PROTEIN DOMAIN ARCHITECTURE OF CYANOBACTERIAL SODIUM-HYDROGEN EXCHANGERS CONTAINING THE UNIVERSAL STRESS PROTEIN DOMAIN

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Abstract: Our previous analysis of the taxonomic distribution of proteins that are annotated to contain domains for universal stress protein (Usp) and sodium/hydrogen exchanger revealed overrepresentation of cyanobacterial proteins. Proteins with the Usp domain are known to provide cells with the ability to respond to environmental stresses such as nutrient starvation, drought, high salinity, extreme temperatures, and exposure to toxic chemical. Na+/H+ exchangers are transmembrane proteins that eject intracellular hydrogen ion in exchange for external sodium ion as an effective means of eliminating excess acid from actively metabolizing cells. We postulate that the Usp domain provides specificity for stress response to the Na+/H+ exchangers in cyanobacteria. Our goal is to identify and understand the biological pathways controlled and coordinated by interaction between the Na+/H+ exchanger (NHX) and the Usp domains. Our objective in this study was to determine the domain architecture of the cyanobacterial Na+/H+ exchangers that contain the Usp domain. We developed a computational pipeline to extract proteins that are annotated with protein domains for Na+/H exchangers (Pfam:PF00999) and Universal Stress Protein (Pfam:PF00582) for the Cyanobacteria (NCBI Taxon ID: 1117) from the iProClass protein classification database. A total of 35 proteins from 22 cyanobacteria genomes (10 genera) were retrieved and analyzed for domain architecture. The length of the sequences ranged from 536aa to 749aa. The count of protein per genome ranged from one to four. The genomes of Anabena viriabilis (strain ATCC 2941/PCC7927) and Nodularia spumigena CCY 9414 had the maximum number of protein contain the two domains. All the protein sequences analyzed contained a single NHX domain which starts within the first 54 amino acid positions. There were sets of sequences in which the start and end positions of the NHX or Usp domain were conserved. A total of 22 sequences had one Usp domain while 13 sequences had two Usp domains arranged in tandem. Our observations provide guidance for additional objectives namely, (i) to determine distinctive features in the sequences, and (ii) compare the expression levels in response to stress conditions of single Usp and double Usp domain containing cyanobacterial sodium hydrogen exchangers.

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