that Line 6 (G13), Gemmiza 12 (G5) and Line 4 (G11) recorded the highest concentration of Chl.a under normal treatment, but under low irrigation Shandweel 1 (G7), Line 1 (G8) and Misr 1 (G1) gave the highest values of this pigment. While, Sids 14 (G6), Misr 2 (G2), Misr 3 (G3), Line 5 (G12) and Line 7 (G14) recorded the lowest values of chl.a under the two treatments the genotype G15 was the best (quarter A). Concerning chl. b Line 5 (G12), Line 1 (G8) and Line 2 (G9) gave the highest concentration of chl. b under normal treatment, ~~while,~~while Gemmiza 12 (G5) and Misr 3 (G3) had the highest values under low irrigation treatment. On the other hand, Sahka 95 (G4), Line 8 (G15), Misr 1 (G1) and Line 9 (G16) were the best genotypes for this trait under both irrigation treatments.

For proline content, Table 9 and Fig. 1 showed also that under low irrigation Line 4 (G11) had the highest content of proline, while under the two irrigation treatments Line 8 (G15) and Line 3 (G10) gave the highest values (quarter A). The genotypes Gemmiza 12 (G5), Misr 3 (G3), Line 4 (G11) and Misr 1 (G1) had the highest values of maximal quantum efficiency (Fv / Fm) under low irrigation treatment (Table 9 and Fig.2), while, Sakha 95 (G4), Line 8 (G15) and Line 2 (G9) gave the highest efficiency under the two irrigation treatments. Regarding the activity of the two enzymes (POD and CAT), they approximately had the same trend under the two treatments, where Line 8 (G15), Sakha 95 (G4) and Line 4 (G11) recorded the highest activity for both enzymes (Table 9 and Fig.2).

Table 9: Effect of the interactions between irrigation treatments and genotypes for physiological characters combined over the two seasons

		Chl. a		Chl. b		~~proliene~~Proline		Fv/fm					
L ~~irr.~~		N ~~irr.~~	L ~~irr.~~	N irr.	L ~~irr.~~	N ~~irr.~~	L ~~irr.~~	N irr.	L ~~irr.~~	N irr.			
80.585		10.965	8.867	4.467	3.558	0.128	0.265	0.828	0.813	2.283	2.902	0.247	0.313
79.267		10.487	8.217	4.153	2.948	0.150	0.272	0.835	0.797	2.205	2.747	0.240	0.302
81.168		10.542	8.212	4.343	3.022	0.162	0.263	0.837	0.818	2.528	3.025	0.287	0.327
83.850		11.998	9.510	5.173	3.035	0.133	0.275	0.872	0.824	2.882	3.548	0.307	0.355
81.965		11.605	8.522	4.405	3.158	0.123	0.287	0.837	0.818	2.603	3.297	0.232	0.320
81.425		10.372	8.573	3.760	2.992	0.123	0.273	0.831	0.805	2.447	2.860	0.228	0.290
79.723		11.213	8.997	4.363	2.882	0.135	0.257	0.831	0.803	2.288	2.895	0.242	0.293
80.768		11.047	9.050	4.613	2.655	0.182	0.260	0.831	0.807	2.553	2.993	0.242	0.287
86.190		12.425	9.800	4.523	2.892	0.140	0.290	0.840	0.827	2.738	3.293	0.268	0.323
83.192		11.982	9.605	4.380	2.822	0.180	0.315	0.838	0.816	2.458	3.365	0.298	0.340
81.238		11.668	8.202	4.053	2.762	0.125	0.305	0.836	0.815	2.838	3.400	0.288	0.347
80.407		10.757	8.355	4.543	2.907	0.168	0.275	0.831	0.805	2.578	3.057	0.290	0.318
80.965		12.020	8.740	4.383	2.773	0.175	0.278	0.845	0.806	2.683	[illegible]	[illegible]	[illegible]
81.765		11.328	8.735	4.388	2.937	0.133	0.245	0.829	0.802	2.433	[illegible]	[illegible]	[illegible]
83.237		13.343	10.102	4.585	3.585	0.160	0.332	0.853	0.820	2.913	[illegible]	[illegible]	[illegible]
82.687		11.678	9.337	4.450	3.088	0.167	0.197	0.837	0.808	2.637	[illegible]	[illegible]	[illegible]
81.78		**11.46**	**8.93**	**4.41**	**3.00**	**0.15**	**0.27**	**0.84**	**0.81**	**2.5**	[illegible]	[illegible]	[illegible]
.95		**0.82**		**0.46**		**0.03**		**0.008**		[illegible]		[illegible]	

N ~~Irr~~ (Normal irrigation), L ~~Irr~~ (Low irrigation), RWC (relative water content),chl.a(chlorophyll a), chl.b (chlorophyll b), POD (peroxidase enzyme activity), CAT (catalase enzyme activity). *, ** and NS = significant at 0.05 and 0.01, probability levels, and not significant respectively

Agronomic characteristics

According to the interaction effects on agronomic trait shown in Table 10 and Fig.3, the tallest genotypes were Sids 14 (G6) under both irrigation treatments and Misr 2 (G2) under low irrigation treatment. On the other hand, the shortest genotypes were Line 1 (G8), Line 2 (G9) under both irrigation treatments and Line 3 (G10) under low irrigation treatment. The highest SM^{-2} recorded by Misr 2 (G2) under both irrigation treatments, Misr 1 (G1), Misr 3 (G3) and Sakha 95 (G4) under low irrigation treatment. Further, the lowest SM^{-2} obtained by Line 5 (G12) under both irrigation treatments and Line 6 (G13) under low irrigation treatment.

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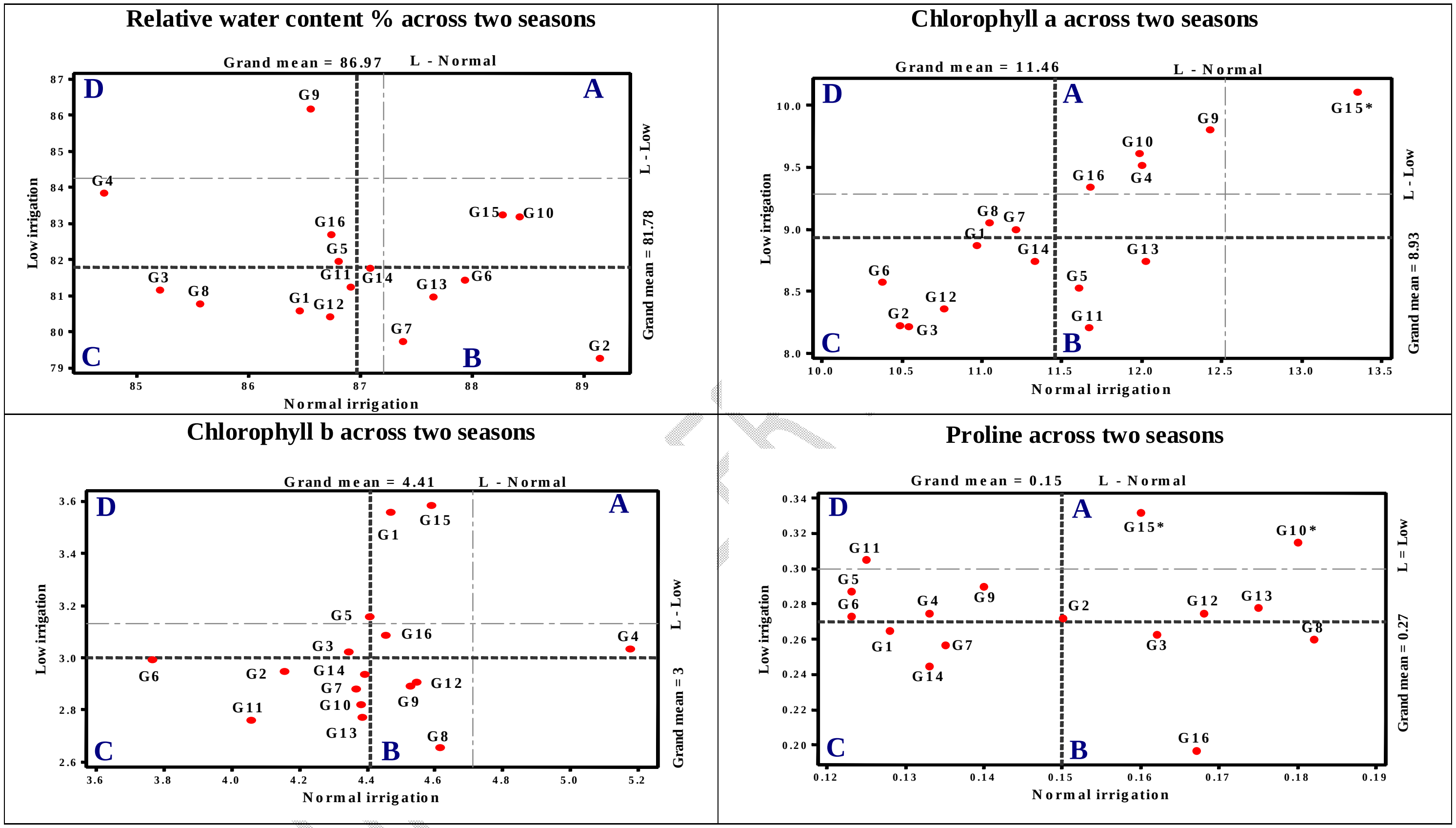

Relative water content % across two seasons

Chlorophyll a across two seasons

Chlorophyll b across two seasons

Proline across two seasons

Figure 1: The mean performance of the genotype × irrigation interaction ~~of~~ forRelative water content, Chlorophyll-a, Chlorophyll-b and Proline contentcombined across two seasons, L- Normal =(LSD for Normal irrigation), L- Low=(LSD for Low irrigation)

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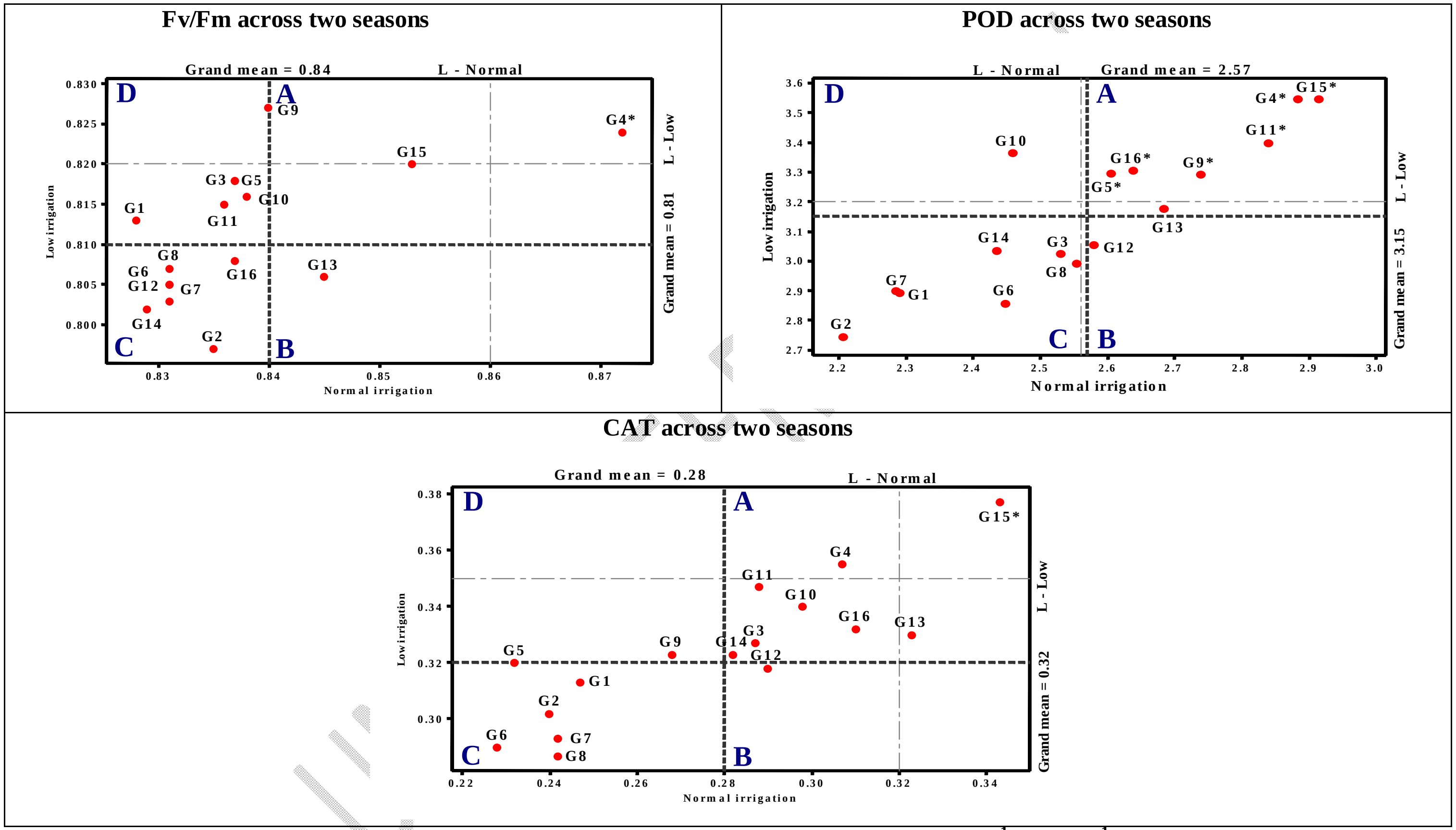

Figure 2: The mean performance of the genotype x Irrigation interaction ~~of~~ forgrain yield plot^{-1} (kg plot^{-1}), Fv/Fm, POD and CAT combined across two seasons, L- Normal= (LSD for Normal irrigation), L- Low= (LSD for Low irrigation)

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Table 10. Effect of the interaction~~s~~ between irrigation treatments and genotypes for agronomic~~y~~ traits combined over the two seasons

Genotypes	PH		SM^{-2}		KS^{-1}		1000 KW		GY	
	N ~~irr.~~	L ~~irr.~~	N ~~irr.~~	L ~~irr.~~	N ~~irr.~~	L ~~irr.~~	N ~~irr.~~	L ~~irr.~~	N ~~irr.~~	L ~~irr~~.
G 1	118	116	446	365	57	51	50.06	53.90	5.18	4.13
G 2	128	126	504	389	60	54	42.05	45.60	5.08	3.96
G 3	119	114	386	363	69	63	50.27	52.89	5.34	4.99
G 4	123	120	394	398	68	60	51.19	53.28	5.48	5.27
G 5	117	113	376	346	63	55	47.92	52.05	4.52	4.11
G 6	134	128	390	341	67	61	51.39	54.02	5.32	4.45
G 7	120	118	423	334	69	65	40.29	45.82	4.69	4.08
G 8	105	98	367	323	62	56	51.16	54.79	4.68	4.03
G 9	112	103	341	327	58	53	55.67	57.89	4.38	4.15
G 10	105	99	335	343	67	55	50.99	54.87	4.58	4.26
G 11	119	118	359	340	74	66	53.37	56.39	5.66	5.20
G 12	123	116	324	275	74	68	49.31	53.26	4.70	4.11
G 13	122	119	358	298	72	68	46.84	50.84	4.98	4.19
G 14	126	122	392	327	74	69	42.98	47.11	5.02	4.40
G 15	123	118	367	359	71	63	52.24	54.99	5.51	5.18
G 16	123	120	343	319	69	61	54.38	55.88	5.17	4.31
Mean	**119.81**	**115.50**	**381.56**	**340.44**	**67**	**61**	**49.38**	**52.72**	**5.02**	**4.43**
LSD	**2.55**		**32.58**		**1.29**		**1.09**		**0.29**	

N irr. =Normal irrigation treatment, L irr. = Low irrigation treatment, PH = Plant height (cm), SM^{-2} = no. spikes m^{-2}, KS^{-1} = no. kernels $spike^{-1}$, 1000KW = 1000-kernel weight (g) and GY = Grain yield (kg $plot^{-1}$)

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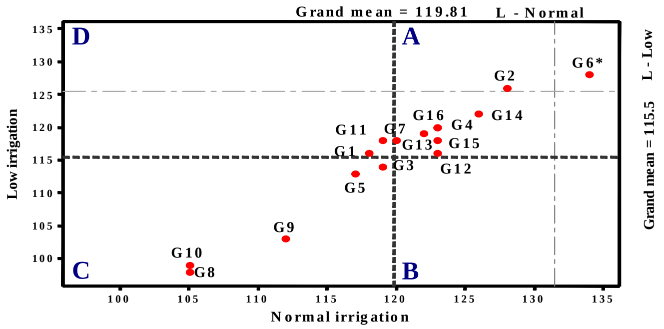
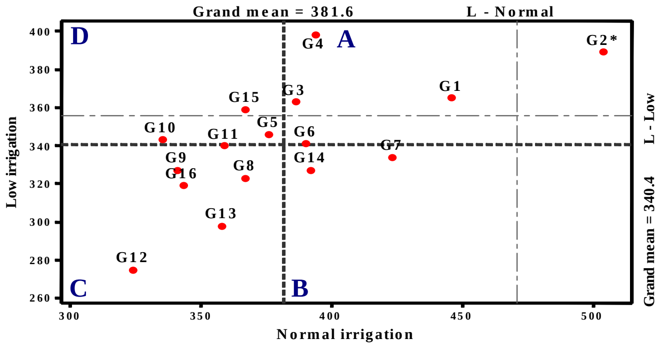
The highest KS^{-1} was recorded by Line 5 (G12), Line 7 (G14) under both irrigation treatments, line 4 (G11) under normal irrigation and Line 6 (G13) under low irrigation treatment. The lowest KS^{-1} was recorded by Misr 1 (G1) under both irrigation treatments and Line 2 (G9) under normal treatment. The heaviest 1000-KW was recorded by Line 2 (G9) under both irrigation treatments. Otherwise, the lightest 1000-KW was obtained by Shandweel 1 (G7) under both treatments and Misr 2 (G2) under low irrigation treatment. Table 10 and Fig.4 showed that Sakha 95 (G4), Line 4 (G11) and Line 8 (G15) gave the highest GY under both irrigation treatments. Furthermore, the lowest GY were showed by Line 2 (G9) and Misr 2 (G2) under normal and low irrigation treatments, respectively.

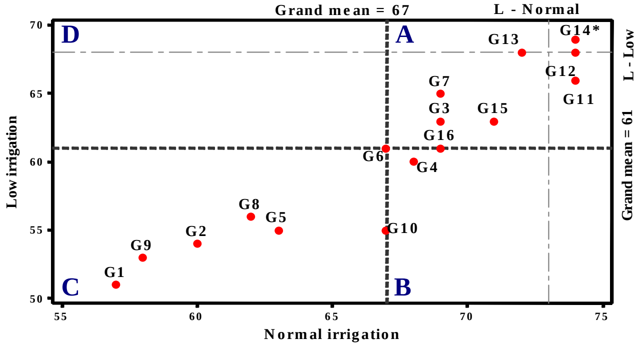
Plant height (cm) across two seasons



No. spikes m^{-2} across two seasons



No. Kernels Spike^{-1} across two seasons



1000 kernel weight (g) across two seasons

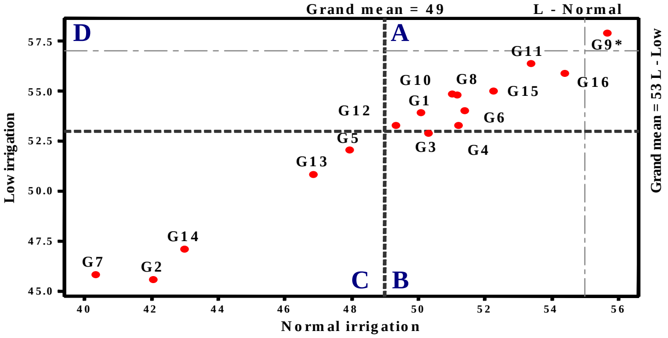


Figure 3: The mean performance of the genotype x irrigation interaction ~~of~~ for Plant height, Number of spikes m^{-2}, Number of kernels spike^{-1} and 1000 kernel weight (g) combined across two seasons, L-Normal = (LSD for Normal irrigation), L-Low = (LSD for Low irrigation)

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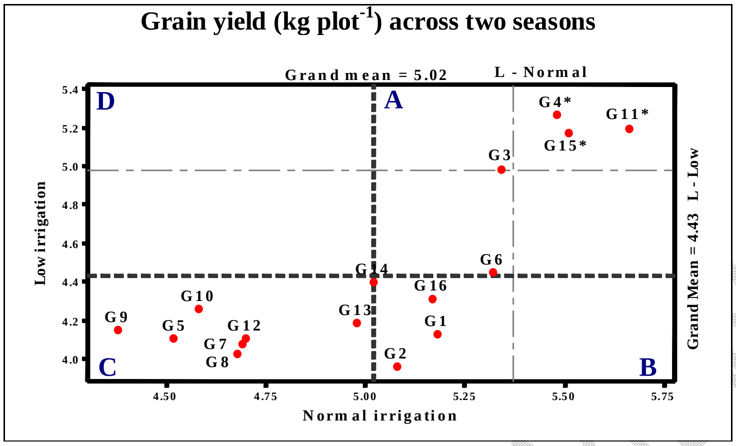

Figure 4: The mean performance of the genotype x Irrigation interaction ~~of~~ forgrain yield plot^{-1} (kg plot^{-1}) combined across two seasons.L-Normal = (LSD for Normal irrigation), L-Low = (LSD for Low irrigation)

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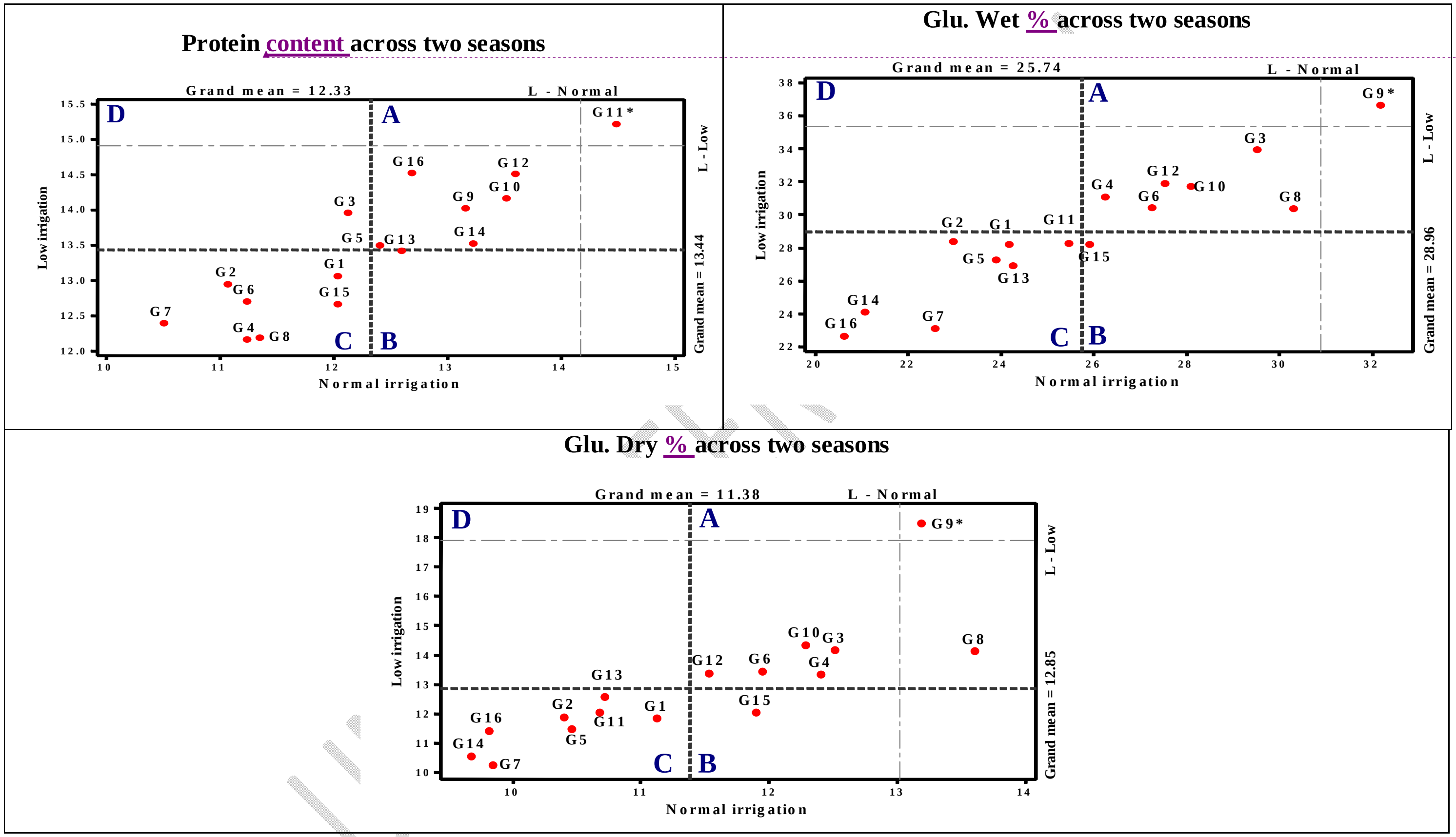
Grain quality characteristics

According to the interaction effects on quality trait shown in Table 11Fig.5,Line 4 (G11) was the highest genotype in protein content under both irrigation treatments. On the other hand, the lowest genotypes in protein content were Shandweel 1 (G7) under both treatments, Sakha 95 (G4), Line 1 (G8), Line 8 (G15), Sids 14 (G6) and Misr 2 (G2) under low irrigation treatment.The highest genotype in wet gluten was Line 2 (G9) under both normal and low irrigation. While, the lowest genotypes wereLine 9 (G16), Line 7 (G14) under both treatments and Shandweel 1 (G7) under low irrigation treatments.


Protein content across two seasons

Glu. Wet % across two seasons

Glu. Dry % across two seasons

Figure 5: The mean performance of the genotype × Irrigation interaction ~~of~~ for protein content, wet and dry gluten percentages combined across two seasons, L-Normal= (LSD for Normal irrigation), L-Low = (LSD for Low irrigation)

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With regard to dry gluten data showed that Line 2 (G9) was the highest genotype under both treatments. As well, Line 1 (G8) under normal treatment. On the other hand, the lowest genotypes in dry gluten were Line 7 (G14), Shandweel 1 (G7) under both treatments and Line 9 (G16) under normal treatment.

Table 11. Effect of the interactions between irrigation treatments and genotypes for grain quality traits combined over the two seasons

Genotypes	Protein content		Wet Gl.%		Dry Gl.%	
	N ~~irr.~~	L ~~irr.~~	N ~~irr.~~	L ~~irr.~~	N ~~irr.~~	L ~~irr.~~
G 1	12.03	13.07	24.16	28.24	11.12	11.86
G 2	11.07	12.95	22.96	28.38	10.40	11.90
G 3	12.12	13.96	29.52	33.95	12.51	14.18
G 4	11.23	12.17	26.22	31.11	12.40	13.35
G 5	12.40	13.50	23.87	27.30	10.46	11.50
G 6	11.23	12.71	27.23	30.43	11.94	13.47
G 7	10.50	12.40	22.58	23.15	9.84	10.27
G 8	11.35	12.20	30.28	30.37	13.60	14.14
G 9	13.16	14.03	32.17	36.62	13.19	18.49
G 10	13.52	14.17	28.07	31.75	12.28	14.37
G 11	14.48	15.22	25.45	28.27	10.67	12.08
G 12	13.60	14.51	27.52	31.93	11.53	13.39
G 13	12.60	13.42	24.25	26.92	10.71	12.61
G 14	13.22	13.53	21.06	24.12	9.67	10.57
G 15	12.03	12.67	25.91	28.20	11.90	12.05
G 16	12.68	14.52	20.60	22.65	9.81	11.44
Mean	**12.33**	**13.44**	**25.74**	**28.96**	**11.38**	**12.85**
LSD G X I	**0.31**		**1.28**		**0.58**	

N ~~Irr.~~ (Normal irrigation), L ~~Irr.~~ (Low irrigation), Protein % (Crude protein), Wet Gl. % (Wet gluten) and Dry Gl. %(dry gluten). *, ** and NS = significant at 0.05 and 0.01 probability levels, and not significant, respectively

Simplified ranks summation index

Results in Table 12 showed that genotypes Line 8 (G15), Sakha 95 (G4) and Line 2(G9) were the superior wheat genotypes over agronomic~~y~~, physiological~~y~~ and quality traits being promising to the breeding program under low irrigation treatment in this study.

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Table ~~(~~12~~)~~: Simplifiedrank Genotype under Low Irrigation

Genotypes	**RWC**	**Chl. a**	**Chl. b**	**proline**	**MDA**	**Fv/fm**	**POD**	**CAT**	**DH**	**DM**	**PH**	**SM^{-2}**	**KS^{-1}**	**1000 KW**	**GY**	**Protein %**	**Wet Gl.%**	**Dry Gl.%**	**Average**	**Mean Rank**
G1	13	8	2	8	12	12	14	14	11	9	11	3	16	8	11	10	11	11	10	13
G2	16	16	12	4	10	10	16	16	16	16	2	2	14	16	16	11	8	12	12	15
G3	10	15	6	2	9	9	11	9	10	13	12	4	5	11	4	6	2	3	8	7
G4	2	4	5	10	1	1	1	1	12	7	4	1	9	9	1	16	5	6	5	2
G5	6	12	3	9	7	7	6	11	7	6	13	6	12	12	13	8	12	13	9	10
G6	8	11	7	11	16	16	13	13	14	12	1	8	10	7	5	13	7	5	10	11
G7	15	7	10	13	13	13	15	15	9	11	8	10	6	15	14	14	15	16	12	16
G8	12	6	16	7	14	14	10	12	2	2	16	13	13	6	15	15	6	4	10	12
G9	1	2	8	12	3	3	5	5	1	1	14	12	15	1	10	5	1	1	6	3
G10	3	3	13	5	4	4	4	4	3	3	15	7	11	5	8	4	4	2	6	4
G11	9	14	15	14	5	5	3	3	13	14	9	9	2	2	2	1	9	10	8	5
G12	14	13	9	3	6	6	9	8	4	4	10	16	3	10	12	2	3	7	8	6
G13	11	9	14	6	8	8	8	7	5	5	6	15	4	13	9	9	13	8	9	9
G14	7	10	11	16	15	15	12	10	15	15	3	11	1	14	6	7	14	15	11	14
G15	4	1	1	1	2	2	2	2	6	10	7	5	7	4	3	12	10	9	5	1
G16	5	5	4	15	11	11	7	6	8	8	5	14	8	3	7	3	16	14	8	8

RWC (relative water content),chl. a(chlorophyll a), chl. b (chlorophyll b), MDA (~~malondealdehyde~~malondialdehyde), POD (peroxidase enzyme) , CAT (catalase enzyme),DH (Days to heading), DM (Days to maturity), PH (Plant height), SM^{-2} (no. of spikes m^{-2}),KS^{-1} (no. of kernels spike^{-1}), 1000KW (1000 kernel weight), GY (Grain yield plot^{-1}), Protein % (Crude protein), Wet Gl.% (Wet gluten) and Dry Gl. % (dry gluten).

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DISCUSSION

Water is necessary for plant growth and diverse metabolic activities and water shortage causes disturbances at morphological, physiological, biochemical and molecular levels **[26].**In the last decades wheat production decreased because of acute water deficiency in wheat-producing areas as a consequence of climatic changes, in addition to the huge increase in human population, these factors made finding out new genotypes have the ability to produce high yield with less amount of water is a very important necessary. The mechanisms of water stress tolerance have to be understudied well, and physiological approach could be the most effective way to improve new varieties **[27].** The breeders can select good adaptive drought genotypes based on morphological and physiological markers **[4].**Plant breeding competence could be ameliorated by using physiological and morphological traits linked with yield components under adverse conditions and used as a standard for selection in traditional plant breeding techniques. **[28] and [29].**

The current study described effects of limited irrigation on physiological and biochemical traits of 16 wheat genotypes. Where some traits had negative decrease under low irrigation like chlorophyll pigments (a, b)leaf relative water content (RWC)and Fv/Fm. These results are in line with those obtained by **[6];[3] and [30].** While negative increases under low irrigation treatment were obtained in ~~malodealdehyde~~malondialdehyde (MDA) **[32] and[7]**. On the contrary, enzymatic and non-enzymatic antioxidants (proline, CAT and POD), respectively in all studied genotypes had positive increases under low irrigation treatments.These results are in good agreement with**[6]; [7] and [30]**.

Chlorophyll content was used as marker for evaluation of genotypes [4]and it decreased significantly under water shortage **[30],**this decrease causes and accelerates leaf senescence in various wheat genotypes (**[5]** and **[4]).**The senescence occurs by accelerating loss of leaf chlorophyll and this loss is more in sensitive genotypes than tolerant one**[26].** From the previous results line 8 (G15), line 2 (G9) and Sakha 95 (G4) had the highest concentrations of both pigments (a, b) underthe two irrigation treatments. Relative water content (RWC) is a measure of plant water status that reflects metabolic activity in plant cells and used as the most significative guide for dryness tolerance **[31].**Water shortage circumstances result in water losses inside the plant, resulting in (RWC) decrease **[32].** Stomata close when RWC (relative water content) leaf and water potential decrease [3] leading to decrease stomata conductance, and decrease stomata conductance is the main cause of the reduction in photosynthesis**[33].** The association between higher RWC and water shortage tolerance for wheat varieties has already been reported by **[34]** and **[35].** In our study, line 2(G9), Sakha 95(G4), line 8 (G15) and line 3(G 10) had the best ratios of relative water content under low irrigation treatment. The variance in photosynthesis may be due to the changes of leaf relative water content, photosynthetic machinery (Fv/ Fm) and chlorophyll content (a~~,~~and b). So genotypes which can tolerate low irrigation stress maintain a higher photosynthetic rate and leaf water status**[36].** In the current study, line 8 (G15), line 2 (G9) and Sakha95 (G4) had these traits which clearly reflected on yield and its components. To cope with water shortage, plants try to adjust the osmotic pressure of the cells by the active accumulation of free amino acids(proline), ions, sugars, and other biochemical substance **[37]**. Proline is also considered a non-enzymatic antioxidant; it has an important role in scavenging and coping with (Reactive Oxygen Species) and stability of cell membranes**[38].** The enzymatic antioxidant system is one of the protective mechanisms against reactive oxygen species (ROS). POD is one of the most important enzymes involved in water stress defense system because it scavenges H_2O_2 in chloroplasts, and genotypes differed in their response to water deficit **[39].**Tolerant genotypes showed the highest enzymatic (CAT and POD) and non-enzymatic (proline) antioxidants **[40] and [7]** and they reported that water shortage tolerant genotypes had higher RWC, proline accumulation, enzymatic activities such as CAT and POD and lower content of malondialdehyde (MDA). Concerning yield and its components traits, significant differences were obtained between the two irrigation treatments, where all traits decreased under low irrigation treatment compared to normal treatment except 1000-kernel weight which increased under low irrigation **[41] and [30]**. Significant decrease in number of days to maturity was observed under low irrigation treatment in all studied genotypes. The reduction in maturity days caused by deficit of irrigation water may be due to a drop in nutrients absorption by plants, which resulted in a decrease in chlorophyll content of leaves due to a shortage of nitrogen required. Selection of early maturing genotypes has been an efficacious strategy for minimizing the yield drop under water deficit in which crop growth duration has been shortened. The reduction in plant height of all genotypes in low irrigation treatment compared to normal irrigation might be attributable to a decrease in relative turgidity and dehydration of protoplasm, which is linked to a decrease in cell division and elongation **[42]**. During the grain development time, flag leaf acts as a primary source of assimilates, accounting for 30 to 50 percent of total assimilates to the wheat grain **[41]**, but water shortage causes and accelerates leaf senescence in various wheat genotypes **[5],**early leaves senescence causing decrease in grain filling duration **[43].**Water scarcity near the end of the growing season produces a fall in grain number rather than grain size, resulting in a considerable reduction in wheat production**[44].** The decrease in the number of grains may be due to premature abortion of florets **[45].** A low number of KS^{-1} in pre-anthesis water deficit stress compared to non-stress conditions led to increase of the average of 1000KW of all genotypes. These results are in agreement with those of **[46]**.Grain protein content is the most important component affecting the grain quality **[47]**. Wheat has individual advantage of gluten protein fraction in the grain **[48]**. Storage proteins such as gliadins and glutenins can determine the baking quality where gliadins decide the dough viscosity and glutenins determine the dough elasticity and strength **[49]**. The effect of water stress on grain quality was studied in wheat lines to evaluate them as a genetic source of high quality under water stress for development in bread wheat.

It was previously shown that water stress causes big changes in grain composition, including an increase in grain protein content **[13].**However, water stress can also affect both the protein composition **[50]**, where the amounts of total proteins increased in wheat under water stress, these results are in agreement with previous findings obtained by (**[36] and [51]).** Also water shortage caused significant increment in wet and dry gluten contents and these results are in line with those obtained by**[11]**who reported that abiotic stresses (salt and drought) increased wet and dry gluten contents.

One of the most important features of this analysis is the possibility of placing superiority index (rank) based on all the studied ~~trait~~traits. Simplified ranks summation index **[25],** was used to obtain the estimates of genetic gains for each characteristic in order to choose the best genotypes.**[52]**Reported the greatest winning in the selection of wheat genotypes using the simplified ranks summation index.

Conclusion~~s~~

Based on the obtained results in this study, it could be concluded that for achieving high grain yield with less irrigation water, cultivation Sakha 95 and Misr 3 will be recommended in the regions which suffering from water deficit conditions, at the same time Line 8 and Line 4 had high physiological, agronomic and grain quality characteristics under low irrigation conditions and can be recommended for release as a cultivars after evaluate them at large scale in multi locations over all Egypt.

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