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Short Communication

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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 vacuole to detoxify the cell from harmful effects [1]. Here, we analyzed 5' UTR of canola *NHX1* gene through computational based methods. To best our knowledge, there is limit reports about the regulatory regions of *NHX1* gene in canola.

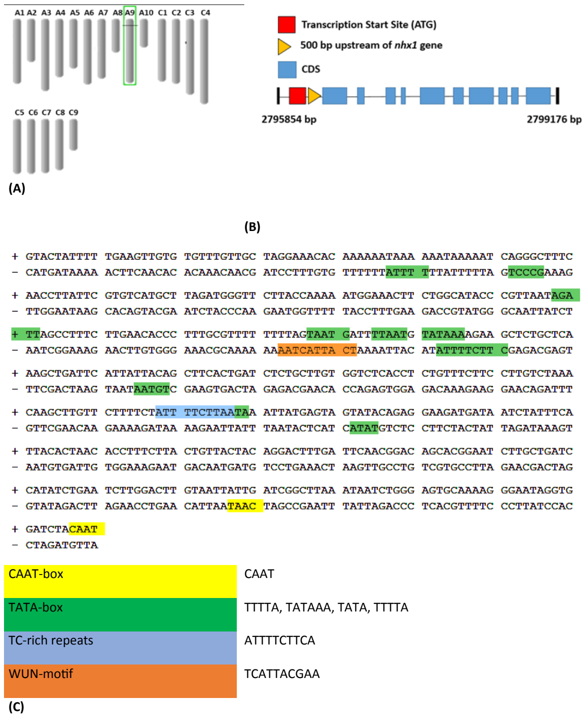
Results and Discussion

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 hints. 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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+ GTACTATTTT TGAAGTTGTG TGTTTGTTGC TAGGAAACAC AAAAAATAAA AAATAAAAAT CAGGGCTTTC
- CATGATAAAA ACTTCAACAC ACAAACAACG ATCCTTTGTG TTTTTTATTT TTTATTTTTA GTCCCGAAAG

+ AACCTTATTC GTGTCATGCT TAGATGGGTT CTTACCAAAA ATGGAAACTT CTGGCATACC CGTTAATAGA
- TTGGAATAAG CACAGTACGA ATCTACCCAA GAATGGTTTT TACCTTTGAA GACCGTATGG GCAATTATCT

+ TTAGCCTTTC TTGAACACCC TTTGCGTTTT TTTTAGTAAT GATTTTAATG TATAAAAGAA GCTCTGCTCA
- AATCGGAAAG AACTTGTGGG AAACGCAAAA AAAATCATTA CTAAAATTAC ATATTTTCTT CGAGACGAGT

+ AAGCTGATTC ATTATTACAG CTTCACTGAT CTCTGCTTGT GGTCTCACCT CTGTTTCTTC CTTGTCTAAA
- TTCGACTAAG TAATAATGTC GAAGTGACTA GAGACGAACA CCAGAGTGGA GACAAAGAAG GAACAGATTT

+ CAAGCTTGTT CTTTTCTATT TTCTTAATAA ATTATGAGTA GTATACAGAG GAAGATGATA ATCTATTTCA
- GTTCGAACAA GAAAAGATAA AAGAATTATT TAATACTCAT CATATGTCTC CTTCTACTAT TAGATAAAGT

+ TTACACTAAC ACCTTTCTTA CTGTTACTAC AGGACTTTGA TTCAACGGAC AGCACGGAAT CTTGCTGATC
- AATGTGATTG TGGAAAGAAT GACAATGATG TCCTGAAACT AAGTTGCCTG TCGTGCCTTA GAACGACTAG

+ CATATCTGAA TCTTGGACTT GTAATTATTG ATCGGCTTAA ATAATCTGGG AGTGCAAAAG GGAATAGGTG
- GTATAGACTT AGAACCTGAA CATTAATAAC TAGCCGAATT TATTAGACCC TCACGTTTTC CCTTATCCAC

+ GATCTACAAT
- CTAGATGTTA
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CAAT-box	CAAT
TATA-box	TTTTA, TATAA, TATA, TTTTA
TC-rich repeats	ATTTTCTTCA
WUN-motif	TCATTACGAA

Figure 1: (A) Location of the *NHX1* gene in canola chromosomes, (B) Gene structure of *NHX1* gene, (C) Some of important cis-acting element found at 500 bp upstream of canola *NHX1* gene.

(a) CAAT box: Common *cis*-acting elements with sequence of GG(T/C) CAATCT and can be found about 75 bp position regarding to transcription start site, acting as binding site for the CCAAT-binding

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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 abs*cis*ic 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].

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