

Expression Analysis of Nickel Responsive Genes in Sunflower Under Stress Conditions

Mahmood-ur-Rahman

Department of Bioinformatics and Biotechnology, Faculty of Life Sciences, GC University, Faisalabad, Pakistan
Corresponding Author E-mail: mahmoodansari@gcuf.edu.pk

Abstract

Heavy metal contaminated soils reduce the production and quality of crop plants. This situation is getting worsened with increasing population and food demand across the world. Many countries including Pakistan face severe environmental problems in most of the agricultural land areas. These severe environmental problems/heavy metal contaminations especially nickel (Ni) adversely affect the sunflower by reducing the yield of the plant substantially. The counterbalancing toxicity due to Ni requires complex mechanisms at molecular, biochemical, physiological, cellular, tissue, and whole plant level, which might manifest in terms of improved crop productivity. Different plant varieties possess variable tolerance to the stress conditions. One of the major adaptations to tolerate the Ni toxicity is enhanced production of anti-oxidant enzymes and the elevated expression of Ni responsive genes in plants. In this study, the expression of metal transporter genes was studied under Ni stress in sunflower. The sunflower plants were grown in pots having 10 Kg of soil each. There were four treatments (0, 50, 100, 200ppm) of Ni doses where 0 is control having no Ni. The experiment was conducted in triplicate using CRD. Total RNA was isolated from leaves at 28 days old plants. First strand cDNA was synthesized and expression of NRAMP1 and NRAMP3 genes was studied using Real Time PCR. The results indicated the up-regulation of NRAMP1 and NRAMP3 genes. This study may help to evaluate the role of NRAMP transporter genes in Ni toxicity tolerance in sunflower.

Key Words: *Expression analysis, Real Time PCR, Nickel, Heavy metal stress, NRAMP genes*