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**A comparative proteomic analysis of an *Arabidopsis thaliana* mutant of the COP9 Signalosome (CSN), to investigate gene specific functions**

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The CSN is a conserved protein complex in higher eukaryotes. In plants the CSN is implicated in regulating a range of developmental pathways and also in hormone and light signalling. Underlying mechanisms of action of the complex is not fully understood and is currently the scope of major research worldwide. Studies on *Arabidopsis* mutant lines of various CSN subunits have disclosed some of the hidden secrets. A bioinformatics study was undertaken to analyse the differential expression of proteins between the wild type (WT) *Arabidopsis* plants and a *csn5* mutant line, with the objective of gaining insights into the influence of the CSN complex or of its sub unit 5 (CSN5) on the plant at the proteome level. A set of gel images previously generated for 200µg cytosolic proteins extracted from shoots (pooled) of the WT and *csn5* mutant seedlings grown under controlled environmental conditions, and separated by two dimensional gel electrophoresis (2-DE) were used in the analysis. First, the spot level deviations in the 2-D gel images were identified mainly with the help of Melanie software tool, and then the identities of those corresponding proteins were determined by Mascot and UniProt data base search using already available Peptide Mass Fingerprints (PMFs) previously generated from the gels. Three categories of protein spot differences were found in the 2-D images: There were 11 protein spots that appeared only in the 2-D gels of the WT, 07 spots that appeared in the 2-D gels of the *csn5* mutant line gels and 10 protein spots showing intensity-wise differences between the WT and the mutant. Of these 28 proteins, identities of 10 spots were confirmed. These include Pathogenesis Related protein 5 (PR5), Beta 1,3- glucanase 2 (PR2), RubisCO Activase (RCA) and Catalase 2 which were highly expressed in the mutant compared to the WT. These proteins, except RCA, are known to be involved in plant defense mechanisms including the systemic acquired resistance (SAR) and hyperactive response (HR) and in responses to reactive oxygen species (ROS). The elevated expressions of these proteins could be due to the mutation in the CSN5 subunit. This indicates that either the CSN5 subunit itself or the CSN complex probably take part in the signal transduction pathways linked with biotic and abiotic stress responses of the plant.

**Keywords:** COP9 signalosome mutant, 2-DE, bioinformatics, stress responses