Karam, M.A., Abd-Elgawad, M.E., Ali, R.M.. 2016. Differential gene expression of salt-stressed *Peganum harmala* L. Journal of Genetic Engineering and Biotechnology, 14: 319-326

Abstract

The response of *Peganum harmala* L. seedlings subjected to salinity was investigated through the observation of germination at the ٤th, ٦th and ٨th days under normal and two salinity levels (١٥٠ and ٢٠٠ 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 ٨٥% in the control to ٧٠ and ٣٠% under the concentration of ١٥٠ and ٢٠٠ 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 cat١, cat٢-٣ and cat٣ 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 $H_٢O_٢$ subsequent to salinity. The stress specific gene expression was interpreted as molecular mechanism by which plants can tolerate salinity stress. The up-regulation of cat٢-٣ gene in relation to stress suggests it crucial role in salinity tolerance in *P. harmala* and further studies are needed for its sequence identification.