Genome-Wide Expression Profiling of Cicer arietinum Heavy Metal Toxicity

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Abstract : Chickpea (Cicer arietinum L.) is an annual, self-pollinating, diploid ($2n = 2x = 16$) pulse crop that ranks second in world legume production after common bean (Phaseolus vulgaris). ICC 4958 flowers approximately 39 days after sowing under peninsular Indian conditions and the crop matures in less than 90 days in rained environments. The estimated collective yield losses due to abiotic stresses (6.4 million t) have been significantly higher than for biotic stresses (4.8 million t). Most legumes are known to be salt sensitive, and therefore, it is becoming increasingly important to produce cultivars tolerant to high-salinity in addition to other abiotic and biotic stresses for sustainable chickpea production. Our aim was to identify the genes that are involved in the defence mechanism against heavy metal toxicity in chickpea and establish the biological network of heavy metal toxicity in chickpea. ICC4958 variety of chick pea was taken and grown in normal condition and 150µM concentration of different heavy metal salt like $CdCl_2$, $K_2Cr_2O_7$, $NaAsO_2$. At 15th day leave samples were collected and stored in RNA Later solution microarray was performed for checking out differential gene expression pattern. Our studies revealed that 111 common genes that involved in defense mechanism were up regulated and 41 genes were commonly down regulated during treatment of 150µM concentration of $CdCl_2$, $K_2Cr_2O_7$, and $NaAsO_2$. Biological network study shows that the genes which are differentially expressed are highly connected and having high betweenness and centrality.

Keywords : abiotic stress, biological network, chickpea, microarray