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COMPARATIVE AND COMPUTATIONAL ANALYSIS OF SOLIBACILLUS KALAMII UV DAMAGE REPAIR PROTEINS

Abstract

Solibacillus kalamii is a gram-positive, rod-shaped, and aerobic bacterium that was found on the International Space station by isolating it from high efficiency particulate arrestance filter system. These spores forming bacterium can withstand high radiation. Not only that, but they are also known to contain distinct UV damage repair proteins (UVDR proteins) which could carry a lot of potential in various biotechnological applications. The main objective of this experiment was to analyze the structural and functional properties of all S. kalamii UVDR proteins that specifically repair damaged DNA sequences. BLASTp was performed to retrieve all DNA UVDR proteins sequences, followed by their physiochemical analysis, subcellular localization, functional annotation, pathway analysis and comparative analysis. Results indicated that a total of five DNA UVDR proteins (UvrA, UvrB, UvrC, UvrX and UvsE) were identified in S. kalamii, all of which are located within the bacterial cytoplasm. UvrA, UvrB and UvrC coordinate their activity via the UvrABC excinuclease system. UvrX appears to prevent transcription of damaged nucleotide sequences in the DNA rather than repair them, whereas UvsE removes both UV and Non-UV induced DNA adducts. It could be hypothesized that UvrA, UvrB and UvrC directly repair damaged DNA sequences, while UvrX and UvsE play a more indirect role by blocking the effects of mutagenesis and eliminating radiation induced DNA adducts respectively. Further analysis via the use of simulation tools like RITRACKS and practical analysis of all identified UVDR proteins is recommended for future studies.

Keywords: Solibacillus kalamii, UVDR, UvrA, UvrB, UvrC, UvrX, UvsE, DinB, motifs, Nucleotide excision repair/NER, domains, excinuclease, adducts, mutagenesis.