Differential physiological responses of three Sesame genotypes to drought stress and the expression of antioxidant genes

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ABSTRACT

This study was conducted to determine the physiological responses and the expression of major antioxidant genes (*Cu/Zn-SOD*, *CAT*, and *APX*) to drought stress in three sesame (*Sesamum indicum* L.) genotypes. Drought conditions were imposed at three levels: D1 (100%), D2 (50%), and D3 (25%) of field capacity on three major Iraqi genotypes of sesame, namely Wadaa, Sumer, and Local. The physiological results indicated that variety Wadaa was characterized by the highest relative water content (82%). The expression of *Cu/Zn-SOD* gene was influenced by drought in Wadaa variety and recorded the lowest gene expression compared to non-stress plants at 50% of field capacity. Gradual increase of expression was recorded in Sumer and Local varieties to reach 43.63 and 50.98-fold over, respectively of the normal expression. The expression for *CAT* gene was up-regulated in both Wadaa and Sumer for treatments D2 and D3, and up-expression for treatment D2 with the Local variety while down-regulated from normalized expression for D3 treatment (1.56-fold). The expression levels of *APX* gene increased in Wadaa variety for the treatment D2 and decreased for the treatment D3 by 83.33-fold. While its expression up-regulated for the treatments D2 and D3 in Sumer variety as well as in treatment D2 in the Local variety. Severe drought at 25% of field capacity caused down-regulated in *APX* in Local variety and scored 1.26-fold than non-stress plants.

Key word : Sesame, Antioxidant enzymes, Gene expression, Drought tolerance, RWC

Introduction

Sesame (*Sesamum indicum* L. 2n = 26) is an essential oil and food crops in many countries in warm and semi-warm temperate regions. Globally, demand for sesame is growing mainly due to three reasons: first sesame has a high medicinal and nutritional value (Anastasi *et al.*, 2017). Second, it is consumed in both the oil and confectionary industries (Peter, 2012), and third, it has been identified as a good source of high-grade oil (high proportion of unsaturated fatty acids, protein content and antioxidants) (Bahrami *et*

al., 2012).

In a persistently changing environment, plants are constantly challenged by various abiotic stresses (Abu-Romman, 2016), such as salinity, drought, temperature extremes, heavy metal toxicity, high light intensity, nutrient deficiency, UV-B radiation, ozone, etc., which cause significant crop yield and quality losses. Drought stress is one of the most prevailing abiotic stress affecting plant growth and development (Abu-Romman and Suwwan, 2012). Drought stress happens when the water available in the soil is limited to such low levels and atmospheric conditions contribute to the constant loss of water. Under water stress conditions, growth is inhabited and a variety of molecular, biochemical and physiological changes are produced (Hsu *et al.*, 2003). However, unlike most of the important food crops, sesame can survive drought but severe and repeated drought episodes, especially occurring during the reproductive stage, significantly curtail the productivity of this high oil crop (Dossa *et al.*, 2019).

According to Gill and Tuteja, (2010), drought stress led to release ROS, which is mainly produced by aerobic respiration in mitochondria, photosynthesis in chloroplasts, and photorespiration in peroxisomes such as singlet oxygen (O), superoxide (O_2^{-}) , hydrogen peroxide (H_2O_2) and hydroxyl radicals (OH). Du et al., (2013) reported that ROS may inactivate biomolecules and initiate autocatalytic peroxidation of the membrane and other macromolecules, such as photosynthetic pigments, proteins, lipids and nucleic acids, resulting in loss of membrane integrity and some functional alterations. Thus, their levels must be closely and carefully monitored inside the cell so that the injury caused by ROS is known as "oxidative stress." Increased production of ROS induces molecular reactions, which are key factors in the determination of plant tolerance to stress (Dudziak *et al.*, 2019). ROS appears to have a dual effect under abiotic stress conditions that depend on their total cell count. If maintained at relatively low levels, they are likely to function as components of the stress-signaling pathway, triggering a stress defense/ acclimation response.

Enhancing antioxidant defense in plants can therefore increase tolerance to different types of reactive oxygen (ROS) stress factors. Defending mechanisms against free radical oxidative stress include:(i) precautionary mechanisms; (ii) repair mechanisms; (iii) physiological defenses; and (iv) antioxidant defenses (Mittova et al., 2003). Antioxidant defense systems that work together to regulate uncontrolled oxidation cascades and protect plant cells from oxidative damage by scavenging ROS (Gill and Tuteja, 2010). In oxidative stress, redox homeostasis is maintained by enzymatic antioxidants such as superoxide dismutase (SOD, EC 1.15.1.1), ascorbate peroxidase (APX, EC 1.11.1.11), guaiacol peroxidase (POD EC 1.11.1.7), glutathionereductase (GR, EC 1.6.4.2), catalase (CAT, EC 1.11.1.6), Dehydroascorbatereductase and monodehydroascorbatereductase) (Noctor and Foyer, 1998), and non-enzymatic low molecular compounds such as ascorbic acid (AA), glutathione, carotenoids and anthocyanins. Additional compounds, such as osmolytes, proteins (e.g. peroxiredoxin) and amphiphilic molecules (e.g. α -tocopherol), may also function as ROS scavengers, reduced glutathione (GSH), carotenoids, phenolics, flavonoids, and proline (Gill and Tuteja, 2010).

The aim of this study was to explore the physiological responses of sesame varieties to different drought levels. Also, gene expression profile of selected antioxidant genes was investigated.

Materials and Methods

The experiment was conducted in the laboratory of College of Science/University of Anbar during the season of 2019. The plant materials included three sesame genotypes: Wadaa, Sumer and Local that were obtained from College of Agriculture/Department of Field Crops and from the Center of Desert Studies/University of Anbar. The soil was mixed with peatmoss in 5:1 ratio. The seeds were sterilized with 10% sodium hypochlorite for 1-2 min and washed two times with sterile distilled water. Five sesame seeds were planted in each of six pits that made in $(25 \times 25 \text{ cm})$ pots containing 9 Kg of the prepared soil. After germination, the seedlings were thinned and the strongest and healthiest one was kept in each pit. The plants were irrigated and fertilized with urea at a concentration of 100 mg/kg soil. The urea fertilizer was divided and applied at planting date and after one month from the first application.

The three sesame genotypes were subjected to drought stress after 55 days from planting date by using tap water for three treatments: 100% irrigation (D1, control), 50% of field capacity (D2), and 25% of field capacity (D3). Irrigation was applied daily at 7-8 AM by using graduated cylinder. For physiological and molecular analysis, the samples were collected after 100 days of the planting date.

Physiological indices

The RWC of the leaves was measured as an indicator of leaf hydration at reproductive stages based on fresh (FW), turgid (TW) and dry (DW) weights (Barr and Weatherley, 1962). RWC was determined according to the formula:(FW–DW)/ (TW–DW) ×100.

Cell membrane permeability was measured as membrane stability index (MSI); electrolyte leakage measured at the reproductive stage. Leaf samples

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were cut into six equal disk sizes of 12 mm and immersed in 10 ml of distilled water for 12 h. The electrical conductivity (EC1) of the solution was measured by EC meter (Trans-BC3020, China). The samples were then heated in a 60°C water bath for 20 minutes, and the second electrical conductivity (EC2) of the heated samples was measured . Electrolyte leakage was estimation by using the del Carmen Rodríguez-Hernández *et al.*, (2013) formula:

MSI%= (EC1/EC2)×100

The proline content was estimated according to Bates *et al.*, (1973) from 0.2 gm of fully expanded leaf collected at reproductive stage. Standard curve of pure proline (0.1 mg. ml⁻¹) was prepared taking different concentrations of proline, using toluene as a blank. The proline content of plant material was calculated on a fresh weight using standard curve as follows:

 $[(\mu g \text{ proline}/ \text{ml} \times \text{ml toluene})/115.5 \ \mu g/ \ \mu \text{moles}]/[(g \text{ sample})/5] = \mu \text{moles proline}/g \text{ of fresh}$ weight material.

Expression analysis of antioxidant genes

Total RNA was isolated from sesame leaf samples using the QIAzol ® reagent and the concentration was quantified using Qubit 4 flourometer. The transcription levels of all genes were analyzed using quantitative real-time PCR(RT-PCR, Bioer, Japan) and the assessment of the melting curves confirmed that all primers generated only a single amplicon and that no primer dimers or unexpected products were found. Actin's gene (*Si*Actin) was used as an internal reference to verify the equivalent loading of cDNA. Primers were designed using Primer3 program (Table 1).

A total of 20 µl of PCR reaction mixture has been prepared for the reaction mix by combining 10 µl of GoTaq® Probe qPCR Master Mix with dUTP with 0.4 μl of GoScriptTM RT Mix for 1-Step RT-qPCR, 2 μl of each gene-specific primer, 5 µl of 10 pg RNA template and Nucleas-free water was added to make up the final volume of 20 µl. Amplifications were performed for 1 cycle of 15 minutes at 37 °C for reverse transcription, 1 minute at 95°C for activation of GoTaq ® DNA polymerase. For denaturation 40 cycles of 10 seconds at 95 °C, 40 cycle at 60 °C for 30 seconds for the Anneal/Collect data, 40 cycles at 72 °C for 30 seconds to Extend, Melting Stage 1 cycle at 95 °C for 5 minutes, 1 cycles at 60 °C for 5 minutes to annealing and final denaturation (Read) step were performed by 1 cycle 10 minute at 95 °C. The relative quantification of the differential expression was carried out using the comparative threshold cycle method as described by Livak and Schmittgen, (2001).

Results and Discussion

Relative water content (RWC)

The decrease in RWC leaves under drought conditions was shown in Table 2. Wadaa variety showed the highest ratio of 82.0%, while Sumer and Local showed the lowest ratio of 77.7% and 77.0%, respectively and was therefore identified as an indicator of drought tolerance in crops (Jones, 2007). The effect of the interaction between the drought and varieties of the RWC of treatments in the reproductive stage shows the distinction of the Local variety in D2 irrigation level with the highest percentage was 91.7%.

High relative water content (RWC) has previously been reported to improve the ability of plants to extract soil water for increased water uptake associated with PIPI and RWC3 aquaporin gene in maize, resulting in improved root water uptake and, as a result, increased drought tolerance (Comas *et al.*, 2013). Hassanzadeh *et al.*, (2009) also reported that the rate of RWC in plants with high resistance to

Gene	Accession Number	Sequence $(5' \rightarrow 3')$	Amplicon size
Cu/Zn-SOD	XM_011090495.2	090495.2 Forward-CCTCTGACTGGTCCTGACTC	151 bp
		Reverse-ACAGGGGAGTCAAACCAACA	
CAT	NM_001304397.1	Forward-GCCCTGCTATTATCGTCCCT	196 bp
		Reverse-ACCTCTTCATCCCTGTGCAT	1
APX	XM_011091553.2	Forward-GCTGGAGTTGTTGCTGTTGA	177 bp
		Reverse-CGCAACAATATCCTGGTCGG	1
SiActin	XM_011076839.2	Forward-CCCAGGTATTGCTGACAGGA	178 bp
	_	Reverse-GCCCAGCCTCATCATACTCT	1

Table 1. List of primers used in the current study.

drought is higher than in others. In other words, plants with higher yields under drought stress should have a high RWC. Therefore, on the basis of the results, the genotypes mentioned, which are classified as high and medium yielding genotypes, should be of high RWC content.

Drought treatment appears to have a significant decrease in the RWC ratio with decreased water irrigation at reproductive stage and a clear decrease in the D3 value of 68.5 % compared to the control and D2 treatment levels were 83.8% and 84.4%. The increase in RWC in irrigation level D2 may be due to the great role of water in increasing the activity of antioxidant enzymes (*CAT* and *APX*), which were over expressed in this treatment, it may also have significance in the acquisition by the plant of an adaptive characteristic in order to resist the shortage of water in this treatment. On the contrary decrease in RWC leaf in D3 may due to limited availability of water for plants use.

RWC also establishes a close relationship with plant water potential, in such a way that the decreasing RWC can be attributed to the imbalance between re-watering and water losses due to canopy evapotranspiration (Jones, 2007). In the study of sesame, Anee *et al.*, (2019); Behzadnejad *et al.*, (2020) reported similar results.

Electrolyte leakage (EL)

Electrolyte leakage results (Table 3) showed no significant differences among sesame varieties. For D3 irrigation water level Wadaa variety recorded highest ratio (59.3%). The degree of cell membrane injury caused by water stress can be easily estimated by measuring electrolyte leakage from the cells (Bajji *et al.*, 2002); In fact, it was assumed that sugars, particularly non-reducing disaccharides such as sucrose and trehalose (in a few species) interact with cell membranes to increase cellular membranes stability of the lipid layers (Nilsen and Orcutt, 1996).

The protection mechanism of these solutes is still uncertain, but one hypothesis suggests that, under desiccation, molecules normally associated with phospholipids head-groups are replaced by sugars (Leopold and Vertucci, 1986). This may prevent the lateral phase transition and the formation of lipid domains that have the potential to form inverted lipid domains and thus increase membrane leakage, increased accumulation of such compatible solutes in drought resistant cultivars' leaf tissues would reduce dehydration damage and promote growth during and after water stress (Bajji *et al.*, 2000).

Significant differences were existed among drought treatments; D3 recorded 51.8% compared with D1 that recorded 28.3%. The increase in electro-

Table 2. Relative water content (%) for sesame varieties that treated with different drought levels

Variety name	RWC (%) in reproductive stage				
	D1 (100% Field Capacity)	D2 (50% Field Capacity)	D3 (25% Field Capacity)	Average	
Wadaa	87.6	90.9	67.4	82.0ª	
Sumer	81.0	70.6	81.3	77.7^{b}	
Local	82.7	91.7	56.6	77.0 ^b	
LSD P≤0.05	10.83				
Average	83.8ª	84.4^{a}	68.5 ^b		
LSD P≤0.05	6.26	6.26			

Table 3. Electrolyte Leakage (%) for sesame varieties that treated with different drought levels

Variety name	EL % in reproductive stage				
	D1	D2	D3	Average	
	(100% Field Capacity)	(50% Field Capacity)	(25% Field Capacity)	0	
Wadaa	26.1	54.6	59.3	46.7 ^{N.S}	
Sumer	32.5	48.9	49.5	43.6 ^{N.S}	
Local	26.4	39.9	46.7	37.6 ^{N.S}	
LSD P≤0.05	36.58				
Average	28.3 ^b	47.8 ^{ab}	51.8ª		
LSD P≤0.05	21.12	21.12			

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lyte leakage as soil water content decreased can be attributed to a consequence of the limitation in photo synthesis imposed by the water deficit, as a result of the disruption of membrane integrity caused by overproduction of reactive oxygen species (ROS). High levels of these compounds may reduce the activity of enzymes, cause lipid peroxidation, oxidize proteins, and kill cells at the most advanced stage (Du *et al.*, 2013). Lima *et al.*, (2018) has found similar result.

Proline content

As shown in Table 4, no significant differences were observed among sesame varieties for proline content. Sumer scored elevated proline content with D3 treatment (8.88 µmole.g plant⁻¹). Proline acts as an osmoprotective molecule, maintaining and improving the water status of plants (Anee *et al.*, 2019); also, proline acts as an antioxidant, defending cells from free radical damage and maintaining the cellular environment for better synthesis of biomolecules that play a major role in stress adaptation (Barickman *et al.*, 2019). Dossa *et al.*, (2017) reported that proline accumulation was significantly higher in drought tolerance plants compared to drought sensitivity, especially when drought stress was severe.

The irrigation water treatments increased proline content in D3 (7.83 µmole.g plant⁻¹) compared to D1 (5.49 µmole.g plant⁻¹). Increases proline proportionately faster than other amino acids in plants under water stress have been suggested as an assessment parameter for irrigation planning and selection of drought-resistant (Bates *et al.*, 1973). Gill and Tuteja, (2010) found that proline is involved in oxidative stress tolerance mechanisms, and this was the plant's main strategy to avoid harmful oxidative stress effects due to water stress. Insufficient availability of the electron acceptor CO₂ slows down the oxidation of nicotinamide adenine dinucleotide phosphate (NADPH) in the Calvin-Benson cycle. Lack of NADP⁺ causes a backlog of electrons and over-reduction of the photosynthetic electron transport which in turn increases the reduction rate of oxygen as alternative electron acceptor in the Mehler reaction at photosystem I (PSI) and enhanced release of superoxide anion (O₂^{•-}) and hydrogen peroxide (H₂O₂) in drought-treated cells during photosynthesis ((Cruz de Carvalho, 2008).

To study the molecular impacts drought stress and the associated ROS release and oxidative damage on sesame, gene expression analyses of *Cu/Zn-SOD*, *CAT*, and *APX* genes were investigated. SOD is considered as a key enzyme for maintaining normal physiological conditions and coping with oxidative stress in the regulation of intracellular levels of ROS, it is the first enzyme in the detoxifying process, converts O₂ radicals to H₂O₂ in plants (Mittler, 2002).

The results presented in Table 5 showed downregulation *Cu/Zn-SOD* gene in Wadaa after treated with drought stress. The treatments of drought led to gradual increase in its expression for Sumer and Local, as the highest expression was in D2 treatment (43.631-fold and 50.984-fold, respectively) and in D3 treatment (7.514-fold and 21.008-fold, respectively). SOD is one of several important antioxidant enzymes with the ability to repair oxidative dam-age on drought tolerant variety of sesame (*Sesamum indicum* L.) under water stress (Fazeli *et al.*, 2007). Mehrabad Pour-Benab *et al.*, (2019) showed that *SOD* expression was increased in all species of wheat under the drought stress treatment compared to the well-watered conditions.

Under drought condition, CAT turns over

Variety name	Proline (μ mole.g plant ⁻¹) in reproductive stage				
	D1 (100% Field Capacity)	D2 (50% Field Capacity)	D3 (25% Field Capacity)	Average	
Wadaa	5.90	6.52	7.00	6.47 ^{N.S}	
Sumer	4.74	6.87	8.88	6.83 ^{N.S}	
Local	5.82	8.16	7.62	7.20 ^{N.S}	
LSD P≤0.05	3.392				
Average	5.49 ^b	7.18^{ab}	7.83ª		
LSD P≤0.05	1.958	1.958			

Table 4. Plants proline content for sesame varieties that tree	ated with different drought levels
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N.S: Non Significant

quickly in leaf cells and is vital for the eliminating of free oxygen radicals formed in the peroxisomes by photorespiration (Mittler, 2002). CAT is a tetrameric, heme-containing enzyme that catalyzes the dismutation of H₂O₂ into H₂O and O₂ in the peroxisome. The results (Table 5) revealed that the expression level CAT gene in Wadaa was increased by 17.895-fold in response to D2 treatment, while the expression level was slightly increased by 1.77-fold in response to D3 treatment. The same applies to the cultivar Sumer, which showed an over expression of CAT gene in D2 treatment (6.453 fold) while in D3 treatment, the expression scored 4.723 fold. CAT gene expression was elevated in D2 treatment for the Local variety by 1.531-fold while it decreased by 1.569-flod than normalized for treatment D3. The increasing trend in H₂O₂ accumulation due to increased stress duration is due to decreased CAT activity as an H₂O₂ scavenging enzyme (Hasanuzzaman et al., 2012). Uzilday et al., (2012) reported that high levels of CAT expression were observed in Cleome gynandra and Cleome spinosa during prolonged drought exposure (10 days). Dudziak et al., (2019) suggested that short-term drought has increased CAT expression as a rapid plant response. However, prolonged exposure to drought could lead to inhibition of expression and lower transcription levels.

APX is widely dispersed in plant cells, and different isoforms are more efficient in removing H_2O_2 under stressor conditions (Sharma *et al.*, 2012). The expression of the *APX* gene (Table 5) varied among the three varieties of sesame under the influence of drought, as the expression in Wadaa reached 4512.403-fold in D2 treatment while it was down-regulated in D3 treatment. *APX* gene expression increased in Sumer variety in both D2 treatment and D3 treatment as it scored a high expression in D2 treatment, 825.001-fold, while it was characterized by a little increase in D3 treatment with 7.693-fold

compared to non-stress plants. *APX* gene of Local variety showed an increase in the expression with 50% irrigation level and scored 12.466 fold, while it decreased from normal for D3 treatment to record a down-regulated with 1.265-fold compared to D1 treatment.

The pattern for APX gene expression was characterized by an initial increase, followed by a decrease with increase drought period (Dudziak et al., 2019). APX, as the main component in the ascorbate- glutathione cycle, has a crucial role in the balancing of the intercellular ROS accumulation. Under the nonstress and drought stress conditions, the expression of APX gene was significantly variable among species (Mehrabad Pour-Benab et al., 2019). Ren et al., (2016) reported that the expression of cytosolic APX and dehydroascorbatereductase (DHAR) was followed by significant up-regulation, indicating that they were regulated at transcriptional level for drought resistant plants exposed to long-term soil drought. In contrast, drought susceptible plants exhibited high ROS levels and poor antioxidant enzyme response, leading to increased membrane damage during long-term soil drought conditions.

Several studies in plants have shown that relatively low levels of ROS act as signaling molecules that induce abiotic stress tolerance by controlling the expression of defense genes. In addition, numerous results have shown that plants with higher levels of antioxidants, whether constitutive or induced, show greater resistance to different types of environmental stress (Hasanuzzaman et al., 2012). Guan and Scandalios, (2000) reported that expression patterns of APX, CAT and SOD in barley under drought conditions depend on the stage of plant development and genotype. The comparison of tolerant with sensitive phenotypes highlights the role of the antioxidant system in drought tolerance. For instance, CAT, APX and SOD levels are up-regulated in the drought-tolerant CE704 genotype (maize), while

Table 5. Relative expression of *Cu/Zn-SOD*, *CAT* and *APX* genes in sesame varieties subjected to different drought levels. Values were normalized to sesame to reference gene using the 2^{-ΔΔCt} method and expressed as ratios relative to D1 treatment (set as 1).

Variety	Cu/Zn-SOD		CAT		APX	
	D2 (50% Field Capacity)	D3 (25% Field Capacity)	D2 (50% Field Capacity)	D3 (25% Field Capacity)	D2 (50% Field Capacity)	D3 (25% Field Capacity)
Wadaa Sumer Local	0.0002 44.631 51.984	0 8.514 22.008	18.895 6.453 2.531	2.770 4.723 0.637	4513.403 826.001 12.466	0.012 8.693 0.790

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CAT and *APX* levels decreased in the drought-sensitive 2023 genotype (Benešová *et al.*, 2012).

Conclusion

The results showed a significant increase in the distinction of the variety Wadaa for RWC. The results also showed differential response of antioxidant enzymes at gene expression, (*Cu-Zn-SOD*) down-regulated in Wadaa variety; the gene expression of *CAT* and *APX* over expression at D2 treatment for the three varieties, indicating that sesame plants tolerance to this level of drought. SOD, CAT, and APX activities particularly in tolerant genotypes, protected them against oxidative damage, as indicated by the lower ROS production, and also specified their role in drought tolerance. This observation warrants further exploration to clarify the complex mechanism underlying the antioxidant defense system of plants for enhanced drought tolerance.

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