PHYLOGENETIC STUDIES ON PLANT COLD SHOCK DOMAIN PROTEINS

[1]ASHUTOSH MANI, [2]DWIJENDRA K. GUPTA

[1]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad-211004, India.
[2]Center of Bioinformatics, Institute of Interdisciplinary Studies, University of Allahabad, Allahabad 211002, India.
E-mail: amani@mnnit.ac.in

Abstract- Cold shock proteins are nucleic acid-binding proteins. They are well conserved in bacteria, animals as well as plants. Prokaryotic CSPs possess a single cold shock domain while animal CSPs are flanked by N- and C-terminal domains. Eukaryotic CSPs are commonly named Y-box proteins. Interestingly, the plants CSPs contain a C-terminal domain in addition to their N-terminal CSD. The CSPs have been reported to have important role in development and stress adaptation in various plant species. Main objective of this study was to perform molecular phylogeny studies on different plant CSPs..

Keywords- CSP, N-terminal, C-terminal. , Phylogeny

I. INTRODUCTION

The comprehensive study of low temperature stress has been done in Escherichia coli and well characterized by the accumulation of cold shock protein. Bacterial CSPs are small proteins that possess a single nucleic acid-binding domain, which is known as the cold shock domain (CSD).

This domain is proposed to be an ancient molecule that was present even before the origin of single-cell life and is one of the most evolutionarily conserved nucleic acid-binding domains within prokaryotes and eukaryotes.

A distinctive class of CSD proteins has been discovered in plants. Plant CSD homologs typically contain two distinct nucleic acid-binding modules (a single N-terminal CSD and variable quantities of C-terminal retroviral-like CCHC zinc fingers), which are interspersed by glycine-rich regions, with a few exceptions (Arabidopsis contains four unique types of CSD proteins and displays differential regulation activity in response to low-temperature stress.

In Arabidopsis thaliana as a model plant, its endogenous CSPs are demonstrated to be important during plant growth and development.

II. METHODOLOGY

Multiple sequence alignment (MSA) and phylogeny:
Amino acid sequences of CSPs from seven plant species; A. thaliana CSD protein 3 (gi|330251603|gb|AEC06697.1|), Eutrema salsugineum CSD protein 3 (gi| 294470716|gb|ADE80750.1), Medicago truncatula Major cold-shock protein (gi|357518027|ref|XP_003629302.1|), Cucumis melo cold-shock DNA-binding family protein (gi|307136096|gb|ADN33944.1|), Ricinus communis CSP putative (gi|255545420|ref|XP_002513770.1|), Triticum aestivum CSP-1 (gi|21322752|dbj|BAB78536.2|), and Oryza sativa Japonica CSD protein 2-like protein (gi| 57900030|dbj| BAD88072.1|) were retrieved from NCBI Genbank (available at ncbi.nlm.nih.gov/genbank).

The retrieved sequences were analyzed by clustalW MSA tool. The MEGA 5.0 software was used to construct phylogenetic tree of above sequences using Close-Neighbor-Interchange algorithm in MEGA 5.0 software.

Sequence analysis:
The MSA of seven plants CSPs resulted into 372 aligned positions. The positions from 14 to 75 were found to be conserved and belong to CSD. Interspersed glycine-rich regions were found prevalently restricted to the C-terminal domain of the proteins.

The CSPs from seven plant species were found to have four signature, motifs consisting of residues K/NGF/YG/SFI, E/ DLFVHQS/T, S/FD/EGFYRS/TL, and GK/RT/SAI/VE/ DVT/I. All these signature motifs belong mostly to the random coil as well as β strands

Phylogenetic studies:
A phylogenetic tree was constructed using MEGA 5.0 for aligned amino acid sequences of the A. thaliana and the known plant CSD proteins.

III. RESULTS

Sequence analysis:
The MSA of seven plants CSPs were aligned . The positions from 14 to 75 were found to be conserved and belong to CSD.

Intervening glycine-rich regions were found prevalently restricted to the C-terminal domain of the proteins.

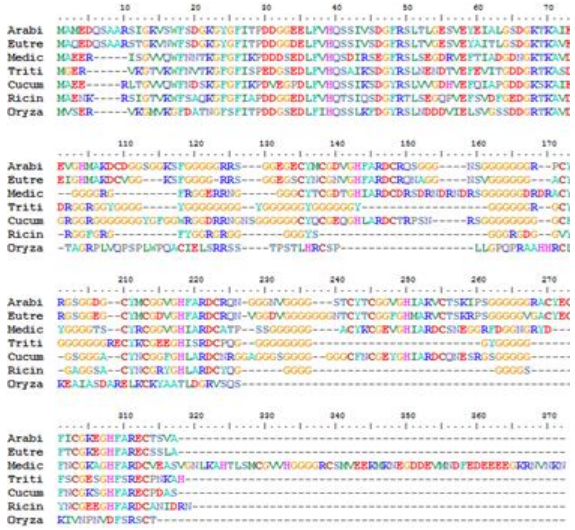


Figure 1: M of plant cold shock proteins

Phylogenetic analysis:
A phylogenetic tree was constructed using MEGA 5.0 for aligned amino acid sequences of the A. thaliana and the known plant CSD proteins. The evolutionary history was inferred using the Maximum Parsimony method.

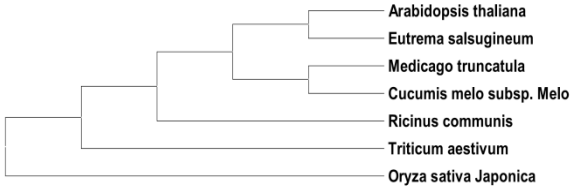


Figure 2: Phylogenetic tree of plant cold shock proteins

CONCLUSION

These results may accelerate the phylogenetic studies on CSPs and help in increasing focus on the sequences involved in different types of nucleic acids binding in plants as well as other organisms.

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