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## Identification of putative cis-regulatory elements of ADP3 protease gene expressed upon thermal-stress in *Arabidopsis thaliana* and its orthologues

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In ATP-dependent protease-3 (ADP3) multifunctional enzyme involved in the proteolysis of complex, abnormal and unstable protein molecules to their units present in mitochondrial matrix. Its expression is increased upon thermal stress, suggesting that it may play a role in the heat shock response. Although, it is up-regulated upon heat stress, the underlying molecular mechanism controlling its expression is still largely unknown. Current research work intends to discover the gene-regulatory-network and molecular base controlling the expression of ADP3 by unraveling the evolutionarily Conserved Non-coding Sequences (CNSs) in the 1000 bp promoter region by analyzing upstream promoter sequences (counted from the translation initiation codon; ATG). Comparative genome-wide bioinformatics analysis performed for identification of evolutionarily preserved regulatory sequences, which revealed three highly conserved upstream non-coding sequences. Consensus sequences from conserved sequence logo showed the position of CNS1 at 371 bp to 390 bp, CNS2 at 476 bp to 486 bp and CNS3 at 654 bp to 674 bp of *Arabidopsis thaliana* promoter counted from the ATG. Thus identified putative cis-regulatory elements in the promoter region of ADP3 gene, are expected to allow physical binding of upstream regulatory proteins which are also yet to be known. This novel putative cis-regulatory might have role in controlling the thermo-tolerance or thermo-memory response upon heat stress in *Arabidopsis thaliana* and in the plant species harboring the orthologues of ADP3 protease.

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