Original Research Articles

Grain protein, oil and starch contents and yields of maize (*Zea mays* L.) as affected by deficit irrigation, genotype and their interaction

ABSTRACT

The main objective of this investigation was to study the effects of deficit irrigation (I) at flowering stage, genotype (G) and G × I interaction on maize grain quality and yield traits of 6 inbred lines and their 15 diallel crosses. The parents and F_1's were evaluated in two seasons. A split plot design was used, where main plots were allotted to two irrigation treatments, *i.e.* well watering by giving all recommended irrigations and water stress by withholding the 4th and 5th irrigations, while sub plots were allotted to genotypes. Water stress caused a significant decrease in protein yield/ha by 25.5 and 13.8%, oil yield/ha by 29.9 and 20.2%, starch yield/ha by 25.0 and 17.03%, grain yield/plant by 32.88 and 19.47% and grain yield/ha by 27.76 and 17.47% for parents and F_1's, respectively, but slightly increased grain protein content of F_1's by 4.19% and grain starch content of parents by 0.63%. On average, means across F_1 crosses were higher than those across inbreds for all studied traits, except for grain protein content, where the opposite was true, under both water stress and non-stress conditions. The rank of inbreds and crosses for studied traits under water stress was changed from that under well watering conditions. Grain yield/ha of drought tolerant (T) was greater than that of sensitive (S) inbreds and crosses by 220.6 and 75.70%, respectively under water stress conditions. This superiority in grain yield/ha was associated with superiority in grain yield/plant, protein yield/ha, oil yield/ha and starch yield/ha. Although there was a negative correlation between grain yield/plant and each of grain protein content and grain oil content in inbreds, it was possible to identify some inbreds and hybrids characterized by high yield and high grain protein or oil content simultaneously under water stress conditions.

Key words: Corn, Grain quality, Tolerance index, Water stress

INTRODUCTION

Grain quality is an important objective in corn (*Zea mays* L.) breeding [1, 2]. In maize grain, a typical hybrid cultivar contains approximately 4% oil, 9% protein, 73% starch, and 14% other constituents (mostly fiber).The oil is stored mainly in the germ, while starch and protein are found primarily in the endosperm, which makes up the majority of the kernel [3]. Some of the most important traits of interest in the maize market are those related to the nutritional quality of the grain, especially protein and oil content [4]. Maize oil is characterized by high levels of unsaturated fatty acids,

especially oleic (18:1); including this grain in the diet would have positive health effects [5, 6].

Corn suffered greater proportional grain yield loss due to deficit irrigation. Timing of water availability is critical for corn production. Denmead and Shaw [7] noted that water stress during the vegetative stage of corn production reduced grain yield by 25%, water stress during silking reduced grain yield by 50%, while water stress during grain fill reduced grain yield by 21%. Grain quality losses are also maximized when drought occurs during flowering time [8-10].

The existence of satisfactory genetic variability is the first prerequisite for successful selection for a given trait. The information on genetic variability of the oil content in maize grain are abundant [11-15], but breeding progress has been limited by an apparent inverse genetic relationship between grain yield and oil concentration in maize [16,17].

Trials have shown that unfavorable conditions, especially drought, might alter the seed composition and related qualities such as oil physicochemical properties [18-20]. It has been reported that lack of water during all stages of growth and development is the limiting factor for seed growth that can influence its composition [20,21]. For example, severe drought has been shown to decrease seed protein and oil contents in soybean [22-24]. In some earlier studies, it has been reported that water deficit can affect seed chemical composition by reducing CO_2 assimilation [25] or through an alteration in the metabolic processes of seed chemical composition [26, 27]. Yang *et al.* [25] reported linear relationships between photosynthetic characteristics and seed chemical composition at different water availabilities. They also reported a positive relationship between plant photosynthetic characteristics and protein and starch contents in grass pea. There are reports that shortage of water has a significant effect on oil fatty acid contents [20], but little work has been reported about the effect of drought stress on maize kernel composition in different genotypes of maize. Therefore, the objectives of this study were: (i) to determine the effects of drought stress at flowering stage on grain composition in relation to protein, oil and starch contents and yields, (ii) to estimate the effects of maize genotype and genotype x irrigation interaction on such traits, (iii) to identify the relationships among grain quality and yield traits in maize under water stress conditions and (iv) to classify

studied genotypes based on efficiency *vs* responsiveness, yielding ability *vs* drought tolerance and grain yield *vs* quality traits.

MATERIALS AND METHODS

This study was carried out at the Agricultural Experiment and Research Station of the Faculty of Agriculture, Cairo University, Giza, Egypt (30° 02'N latitude and 31° 13'E longitude with an altitude of 22.50 meters above sea level), in 2012, 2013 and 2014 seasons.

Plant material

Based on the results of previous experiments, six maize (*Zea mays* L.) inbred lines showing clear differences in performance and general combining ability for grain yield under drought stress; two of them were obtained from Maize Research Department, of the Agricultural Research Center, Egypt as parents of commercial hybrids and four were obtained from Toshki Agricultural Co., Egypt in the 8th selfing generation, were chosen in this study to be used as parents of diallel crosses (Table 1).

Table 1. Designation, origin and most important traits of 6 inbred lines (L) used for making diallel crosses in this study.

Inbred designation	Origin	Institution / country	Productivity under water stress
L20-Y	SC30N11	Pion. Int. Co.	High
L53-W	SC 30K8	Pion. Int. Co.	High
Sk 5-W	Tepalcinqo -5 (Tep # 5)	ARC-Egypt	High
L18-Y	SC30N11	Pion. Int. Co.	Low
L28-Y	Population-59	ARC-Thailand	Low
Sd 7-W	American Early Dent (AED)	ARC-Egypt	Low

ARC = Agricultural Research Center, Pion. Int. Co. = Pioneer International Company in Egypt, SC = Single cross, W = White grains and Y = Yellow grains.

Making F$_1$ diallel crosses

In 2012 season, all possible diallel crosses (except reciprocals) were made among the six parents, so seeds of 15 direct F$_1$ crosses were obtained. Seeds of the 6 parents were also increased by selfing in the same season (2012) to obtain enough seeds of the inbreds in the 9th selfing generation.

Evaluation of parents and F$_1$`s

Two field evaluation experiments were carried out in 2013 and 2014 seasons at the Agricultural Experiment and Research Station of the Faculty of Agriculture, Cairo

University. Each experiment included 15 F_1 crosses, their 6 parents and 2 check cultivars, *i.e.* SC 130 (white corn), obtained from the Agricultural Research Center (ARC) and SC 2055 (yellow corn) obtained from Hi-Tech. Company, Egypt. Evaluation in each season was carried out under two environments, *i.e.* two irrigation regimes; well watering (WW) by giving all required irrigations during the whole season and water stress (WS) by withholding the 4th and 5th irrigations, thus irrigation was withheld for 40 days, including a water stress period of 25 days just before and during flowering stage. A split plot design in randomized complete block arrangement with four replications was used. Main plots were devoted to irrigation regimes (WW and WS). Sub plots were devoted to 23 maize genotypes (6 parents, 15 F_1`s and 2 checks). Each subplot consisted of one ridge of 4 m long and 0.7 m width; the experimental plot area was 2.8 m^2. The distance between each two hills was 20 cm. Thinning was done after 21 days from sowing and one plant was left in each hill. Each main plot was surrounded with a wide alley (3.5 m width) to avoid interference of the two water treatments with irrigation water. Sowing date was done on May 5 and May 8 in 2013 and 2014 seasons, respectively.

The soil analysis of the experimental soil at the Agricultural Experiment and Research Station of the Faculty of Agriculture, Cairo University, Giza, Egypt, as an average of the two growing seasons 2013 and 2014, indicated that the soil is clay loam (4.00% coarse sand, 30.90% fine sand, 31.20% silt, and 33.90% clay), the pH (paste extract) is 7.73, the EC is 1.91 dSm-1, soil bulk density is 1.2 g cm-3, calcium carbonate is 3.47%, organic matter is 2.09%, the available nutrient in mg kg-1are Nitrogen (34.20), Phosphorous (8.86), Potassium (242), hot water extractable B (0.49), DTPA - extractable Zn (0.52), DTPA - extractable Mn (0.75) and DTPA - extractable Fe (3.17). Meteorological variables in the 2013 and 2014 growing seasons of maize were obtained from Agro-meteorological Station at Giza, Egypt. For May, June, July and August, mean temperature was 27.87, 29.49, 28.47 and 30.33°C, maximum temperature was 35.7, 35.97, 34.93 and 37.07°C and relative humidity was 47.0, 53.0, 60.33 and 60.67% respectively, in 2013 season. In 2014 season, mean temperature was 26.1, 28.5, 29.1 and 29.9°C, maximum temperature was 38.8, 35.2, 35.6 and 36.4°C and relative humidity was 32.8, 35.2, 35.6 and 36.4%, respectively. Precipitation was nil in all months of maize growing season for both seasons. All other agricultural practices were followed according to the recommendations of ARC,

Egypt. Sibbing was carried out in each entry for the purpose of determining the grain contents of protein, oil and starch.

The following traits were measured at harvest: **1. Grain yield per plant (GYPP)** in g estimated by dividing the grain yield per plot (adjusted at 15.5% grain moisture) on number of plants/plot at harvest. **2. Grain yield per hectare (GYPH)** in ton, by adjusting grain yield/plot to grain yield per hectare. **3. Grain protein content (GPC%). 4. Grain oil content (GOC%). 5. Grain starch content (GSC%).** The three traits GPC, GOC and GSC were determined using the non-destructive grain analyzer, Model Infratec TM 1241 Grain Analyzer, ISW 5.00 valid from S/N 12414500, 1002 5017/Rev.1, manufactured by Foss Analytical AB, Hoganas, Sweden. **6. Protein yield per hectare (PYPH)** in kg, by multiplying grain protein content by grain yield per hectare. **7. Oil yield per hectare (OYPH)** in kg, by multiplying grain oil content by grain yield per hectare. **8. Starch yield per hectare (SYPH)** in kg, by multiplying grain starch content by grain yield per hectare.

Tolerance index: Tolerance index (T), a general measure of stress intensity in the experiment, was calculated according to Fisher and Maurer [28] as follows: $T = (Li/Hi) / D$, where: $Li =$ Grain yield of ith genotype under WS. $Hi =$ Grain yield of ith genotype under WW. $D =$ Overall mean grain yield of L / overall mean grain yield of H.

Biometrical analysis

The analysis of variance (ANOVA) of the split plot design was performed on the basis of individual plot observation using the MIXED procedure of SAS ® [29]. Combined analysis of variance across the two seasons was performed if the homogeneity test was non-significant. Moreover, each environment (well watering; WW and water stress; WS) was analyzed separately across seasons as randomized complete block design (RCBD) for the purpose of determining genetic parameters using GENSTAT 10th addition windows software. Least significant differences (LSD) values were calculated to test the significance of differences between means according to Steel *et al.* [30]. Genotypic (r_g) correlation coefficients were calculated between grain quality and yield traits under each environment (WW and WS) according to Singh and Chaudhary [31] using the following formula: $r_g = \delta^2_{gxy}/(\delta^2_{gx} . \delta^2_{gy})^{1/2}$ Where: $\delta^2_{gxy} =$ the genotypic covariance of the two traits, X and Y,

respectively. δ^2_{gx} and δ^2_{gy} = the genotypic variance of the two traits, X and Y, respectively.

RESULTS AND DISCUSSION

1. Analysis of variance

Combined analysis of variance across years (2013 and 2014) for studied grain quality and yield traits of 23 maize genotypes (6 inbred lines, their 15 diallel F_1 crosses and two checks) under two irrigation regimes using a split plot design is presented in Table (2). The variances due to the irrigation treatments for grain protein content (GPC), grain oil content (GOC) and grain starch content (GSC) were not significant, indicating that irrigation treatments did not differ significantly for these three grain quality traits.

On the contrary, variances due to irrigation treatments for the studied yield traits, *i.e.* grain yield/ plant (GYPP), protein yield/ha (PYPH), oil yield/ha (OYPH), starch yield/ha (SYPH) and grain yield/ha (GYPH) were significant (P≤0.01), indicating that water stress had a significant effect on these traits. The main effects of years were not significant for all studied traits, except grain yield/ plant, indicating that environmental conditions prevailed in the two seasons (weather and soil conditions) were not different to the extent that affected all studied traits, except grain yield/ plant, which was significantly affected by years.

The main effects of genotypes were significant (P≤0.01) for all studied traits, indicating that studied genotypes exhibited significant differences in all studied quality and yield characters. It is observed that genotype effects were more pronounced than irrigation effects on all studied traits (Table 2). This was expressed *via* the percentage of sum of squares (SS) for each component to the total sum of squares, which indicated that genotypes contributed the highest percentage to the total variance as compared to other components.

Table 2. Combined analysis of variance (% sum of squares) of split plot design for studied grain traits of 23 maize genotypes under two irrigation regimes across 2013 and 2014 years.

SOV	df	Sum of squares (SS) %			
		GPC%	GOC%	GSC%	GYPP
Years (Y)	1	0.66 ns	0.03 ns	1.81 ns	1.12**
Irrigations (I)	1	2.63 ns	4.13 ns	3.19 ns	9.21**
I × Y	1	0.0004 ns	0.06 ns	0.09 ns	0.01 ns
Error	8	6.71	13.20	6.68	0.29

	22	60.43**	44.75**	42.53**	83.38**
Genotypes (G)	22	60.43**	44.75**	42.53**	83.38**
G × Y	22	4.31**	9.77**	8.65**	1.25**
G × I	22	4.99**	6.14**	12.10**	1.75**
G × I × Y	22	11.25**	9.47**	10.21**	0.94**
Error	176	9.00	12.44	14.74	2.05
Total SS	275	308.98	47.66	193.81	1420737
		PYPH	**OYPH**	**SYPH**	**GYPH**
Years (Y)	1	0.03 ns	0.06 ns	0.10 ns	0.12 ns
Irrigations (I)	1	4.40**	6.92**	5.84**	6.02**
I × Y	1	0.04 ns	0.04 ns	0.002 ns	0.001ns
Error	8	0.47	0.47	0.30	0.30
Genotypes (G)	22	87.27**	85.75**	87.66**	87.58**
G × Y	22	0.49*	1.36**	0.51**	0.55**
G × I	22	3.46**	2.87**	3.16**	3.14**
G × I × Y	22	1.63**	0.78**	1.04**	0.96**
Error	176	2.20	1.74	1.40	1.34
Total SS	275	39158981	7514703	1757058593	3518

GPC = grain protein content, GOC = grain oil content, GSC = grain starch content, GYPP = grain yield/ plant , PYPH = protein yield/ha, OYPH = oil yield/ha, SYPH = starch yield/ha, GYPH = grain yield/ha, * and ** indicate significance at 0.05 and 0.01 probability levels, respectively, ns = non-significance.

Mean squares due to genotype × years, genotype × irrigations and genotype × irrigations × years were significant (P≤ 0.01) for all studied traits, suggesting that rank of genotypes is different from year to year, from one irrigation regime to another and from one combination of irrigation × year to another.

Significance of main effects of maize genotypes, irrigation treatments and their interactions of the present study confirms the findings of pervious investigators; i.e. Al-Naggar et al. [32-36] for genotypes, Al-Naggar et al. [10, 37,38] for irrigation regimes and Mittelmann et al. [4], Berke and Rocheford [39], Pixley and Bjarnason [40] and Munamava et al. [41] for genotype × irrigation interaction.

Moreover, significant interaction between genotypes and irrigation treatments indicated that selection is possible to be practiced under a specific irrigation treatment [10, 35, 42-45].

## 2. Effect of deficit irrigation at flowering stage

The effects of drought at flowering stage on the means of studied traits across inbreds, hybrids (F$_1$'s) and checks across two years are illustrated in Fig.(1). Mean grain yield/plant (GYPP) was significantly decreased due to water stress at flowering stage by 32.8, 19.74 and 22.82% for parents, F$_1$'s and checks, respectively. Effects of water stress on the mean performance of grain yield/ plant were approximately in the same trend to those effects on grain yield/ha (27.76, 17.74 and 24.20%), protein yield/ ha (25.5, 13.8 and 18.5%), oil yield/ha (29.9, 20.2 and 26.3%), and starch yield/ ha

(25.0, 17.03 and 23.7%) for parents, F_1 crosses and checks, respectively. Consistent to these results, several investigators reported reductions due to drought stress in grain yield [35, 45, 46], protein yield [14] and oil yield [36, 38].

Moreover, drought stress at flowering caused a slight, but not significant reduction in grain oil content by 5.20, 4.22 and 3.20% for inbred parents, F_1's and checks, respectively. This reduction in grain oil content due to water stress at flowering was previously reported by some investigators [36, 38].

On the contrary, water stress caused a significant, but slight increase in grain protein content of F_1's (4.17%) and checks (7.07%) and grain starch content of parents (0.63%) and checks (0.65%). It seems that under drought stress conditions, plants instead of using available energy for producing oil in their grains, they use it for producing starch and/or protein, which might consume less energy for their metabolism.

It is observed from Fig (1) that F_1's showed the least reduction due to drought in grain yield/ plant, grain yield/ ha, oil yield/ ha, protein yield/ ha and starch yield/ ha, while parental inbreds showed maximum reduction in these traits, indicating that heterozygotes are more drought tolerant than homozygotes. Superiority of heterozygotes over homozygotes in abiotic stress tolerance may be due to heterosis phenomenon and was reported by several investigators [32-34].
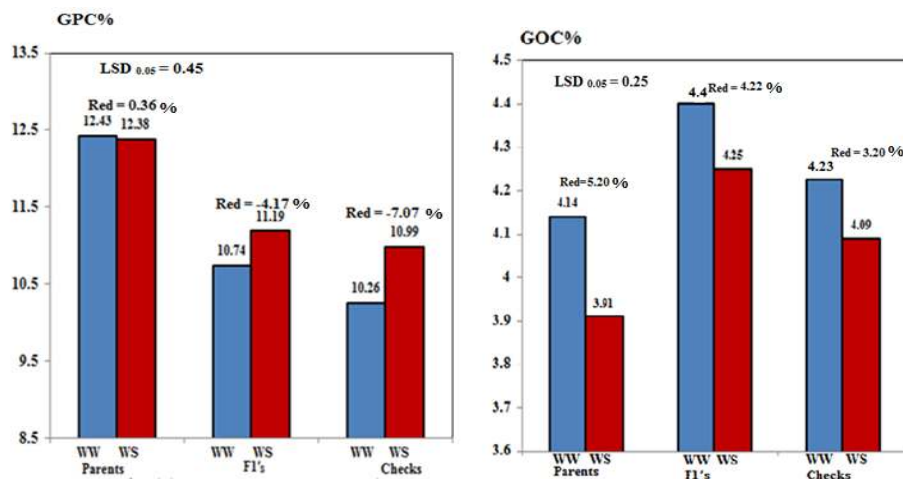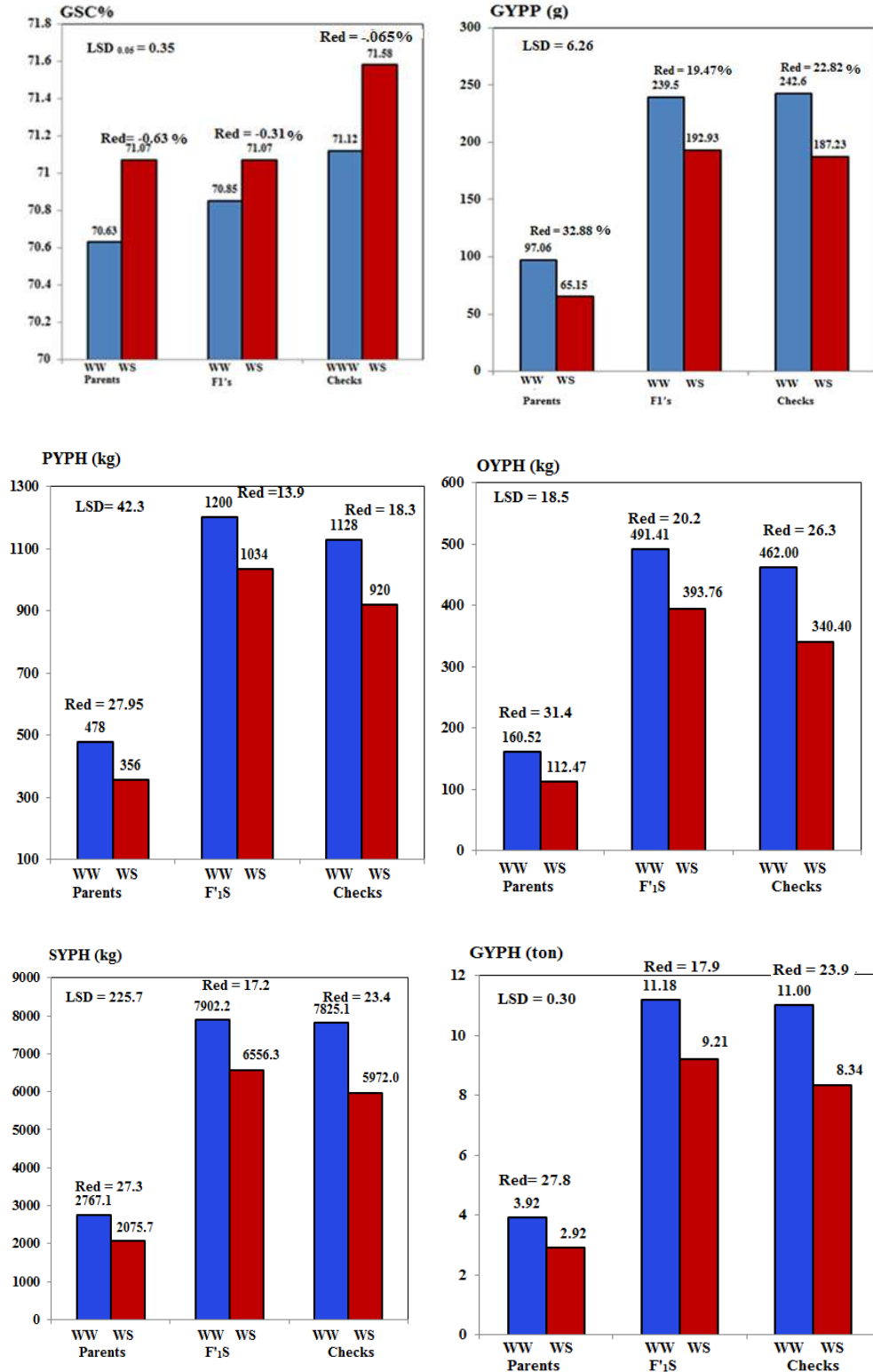
Fig. 1.**Effect of drought at silking on means of grain quality and yield traits of parental inbreds, F$_1$ crosses and checks across two seasons. GPC= grain protein content, GOC= grain oil content, GSC= grain starch content, GYPP= grain yield / plant, PYPH= protein yield /ha, OYPP= oil yield /ha, SYPH= starch yield /ha, GYPH= grain yield /ha, Red= Reduction %= 100×(WW − WS)/WW. Checks= The single crosses SC130 and SC2055.**

Effect of maize genotype

In general, inbreds varied significantly in all studied traits (Table 3). High values of all studied traits were considered favorable. The inbred line L53 showed the highest (most favorable) means for grain yield/plant, grain yield/ha, oil yield/ha, protein yield/ha and starch yield/ha. The inbreds L20 and Sk5 ranked second and third, respectively for the same traits. For grain contents of protein (GPC), oil (GOC) and starch (GSC), the inbreds L18, L28 and L20, respectively came in the first rank and showed the highest means for these traits.

Table 3. Means of studied grain quality and yield traits of inbreds and crosses across two irrigation regimes combined across 2013 and 2014 seasons.

Genotypes	GPC %	GOC %	GSC %	GYPP g	PYPH kg	OYPH kg	SYPH kg	GYPH ton
Parents								
L20	11.43	3.95	71.57	103.64	531.73	188.45	3358.9	4.70
L53	11.50	4.15	70.72	128.8	645.77	229.61	3912.4	5.54
Sk5	12.94	3.53	70.9	86.30	521.36	141.40	2863.3	4.03
L18	13.32	3.96	70.71	60.74	333.62	99.03	1775.6	2.51
L28	12.76	4.35	70.22	53.73	278.45	95.13	1538.1	2.19
Sd7	12.48	4.22	70.99	53.40	191.16	65.29	1080.0	1.52
Average	12.4	4.03	70.85	81.1	417.02	136.48	2421.40	3.42
Crosses								
L20 X L53	10.05	4.23	71.65	167.23	691.3	293.5	4956.2	6.92
L20 X Sk5	10.43	4.08	71.70	200.6	979.4	383.3	6702.4	9.35
L20 X L18	10.88	3.88	72.32	223.63	1228.6	438.5	8172.1	11.30
L20 X L28	10.85	4.46	70.91	191.43	1006.3	412.2	6595.5	9.29
L20 X Sd7	10.67	4.31	70.88	241.12	1187.3	479.8	7890.6	11.14
L 53 X Sk5	10.82	4.27	70.64	231.23	1111.5	437.2	7283.9	10.31
L53 X L18	11.08	4.33	70.73	250.72	1406.7	552.2	9000.0	12.73
L53 X L28	11.04	4.43	70.81	191.44	934.1	378.3	6038.0	8.53
L53 X Sd7	10.91	4.52	70.88	177.04	941.8	392.6	6147.7	8.68
Sk5 X L18	11.47	3.98	71.56	208.45	1066.3	372.7	6661.7	9.32
Sk5 X L28	11.33	4.28	70.78	220.37	1225.2	464.4	7665.5	10.83
Sk5 X Sd7	10.93	4.72	69.89	248.68	1331.7	576.3	8533.5	12.21
L18 X L28	11.94	4.31	70.7	193.22	1113.8	403.1	6609.6	9.35
L18 X Sd7	11.19	4.33	70.87	220.88	1063.1	413.2	6749.3	9.52
L28 X Sd7	10.93	4.75	70.14	277.8	1468.1	641.5	9432.5	13.46
Average	10.97	4.32	70.96	216.26	1117.0	442.6	7229.2	10.20
Checks								
S.C. 130	10.67	3.87	71.65	224.64	1091.4	398.64	7357.1	10.28
S.C. 2055	10.58	4.45	71.05	205.18	956.2	403.83	6440.0	9.07
LSD (G)0.05	0.32	0.15	0.32	10.29	48.44	18.91	258.61	0.36
LSD (G)0.01	0.42	0.19	0.42	13.53	63.66	24.85	339.89	0.47

GPC= grain protein content, GOC= grain oil content, GSC= grain starch content, GYPP= grain yield/plant, PYPH= protein yield/ha, OYPH= oil yield/ha, SYPH= starch yield/ha, GYPH= grain yield/ha. G= genotypes.

On the contrary, the inbred line Sd7 showed the lowest means for all yield traits, *i.e.* grain yield/ha, protein yield/ha, oil yield/ha and starch yield/ha. For grain protein content, grain oil content and grain starch content traits, the inbreds L20, Sk5 ad L28, respectively came in the last rank and achieved the lowest means among all inbreds parents in this study. It is worthy to note that the inbred line Sd7 is one of the most

commonly used as a parent of many commercial single and 3-way cross hybrids in Egypt. It seems that its superiority is not in their characters *per se*, but for its superiority in combining ability.

The F_1 crosses varied greatly in all studied traits (Table 3). The highest means for all yield traits (grain yield/plant, grain yield/ha, protein yield/ha, oil yield/ha and starch yield/ha) were shown by the F_1 cross L28 × Sd7 followed by L53 × L18 and Sk5 × Sd7. In contrast, the lowest means among all crosses for these yield traits were observed in the cross L20 × L53 followed by L53 × L28. The best check cultivar, in this study across the two irrigation regimes was the variety SC130 developed by ARC, Egypt for grain yield/plant, grain yield/ha, protein yield/ ha and starch yield/ ha and HI Tec. cultivar SC2055 for oil yield/ ha. The best F_1 in this study (L28 × Sd7), across WW and WS environments, excelled significantly the best check by 23.66% for grain yield/plant, 31.01% for grain yield/ha, 34.51% for protein yield/ha, 58.85% for oil yield/ha and 28.21% for starch yield/ha. This cross was also the best one among F_1's for grain oil content. This result indicated that it is possible to obtain a high yielding and high grain oil content simultaneously, in spite of the negative correlation mentioned in the review between grain yield and grain oil percent, confirming the results of Mittelmann *et al.* [4]. High grain yield and high oil content were recorded in some maize hybrids [47,48]

For grain protein content and grain starch content, the two crosses L18 × L28 and L20 × L18, respectively came in the first rank. On the contrary, the F_1 cross L20 × L53 showed the lowest means of grain yield/plant, grain yield/ha, protein yield/ha, starch yield/ha and grain protein content. For grain oil content and grain starch content, the two crosses L20 × L18 and Sk5 × Sd7, respectively showed the lowest means among all F_1's.

In general, mean grain protein content across all F_1crosses was lower than that across parental inbreds, and the highest mean grain protein content of the best inbred (13.32%) was higher than that of the best F_1 cross (11.94%). This result agrees with that reported by Al-Naggar *et al.* [32]. They also found that average heterosis relative to the higher parent (heterobeltiosis) across all 76 testcrosses was in the negative direction (-0.47 % for protein and -24.5 % for oil content), indicating average dominance of the alleles for both low oil and low protein contents. This negative

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average heterosis was also reported by Mittelmann e*t al.* [49] for oil content and Oliveira *et al.* [50] for protein content.

Genotypic variation in maize quality and yield traits was reported by several investigators [12,13, 32-34, 51-54]for protein content, Dudley and Lambert [12], Al-Naggar *et al.* [32-34], Misevic and Alexander [55] and Song *et al* [59] and for oil content and Gutierrez-Rojas *et al.* [57] for starch content). The existence of genetic variability for grain protein and oil content indicates that these traits of maize grain could be improved by conventional breeding programs.

Genotype × irrigation regime interaction

Means of each inbred, cross and check for studied grain quality and yield traits under contrasting irrigation regimes, *i.e.* well watering and water stress at flowering across two years are presented in Table (4). The highest mean grain yield per plant and per hectare, protein yield, oil yield and starch yield per hectare was recorded for the inbred line L53 followed by L20 and Sk5 under both irrigation regimes, while the lowest ones were exhibited by Sd7, L28 and L18. The first three inbreds are high yielding under both water stress and non-stress conditions; two of them, namely L53 and Sk5 are tolerant (TI >1.00). The second three inbreds are low-yielders under both irrigation regimes; one of them (L18) is tolerant to drought (TI = 1.224) and the other two, i.e. Sd7 and L28 are drought sensitive (TI <1.00). The present results assure the diversity of the parental inbreds in tolerance to drought at silking stage.

It is observed that the inbred L18 showed the highest grain protein content under both water stress and non-stress conditions and the highest tolerance index. Moreover, the highest grain oil content and starch content were shown by the parental inbreds L28 and L20, respectively under water stress conditions.

Results in Table (4) indicated the existence of cross × irrigation regime interaction in most studied F_1 crosses for all studied traits. The rank of crosses for studied traits under well watering was changed from that under water stress conditions. The highest mean grain yield per hectare under water stress was shown by the F_1 cross L53 × L18 (12.19 ton/ha) followed by L28 × Sd7 (12.02 ton/ha) and Sk5 × Sd7 (11.52 ton/ha). The three crosses excelled the best check (SC130) in grain yield/ha (8.66 ton/ha) by 40.67, 38.70 and 32.94%, respectively under WS

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conditions at flowering stages; these three crosses also out-yielded SC130 under well watering, but in less magnitude, *i.e.* by 11.69, 25.44 and 8.52%, respectively.

Table 4. Means of studied grain quality and yield traits of each inbred and cross under two water regimes and change (%) across two seasons.

Genotype	WW	WS	Change %	WW	WS	Change %	WW	WS	Change %
	GPC %			GOC %			GSC %		
				Parents					
L20	10.97	11.88	8.36**	4.23	3.67	-13.39**	71.00	72.13	1.60**
L53	11.82	11.18	-5.36*	4.15	4.15	0.00	70.48	70.95	0.66*
Sk5	12.80	13.08	2.21	3.48	3.57	2.39	71.25	70.55	-0.98**
L18	13.52	13.12	-2.96	4.03	3.88	-3.72	70.35	71.07	1.02**
L28	12.88	12.63	-1.94	4.55	4.15	-8.79**	69.93	70.50	0.81*
Sd7	12.57	12.38	-1.46	4.40	4.03	-8.33**	70.75	71.23	0.68*
				Crosses					
L20 × L53	9.73	10.37	6.51*	4.38	4.07	-7.22**	71.67	71.63	-0.05
L20 × Sk5	10.55	10.32	-2.21	4.20	3.95	-5.95*	71.52	71.88	0.51*
L20 × L18	10.95	10.82	-1.22	4.05	3.72	-8.23**	71.63	73.00	1.91*
L20 × L28	10.63	11.07	4.08	4.38	4.53	3.42	71.15	70.67	-0.68*
L20 × Sd7	10.33	11.00	6.45**	4.50	4.12	-8.52**	70.97	70.78	-0.26
L53 × Sk5	10.58	11.05	4.41*	4.12	4.42	7.29**	70.80	70.48	-0.45
L53 × L18	10.57	11.60	9.78**	4.27	4.40	3.12	70.75	70.70	-0.07
L53 × L28	10.63	11.45	7.68**	4.53	4.32	-4.78*	70.77	70.85	0.12
L53 × Sd7	10.50	11.32	7.78**	4.57	4.47	-2.19	70.87	70.88	0.02
Sk5 × L18	11.35	11.58	2.06	4.10	3.85	-6.10*	71.13	71.98	1.19**
Sk5 × L28	11.42	11.23	-1.61	4.40	4.17	-5.30*	70.40	71.17	1.09**
Sk5 × Sd7	10.83	11.03	1.85	4.68	4.75	1.42	70.00	69.78	-0.31
L18 × L28	11.57	12.32	6.48**	4.45	4.17	-6.37**	70.72	70.68	-0.05
L18 × Sd7	10.85	11.53	6.30**	4.42	4.25	-3.77	71.07	70.67	-0.56*
L28 × Sd7	10.67	11.20	5.00*	4.92	4.58	-6.78**	69.37	70.92	2.23**
				Checks					
S.C 130	10.22	11.12	8.81**	3.95	3.78	-4.22*	71.32	71.98	0.93**
S.C 2055	10.30	10.85	5.34*	4.50	4.40	-2.22	70.92	71.18	0.38
LSD 0.05	G=0.32, G×I=0.45,I=0.45			G=0.15, G×I=0.21,I=0.25			G=0.32, G×I=0.46,I=0.35		
LSD 0.01	G=0.42, G×I=0.59,I=0.65			G=0.19, G×I=0.27,I=0.36			G=0.42, G×I=0.60,I=0.51		
Genotype	PYPH(kg)			OYPH (kg)			SYPH(kg)		
				Parents					
L20	589.6	473.9	-19.6**	229.7	147.2	-35.9**	3838.2	2879.6	-24.97**
L53	771.3	520.3	-32.5**	266.4	192.9	-27.6**	4534.6	3290.3	-27.44**
Sk5	530.2	512.5	-3.3	144.3	138.5	-4.0	2950.7	2775.9	-5.92
L18	370.1	297.1	-19.7**	111.0	87.1	-21.5*	1933.3	1618.0	-16.31*
L28	321.8	235.1	-26.9**	112.9	77.3	-31.6**	1747.9	1328.4	-24.00**
Sd7	284.6	97.7	-65.7**	98.8	31.8	-67.8**	1597.9	562.0	-64.83**
				Crosses					
L20 × L53	775.3	607.4	-21.7**	348.2	238.8	-31.4**	5710.8	4201.6	-26.43**
L20 × Sk5	1285.9	673.0	-47.7**	508.5	258.2	-49.2**	8715.8	4689.0	-46.20**
L20 × L18	1248.6	1208.6	-3.2	461.3	415.6	-9.9**	8169.8	8174.4	0.06
L20 × L28	1095.5	917.1	-16.3**	451.7	372.8	-17.5**	7342.8	5848.1	-20.36**
L20 × Sd7	1131.8	1242.7	9.8**	494.6	465.1	-6.0**	7778.9	8002.4	2.87
L53 × Sk5	1208.2	1014.7	-16.0**	469.7	404.8	-13.8**	8081.6	6486.1	-19.74**
L53 × L18	1401.8	1411.5	0.7	567.3	537.0	-5.3**	9384.6	8615.3	-8.20**
L53 × L28	1055.5	812.7	-23.0**	450.8	305.5	-32.2**	7054.7	5021.4	-28.82**
L53 × Sd7	987.6	896.1	-9.3**	430.0	355.3	-17.4**	6667.4	5628.1	-15.59**
Sk5 × L18	1251.1	881.5	-29.5**	451.6	293.7	-35.0**	7846.2	5477.3	-30.19**
Sk5 × L28	1313.6	1136.9	-13.4**	506.6	422.1	-16.7**	8109.0	7222.0	-10.94**
Sk5 × Sd7	1394.3	1269.1	-9.0**	604.4	548.1	-9.3**	9031.6	8035.4	-11.03**
L18 × L28	1142.4	1085.2	-5.0**	438.9	367.3	-16.3**	6988.1	6231.1	-10.83**
L18 × Sd7	1117.8	1008.5	-9.8**	454.3	372.1	-18.1**	7308.8	6189.8	-15.31**
L28 × Sd7	1590.3	1345.9	-15.4**	733.2	549.8	-25.0**	10343.1	8521.8	-17.61**
				Checks					
S.C 130	1214.1	968.7	-20.21**	469.3	327.9	-30.13**	8478.6	6235.6	-26.46**
S.C 2055	1041.8	870.5	-16.44**	454.7	352.9	-22.38**	7171.6	5708.4	-20.40**
LSD 0.05	G=55.93, G×I=79.1,I=42.3			G=21.83, G×I=30.9,I=18.5			G=298.62, G×I=422.3,I=225.7		
LSD 0.01	G=73.50, G×I=104.0.,I=61.5			G=28.70, G×I=40.6,I=26.9			G=393.47, G×I=555.0,I=328.4		

Table 4.Continued.

	WW	WS	Change%	WW	WS	Change%	TI
Genotype	GYPH(ton)			GYPP(g)			
			Parents				
L20	5.41	3.99	-26.2**	126.58	80.71	-36.24**	0.95

L53	6.44	4.64	-28.0**	152.05	105.54	-30.59**	1.03
Sk5	4.14	3.92	-5.3	97.56	75.04	-23.09**	1.15
L18	2.75	2.28	-17.2**	66.69	54.79	-17.85**	1.22
L28	2.50	1.88	-24.8**	64.37	43.09	-33.05**	1.00
Sd7	2.26	0.79	-65.1**	75.10	31.70	-57.79**	0.63
Crosses							
L20 × L53	7.97	5.87	-26.4**	185.33	149.14	-19.53**	1.00
L20 × Sk5	12.18	6.52	-46.5**	250.79	150.41	-40.03**	0.75
L20 × L18	11.40	11.19	-1.8	244.60	202.65	-17.15**	1.03
L20 × L28	10.32	8.27	-19.8**	214.05	168.82	-21.13**	0.98
L20 × Sd7	11.30	11.00	-2.7*	246.25	235.98	-4.17**	1.19
L53 × Sk5	11.41	9.20	-19.4**	253.82	208.63	-17.81**	1.02
L53 × L18	13.27	12.19	-8.1**	264.87	236.56	-10.69**	1.11
L53 × L28	9.97	7.09	-28.9**	213.97	168.91	-21.06**	0.98
L53 × Sd7	9.41	7.94	-15.6**	209.01	145.06	-30.60**	0.86
Sk5 × L18	11.03	7.61	-31.0**	241.40	175.50	-27.30**	0.90
Sk5 × L28	11.52	10.15	-11.9**	233.93	206.81	-11.59**	1.10
Sk5 × Sd7	12.90	11.52	-10.7**	268.76	228.61	-14.94**	1.06
L18 × L28	9.88	8.81	-10.8**	220.44	166.01	-24.69**	0.94
L18 × Sd7	10.29	8.76	-14.8**	246.34	195.41	-20.67**	0.99
L28 × Sd7	14.91	12.02	-19.4**	300.09	255.50	-14.86**	1.06
Checks							
S.C 130	11.89	8.66	-27.11**	249.77	199.51	-20.12**	1.03
S.C 2055	10.11	8.02	-20.69**	235.40	174.95	-25.68**	0.96
LSD 0.05	G=0.41, G×I=0.6,I=0.3			G=10.29, G×I=14.56,I=6.26			
LSD 0.01	G=0.54, G×I=0.8,I=0.5			G=13.53, G×I=19.1,I=9.10			

GPC= grain protein content, GOC= grain oil content, GSC= grain starch content, GYPP= grain yield/plant, PYPH= protein yield/ha, OYPP= oil yield /ha, SYPH= starch yield /ha, GYPH= grain yield /ha, Change%= 100×(WS − WW)/WW. G= genotypes, I= irrigations. * andsignificant at 0.05 and 0.01 levels, respectively.**

The superiority of these three crosses in grain yield/ha over the best check under water stress was associated with superiority in grain yield/plant, protein yield/ha, grain oil yield/ha and grain starch yield/ha and reached maximum in grain oil yield/ha (52.23. 55.81 and 55.33% for L53 × L18, L28 × Sd7 and Sk5 × Sd7, respectively).

It is observed that the cross L53 × l8 was the highest in drought tolerance index among all F_1 crosses and showed the highest grain protein content, indicating the possibility of obtaining a drought tolerant genotype with high yield under water stress as well as high grain protein content. Also, the cross Sk5 × Sd7; one of the three highest yielding crosses under water stress, occupied the first rank in grain oil content, the second rank in grain oil yield/ha and the third rank in grain protein yield/ha. Several investigators [12, 55] reported a negative correlation between grain yield and either grain protein content or grain oil content, but our results indicated that it is possible to break such linkage between high yield and low grain protein or oil content genes of maize and obtain genotypes of high grain yield and high oil or protein content simultaneously. High grain yield and high oil content were recorded in some maize hybrids, such as L53 × Sk5.

It is worthy to note that the three highest yielding crosses under water stress (L53 × L18, L28 × Sd7 and Sk5 × Sd7) were tolerant to drought at flowering (TI >1.00) and reduction in GYPH due to water stress was low (10.69, 14.88 and 14.94%,

respectively). The cross L20 × Sd7 was the best in tolerance index and showed the lowest reduction (4.17%) in grain yield due to water stress. It is worth noting that the highest tolerant crosses were among tolerant × tolerant inbreds (L53 × L18), tolerant × sensitive (L20 × L18 and Sk5 × Sd7) and sensitive × sensitive (L2 × Sd7). The tolerant cross (tolerant × tolerant) could be due to accumulating additive genes of drought tolerance. The tolerant cross (tolerant × sensitive) could be due to dominance gene action. The tolerant cross (sensitive × sensitive) could be due to epsitasis, one of the theories that might explain heterosis phenomenon. On the contrary, the lowest grain yield/ha was exhibited by the cross L20 × L53 (5.87 ton /ha) followed by L20 × Sk5 (6.52 ton /ha). The latter cross showed maximum reduction (46.50%) in grain yield/ha due to water stress and the lowest TI value in this study (TI= 0.75).

Superiority of drought tolerant (T) over sensitive (S) genotypes

To describe the differences between tolerant (T) and sensitive (S) inbreds and hybrids, data of studied characters were averaged for the two groups of inbreds and hybrids differing in their drought tolerance expressed by higher TI value than unity mean grain yield under water stress and low reduction in grain yield due to water stress (Table 5). Based on these parameters, the drought tolerant (T) inbred lines were L53 and Sk5 and the drought sensitive (S) inbred lines Sd7 and L28. Moreover, the three F_1 crosses L53 × L18 (grain yield/ha under WS = 12.19 ton), L28 × Sd7 (grain yield/ha under WS = 12.02 ton) and Sk5 × Sd7 (grain yield/ha under WS = 11.52 ton) (Table 5) were considered the most tolerant to drought at flowering stage, while the F_1 crosses L20 × L53 (grain yield/ha under WS = 5.87 ton), L20× Sk5 (GYPH under WS = 6.52 ton) and L53 × Sd7 (grain yield/ha under WS = 7.94 ton) could be considered the most high drought sensitive crosses (Table 4).

Data averaged for each of the two groups (T and S) of inbreds and crosses differing in tolerance to drought indicate that grain yield/ha of drought tolerant (T) were greater than that of the sensitive (S) inbreds and crosses by 220.6 and 75.70%, respectively under WS and 122.3 and 38.96%, respectively under WW conditions. Superiority of drought tolerant (T) over sensitive (S) inbreds in grain yield/ha was associated with their superiority in grain yield/plant (141.45 and 78.97%), starch yield/ha (220.92 and 123.73%), oil yield/ha (203.64 and 93.95%) and protein yield/ha (210.23 and 114.69%) under water stress and non-stress, respectively. Superiority of

T over S hybrids in grain yield/ha was associated with their superiority in grain yield/plant (62.09 and 29.23%), protein yield/ha (85.0 and 43.88%), oil yield/ha (91.86 and 48.05%) and starch yield/ha (73.38 and 36.34%) under WS and WW, respectively.

Table 5. Superiority (%) of the most tolerant inbreds (2) and most tolerant hybrids (3) over the most sensitive inbreds (2) and most sensitive hybrids (3) for studied characters under water stress (WS) and well watering (WW) conditions across two seasons.

Genotype	Inbreds			Crosses		
	T	S	Superiority	T	S	Superiority
			WS			
GYPH(ton)	4.28	1.34	220.60**	11.91	6.78	75.70**
GYPP(g)	90.29	37.4	141.45**	240.22	148.2	62.09**
PYPH(kg)	516.3	166.4	210.23**	1342.1	725.5	85.00**
OYPH (kg)	165.7	54.6	203.64**	545.0	284.1	91.86**
SYPH(kg)	3033.1	945.1	220.92**	8390.8	4839.6	73.38**
GPC %	12.13	12.51	-3.00*	11.28	10.67	5.69*
GOC %	3.86	4.09	-5.62*	4.58	4.16	9.93*
GSC %	70.75	70.87	-0.16	70.47	71.46	-1.39
			WW			
GYPH(ton)	5.29	2.38	122.34**	13.69	9.85	38.96**
GYPP(g)	124.81	69.74	78.97**	277.91	215.04	29.23**
PYPH(kg)	650.7	303.1	114.69**	1462.1	1016.2	43.88**
OYPH (kg)	205.3	105.9	93.95**	635.0	428.9	48.05**
SYPH(kg)	3742.6	1672.9	123.73**	9586.4	7031.3	36.34**
GPC %	12.31	12.73	-3.26*	10.69	10.26	4.19*
GOC %	3.82	4.48	-14.75**	4.62	4.38	5.48*
GSC %	70.87	70.34	0.75	70.04	71.35	-1.84

% Superiority = 100 × [(T – S)/S]. GPC= grain protein content, GOC= grain oil content, GSC= grain starch content, GYPP= grain yield /plant, PYPH= protein yield /ha, OYPH= oil yield /ha, SYPH= starch yield /ha, GYPH= grain yield /ha. * andsignificant at 0.05 and 0.01 levels, respectively,**

In general, for yield characters (grain yield/ha, grain yield/plant, protein yield/ha, oil yield/ha and starch yield/ha), superiority of T over S for inbreds was more pronounced than hybrids and that under water stress (WS) was more pronounced than well watering (WW) conditions. This could be attributed to the severest effect of drought on inbreds than hybrids (refer to Fig.1) and to the heterozygote phase of hybrids which helps for more adaptation to water stress compared to homozygote phase. On the contrary, superiority of T over S in yield characters did not reflect superiority in grain quality characters (grain protein content, grain oil content and grain starch content), except a slight superiority in grain oil content of F_1 crosses (6.8 and 6.4% under WS and WW, respectively. This slight superiority in grain oil content might be attributed to the inferiority of T crosses

compared to S crosses in grain starch content under WS and grain protein content and grain starch content under WW conditions. Al-Naggar *et al.* [35] also reported that when drought was imposed at flowering stage, tolerant genotypes of maize showed 118.3% more grain yield/plant, 25.78% more kernels/plant and 27.71% more ears/plant.

Trait interrelationships

In general, all correlation coefficients of pair combinations among studied traits (24 combinations) calculated under well watering took the same sign taken by those calculated under water stress conditions; but were little higher in magnitude under well watering than water stress in 11combinations for both hybrids and inbreds, namely between grain protein content and each of grain yield/plant, grain yield/ha, protein yield/ha and starch yield/ha, between grain starch content and each of grain yield/plant, grain yield/ha, oil yield/ha, protein yield/ha and starch yield/ha and between grain yield/plant and each of protein yield/ha and starch yield/ha (Table 6). Change in magnitude of correlation coefficient due to water stress was previously reported by some investigators and ranged between increase and decrease [42,58,59].

Grain yield/plant showed a significant (P ≤ 0.01), positive and strong association with grain yield/ha (GYPH) under both irrigation regimes WW and WS across inbreds and F_1 crosses and across 2013 and 2014 years (Table 6), ranging from 0.92 for crosses under WS to 0.99 for inbreds under WW conditions. The pair correlations among all studied yield characters, namely grain yield/plant, grain yield/ha, protein yield/ha (PYPH), oil yield/ha (OYPH) and starch yield/ha (SYPH) were very strong, highly significant and positive (r_g = > 0.91) and reached perfect association (r_g= 1.00) between grain yield/ha and starch yield/ha in both inbreds and hybrids. The reason of perfect association between grain yield/ha and starch yield/ha might be due to that starch is the main component of grain yield. Thus, selection for any one of these yield traits would result in improving the other trait(s), *i.e.* protein, oil and/or starch yield per hectare. These correlations might mainly be attributed to the calculation of these traits, where grain yield/ha is a common component in all these traits, *i.e.* oil yield/ha, protein yield/ha and starch yield/ha.

There is a negative and significant correlation between grain yield/plant and each of grain protein content of inbreds under WW (-0.81) and WS (-0.65) and grain

starch content of crosses under WW (-0.69). An apparent inverse genetic relationship was also reported between grain yield and oil concentration in maize by Simmonds [16] and Feil [17].

Table 6. Genotypic correlation coefficients between studied grain quality and yield traits under well water (WW) and water stress (WS) across 2013 and 2014 seasons.

Pair of traits	Parents		Crosses	
	WW	WS	WW	WS
GYPP vs GYPH	0.99**	0.98**	0.96**	0.92**
GYPP vs GOC%	-0.20	-0.20	0.25	0.35
GYPP vs GPC%	-0.81**	-0.65*	0.22	0.11
GYPP vs GSC%	0.44	0.17	-0.69**	-0.30
GYPP vs OYPH	0.98**	1.00**	0.92**	0.91**
GYPP vs PYPH	0.98**	0.93**	0.94**	0.90**
GYPP vs SYPH	0.99**	0.97**	0.96**	0.92**
GYPH vs GOC%	-0.28	-0.39	0.27	0.33
GYPH vs GPC%	-0.78*	-0.49	0.23	0.21
GYPH vs GSC%	0.43	0.16	-0.72**	-0.24
GYPH vs OYPH	0.98**	0.99**	0.95**	0.96**
GYPH vs PYPH	0.99**	0.99**	0.98**	0.99**
GYPH vs SYPH	1.00**	1.00**	1.00**	0.999**
GOC% vs GPC%	-0.18	-0.43	-0.15	-0.20
GOC% vs GSC%	-0.74*	-0.28	-0.77**	-0.90**
GOC% vs OYPH	-0.10	-0.24	0.56*	0.56*
GOC% vs PYPH	-0.37	-0.50	0.22	0.34
GOC% vs SYPH	-0.29	-0.40	0.23	0.28
GPC% vs GSC%	-0.39	-0.42	-0.26	-0.37
GPC% vs OYPH	-0.84**	-0.59	0.15	0.23
GPC% vs PYPH	-0.69*	-0.36	0.44	0.37
GPC% vs SYPH	-0.78*	-0.50	0.23	0.20
GSC% vs OYPH	0.30	0.13	-0.87**	-0.46
GSC% vs PYPH	0.42	0.10	-0.72**	-0.30
GSC% vs SYPH	0.44	0.17	-0.68**	-0.19
OYPH vs PYPH	0.95**	0.96**	0.91**	0.96**
OYPH vs SYPH	0.98**	0.99**	0.94**	0.95**
PYPH vs SYPH	0.99**	0.99**	0.97**	0.98**

WW= well watering, WS= water stress and *and ** indicate that r_g estimate exceeds once and twice its standard error, respectively. GPC= grain protein content, GOC= grain oil content, GSC= grain starch content, GYPP= grain yield per plant, PYPH= protein yield/ha, OYPH= oil yield yield/ha, SYPH= starch yield/ha, GYPH= grain yield/ha.

It is observed that a significant and positive correlation existed between grain oil content (%) and oil yield/ha across crosses under WW (r_g = 0.56) and WS (r_g =0.56). However, there is a trend of negative correlation between grain protein content% and grain starch content %, but such correlation did not reach to the significance level (r_g = -0.39 and -0.42 for inbreds and -0.26 and 0.37 for crosses, under WW and WS, respectively. Moreover, a trend of negative but not significant between grain oil content and grain protein content was shown across inbreds (-0.18 and -0.43) and crosses (-0.50 and -0.20) under WW and WS, respectively. In the literature, investigators reported that associations between grain protein and oil

content in maize varied from insignificant [60, 61] to highly positive values [56].

It is worthy to mention that in the present investigation the correlation coefficient varied from inbreds to hybrids in direction (sign) in 15 out of 28 cases, namely between grain yield/plant and each of grain oil content, grain protein content and grain starch content; sign was -, - and + in inbreds but was +, + and – in hybrids, respectively, between grain yield/ha and each of grain oil content, grain protein content and grain starch content; sign was -, - and + in inbreds, but was +, + and – in hybrids, respectively, between GOC and each of OYPH, PYPH and SYPH and between GPC and each of OYPH, PYPH and SYPH; sign was -, - and - in inbreds but was +, + and + in hybrids, respectively and between GSC and each of OYPH, PYPH and SYPH ; sign was +, + and + in inbreds, but was -, - and - in hybrids, respectively. Change in the sign of associations between genotypes involved was reported in different studies and might be attributed to differences in trait combination and/or genetic background of the genotypes under study.

Grouping genotypes

1. Based on relationships between means under water stress and well watering

Mean of grain yield per hectare across years of studied genotypes under well watering (WW) or water stress (WS) was plotted against same trait of the same genotypes under well watering (WW) or water stress (WS) and illustrated in Fig.(2), where numbers from 1 to 6 refer to inbred names: 1= L20, 2= L53, 3= Sk5, 4=L18, 5=L28 and 6=Sd7 and numbers from 1 to 15 refer to cross names: 1= L20 × L 53, 2= L20 × Sk5, 3= L20 × L18,4= L20 × L28, 5= L20 × Sd7, 6= L53 × Sk5, 7= L53 × L18, 8 = L53 × L28, 9 =L53 × Sd7, 10= Sk5 × L18, 11 = Sk5 × L28, 12= Sk5 × Sd7, 13= L18 × L28, 14= L18 × Sd7and 15= L28 × Sd7. This made it possible to distinguish between efficient and inefficient genotypes on the basis of above-average and below-average studied trait under WW or WS together, respectively and responsive and non-responsive genotypes on the bases of above-average and below-average same trait under WW or WS together, respectively [35,62,63].Similarly, means of other studied yield traits (PYPH, OYPH and SYPH) under WS were plotted against means of the same traits for the same genotypes under WW conditions.

According to Fig. 2, studied inbreds or crosses were classified into four groups, *i.e.* water efficient and responsive, water efficient and non-responsive, water

inefficient and responsive and water inefficient and non-responsive based on grain yield/ha, protein yield/ha, oil yield/ha and starch yield/ha.
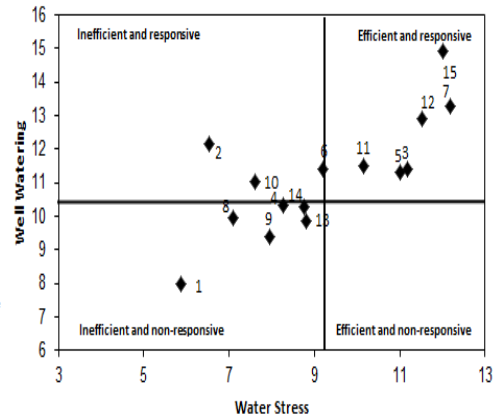
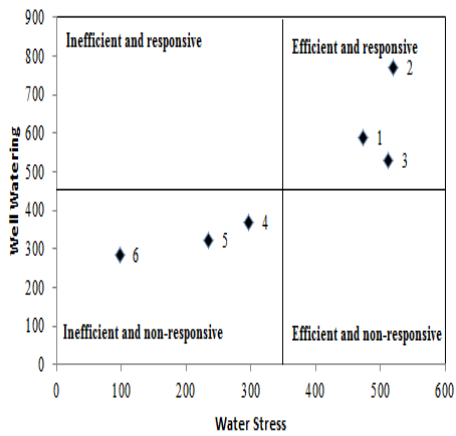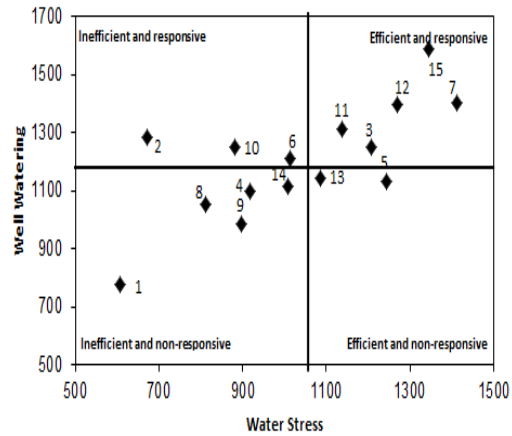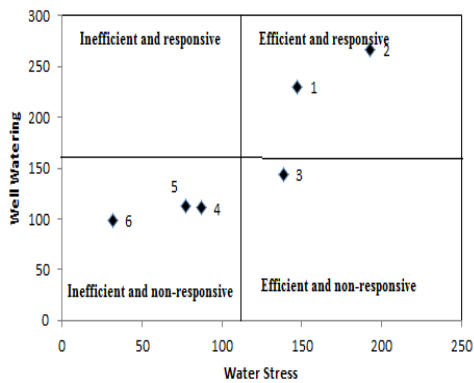**Inbreds**   **Crosses**
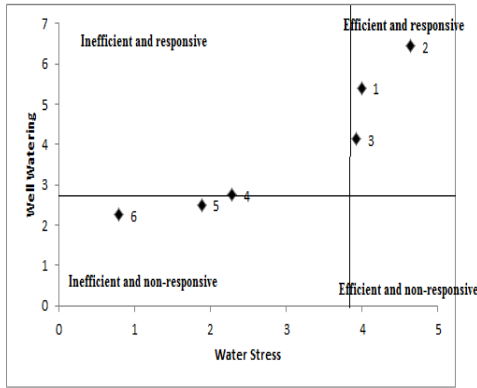
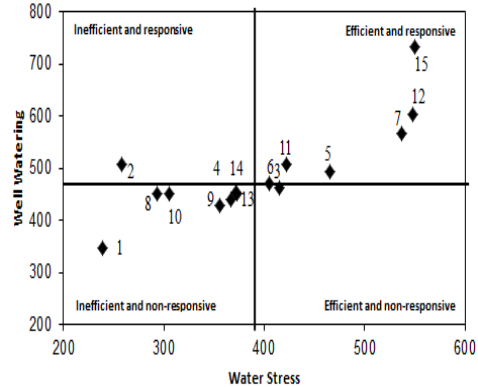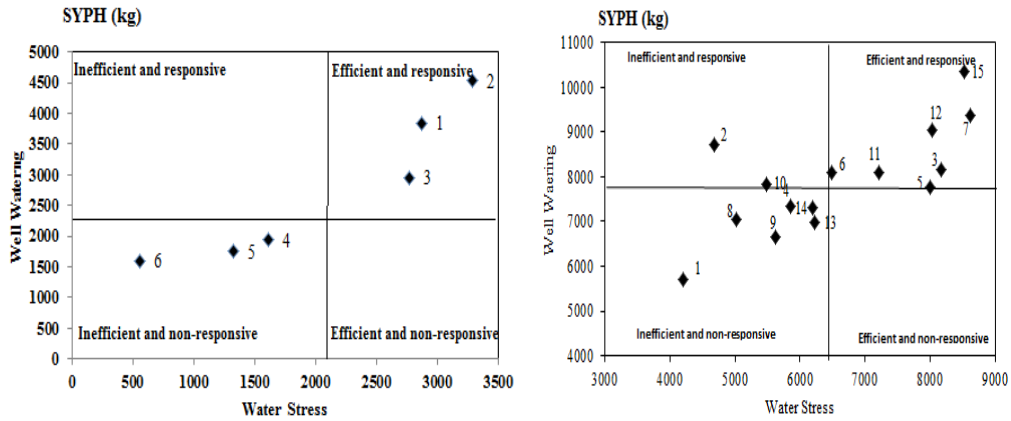**Fig.2. Relationships between efficiency and responsiveness for grain yield/ha (GYPH), protein yield/ha (PYPH), oil yield/ha (OYPH) and starch yield/ha (SYPH) of 6 inbred lines and 15 F₁ maize hybrids under water stress and well watering, combined across two seasons. Broken lines represent means of all inbreds or F₁'s. Numbers from 1 to 5 refer to inbred names and from 1 to 15 refer to F₁ hybrid names.**

Based on this classification, the inbreds No. 2(L53), No.1(L20) and No.3(Sk5) had the highest *per se* means of grain yield/ha, protein yield/ha, oil yield/ha and starch yield/ha under WW and WS simultaneously, *i.e.* they could be considered as the most water use efficient and the most responsive inbreds in this study (Fig.2).On the contrary, the inbreds No.6 (Sd7), No.5(L28) and No.4 (L18) had the lowest means of grain yield/ha, protein yield/ha, oil yield/ha and starch yield/ha under both WW and WS and could therefore be considered inefficient and non-responsive inbred lines (Fig.2). The F₁ crosses No. 15 (L28 × Sd7), No.7 (L53 × L18), No.12 (Sk5 × Sd7), No.11(Sk5 × L28) and No.3 (L20 × L18) had the highest means of studied yield traits under both WW and WS, *i.e.* they could be considered as the most water use efficient and the most responsive crosses in this study (Fig.2).

On the contrary, the F₁ crosses No.1 (L20 × L53), No.8 (L53 × L28), No.9(L53 × Sd7), No.10(Sk5 × L18) and No.4 (L20 × L28) had the lowest means of yield traits under both WW and WS and therefore could be considered water use inefficient and non-responsive (Fig.2). Classification of the studied crosses into the previous mentioned groups based on GYPH was similar to that based on other studied yield traits.

Based on GYPH, PYPH and SYPH traits, the cross No.5(L20 × Sd7) and on OYPH the crosses No.3 and 6 were classified as water use efficient but non-

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responsive genotypes, while the cross No.2 (L20 × Sk5) was classified as responsive to well watering, but water inefficient genotypes (Fig. 2).

2. Based on relationships between drought tolerance and trait means

According to drought tolerance index and mean of each GYPH, PYPH, OYPH and SYPH under water stress, studied crosses were classified into four groups, *i.e.* tolerant and high-yielding, tolerant and low-yielding, sensitive and high-yielding and sensitive and low-yielding (Fig.3). Based on this classification, the inbreds No. 2 (L53) and No. 3(Sk5) and the crosses No.7 (L53 × L18), No.15 (L28 × Sd7), No.12 (Sk5 × Sd7), No.5 (L20 × Sd7),No. 3(L20 × L18), No.11 (Sk5 × L25) and No.6 (L53 × Sk5) exhibited tolerance and high yield, expressed in GYPH, PYPH, OYPH and SYPH, under water stress conditions. By contrary, the inbred No. 6 (Sd7) and the F_1 crosses No. (L20 × Sk5), No.9 (L53 × Sd7), No.10 (Sk5 × L18) and No.13 (L18 × L28) occupied the sensitive and low-yielding group (Fig.3). The inbred No.1 (L20) was classified as high-yielding, but sensitive genotype. While the inbred No.4 (L18) was classified as tolerant, but low-yielding genotype.
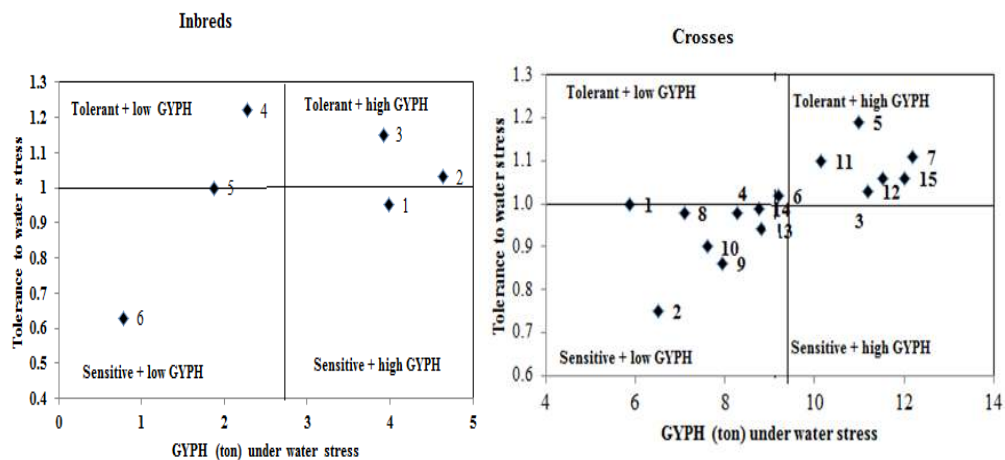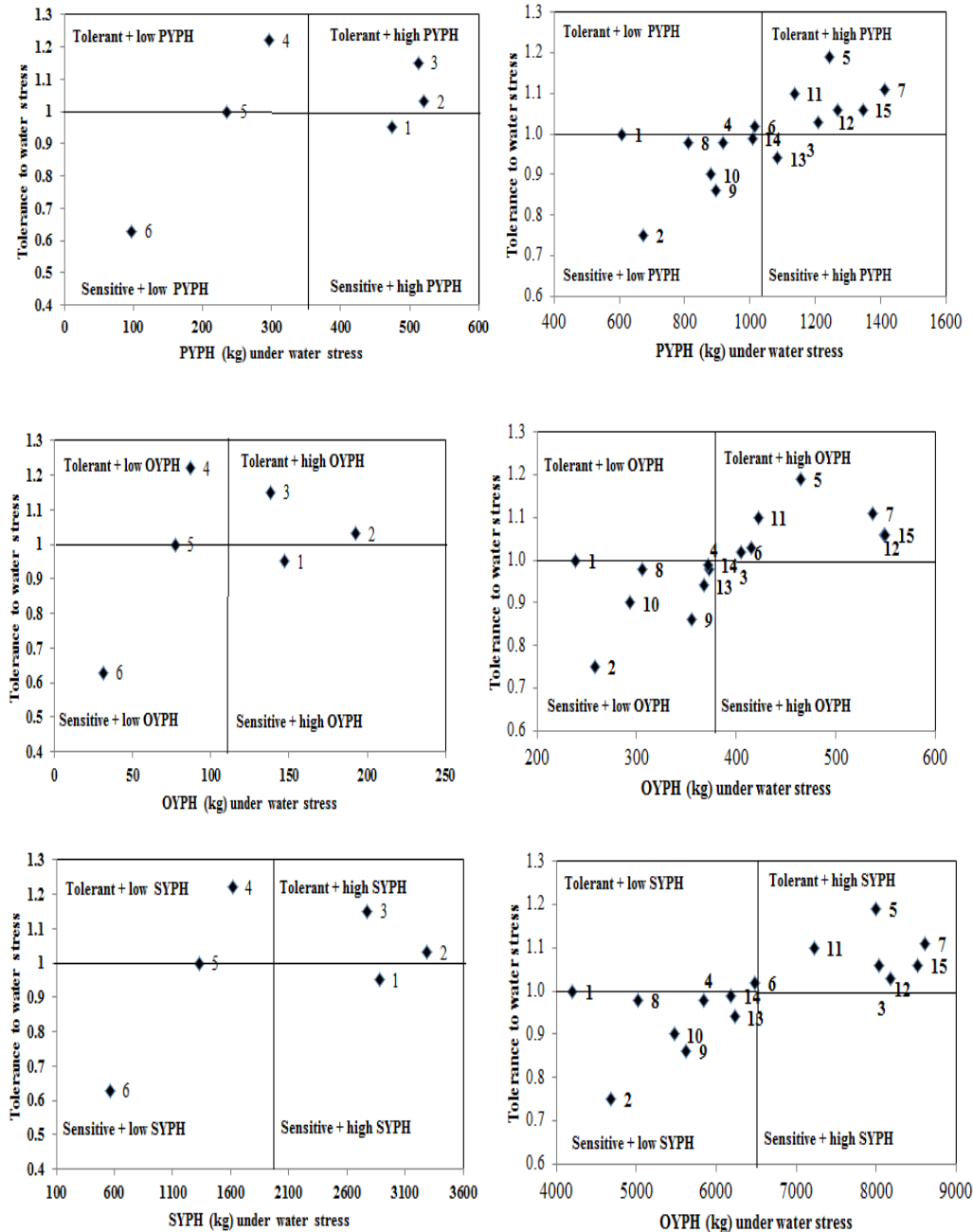
Fig.3. Relationships between tolerance index (TI) and means of grain yield/ha (GYPH), protein yield/ha (PYPH), oil yield/ha (OYPH) and starch yield/ha (SYPH) under water stress, combined across two seasons. Broken lines represent means of all inbreds or F$_1$'s. Numbers from 1 to 5 refer to inbred names and from 1 to 15 refer to F$_1$ hybrid names.

3. Based on relationships between mean grain yield and grain quality

Mean of grain yield per plant across years of studied genotypes was plotted against each of the three grain quality traits, *i.e.* grain protein content, grain oil content or grain starch content (Fig.4) . This made it possible to distinguish four groups, *i.e.* high yield and high quality, high yield and low quality, low yield and high

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quality and low yield and low quality. Based on this classification, the inbred No.3 (Sk5) is characterized by high grain yield per plant and high grain protein content %, No.2 (L53) had high grain yield per plant and high grain oil content, and No. 1(L20) had high grain yield per plant and high grain starch content, simultaneously.

The cross No.7 (L53 × L18) had high grain yield per plant and high grain protein content, No.15 (L28 × Sd7), No.12 (Sk5 × Sd7), No.7 (L53 × L18) and No. 6 (L53 × Sk5) had high grain yield per plant and high grain oil content and the crosses No.3 (L20 × L18) and No.11 (Sk5 × L28) had grain yield per plant and high grain starch content simultaneously. The possibility of obtaining high-yielding maize genotype and high grain quality was reported in the literature [4, 38, 47, 48]. It is therefore possible to select simultaneously for both high yield and high oil or protein content under water stress and non-stress conditions in maize breeding programs.
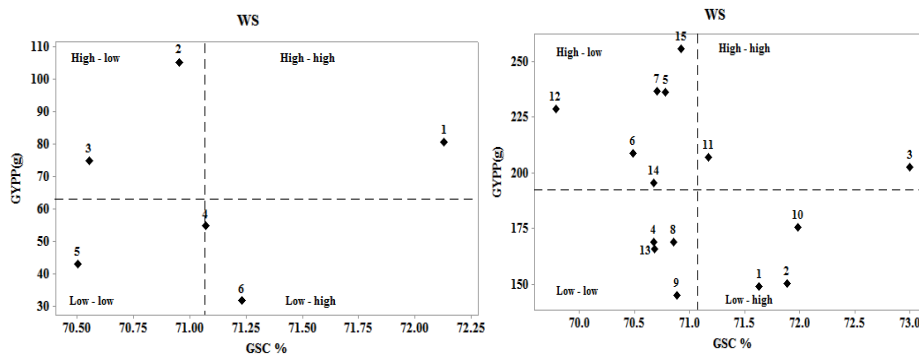
Inbreds   **Crosses**
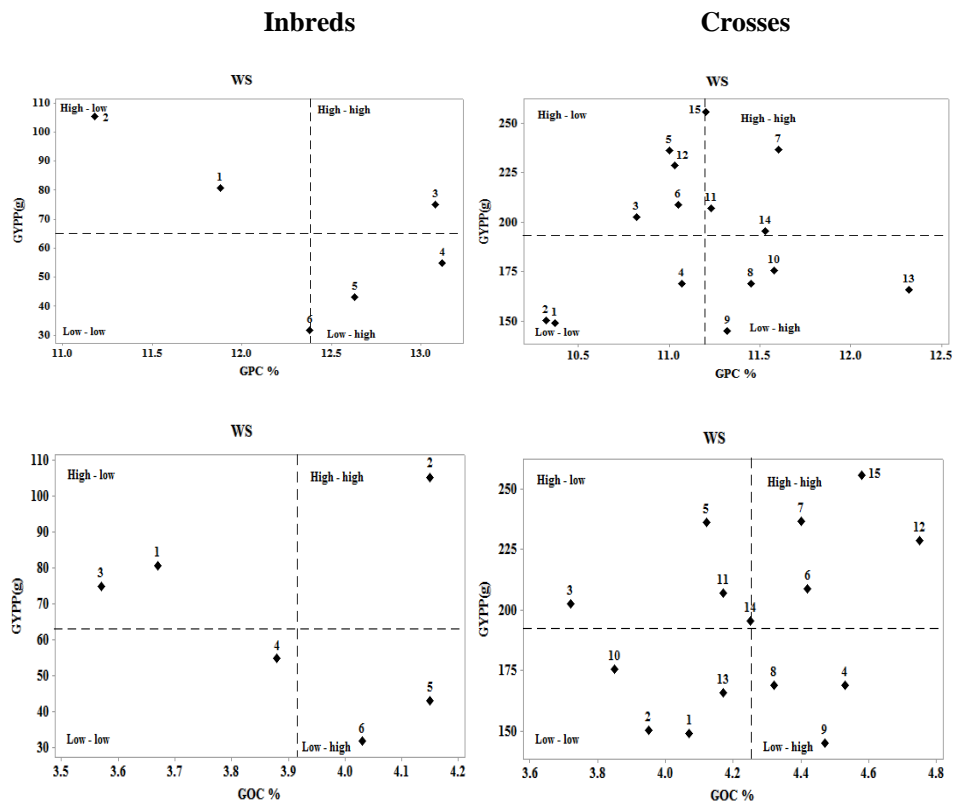
Fig.4. Relationships between means of grain yield per plant (GYPP) and each of grain protein content (GPC), grain oil content (GOC) and grain starch content (GSC) of 6 inbreds and their 15 F$_1$'s under water stress combined across two seasons. Broken lines represent means of all inbreds or F1's. Numbers from 1 to 5 refer to inbred names and from 1 to 15 refer to F$_1$ hybrid names.

CONCLUSIONS

This investigation concluded that water stress causes a significant reduction in maize protein yield/ha, oil yield/ha, starch yield/ha, grain yield/plant and grain yield/ha for inbreds and F$_1$'s, but slightly increased grain protein content of F$_1$'s and grain starch content of inbreds. The rank of inbreds and crosses for studied traits under WS was changed from that under well watering conditions. Developing drought tolerant (T) genotypes of maize gave them superiority over sensitive (S) ones in all studied yield parameters (grain yield/ha, grain yield/plant, protein yield/ha, oil yield/ha and starch yield/ha) under water stress conditions. Although there was a negative correlation between grain yield/plant and each of grain protein content and grain oil content in inbreds and a slight non-significant positive correlation in hybrids, it is possible to select for high yield and high grain protein content or grain oil content simultaneously under WS conditions. It was possible to identify the best water-efficient and responsive genotypes (inbreds L20 and Sk5 and crosses L28 x Sd7 and L53 x L18), the best tolerant and high-yielding genotypes (inbred L53 and hybrid L20 x Sd7), high-yielding and high-protein content genotypes (inbred Sk 5 and cross L53 x L18) and high yielding and high-oil content genotypes (inbred L53 and crosses L28 × Sd7, Sk5 × Sd7, L53 × L18 and L53 × Sk5). They could be offered to future breeding programs for improving water stress tolerance, yielding ability and grain quality traits of maize.

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