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Analysis of the genome and proteome composition of Bdellovibrio bacteriovorus: indication for recent prey-derived horizontal gene transfer

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Abstract

The genome/proteome composition of Bdellovibrio bacteriovorus, the predatory microorganism that preys on other Gram-negative bacteria, has been analyzed. The study elucidates that translational selection plays a major role in genome compositional variation with higher intensity compared to other deltaproteobacteria. Other sources of variations having relatively minor contributions are local GC-bias, horizontal gene transfer and strand-specific mutational bias. The study identifies a group of AT-rich genes with distinct codon composition that is presumably acquired by Bdellovibrio recently from Gram-negative prey-bacteria other than deltaproteobacteria. The proteome composition of this species is influenced by various physico-chemical factors, viz, alcoholicity, residue-charge, aromaticity and hydropathy. Cell-wall-surface-anchor-family (CSAPs) and transporter proteins with distinct amino acid composition and specific secondary-structure also contribute notably to proteome compositional variation. CSAPs, which are low molecular-weight, outer-membrane proteins with highly disordered secondary-structure, have preference toward polar-uncharged residues and cysteine that presumably help in prey-predator interaction by providing particular bonds of attachment.

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