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ASSESSMENT OF SALINITY-INDUCED CHANGES IN PHYSIO-BIOCHEMICALS AND ANTIOXIDANT ENZYMES IN SESAME (*Sesamum indicum* L.)

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ABSTRACT

Salinity stress is a major constraint limiting sesame (*Sesamum indicum* L.) productivity, particularly in arid and semi-arid regions. The present study was conducted to evaluate the morpho-physiological and biochemical responses of fifteen sesame genotypes under varying salinity levels (0, 2, 4, 6 and 8 dS m^{-1}) at the seedling stage. The experiment was laid out in a factorial completely randomized design to assess morpho-physiological parameters, osmolyte accumulation and antioxidant enzyme activities. Significant variation among genotypes and treatments was observed for morpho-physiological and biochemical parameters. Increasing salinity adversely affected germination, vigour index, chlorophyll content and total soluble protein, whereas osmolytes such as proline and glycine betaine and antioxidant enzymes showed a marked increase. Among the genotypes, AT-518 and Guj. Til 11 performed superior under stress, maintaining higher vigour, relative water content, protein stability and chlorophyll retention. These genotypes also exhibited enhanced accumulation of glycine betaine and higher activities of antioxidant enzymes such as superoxide dismutase, catalase and ascorbate peroxidase, indicating efficient osmotic adjustment and reactive oxygen species scavenging. Correlation analysis revealed strong positive associations of salt tolerance index with vigour index, protein content, glycine betaine and key antioxidant enzymes, highlighting their role in stress adaptation. In contrast, genotypes like Guj. Til 6 and Guj. Til 8 were found to be more sensitive to salinity stress. The study concludes that salinity tolerance in sesame is a complex trait governed by integrated physiological and biochemical mechanisms, and traits such as protein stability, glycine betaine accumulation and antioxidant defense can serve as reliable selection criteria for developing salt-tolerant cultivars.

Keywords **:** Salinity stress; Sesame (*Sesamum indicum* L.); Antioxidant enzymes; Glycine betaine; Salt tolerance index.

Introduction

Sesame (*Sesamum indicum* L.) is one of the most important oilseed crops cultivated globally and holds a prominent position in Indian agriculture next only to groundnut and rapeseed–mustard. It is particularly well adapted to arid and semi-arid agro-ecological regions, where its drought tolerance and ability to thrive under marginal conditions make it a valuable crop for resource-poor farmers. Belonging to the family Pedaliaceae, sesame is considered one of the oldest oilseed crops known to mankind, with a long history of cultivation and utilization across Asia and Africa (Debnath *et al*., 2025).

Sesame seeds are highly valued for their rich nutritional composition and functional properties. Chemically, the seeds contain approximately 44–57% oil, 18–25% protein, and 13–14% carbohydrates, making them an excellent source of energy and nutrition (Borchani *et al*., 2010). The oil fraction is particularly notable for its fatty acid composition, consisting of about 35% monounsaturated fatty acids and 44% polyunsaturated fatty acids, which are beneficial for human health. Moreover, sesame oil exhibits remarkable oxidative stability due to the presence of naturally occurring antioxidants such as lignans (e.g., sesamin and sesamol) and tocopherols, which contribute to its long shelf life and resistance to rancidity (Elleuch *et al*., 2007). Beyond oil extraction, sesame seeds are widely used in confectionery products and hold significant cultural and religious importance in many societies (Xu *et al*., 2005).

Globally, sesame is cultivated over an area of approximately 7.54 million hectares, with an annual production of about 3.34 million tons and an average productivity of 443 kg ha^{-1}. The crop is grown in nearly 60–65 countries, with Asian and African regions accounting for the majority of production. Major sesame-exporting countries include India, China, and Mexico, while Japan is recognized as the largest importer of sesame seeds in the international market. In India, sesame occupies a significant share of oilseed cultivation. During 2014–15, it was grown on about 1.74 million hectares, producing 0.827 million tons with an average productivity of 474 kg ha^{-1}. In the state of Gujarat, sesame cultivation covered approximately 0.181 million hectares with a production of 0.102 million tons and a productivity of 564 kg ha^{-1} during the summer season (Anon., 2023). These statistics highlight the economic importance of sesame both at national and regional levels.

Despite its adaptability, sesame productivity is severely constrained by several abiotic stresses, among which soil salinity is a major limiting factor. Soil salinity is one of the most critical challenges facing irrigated agriculture worldwide, significantly reducing crop growth, yield, and quality. It primarily arises due to low precipitation, high evapotranspiration rates, and improper irrigation practices, which lead to the accumulation of soluble salts in the soil profile. This imbalance not only deteriorates soil health but also renders groundwater brackish, further aggravating the problem (Parida and Das, 2005).

Globally, it is estimated that around 80 million hectares of arable land are affected by salinity, posing a serious threat to food security and sustainable agriculture. The impact of salinity is particularly severe in arid and semi-arid regions, where limited rainfall, high temperatures, and increased evaporation demand accelerate salt accumulation in the root zone (Azevedo *et al.*, 2006). Under saline conditions, plants experience osmotic stress, ion toxicity, and nutrient imbalance, which collectively impair physiological and biochemical processes, ultimately reducing crop productivity.

It is hypothesized that increasing levels of salinity adversely affect growth, physiological efficiency and biochemical processes in sesame, while genotypic variability plays a crucial role in determining the degree of tolerance through differential osmotic adjustment and antioxidant defence mechanisms. Genotypes capable of maintaining higher protein stability, osmolyte accumulation (particularly glycine betaine) and enhanced antioxidant enzyme activity are expected to exhibit superior performance under saline conditions. Therefore, the present study was undertaken to evaluate the response of different sesame genotypes to varying salinity levels, to assess their growth, physiological and biochemical behaviour under stress, and to identify key traits associated with salinity tolerance. The study also aims to screen and identify salt-tolerant genotypes that can be utilized in future breeding programs for improving sesame productivity in salt-affected areas.

Materials and Methods

Fifteen genotypes of sesame (*Sesamum indicum* L.), namely G. Til 1, G. Til 2, G. Til 3, G. Til 4, G. Til 5, G. Til 6, G. Til 8, G. Til 10, G. Til 11, Purva 1, AT 468, AT 475, AT 482, AT 513 and AT 518, were procured from the Agricultural Research Station, Junagadh Agricultural University, Amreli, and evaluated under laboratory conditions at the Department of Biochemistry, Junagadh Agricultural University, Junagadh. The experiment was conducted in three replications using petriplate culture under five salinity levels, *viz*., tap water 0 (control), 2, 4, 6 and 8 dS/m, prepared using seawater, and arranged in a factorial completely randomized design (FCRD) to study the individual and interaction effects of genotypes and salinity stress.

Physiological parameters

Germination parameters such as germination index and vigor index were recorded based on daily germination counts until stabilization (Sivakumar *et al*., 2021; Ahmed *et al*., 2021), while salt tolerance index (STI) was calculated using root and shoot length measured at 10 days after sowing (Sanjay *et al*., 2015). Relative water content (RWC) of leaves was determined using the method of Weatherley (1962). Sodium and potassium contents were estimated after acid digestion of dried plant samples using a flame photometer, and the Na^{+}/K^{+} ratio was computed (Abdulfatah *et al*., 2021). Stomatal morphology was studied using scanning electron microscopy after fixation, dehydration through graded ethanol series, and gold coating of leaf samples (Jayaprakasan*et al*., 2013).

Biochemical parameters

Total chlorophyll content was estimated spectrophotometrically in 80% acetone extract using absorbance at 645 and 663 nm (Arnon, 1949). Free proline content was determined following the ninhydrin method described by Bates *et al*. (1973), while glycine betaine content was estimated according to Grieve and Grattan (1983). For antioxidant enzyme analysis, fresh leaf tissues were homogenized in phosphate buffer and centrifuged to obtain enzyme extracts. Peroxidase (POX) activity was measured by recording the increase in absorbance at 460 nm (Wang *et al*., 2017), and polyphenol oxidase (PPO) activity was determined at 490 nm (Mayer *et al*., 1965). Catalase (CAT) activity was estimated by titration of residual hydrogen peroxide (Patra *et al*., 1978), whereas superoxide dismutase (SOD) activity was determined based on inhibition of nitro blue tetrazolium reduction at 560 nm (Mishra and Fridovich, 1972). Glutathione peroxidase (GPx) activity was measured at 412 nm following the method of Smith *et al.* (1988), and ascorbate peroxidase (APX) activity was estimated by monitoring the decrease in absorbance at 290 nm (Mehr and Bahabadi, 2013).

Results and Discussion

The performance of various sesame genotypes was evaluated across several physiological and growth parameters. The data revealed significant variations among the genotypes at a 5% level of significance (CD at 5%). The overall mean values for the evaluated parameters across all 15 genotypes provide a level for sesame seedling performance. Based on the experimental data, the overall mean values for the primary growth and physiological traits are as follows:

Physiological parameters

Significant differences among the fifteen sesame (*Sesamum indicum* L.) genotypes were observed for all studied parameters at the 5% level of significance (CD at 5%), indicating substantial genetic variability. The vigour index varied widely from 192 in Guj. Til 6 to 829 in AT-518, reflecting marked differences in seedling establishment among genotypes (Table 1).

Relative water content (RWC) remained comparatively high across genotypes, ranging from 77.55% (Guj. Til 1) to 91.43% (AT-518), suggesting efficient water retention capacity. The Na^+/K^+ratio showed minimal variation (0.95–0.99), indicating maintenance of ionic balance under the imposed conditions. Stomatal size also exhibited considerable variation, ranging from 35.07 (Guj. Til 6) to 70.85 (AT-468), with higher values recorded in AT-468, AT-518, and AT-513 (Table 1).

Among the genotypes, AT-518 emerged as the best performer, recording the highest vigour index (829) and salt tolerance index (83.31), indicating superior adaptability under stress conditions. In contrast, Guj. Til 6 and Guj. Til 8 showed comparatively poor performance, suggesting higher sensitivity to salinity. Higher RWC observed in AT-518, Guj. Til 11, AT-468, and AT-482 indicates better cellular turgidity and physiological efficiency. The consistently low Na^+/K^+ratio across genotypes further suggests effective ion regulation, a key mechanism for stress tolerance.

The low coefficient of variation (1.22–5.54%) indicates reliability and precision of the experimental data, while significant CD values confirm the statistical validity of observed differences. Stomatal characteristics revealed that genotypes with larger stomata (AT-518 and AT-468) also exhibited higher vigour and RWC, possibly due to enhanced gas exchange and photosynthetic efficiency. Conversely, genotypes with smaller stomata (Guj. Til 6 and Guj. Til 8) showed lower vigour and tolerance indices, suggesting that reduced stomatal size in these cases may be associated with overall lower physiological performance rather than adaptive advantage. Overall, the results highlight AT-518 and related genotypes as promising candidates for salinity tolerance, while Guj. Til 6 and Guj. Til 8 appear less suitable under such conditions.

Biochemical parameters

Total soluble protein content decreased significantly with increasing salinity in all genotypes. The mean value of total soluble protein content in sesamum genotypes ranged from 0.25% (Guj. Til 6) to 0.44% (AT-518). High protein content was observed in AT-518 (0.44%) followed by Guj. Til 11 (0.41%), whereas the lowest protein accumulation was recorded in Guj. Til 6 (0.25%) and Guj. Til 8 (0.26%) (Table 2). In interaction effect, tolerant genotypes (AT-518, Guj. Til 11) maintained higher protein levels, while Guj. Til 6 showed maximum decline in protein under severe salinity stress (8 dS mv^{-1}) (Fig. 1). This reduction may be attributed to enhanced protease activity, inhibition of protein synthesis, and oxidative damage under salinity (Ashraf and Harris, 2004; Munns and Tester, 2008; Gill and Tuteja, 2010). Higher protein retention in tolerant genotypes may be due to synthesis of stress proteins such as dehydrins and HSPs (Kosová *et al.*, 2011).

Chlorophyll content varied between 0.08 $mg.g^{-1}$ FW (Guj. Til 6 and 8) and 0.17 $mg.g^{-1}$ FW (Guj. Til 2). Genotypes such as Guj. Til 11 (0.16 $mg.g^{-1}$ FW) and Purva 1 (0.14 $mg.g^{-1}$ FW) showed relatively higher chlorophyll content. Lower chlorophyll levels were observed in Guj. Til 6 and 8, suggesting possible susceptibility to stress or lower photosynthetic capacity. The variability was moderate, with a coefficient of variation (CV%) of 4.21% (Table 2). During the interaction effect, chlorophyll content declined progressively with increasing salinity. GenotypesGuj. Til 2 and Guj. Til 11 were recorded higher chlorophyll content, whereas Guj. Til 6 and Guj. Til 8 were found most affected under high salinity stress (8 dS mv^{-1})(Fig. 2). The decline in chlorophyll may be due to increased chlorophyllase activity, ion toxicity, membrane damage, and reduced Mg^{+2} uptake (Santos, 2004; Parida *et al.*, 2004; Ashraf, 2009; Atta *et al*., 2023).

In contrast, free proline content increased significantly, rising from 0.19 mg.g^{-1} FW (AT-475)to 0.28 mg.g^{-1} FW (Guj. Til 5, Guj. Til 6, Guj. Til 11, and AT-518)(Table 2). At maximum stress (8 dS mv^{-1}), Guj. Til 11 and AT-518 recorded peak accumulation (0.60 mg g^{-1}), indicating superior stress adaptation (Fig. 3). Proline accumulation acts as an osmoprotectant, stabilizes proteins and membranes, and scavenges reactive oxygen species under stress (Hayat *et al*., 2012; Szabados and Savoure, 2010; Liang *et al*., 2013).

GB content among genotypes varied from 0.27 mg.g^{-1} FW (Guj. Til 6 and 8) to 0.44 mg.g^{-1} FW (AT-518) (Table 2).Glycine betaine content increased significantly with increasing salinity levels in all sesame genotypes. Under severe stress, Guj. Til 2 exhibited maximum accumulation (0.53 mg g^{-1}), while Guj. Til 8 remained lowest, indicating variation in osmotic adjustment capacity (Fig. 4). The increased accumulation of glycine betaine under salinity stress reflects its role as an effective osmoprotectant. It helps maintain cellular osmotic balance, stabilizes proteins and membranes, and protects the photosynthetic apparatus, particularly Photosystem II, from salt-induced damage. Higher accumulation in tolerant genotypes (AT-518, Guj. Til 11) suggests efficient biosynthesis and better stress adaptation, whereas lower levels in sensitive genotypes may result in reduced cellular stability and vigor (Ashraf and Foolad, 2007; Chen and Murata, 2011). Overall, significant differences ($P < 0.05$) among genotypes and treatments confirm the role of glycine betaine in salinity tolerance.

Antioxidant Enzymes Systems

Superoxide Dismutase (SOD) activity ranged from 6.15ΔOD min^{-1} g^{-1} FW (Guj. Til 6) to 8.44 ΔOD min^{-1} g^{-1} FW (AT-518). High antioxidant enzyme activity was recorded in AT-518, Guj. Til 10 (8.22ΔOD min^{-1} g^{-1} FW), and Guj. Til 5 (7.95ΔOD min^{-1} g^{-1} FW), indicating their potential ability to detoxify reactive oxygen species under stress. Genotypes Guj. Til 6 and AT-468 showed the lowest SOD activity, suggesting lower antioxidant defense (Table 2). Under severe stress, AT-518 recorded maximum activity (9.65ΔOD min^{-1} g^{-1} FW), indicating efficient ROS scavenging(Fig. 5). Increased SOD reflects its role in dismutating superoxide radicals and initiating antioxidant defence (Derbali*et al*., 2020; Mittler, 2002). Ascorbate Peroxidase (APX) activity activity ranged from 44.51 (AT-475) to 69.51 ΔO.D. min^{-1}·g^{-1} FW (Guj. Til 5) (Table 2). Guj. Til 11 and AT-518 exhibited highest activity, while AT-475 showed lowest responseunder high slinity stress condition(Fig. 6). Higher APX activity indicates efficient detoxification of H_2O_2 via the ascorbate–glutathione cycle, protecting photosynthetic machinery (Hussain*et al*., 2024; Murshed *et al*., 2013).

Glutathione peroxidase (GPX) activity increased from 44.51 (AT-475) to 69.51 ΔOD min^{-1} g^{-1} FW (Guj. Til 5) (Table 2). Enhanced GPX activity under higher salinity stress was observed in AT-518 (Fig. 7) that reflects improved detoxification of peroxides and maintenance of redox balance (Gaber *et al*., 2023; Hasanuzzaman *et al*., 2017). Catalase (CAT) activity was varied widely from25.92 (Guj. Til 6) to 40.06 ΔOD min^{-1} g^{-1} FW (AT-518). AT-518 and Guj. Til 11 showed highest activity, whereas Guj. Til 6 recorded lowest (Table 2).Under severe stress, AT-518 recorded maximum activity(Fig. 8), indicates rapid breakdown of H_2O_2, protecting cellular components under stress (Gill and Tuteja, 2010; Das and Roychoudhury, 2014). Polyphenol Oxidase (PPO) activity was increased significantly from 3.59 (Guj. Til 10) to 8.09 ΔOD min^{-1} g^{-1} FW (AT-518) (Table 2). Genotype AT-518 exhibited the highest PPO activity, followed by Guj. Til 11 and Guj. Til 1 under sevear stress (Fig. 9). Increased PPO activity suggests enhanced phenolic metabolism and protective responses against oxidative stress (Azzam *et al*., 2021; Hasanuzzaman *et al*., 2021).

Salinity stress induces excessive generation of reactive oxygen species (ROS), including superoxide radicals (O_2^-) and hydrogen peroxide (H_2O_2), which can severely damage cellular components if not efficiently scavenged. The present study demonstrated a coordinated and significant upregulation of antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX), glutathione peroxidase (GPX), and polyphenol oxidase (PPO) with increasing salinity, indicating activation of an integrated defense mechanism. SOD acts as the first line of defense by converting superoxide radicals into H_2O_2, which is subsequently detoxified by CAT and APX, thereby maintaining cellular redox homeostasis (Mittler, 2002). The substantial increase in APX activity suggests an efficient operation of the ascorbate–glutathione cycle, particularly in chloroplasts, protecting the photosynthetic apparatus from oxidative damage (Miller*et al*., 2010; Murshed *et al*., 2013). Similarly, enhanced GPX activity reflects improved removal of lipid hydroperoxides and stabilization of membrane integrity through glutathione-mediated redox regulation (Hasanuzzaman *et al*., 2017; Gaber *et al*., 2023).

The rise in CAT activity further supports rapid decomposition of H_2O_2 into water and oxygen, preventing its accumulation to toxic levels (Gill and Tuteja, 2010). Increased PPO activity indicates activation of phenolic metabolism and secondary defense pathways, contributing to lignification and protection against stress-induced damage (Azzam *et al*., 2021; Hasanuzzaman *et al*., 2021). Notably, genotypes such as AT-518 and Guj. Til 11 exhibited higher antioxidant enzyme activities, suggesting a more efficient ROS-scavenging system and better stress adaptation, whereas lower enzyme induction in sensitive genotypes like Guj. Til 6 may lead to oxidative damage due to imbalance between ROS production and detoxification (Derbali *et al*., 2020). Thus, the enhanced antioxidant enzyme system plays a crucial role in conferring salinity tolerance by maintaining cellular integrity, metabolic stability, and overall seedling performance.

Overall, antioxidant enzymes showed coordinated upregulation under salinity stress. Genotypes like AT-518 and Guj. Til 11 exhibited higher enzymatic activity along with better osmolyte accumulation and pigment retention, indicating superior stress tolerance. In contrast, Guj. Til 6 and Guj. Til 8 showed weaker antioxidant responses, leading to reduced physiological performance. These findings highlight the importance of an efficient antioxidant defence system in salinity tolerance.

Correlation Analysis of Morpho-Physiological and Biochemical Markers

Correlation analysis revealed strong functional linkages among growth, physiological and biochemical traits governing salinity tolerance in sesame. The Salt Tolerance Index (STI) showed a highly significant positive association with vigour index (r = 0.86) and germination index (r = 0.85), indicating that rapid and uniform seedling establishment is a primary adaptive strategy under saline conditions, likely driven by efficient reserve mobilization and early metabolic activation (Table 3). Among biochemical traits, total soluble protein exhibited the strongest correlation with STI (r = 0.92), highlighting the importance of protein stability and synthesis in maintaining enzymatic functions and structural integrity under ionic and osmotic stress (Munns and Tester, 2008). The differential behavior of osmolytes was evident, where glycine betaine showed a strong positive correlation (r = 0.77), suggesting its key role in osmotic adjustment, membrane stabilization, and protection of photosynthetic machinery, whereas proline showed a weak association (r = 0.19), implying that its accumulation may reflect stress injury rather than effective tolerance (Ashraf and Foolad, 2007).

The antioxidant system also contributed significantly to salinity tolerance, with SOD (r = 0.71) and CAT (r = 0.69) showing positive correlations with STI, indicating an efficient ROS-scavenging mechanism where SOD converts superoxide radicals into H_2O_2 and CAT rapidly detoxifies it, thus preventing oxidative damage (Table 3). In contrast, the negligible correlation of APX (r = 0.03) suggests a relatively lesser role of the ascorbate–glutathione cycle in these genotypes, possibly indicating reliance on catalase-mediated detoxification under high salinity (Mittler, 2002; Gill and Tuteja, 2010).

Moderate positive correlations of STI with chlorophyll content (r = 0.55) and stomatal size (r = 0.64) further emphasize that maintenance of photosynthetic efficiency and gas exchange contributes to sustained growth under stress. Larger stomatal size may facilitate CO_2 uptake, supporting carbon assimilation, while higher chlorophyll retention reflects protection of the photosynthetic apparatus from salt-induced oxidative damage (Parida and Das, 2005). Overall, the results indicate that salinity tolerance in sesame is a complex trait governed by integrated mechanisms involving efficient germination, protein stability, osmotic regulation (primarily via glycine betaine), and a robust antioxidant defense system, particularly the SOD–CAT pathway.

Conclusion

The present study demonstrates that salinity tolerance in sesame (*Sesamum indicum* L.) is governed by a coordinated interaction of morphological, physiological and biochemical mechanisms. Genotypes such as AT-518 and Guj. Til 11 exhibited superior performance under saline conditions, characterized by higher germination and vigour indices, better maintenance of relative water content, chlorophyll and total soluble protein, and enhanced accumulation of glycine betaine. These biochemical markers collectively contribute to improved osmotic adjustment, cellular stability and sustained metabolic activity. The strong positive association of salt tolerance index with protein content and antioxidant enzymes, particularly superoxide dismutase and catalase, highlights the critical role of efficient ROS scavenging in mitigating oxidative damage. In contrast, the weaker response of genotypes like Guj. Til 6 and Guj. Til 8 indicates limited adaptive capacity under salinity stress. Overall, the findings suggest that traits such as protein stability, glycine betaine accumulation and a robust antioxidant defense system are reliable indicators of salinity tolerance and can be effectively utilized in breeding programs aimed at developing salt-tolerant sesame cultivars.

Table 1: Mean performance of morpho-physiological parameters of sesamum genotypes.

Genotype	**Germination Index**	**Vigour Index**	**Salt Tolerance Index (%)**	**Relative Water Content (%)**	**Na/K Ratio (Leaves)**	**Stomatal Size (µm)**
Guj. Til 1	8.29	656	73.37	77.55	0.96	49.54
Guj. Til 2	8.82	737	72.5	80.88	0.95	43.35
Guj. Til 3	8.83	689	76.29	84.86	0.95	49.74
Guj. Til 4	9.59	680	71.08	84.7	0.97	54.06
Guj. Til 5	9.72	709	79.37	83.19	0.98	54.61
Guj. Til 6	3.17	192	61.74	80.18	0.96	35.07
Guj. Til 8	3.44	218	62.38	83.91	0.95	42.93
Guj. Til 10	9.84	697	75.41	91.09	0.95	46.25
Guj. Til 11	9.79	789	76.39	91.01	0.98	57.71
Purva 1	9.3	777	73.46	84.91	0.97	59.02
AT-468	9.7	763	74.8	90.99	0.96	70.85
AT-475	10.04	790	72.58	86.6	0.95	57.17
AT-482	9.79	747	73.36	90.99	0.97	53.01
AT-513	9.34	675	74.47	90.6	0.98	62.00
AT-518	9.86	829	83.31	91.43	0.99	68.03
S.Em. ±	0.120	3.660	0.260	0.270	0.000	-
CD at 5%	0.350	10.220	0.710	0.750	0.010	-
CV %	5.540	2.060	1.300	1.220	1.520	-

Table 2: Mean performance of biochemical parameters of sesamum genotypes

Genotypes	**Total Soluble Protein (%)**	**Chlorophyll Content (mg.g^{-1} FW)**	**Free Proline (mg.g^{-1} FW)**	**Glycine Betaine (mg.g^{-1} FW)**	**Superoxide Dismutase (ΔO.D. min^{-1} . g^{-1} FW)**	**Ascorbate Peroxidase (ΔO.D. min^{-1}. g^{-1} FW)**	**Glutathione Peroxidase (ΔO.D. min^{-1}. g^{-1} FW)**	**Catalase (ΔO.D. min^{-1}. g^{-1} FW)**	**Polyphenol Oxidase (ΔO.D. min^{-1}. g^{-1} FW)**
Guj. Til 1	0.39	0.11	0.24	0.32	7.40	65.79	13.03	38.83	7.66
Guj. Til 2	0.39	0.17	0.22	0.33	7.04	64.19	12.77	38.99	7.51
Guj. Til 3	0.37	0.11	0.25	0.32	7.13	66.89	7.25	38.73	4.26
Guj. Til 4	0.37	0.14	0.22	0.30	7.62	64.02	7.80	37.66	4.59
Guj. Til 5	0.38	0.12	0.28	0.34	7.95	69.51	6.82	37.45	4.01
Guj. Til 6	0.25	0.08	0.28	0.27	6.15	63.00	6.53	25.92	3.84
Guj. Til 8	0.26	0.08	0.24	0.27	6.33	68.49	7.08	26.79	4.16
Guj. Til 10	0.38	0.11	0.25	0.32	8.22	62.24	6.10	37.96	3.59
Guj. Til 11	0.41	0.16	0.28	0.40	7.07	59.45	13.20	39.19	7.76
Purva 1	0.38	0.14	0.21	0.34	7.37	61.32	7.94	37.5	4.67
AT-468	0.38	0.12	0.24	0.30	6.35	66.81	6.96	36.43	4.09
AT-475	0.34	0.14	0.19	0.34	6.84	44.51	12.48	36.22	7.34
AT-482	0.38	0.11	0.22	0.37	7.17	65.79	12.05	27.15	7.09
AT-513	0.38	0.13	0.22	0.31	6.55	63.32	7.39	28.02	4.35
AT-518	0.44	0.14	0.28	0.44	8.44	64.94	13.75	40.06	8.09
S.Em. ±	0.009	0.001	0.001	0.004	0.090	0.480	0.120	0.270	0.070
CD at 5%	0.026	0.004	0.004	0.012	0.250	1.350	0.340	0.750	0.200
CV %	10.133	4.210	2.160	4.910	4.700	2.590	4.510	3.080	4.510

Table 3: Pearson's Correlation coefficients (r)matrix of morpho-physiological and biochemical parameters associated with salinity tolerance in sesamum.

	STI	GI	VI	RWC	Na/K	Stomatal size	Total soluble protein	Total Chl.	Free proline	CAT	SOD	APX	GPX	PPO	GB
STI	1.000														
GI	0.849	1.000													
VI	0.863	0.975	1.000												
RWC	0.475	0.51	0.465	1.000											
Na/K	0.533	0.346	0.346	0.385	1.000										
Stomatal size	0.643	0.651	0.682	0.631	0.704	1.000									
Total soluble protein	0.917	0.883	0.915	0.428	0.508	0.752	1.000								
Total Chl.	0.55	0.695	0.763	0.219	0.313	0.743	0.708	1.000							
Free proline	0.19	-0.242	-0.235	0.025	0.386	0	0.028	-0.241	1.000						
CAT	0.686	0.638	0.696	-0.001	0.073	0.362	0.708	0.635	0.094	1.000					
SOD	0.715	0.573	0.548	0.182	0.372	0.35	0.662	0.313	0.231	0.638	1.000				
APX	0.031	-0.235	-0.255	-0.138	0.187	-0.094	0.037	-0.358	0.462	-0.117	0.101	1.000			
GPX	0.338	0.329	0.456	0.031	0.210	0.404	0.461	0.538	-0.081	0.39	0.218	-0.347	1.000		
PPO	0.329	0.321	0.443	0.034	0.218	0.415	0.484	0.549	-0.088	0.33	0.209	-0.328	1.000	1.000	
GB	0.768	0.605	0.689	0.488	0.619	0.675	0.753	0.57	0.24	0.469	0.605	-0.164	0.705	0.705	1.000

n=45 *P0.05=0.288 **P0.01= 0.372 ***P0.001=0.465

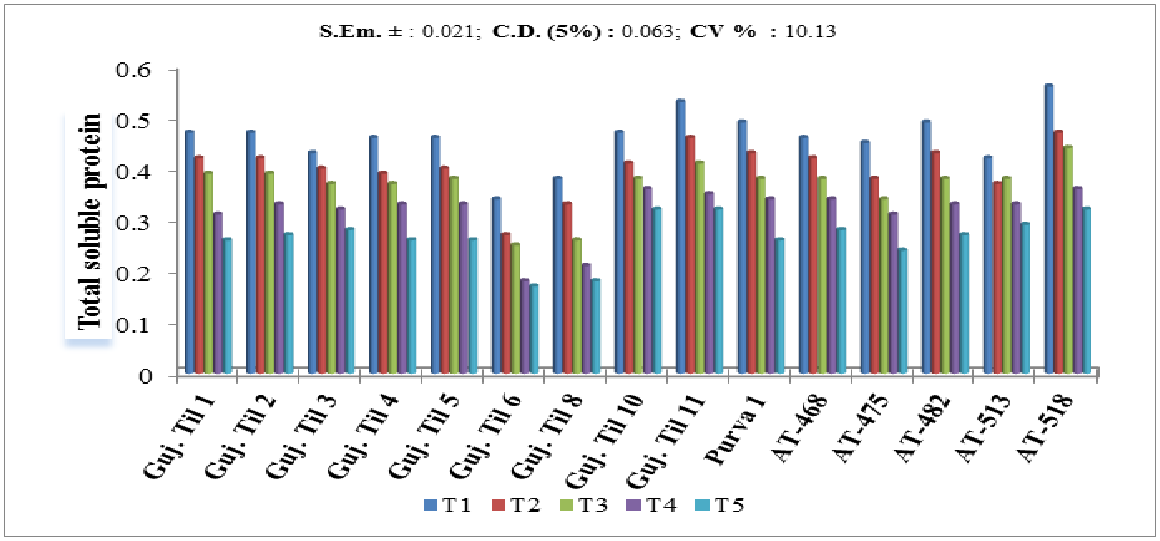

Fig. 1: Interaction effect between sesamum genotype (G) and different concentrations ofsalinity stress (T) on total soluble protein (%) at 7 DAS.
T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

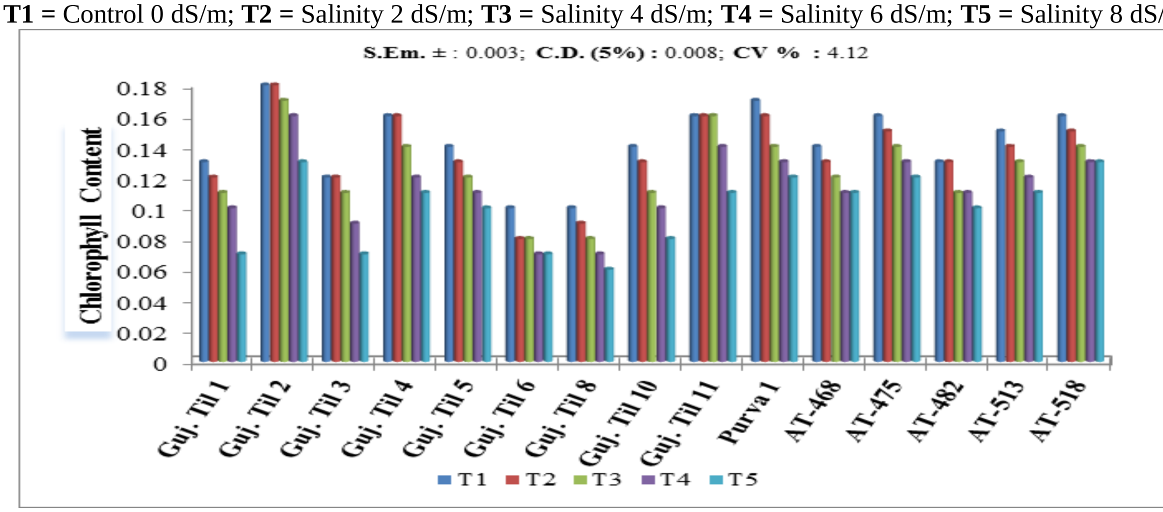

Fig. 2: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on chlorophyll content ($mg.g^{-1}$ FW) at 7 DAS.
T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

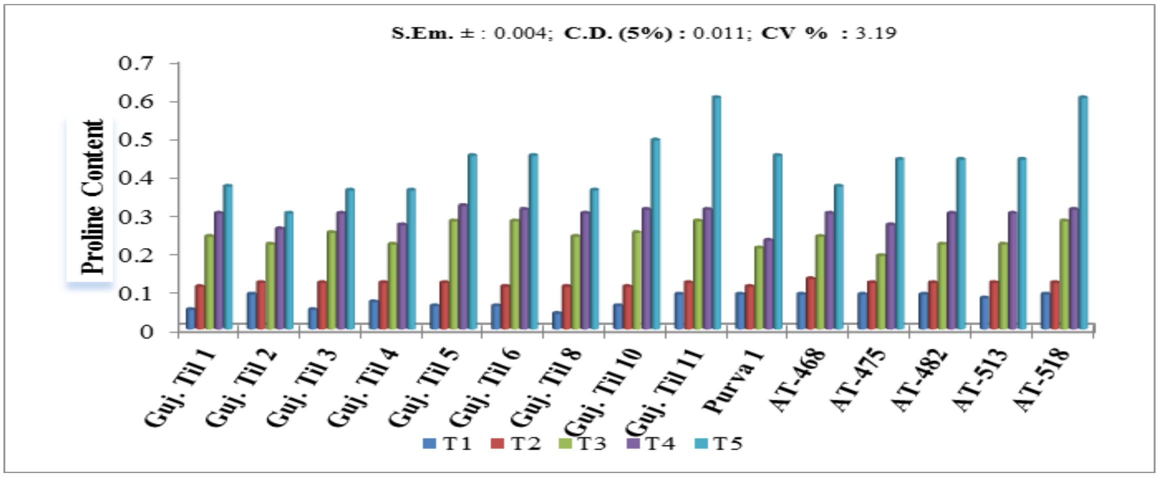

Fig. 3: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on free proline content (mg.g^{-1} FW) at 7 DAS.

T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

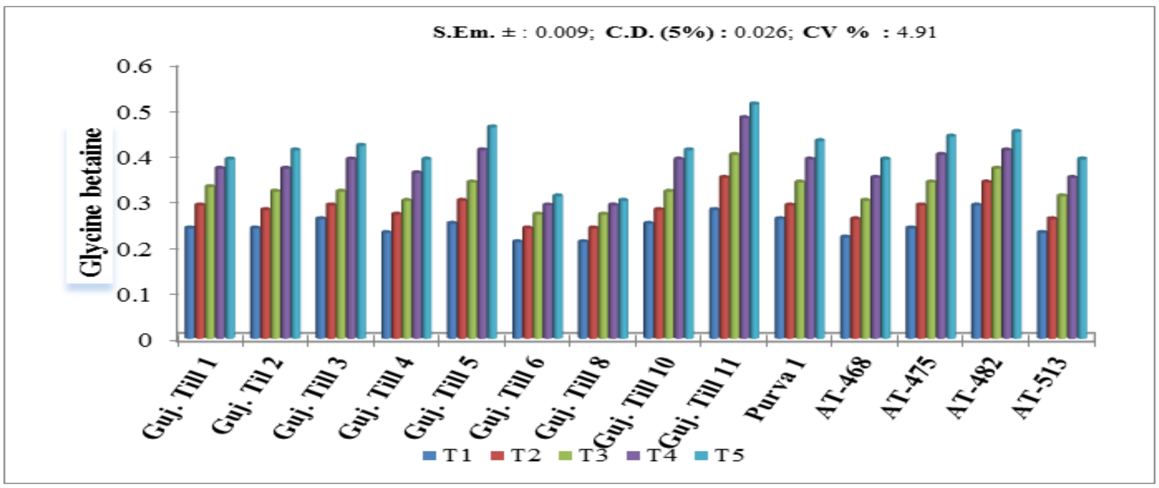

Fig. 4: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on Glycine betaine (mg.g^{-1} FW) activity at 7 DAS.

T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m;**T5** = Salinity 8 dS/m

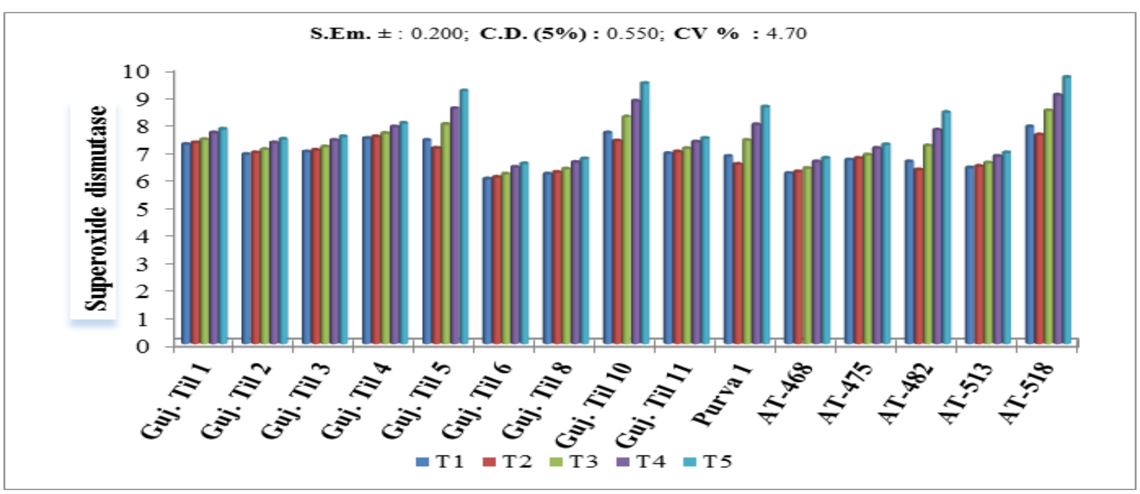

Fig. 5: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on superoxide dismutase activity at 7 DAS.

T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

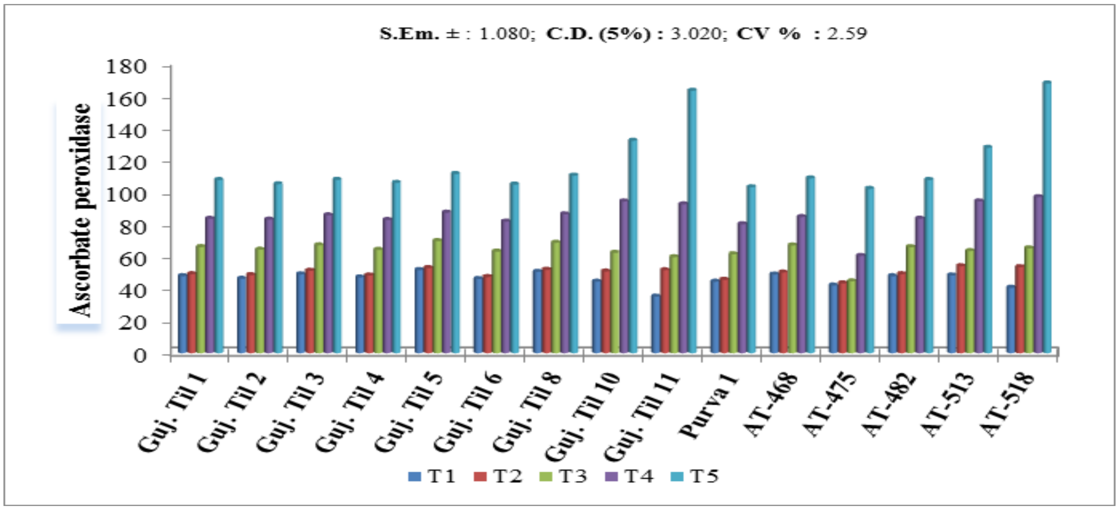

Fig. 6: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on ascorbate peroxidase activity (ΔO.D. min^{-1}. g^{-1} FW) at 7 DAS.
T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

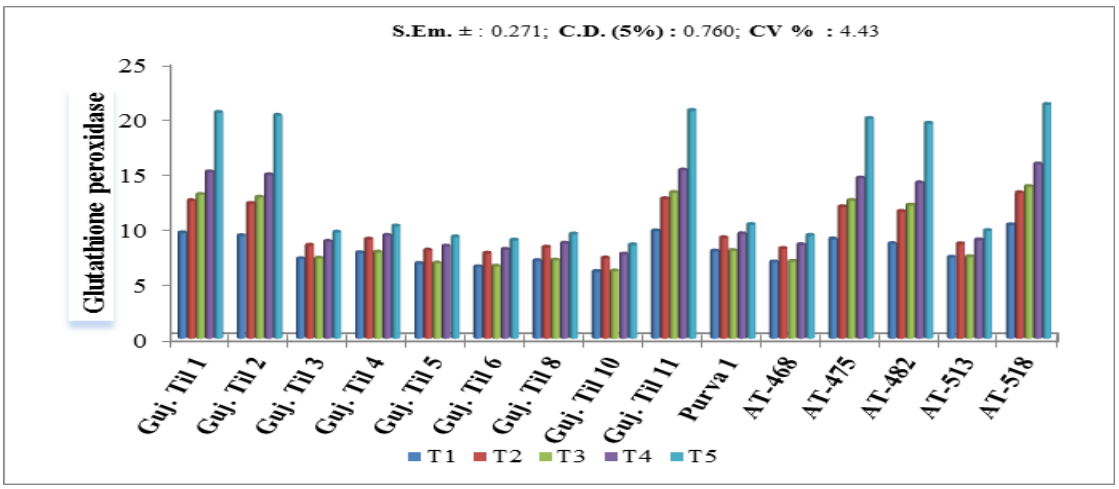

Fig. 7: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on glutathione peroxidase activity (ΔO.D. min^{-1}. g^{-1} FW) at 7 DAS.
T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m;**T5** = Salinity 8 dS/m

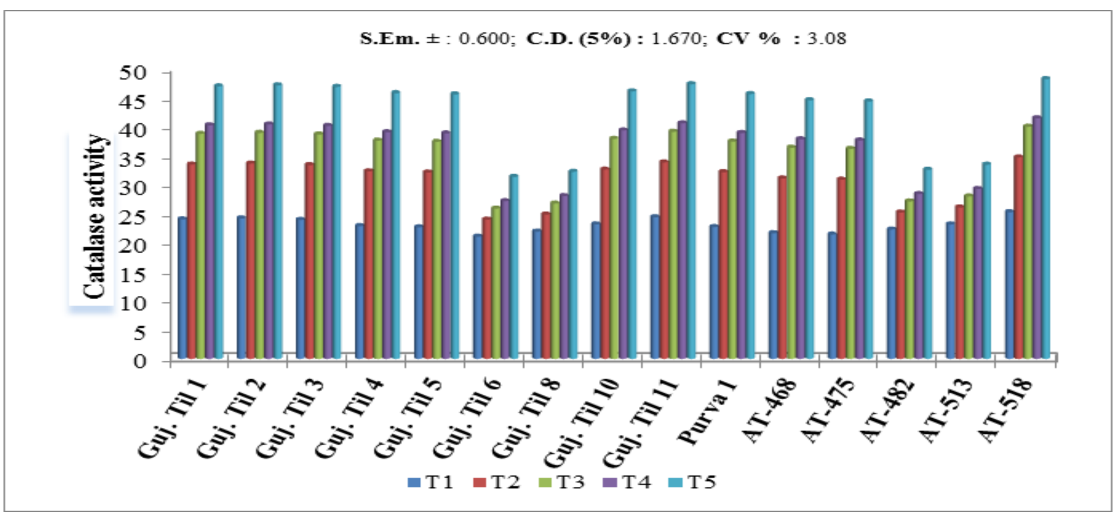

Fig. 8: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on catalase activity (ΔO.D. min^{-1}. g^{-1} FW)at 7 DAS.
T1 = Control 0 dS/m; **T2** = Salinity 2dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

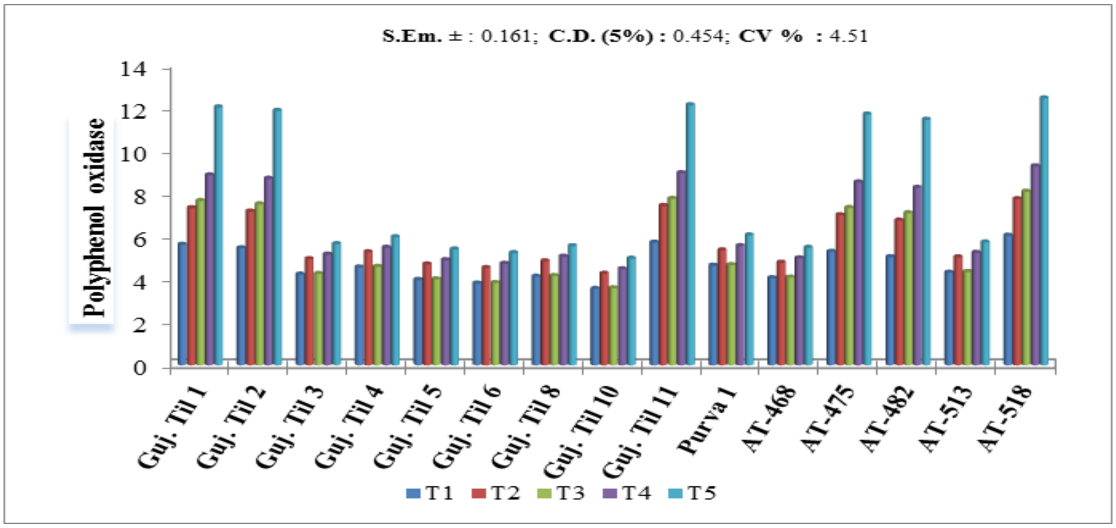

Fig. 9: Interaction effect between sesamum genotype (G) and different concentrations of salinity stress (T) on polyphenol oxidase activity (ΔO.D. min^{-1}. g^{-1} FW) at 7 DAS.
T1 = Control 0 dS/m; **T2** = Salinity 2 dS/m; **T3** = Salinity 4 dS/m; **T4** = Salinity 6 dS/m; **T5** = Salinity 8 dS/m

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