Information system of regulatory elements

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The plant response to biotic and abiotic stresses has been the target for further research of strategic interest. The study of the transcriptome of a particular plant species, associated with these stresses, is a powerful tool in the new sequencing technologies that enable mass scanning of the genome at a speed, accuracy and unprecedented scale generating a huge accumulation of information. These are analyzed as a whole to assist the interpretation of biological data and identify potential candidate genes associated with stress studied. It is therefore essential to carefully analyze this information in order to a closer study of candidate genes to be identified. In this sense, knowledge of which cis-elements are essential for transcriptional regulation of the gene, controlling many biological processes and responses to stress, can be used to supplement the identification of candidate genes responsive to certain conditions. Therefore, the aim of this study was to develop a computer system capable of identifying the presence of known cis-elements, modeled on the family of genes ERDs (Early Responsive to Dehydration) expressed in Arabidopsis thaliana during drought stress. This computer system can also be used for other crops such as beans, rice, wheat, and so on.