

## IDENTIFICATION OF *CIS*-ELEMENTS AND TRANSACTING FACTORS INVOLVED IN THE ABIOTIC STRESS RESPONSES OF PLANTS

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Many stress situations limit plant growth resulting in crop production difficulties. Population growth, limited availability and over-utilization of arable land, and intolerant crop species have resulted in tremendous strain being placed on agriculturalists to produce enough to sustain the worlds population. An understanding of the principles involved in plant resistance to environmental stress will enable scientists to harness these mechanisms to create stress-tolerant crop species, thus increasing crop production, and enabling the farming of previously unproductive land.

This research project uses computational and bioinformatics techniques to explore the promoter regions of genes, encoding proteins that are up-regulated in response to specific abiotic stresses, with the aim of identifying common patterns, which can then be used to identify novel genes involved in specific plant stress responses. Known genes encoding for proteins reported to be up-regulated in response to drought, low temperature, and salinity plant stresses were identified, and a postgresQL database created to store relevant information pertaining to these genes and the proteins encoded by them. The genomic DNA was obtained where possible, and the upstream region identified using the NNPP promoter prediction software package.

Research objectives include: promoter searching using the TRES and TESS software tools to identify known and possible novel *cis*-elements within these genes; identification of significant patterns in the *cis*-elements with regards to order, distance and presence of specific *cis*-elements; and identification of possible novel genes that may be involved in drought, low temperature and salinity plant stress response by developing a consensus nucleotide sequence and doing a sequence homology search against the available plant genomes.

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