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Importance of DNA-Methylation in Entomopathogenic Bacteria with similar lifestyle

Abstract:

DNA methylation plays various roles in bacteria and can contribute to bacterial interactions with their hosts, through diverse mechanisms such as genome maintenance or epigenetic regulations. The bacteria *Xenorhabdus* and *Photorhabdus* are pathogenic for insects and are found in the gut of soil nematodes with whom they are symbiotically associated. The roles of a conserved DNA-Methyltransferase (MTase) were investigated in these bacteria using deregulated strains and methylomic approaches.

Great diversity was observed in the distribution of MTase-encoding genes, and a single MTase (Dam, for DNA-adenine MTase) was identified in all the species of these two genera. Methylome analysis showed that the GATC motifs recognized by Dam reached a high methylation rate (>99%) in the studied strains. Enrichment of unmethylated motifs in promoter regions was observed and may reveal mechanisms of epigenetic regulation. The Dam overexpression was associated with a reduced swimming motility, caused by a downregulation of flagellar genes, in both *Xenorhabdus* and *Photorhabdus*. In contrast, alteration of various major phenotypes such as hemolysis or virulence depended on the species studied.

Our work revealed the diverse roles played by a conserved DNA MTase during the life cycle of entomopathogenic bacteria.