
Abstract

The response of Peganum harmala L. seedlings subjected to salinity was investigated through the observation of germination at the 4th, 6th and 8th days under normal and two salinity levels (151 and 200 mM NaCl). Genetic response of P. harmala was examined by quantitative estimation and electrophoretic separation of catalase and salt-soluble proteins. The gene expression of catalase and osmotin were investigated using RT-PCR. Final percentage of germination at the eighth day of germination was reduced from 80% in the control to 70% and 30% under the concentration of 151 and 200 mM.

The catalase activity and protein content increased as the salinity increased compared to control seedlings. The electrophoretic separation of catalase and salt-soluble proteins exhibited stress-related isozymes and protein bands. RT-PCR of cat\(^1\), cat\(^2-3\) and cat\(^3\) and osmotin genes exhibited up-regulation and down-regulation of genes subsequent to salinity. The reduced germination percentage of salt stressed seedlings was attributed to oxidative damage and osmotic imbalance. The increased catalase activity and protein content were concluded as protective response of P. harmala seedlings to salinity induced oxidative stress and osmoregulation. The additional isozyme bands in the salt-stressed seedlings indicated modulation of CAT gene expression in response to elevated H\(_2\)O\(_2\) subsequent to salinity. The stress specific gene expression was interpreted as molecular mechanism by which plants can tolerate salinity stress. The up-regulation of cat\(^2-3\) gene in relation to stress suggests it crucial role in salinity tolerance in P. harmala and further studies are needed for its sequence identification.