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**EVALUATION OF WATER DEFICIT ON YIELD COMPONENT AND
BIOCHEMICAL TRAITS OF CANOLA GENOTYPES (*BRASSICA NAPUS* L.)**

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ABSTRACT

This study was conducted to study the reactions of canola genotypes to the drought stress in two experiments as randomized complete block design in four replications. Twenty two canola genotypes were cultivated in the first experiment and Twenty two canola genotypes were cultivated in the second experiment and drought stress was used in the flowering stage. Field experimental located in Karaj region. Variance analysis of normal experiments indicated that there are significant differences in 1% level among canola genotypes for pod number per plant, grain per pod, thousandseedweight (TSW), oil percentage, CAT, GPX and chlorophyll. Variance analysis of normal experiments indicated that there are no significant differences among canola genotypes for proline and Soluble carbohydrates. Variance analysis of drought stress experiments indicated that there are significant differences in 1% level among canola genotypes for pod number per plant, grain per pod, thousand kernel weight (TSW), oil percentage, CAT, GPX, soluble carbohydrates and chlorophyll.

Keywords: Drought Stress, Canola (*Brassica napus* L.), Genotypes

INTRODUCTION

Oilseeds after cereal are noteworthy as the second important source of human energy in the world. There for in order to secure the

needed oil, necessity in planning to attain self-sufficiency production of edible oil in developing countries is undeniable. In the

recent years regarding to emphasis on the sustainable agriculture and crop rotation, researchers has been focused on canola as an appropriate crop, which can be in rotation with winter cereals. One of the important factors which endanger development of under cultivation and successful production of canola plant is water deficiency because water deficiency is one of the most important factors which limit the growth and production of plant. Some studies in this area indicated that the average annual yield reduction was 17% in the world through the drought which can increase till more than 70% in every year (Edmeades et al., 1994).

So the best way of combating with the drought is using the suitable agricultural operations and using the varieties which have more tolerance against drought (Ahmadi and far Javid, 2000). Drought enormously damages crops and horticultural products in the word, especially in Iran, every year. In Iran, decreasing the available water per capita caused by population growth, climate change, excessive utilization and reduced quality of water resources has caused a significant increase of the drought damage. The available water per capita has noticeably dropped from 7000 m³ in 1950 to 1900 m³ in the recent years 2000. Taking into consideration the

strong population growth it is expected that the available water per capita in Iran with a decreasing trend will approach to 1300 m³ up to 2025 (Keshavarz et al., 2003). Drought stress influences on plant growth in the all stages of plant life. However, the amount and severity of damage, capacity of compensation and its effects on yield are depending on the stage of plant life in stress (Farooq et al., 2009). According many researches it was found out that the drought stress influences on growth, photosynthesis, breathing and aging plant.

In order to achieve an optimum yield in arid and semi-arid like Iran, using the new methods of irrigation is suggested to overcome water scarcity. Using the new technologies can significantly enhance water use efficiency and prevent accumulation of salts in the root growth zone resulting in a yield increment. In view of the fact that occurrence of drought stress is often coincident with the stages of flowering and pod formation (filling grain) of canola in the most agricultural areas of Iran, the present study has focused on the investigation of the drought stress effects on quantitative and qualitative traits.

MATERIALS AND METHODS

To evaluate tolerance against water deficiency stress of canola genotypes, two separate experiments were conducted in randomized complete block design with 4 replications. Every experiment includes, 16 genotypes canola with six control varieties by the names Okapi (mid tolerant to the water deficiency), Zarfam (tolerant to the water deficiency), Modena (sensitive to water deficiency), Talaye (sensitive to water deficiency), Licord (Mid tolerant to water deficiency), SLM046 (tolerant to water deficiency). One experiment was conducted in the common irrigation condition, (Irrigation on the basis of 80mm evaporation from the pan class A) and the other experimental was conducted in water deficiency stress (drought stress from the flowering stage forward). Catalase and peroxidase activity and viscosity of malondialdehyde were measured according to basic methods (Chance, 1995; Valentovicet al., 2006). Total lipid extraction was performed according to AOAC (2000) (Chance, 1995). Catalase and peroxidase are important antioxidant enzyme for scavenge plant cell. CAT (EC:1.11.6) and POD (EC:1.11.1.3) were extracted by homogenizing frozen fresh leaf material in ice-cold solution containing 100mM Tris (pH 7.0), 10 mM D-threo-ascorbic acid, 20 g L-1

PVP- 10, 1.5 g insoluble PVP, 0.1mM EDTA and 2mL L-1 Triton X-100. CAT activity was determined following Chanes (1995) by monitoring the disappearance of H₂O₂ by measuring the decrease in absorbance at 240 nm of a reaction mixture containing 1.9mL H₂O, 1.0mL of 5.9mM H₂O₂ in potassium phosphate buffer (pH 7.0), and 1.0mL extract. POD activity was determined following the protocol of Chanes (1995) using guaiacol as a reactant. POD activity was measured by monitoring the H₂O₂ – dependent oxidation of reduced 2,3,6-trichloroindophenol at 675 nm using a UV-vis spectrophotometer (Model U-2001, Hitachi, Tokyo, Japan).

The proline content of leaf was extracted according to the method presented by Bates et al., 1973. Chlorophyll content of leaf was determined based on the method explained by Arnon. The observed data, as the primary data of the absorption of light wavelengths related to chlorophylls a & b, were used in the following questions to calculate the content of chlorophyll a and b.

$$C_{\text{chl}a} = (0.0127 \times (\text{OD } 663) - 0.000259 \times (\text{OD } 645)) \times V/W \quad (1)$$

$$C_{\text{chl}a} = (0.0229 \times (\text{OD } 645) - 0.000469 \times (\text{OD } 663)) \times V/W \quad (2)$$

After two years, the combined analysis of variance for the mentioned characteristics as

well as comparison of means based on Duncan's multiple range test were performed at the five percent level. The statistical analysis was performed using MSTATC software.

RESULTS AND DISCUSSION

Pod number per plant: Variance analysis of normal experiment and drought stress indicated that there is significant difference in 1% level among canola genotypes (Table2, 3). Using the results of means comparison of normal experiment indicated that the genotypes number 3 and 5 respectively with 145 and 141.8 had the highest and lowest Pod number per plant (Table 4). The mean comparison of drought stress experiment indicated that the genotype number 5 had the greatest pod number with the average of 119 and the genotype number 7 had the least pod number with the average of 57.92 (Table 5).

Seed number per pod: Variance analysis of normal and drought stress experiments indicated that there are significant difference in 1% level among canola genotypes (Table2, 3). Using the results of means comparison of normal experiment indicated that the genotypes number 11 and 5 respectively with 33.50 and 21.5 had the highest and lowest Seed number per pod (Table4). The result of means comparison of drought stress

experiment indicated that the genotypes number 18 and 5 respectively with the averages of 20.67 and 13.33 had the greatest and least Seed number per pod (Table 5).

1000 seed weigh: Variance analysis of normal experiment indicated that there is significant difference in 1% level among canola genotypes (Table2, 3). Using the results of means comparison of normal experiment indicated that the genotypes number 12 and 19 respectively with 3.975 and 2.638 had the highest and lowest Seed number per pod (Table 4). The result of means comparison of drought stress experiment indicated that the genotypes number 20 and 5 respectively with the averages of 4.300(g) and 2.500(g) had the greatest and least 1000 seed weigh (Table 5). The results indicated that maximum grain yield was obtained in normal condition and without stress which were conformed to the report by other researcher (Sinaki et al., 2007). The reason of grain yield reduction in different genotypes can be due to level of used stress and its effect on some yield components such as pod per plant, seed per pods and the weight of thousand seed. In general, crop is susceptible to drought stress during the flowering period, but genotypes differ in their sensitivity (Richards and

Thurling, 1978). There are significant differences among canola genotypes in grain yield (Khoshnazar et al., 2000; Reddy and Ruddy, 1998).

Oil percentage: Variance analysis of normal experiment and drought stress indicated that there are significant difference in 1% level among canola genotypes (Table 2,3). Using the results of means comparison of normal experiment indicated that the genotypes number 12 and 8 respectively with 43.19% and 37.52% had the highest and lowest Oil percentage (Table 4). The result of means comparison of drought stress experiment indicated that the highest oil percentage of genotypes number 10 with the average of 41.78% while the lowest oil percentage of genotype number 19 with the averages of 36.67% (Table 5). It was observed that seed oil percentage was decrease in the drought stress when compared with the normal experiment. Occurrence of drought stress in flowering stage during pod number and the stress after pollination stage by reduction of seed size resulted in the reduction of grain yield and canola oil (Shirani and Daneshian, 2006).

Proline content: Variance analysis of normal experiment indicated that there are no significant difference among canola

genotypes but the effects of drought stress on the proline content were significant at the five percent level (Table 6, 7). Using the results of means comparison of normal experiment indicated that the genotypes number 3 and 5 respectively with 20.10 mg.kg⁻¹ wet weight and 16.59 mg.kg⁻¹ wet weight had the highest and lowest proline content (Table 8). The result of means comparison of drought stress experiment indicated that the highest proline content of genotypes number 13 with the average of 31.47 mg.kg⁻¹ wet weight while the lowest proline content of genotype number 21 with the averages of 26.99 mg.kg⁻¹ wet weight (Table 9). It can be seen that the drought stress causes an increase in proline content either condition of normal irrigation.

As can be seen from regardless of stress, the proline content of leaves slowly increases then in the reproductive stage and flowering stage approaches to the peak, finally have a descending trend in the end of plant life. It seems in the early growth stages, limitation of soil moisture was not intense enough up to the plant have to provide a biochemical reaction. However, in the next stages of growth with being hard condition, plants accumulate more proline content in leaves. Reduction in proline content of leaves in the late stages of plant growth can be caused by leaf senescence,

destruction of cell organelles and reduction of metabolic activity in leaves. Mostajerani and Rahimi-Eichireported the ability to collect compatible components is depending on age leave (Mostajeran and Rahimi-Eichi, 2009). A significant increment in proline content was accrued in the drought stress. Although this increment occurred in all growth stages, the amount of increment in proline content was depending on the intense stress, duration stress and growth stage of plant. The proline content of leaves increased at the stages of 50% flowering and full pod formation in comparison with the vegetative growth stage (Ma et al., 2006). Proline accumulation in drought stress can be caused by reducing oxidation proline, stimulation of glutamate and increasing activity protease enzyme. Proline is responsible for the protective role of cytosolic enzymes (protection of the enzyme carboxylase) and cell structure. Therefore it can be resulted that proline accumulation in drought stress is caused by its oxidation, binding and incomplete combination within protein complex.

Soluble carbohydrate: Variance analysis of normal experiment indicated that there is no significant difference among canola genotypes (Table6, 7). Using the results of means comparison of normal experiment

indicated that the genotypes number 4 and 17 respectively with 99.36 and 82.87 mg.g⁻¹ dry weight had the highest and lowest Soluble carbohydrate (Table 8). The result of means comparison of drought stress experiment indicated that the genotypes number 10 and 3 respectively with the averages of 148.5 and 125.6 mg.g⁻¹ dry weight had the greatest and least Soluble carbohydrate (Table 9).

Antioxidant enzymes: The statically analysis of normal experiment for CAT enzyme activity and GPX enzyme activity showed that there are significant difference in 1% level among canola genotypes (Table6, 10). The highest CAT enzyme activity was obtained from genotype number 6 with average 20.12 while the lowest CAT enzyme activity of 17.22 was produced in genotype number 9 (Table8). Means comparison of normal experiment indicated that the genotypes number 10 and 18 respectively with 45.71 and 42 had the highest and lowest GPX enzyme activity (Table12). Variance analysis of drought stress experiment for CAT enzyme activity and GPX enzyme activity indicated that there are significant differences in 1% levels among canola genotypes (Table7, 11). The results of means comparison of drought stress experiment indicated that the genotypes number 12 and 13 respectively

with 25.96 and 21.85 had the highest and lowest CAT enzyme activity (Table9). The highest GPX was obtained from genotype number 16 with average 56.37 while the lowest GPX enzyme activity with average 51.77 was produced in genotype number 3 (Table13). Plants under drought stress showed significant in CAT and GPX activity in leaves compared to normal condition. Increase in CAT and GPX activity and decrease in oxidative damage were closely related (Candan and Tarhan, 2003; Esfandiari et al., 2007).

Content of chlorophyll a and b: The statically analysis of normal experiment and drought stress for Content of chlorophyll a and b showed that there are significant difference in 1% level among canola genotypes (Table10, 11). In the normal experiment highest chlorophyll a was obtained from genotype number 2 with average 3.863 mg g⁻¹ wet weight while the lowest chlorophyll a of 3.016 mg g⁻¹ wet weight was produced in genotype number 20 (Table12). The results of means comparison of drought stress experiment indicated that the genotypes number 14 and 20 respectively with 3.431 mg g⁻¹ wet weight and 1.955 mg g⁻¹ wet weight had the highest and lowest chlorophyll a (Table13). Means comparison of normal

experiment indicated that the genotypes number 6 and 21 respectively with 2.909 mg g⁻¹ wet weight and 2.245 mg g⁻¹ wet weight had the highest and lowest chlorophyll b (Table12). The results of means comparison of drought stress experiment indicated that the genotypes number 21 and 20 respectively with 2.526 mg g⁻¹ wet weight and 1.102 mg g⁻¹ wet weight had the highest and lowest chlorophyll b (Table13).

Content of chlorophyll a and b decreased with more delay in planting in both conditions of normal (control) and stress. The most content of chlorophyll a and b was observed in the normal condition. The reduction of photosynthetic pigments, like chlorophyll of a, in drought stress can be caused by reduction in synthesis of the main complex of chlorophyll II (Paseban-Islam et al., 2000). The results showed the drought stress causes decreasing chlorophyll content in leaves. It seems the significant reduced chlorophyll content in the present research is caused by decreasing the necessary factors for chlorophyll synthesis as well as structure degradation of chlorophyll that means chlorophyll catabolism in low water condition enhances. The drought stress causes to change the ratio of chlorophyll a and b. However, limitation of photosynthesis caused by

metabolically degradation is a complex energy decreases with losing chlorophyll phenomenon that pigments often have a caused by drought stress resulting in protective role in this case. As a consistent reduction of damages caused by formation of and useful aspect, the absorption of solar free radical oxygen.

Table 1: Names of genotypes

GENOTYPES	1	2	3	4	5	6	7	8	9	10	11
NAME	KR4	KR18	KS21	KS11	KR7	KS13	KR21	KS1	KS2	KS7	KS17
GENOTYPES	12	13	14	15	16	17	18	19	20	21	22
NAME	KS20	KS6	KS18	KS21	KS4	Okapi	Zarfam	Modena	Talaye	Licord	SLM046

Table 2: Variance analysis of normal experiment

SOV	df	Pod number per plant	Seed number per pod	100seed weigh(g)	Grain Oil (%)
Replication	3	1017.557*	23.106*	0.051 ^{ns}	5.875 ^{ns}
Genotypes	21	955.379**	31.989**	0.477**	9.121**
Error	63	344.922	7.185	0.135	2.673
CV%		15.63	9.80	11.55	4.11

*, ** and ^{ns}: Significant at 5%, 1% probability levels, and Non-significant.

Table 3: Variance analysis of drought stress experiment

SOV	df	Pod number per plant	Seed number per pod	1000 seed weigh(g)	Grain Oil (%)
Replication	3	310.861*	8.776 ^{ns}	0.057 ^{ns}	2.201 ^{ns}
genotypes	21	757.374**	9.831**	0.969**	7.184**
error	63	109.490	3.750	0.254	1.729
CV%		13.09	11.87	14.49	3.36

*, ** and ^{ns}: Significant at 5%, 1% probability levels, and Non-significant.

Table 4: Mean comparison of normal experiment

Genotypes	Pod number per plant	Seed number per pod	1000 seed weigh(g)	Grain Oil (%)
1	102.5 def	24 ef	3.838 ab	39.15 c-g
2	104.8def	27.25 cde	3.013 cd	38.84 d-g
3	145 a	25.50 def	3.213 cd	40.86 a-e
4	118.5 a-f	26 de	2.912 cd	38.85 d-g
5	137.5 abc	21.50 f	3 cd	39.12 c-g
6	117.8 a-f	31 abc	3.188 cd	40.75 a-e
7	96.25 ef	29 bcd	3.225 cd	40.58 a-f
8	108 c-f	25.50 def	3.075 cd	37.52 g
9	93 f	30.75 abc	3 cd	39.34 b-g
10	110 c-f	25.50 def	3.362 bc	42 ab
11	132.5 a-d	33.50 a	3.275 bc	41.08 a-d
12	113 b-f	26 de	3.975 a	43.19 a
13	125.8 a-e	28.75 bcd	3.100 cd	40.11 b-g
14	108 c-f	26.75 cde	3.188 cd	38.08 efg
15	130.5 a-d	25.25 def	3.300 bc	37.88 fg
16	138.5 abc	27 cde	2.787 cd	39.94 b-g
17	105 def	28.25 b-e	2.987 cd	41.15 a-d
18	107.5 c-f	25.50 def	3.963 a	41.67 abc
19	138.5 abc	27.25 cde	2.638 d	38.91 c-g
20	141.8 ab	29.50 a-d	2.950 cd	38.07 efg
21	119 a-f	32.25 ab	2.975 cd	38.92 c-g
22	120.5 a-f	25.50 def	3.100 cd	38.20 efg

Means in each column having similar letter (s), are not significantly at the 5% level.

Table 5: Mean comparison of drought stress experiment

Genotypes	Podnumber per plant	Seed number per pod	1000 seed weigh(g)	Grain Oil (%)
1	81.53 b-f	15.32 bcd	3.075 d-g	39.25 b-f
2	82.72 b-e	17.67 b	3.925 a-d	38.17 fgh
3	70.63 d-g	14.27 cd	3.70 a-d	38.17 fgh
4	91.30 bc	14.82 bcd	3.575 a-d	38.90 c-g
5	119 a	13.32 d	2.50 g	38.97 c-f
6	78.20 b-f	17.83 b	3.50 a-e	37.97 fgh
7	57.92 g	16.33 bcd	3.075 d-g	38.70 d-h
8	87.07 bcd	17.33 bc	4.00 abc	39.17 b-f
9	60.70 g	16 bcd	3.325 c-f	38.78 d-h
10	67.28 efg	16.33 bcd	3.625 a-d	41.78 a
11	66.78 efg	15.68 bcd	3.50 a-e	39.38 b-f
12	93.97 b	16.83 bc	3.40 b-e	41.20 ab
13	71.72 d-g	16.17 bcd	2.575 fg	40.00 a-f
14	94.43 b	14.82 bcd	3.525 a-d	38.05 fgh
15	84.03 b-e	14.50 bcd	4.025 abc	41.08 abc
16	74.40 c-g	17.33 bc	3.70 a-d	40.42 a-e
17	82.80 b-e	15.82 bcd	3.125 d-g	40.60 a-d
18	80.68 b-f	20.67 a	3.425 b-e	40.13 a-f
19	93.78 b	17.33 bc	2.675 efg	36.67 h
20	81 b-f	15.82 bcd	4.30 a	36.78 gh
21	74.28 c-g	17.50 bc	3.70 a-d	39.38 b-f
22	64.88 fg	17.27 bc	4.225 ab	38.30 e-h

Means in each column having similar letter (s), are not significantly at the 5% level.

Table 6: Variance analysis of normal experiment

SOV	df	Proline (mg.kg ⁻¹ FW)	Soluble carbohydrates (mg.g ⁻¹ DW)	CATactivity
Replication	3	3.839 ^{NS}	228.892*	2.015*
genotypes	21	3.679 ^{NS}	90.334 ^{NS}	4.283**
error	63	2.537	68.770	0.521
CV%		8.74	8.87	3.87

*, ** and ^{NS}: Significant at 5%, 1% probability levels, and Non-significant.

Table 7: Variance analysis of drought stress experiment

SOV	df	Proline (mg.kg ⁻¹ FW)	Soluble carbohydrates (mg.g ⁻¹ DW)	CAT activity
Replication	3	8.296 ^{NS}	69.347 ^{NS}	5.441*
genotypes	21	7.588*	260.487**	7.959**
error	63	4.149	58.652	1.403
CV%		7.00	5.60	4.92

*, ** and ^{NS}: Significant at 5%, 1% probability levels, and Non-significant.

Table 8: Mean comparison of normal experiment

Genotypes	Proline (mg.kg ⁻¹ FW)	Soluble carbohydrate(mg.g ⁻¹ DW)	CAT activity
1	18.62 abc	92.69 ab	18.98 a-d
2	16.61 c	96.11 ab	18.85 b-e
3	20.10 a	86.54 ab	18.35 c-f
4	18.81 abc	99.36 a	19.80 ab
5	16.59 c	94.68 ab	18.38 c-f
6	17.72 abc	98.47 a	20.12 a
7	18.29 abc	99.05 a	19.91 ab
8	18.28 abc	96.90 ab	20.05 a
9	18.74 abc	91.02 ab	17.22 f
10	16.99 c	98.73 a	19.64 ab
11	17.37 abc	97.45 a	19.43 abc
12	17.35 abc	97.70 a	20.03 ab

13	17.25 bc	95.61 ab	19.70 ab
14	18.08 abc	96.05 ab	18.99 a-d
15	19.31 abc	87.38 ab	17.54 f
16	17.68 abc	95.12 ab	18.25 def
17	18.43 abc	82.87 b	17.45 f
18	18.57 abc	93.97 ab	17.51 f
19	19.18 abc	88.56 ab	17.98 def
20	18.19 abc	90.04 ab	17.77 ef
21	18.72 abc	90.20 ab	17.36 f
22	19.87 ab	87.38 ab	17.49 f

Means in each column having similar letter (s), are not significantly at the 5% level.

Table 9: Mean comparison of drought stress experiment

Genotypes	Proline (mg.kg ⁻¹ FW)	Soluble carbohydrate (mg.g ⁻¹ DW)	CATactivity
1	28.44 a-d	143.2 abc	25.75 ab
2	29.59 a-d	135.3 bcd	23.02 c-f
3	30.40 a-d	125.6 d	22.97 c-f
4	27.90 bcd	138.7 a-d	24.21 a-d
5	29.30 a-d	134.7 bcd	24.47 a-d
6	29.81 a-d	136.8 a-d	23.91 b-e
7	29.53 a-d	133.6 cd	24.38 a-d
8	30.64 abc	128.9 d	22.89 c-f
9	29.86 a-d	127.2 d	22.56 def
10	27.00 d	148.5 a	25.90 ab
11	30.36 a-d	126.5 d	22.92 c-f
12	27.49 cd	145.0 abc	25.96 a
13	31.47 a	127.2 d	21.85 f
14	29.13 a-d	145.0 abc	24.58 abc
15	29.03 a-d	147.0 ab	25.74 ab
16	27.33 cd	145.6 abc	25.74 ab
17	27.97 bcd	134.8 bcd	24.07 a-d
18	28.43 a-d	147.7 ab	25.83 ab
19	31.25 ab	128.9 d	21.92 f
20	30.57 abc	126.6 d	21.99 ef
21	26.99 d	146.2 abc	25.33 ab
22	27.67 cd	136.3 a-d	23.92 b-e

Means in each column having similar letter (s), are not significantly at the 5% level.

Table 10: Variance analysis of normal experiment

SOV	df	GPXactivity	Chlorophyll a (mg.g ⁻¹ FW)	Chlorophyll b (mg.g ⁻¹ FW)
Replication	3	3.074ns	1.177**	0.066**
genotypes	21	5.561**	0.323**	0.162**
error	63	1.236	0.017	0.013
CV%		2.54	3.84	4.44

*, ** and ^{ns}: Significant at 5%, 1% probability levels, and Non-significant.

Table 11: Variance analysis of drought stress experiment

SOV	df	GPXactivity	Chlorophyll a (mg.g ⁻¹ FW)	Chlorophyll b (mg.g ⁻¹ FW)
Replication	3	23.001	0.005	0.051
genotypes	21	7.234	0.688	0.747
error	63	2.817	0.044	0.030
CV%		3.06	7.50	10.05

*, ** and ^{ns}: Significant at 5%, 1% probability levels, and Non-significant.

Table 12: Mean comparison of normal experiment

Genotypes	GPXactivity	Chlorophyll a (mg.g ⁻¹ FW)	Chlorophyll b (mg.g ⁻¹ FW)
1	45.45 ab	3.108 kl	2.482 g-k
2	44.03 a-g	3.863 a	2.576 e-h
3	43.20 d-h	3.857 a	2.33 j-m
4	45.34 ab	3.762 abc	2.88 ab
5	43.45 c-h	3.142 jkl	2.50 f-j
6	43.83 b-h	3.761 abc	2.909 a
7	45.55 ab	3.806 ab	2.768 a-d
8	43.18 d-h	3.687 a-d	2.797 abc
9	42.60 fgh	3.323 g-j	2.365 i-m
10	45.71 a	3.594 c-f	2.834 abc
11	45.05 abc	3.175 i-l	2.419 h-m
12	44.42 a-f	3.638 b-e	2.675 c-f
13	44.48 a-e	3.406 fgh	2.612 d-g
14	44.94 a-d	3.502 d-g	2.566 e-h
15	43.71 b-h	3.234 h-k	2.404 h-m
16	43.07 e-h	3.449 efg	2.712 b-e
17	42.89 e-h	3.041 kl	2.308 klm
18	42.00 h	3.109 kl	2.46 g-l
19	42.82 e-h	3.324 g-j	2.423 h-m
20	42.52 gh	3.016 l	2.523 f-i
21	42.12 h	3.351 ghi	2.245 m
22	42.67 e-h	3.066 kl	2.275 lm

Means in each column having similar letter (s), are not significantly at the 5% level

Table 13: Mean comparison of normal experiment

Genotypes	GPXactivity	Chlorophyll a (mg.g ⁻¹ FW)	Chlorophyll b (mg.g ⁻¹ FW)
1	56.17 ab	3.097 a-d	2.268 bc
2	55.47 abc	2.592 f-i	1.409 jkl
3	51.77 d	3.366 ab	2.194 bcd
4	54.50 a-d	2.311 ijk	1.244 lm
5	55.63 abc	2.509 g-j	1.521 ijk
6	55.04 abc	2.238 jk	1.156 lm
7	54.71 abc	2.376 ij	1.265 klm
8	53.35 bcd	2.819 d-g	1.721 ghi
9	53.02 cd	3.053 bcd	1.929 d-h
10	56.37 a	2.295 ijk	1.173 lm
11	53.01 cd	2.820 d-g	1.781 ghi
12	55.99 ab	3.064 bcd	2.103 c-f
13	53.62 a-d	3.112 a-d	1.881 e-h
14	55.55 abc	3.431 a	2.425 ab
15	56.04 ab	2.987 cde	1.951 d-g
16	56.37 a	2.712 e-h	1.570 ij
17	55.06 abc	3.307 abc	2.140 cde
18	55.91 ab	2.981 cde	1.856 fgh
19	53.75 a-d	2.434 hij	1.281 klm
20	52.99 cd	1.995 k	1.102 m
21	56.06 ab	3.376 ab	2.526 a
22	54.95 abc	2.913 def	1.669 hij

Means in each column having similar letter (s), are not significantly at the 5% level

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