Analysis of the Promoter Region of the Gene Encoding Sodium/Hydrogen Exchanger 1 Protein

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Abstract

Understudying gene regulatory network in different plants is essential to engineer plants against biotic/abiotic stress. Here, we analyzed 5'UTR to determine which cis-acting elements present at the promoter of canola NHX1 gene, a salt responsive gene. Arabidopsis NHX1 gene sequence was searched in canola (Brassica napus) genome. The putative sequence of NHX1 gene was extracted and analyzed. Many elements were identified that some of them discussed here.

Keywords: Brassica; cis-acting element; Gene regulatory network; Transcription factor

Introduction

Soil salinization is one of the main growing problems in the agriculture section around the world. Presence of sodium chloride (NaCl) in irrigation water leads to accumulation of ions, such as Na+ and Cl-, in soil. Soils with high level of salinization impair the plant growth by limiting access to water for the plant, osmotic stress. In addition, Na+ and Cl- ions taken up in large amount by root interrupts metabolic processes and declines photosynthetic efficiency [1]. In response to such environmental stresses, plants have evolved complex morphological, physiological and biochemical mechanisms that are regulated by gene regulatory networks. Transcription factors are major player in the network controlling a set of gene expression through binding some specific regulatory regions in the genome [2]. One of the main genes are expressed in response to the high level of Na+ and Cl- ions in the cell is the NHX1 gene encoding Na+ and Cl- exchanger 1 protein. This membranous protein sequestrates excessive Na+ to cell is the NHX1 gene encoding Na+ and Cl- exchanger 1 protein. This membranous protein sequestrates excessive Na+ to

Results and Discussion

In this study, the NHX1 gene from Arabidopsis (id: AT5G27150.1) was blasted against Brassica napus genome (https://www.ncbi.nlm.nih.gov/genome/?term=brassica%20napus). Canola putative NHX1 gene sequence was extracted from the genome. Using this sequence, the promoter region was predicted by PlantProm (available at http://mendel.cs.rhul.ac.uk/ and http://www.softberry.com/) and analyzed for presence of cis-acting regulatory elements by PlantCARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/).

Our results are represented in Figure 1. Blast results showed many hits. The first hit with high score was selected and all genomic sequence of NHX1 gene extracted from Brassica napus genome. NHX1 gene located between 2795854 bp and 2799176 bp at chromosome A6 (NC_027765.2).

Conclusions

The promoter region was predicted and 500 bp upstream from transcription start site scanned. This region of NHX1 gene showed many cis-acting elements. Three of these important cis-acting elements are described below:

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factor (CBF), also known as the Nuclear Factor Y (NF-Y) or Hem Activator Protein (HAP). This element has been found at promoter of many genes, including genes regulating flowering in *Arabidopsis* [3], photosynthetic genes [4], genes encoding heat shock proteins [5] and abiotic stress responsive genes [6].

(b) TC-rich repeats: TC-rich repeat is involved in defense and stress responsiveness. It has found at promoter of osa-MIR396c salt responsive transcript [7], the transcription factor gene TaMYB33 responsive to salt, drought and abscisic acid [8] and copper-containing amine oxidase genes [9].

c) WUN motifs: The genes harboring this *cis*-acting element act as wound responsive gene [10]. In addition, studies have demonstrated that WUN-motif is also present at the promoter of the genes responding to drought stress [11], TMV-infection [12], and salinity [13].

References