

PUBLICATIONS

OXIDATIVE STRESS RESPONSES AND ANTIOXIDANT DEFENCE AS INDICATORS OF DROUGHT TOLERANCE IN EXTRA-LONG STAPLE COTTON GENOTYPES

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Extra-long staple cotton (*Gossypium barbadense* L.) is a strategically important industrial crop in Central Asia, where drought reduces yields by 40–60% and constitutes the principal abiotic constraint on productivity. Under water deficit, an imbalance between reactive oxygen species (ROS) generation and antioxidant neutralisation leads to oxidative stress, manifesting as lipid peroxidation, pigment degradation, and cellular damage. Elucidating the biochemical basis of drought tolerance at early ontogenetic stages is essential for developing cost-effective germplasm screening approaches applicable in breeding programmes.

The antioxidant system responses of four *G. barbadense* L. genotypes - drought-tolerant cultivar Surkhan-103 and three breeding lines (L-157, L-474, L-1000) - were investigated under PEG-6000-induced osmotic stress (10%) at the cotyledon stage. Catalase (CAT), superoxide dismutase (SOD), and peroxidase (POD) activities, alongside malondialdehyde (MDA), hydrogen peroxide (H₂O₂), chlorophyll a and b, and carotenoid contents, were determined at 0, 6, 12, and 24 h post-stress initiation. Each treatment included three independent biological replicates; data were analysed by one-way ANOVA and LSD test ($p < 0.05$).

Significant genotype-dependent differences were identified. Cultivar Surkhan-103 demonstrated the most coordinated antioxidant response: synchronous peaks in CAT ($\times 1.4$) and SOD ($\times 1.7$) activities at 12 h ensured effective H₂O₂ neutralisation and limitation of membrane lipid peroxidation, with MDA returning to near-control levels by 24 h. Among breeding lines, L-157 showed the greatest drought tolerance, characterised by moderate MDA accumulation ($\times 1.5$), stable H₂O₂, coordinated enzyme activation, and compensatory increases in chlorophyll a ($\times 2.4$) and b ($\times 2.1$) contents. Line L-474 exhibited progressive 2.4-fold SOD suppression, 5.7-fold carotenoid depletion, and H₂O₂-mediated lipid peroxidation via the classical Fenton pathway. Line L-1000 showed the highest MDA accumulation ($\times 2.2$) concurrent with sub-control H₂O₂, suggesting involvement of H₂O₂-independent lipoxygenase-mediated lipid oxidation pathways. Pearson correlation analysis ($n = 16$) revealed a strong negative MDA–carotenoid relationship ($r = -0.71$; $p < 0.01$), confirming carotenoid content as a reliable non-enzymatic oxidative damage marker, and a moderate negative CAT–H₂O₂ correlation ($r = -0.55$; $p < 0.05$). The weak, non-significant MDA–H₂O₂ correlation ($r = +0.18$; $p > 0.05$) challenged the classical model of H₂O₂-dependent lipid peroxidation and highlighted mechanistically distinct oxidative pathways across genotypes.

The findings demonstrate that temporal coordination of antioxidant enzyme activation - rather than absolute activity levels — is the primary determinant of drought tolerance in *G. barbadense*. The genotypes ranked in decreasing tolerance order: Surkhan-103 > L-157 > L-474 $\approx$ L-1000. Line L-157 represents promising breeding material for drought-tolerance programmes. Cotyledon-stage biochemical screening under controlled conditions provides a rapid, resource-efficient tool for early differentiation of germplasm without field sowing, offering substantial practical advantages for large-scale selection in natural compound biotechnology and crop improvement research.