

Deciphering the role of stress responsive genes in chickpea (*Cicer arietinum* L.)

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Abstract

Chickpea, an important legume crop is seriously challenged by several abiotic and biotic stresses. Understanding the mechanisms that regulate the expression of stress-related genes is a fundamental issue and is necessary for the genetic improvement of chickpea. In separate studies based on *in silico* expression analysis of Illumina GA and Sanger sequencing data generated from drought and *Helicoverpa* challenged tissues of contrasting parental genotypes provided differentially expressed stress-responsive genes that are involved in stress signaling pathways. This work presents deciphering the role of *in silico* identified stress-responsive genes for conferring resistance to drought stress and *Helicoverpa* infestation. A set of 111 and 55 candidate genes for insect resistance and drought tolerance, respectively, were targeted for experimental validation using quantitative real time-PCR (qRT-PCR). Total RNA of root (drought) and leaf (*Helicoverpa*) tissues from stressed and unstressed plants were analysed in the context of tolerant/sensitive genotypes. qRT-PCR analysis confirmed *in silico* predicted expression analysis for a total of 24 genes. This set of genes includes 15 known stress-responsive genes and 9 novel unreported genes. In terms of cross-talking between genes under these two stresses three genes encoding for mannitol dehydrogenase, NADPH quinone oxidoreductase and cytochrome P-450 showed differential expression. Emerging evidence suggests that stress signaling pathways regulated by ABA pathway, Oxidative phosphorylation pathway as well as ROS signaling pathways play key roles in the crosstalk between abiotic and biotic stress signaling. The identified genes could be used to improve resistance to important constraints affecting chickpea production.