Genetic diversity, expression and characteristics of protease genes of haloalkaliphilic bacteria from the saline habitats

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Over the years, haloalkaliphilic bacteria from the saline habitats of coastal gujarat, India have been investigated with the focus on their distribution, diversity and enzymatic characteristics. These microorganisms widely produce extracellular proteases. The proteases share certain unique characteristics; such as salt-dependent temperature profiling, resistance against chemical denaturation and ability to function under multitudes of extreme conditions. Catalytic efficiency of the proteases is enhanced at high temperatures in the presence of salt. The bacteria widely produce extracellular proteases with the diversity of their genes and expression. By designing 12 different specific primers and using gradient PCR, proteases from different haloalkaliphilic bacteria and actinomycetes were amplified. The study reflected diversity of the protease genes with respect to length (~ 400 bp to ~ 2000 bp), amino acids and other characteristics. The ORF of a protease gene on the blastp analysis revealed highest homology with a known serine protease of *Bacillus megaterium* strain corresponding to the peptidase domain of the S8 and S53 families. The halostablity of the protease was identified with the greater negatively charged amino acids and low GRAVY index. Similarly, a highly thermostable alkaline serine protease of nocardiopsis alba tata-5 was cloned using TA cloning and expressed into *E. Coli* (BL21), a mesophilic expression. The MALDI-TOF mass spectroscopic analysis revealed insight into the peptide masses. Further, the 3-D structures of the enzyme were created by SWISS MODEL and the stability of the protease structure was confirmed by the analysis of the ramachandran plot. On accounts of the metagenomics, protocols for the extraction of quality environmental genomic DNA from different saline habitats were established. The metagenomically derived protease genes were cloned, expressed and characterized using degenerative primers that revealed sequence and function-based diversity.

Profiling, cloning and expression of protease genes facilitated the elucidation of the structural and functional attributes of the enzymes.

Biography

Satya P Singh, currently working as UGC-BSR faculty at the department of biosciences, Saurashtra University, Rajkot, India, Worked as professor & amp; Head in the same department from 2003-2020. He was also coordinator of the UGC- CAS program. Having a master's in microbiology from the G. B. Pant University of Agriculture and amp; Technology, Pantnagar, India, He carried out his doctoral research at the Griffith University, Brisbane, Australia. He worked at the National Food Research Institute, Tsukuba, Japan as visiting scientist and as visiting professor at Vangon University, Myanmar. He has published 104 research papers, 24 book chapters and 1 edited book, with H-Index and citations of 31 and around 3000.

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