Whole genome DNA methylation (Methylome), transcriptomic and phenotypic analysis revealed involvement of Dam DNA methyltransferase in gene regulation in Photorhabdus luminescens

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Titre de la présentation :

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DNA Methylation, Gene regulation, Pathogeny, Dam, Phenotypic heterogeneity

Résumé (250 mots max.) :

Dam DNA methylation is an epigenetic mechanism as it can regulate genes expression by reducing the affinity of transcriptional regulators for their binding site (Casadesus and Low, 2006). This Dam DNA methylation has been shown to be involved in pathogenicity and phenotypic heterogeneity of several bacteria (Casadesus and Low, 2013).
Photorhabdus luminescens is an entomopathogenic bacteria switching from symbiosis, with a nematode, to pathogenicity, in the insect (Boemare et al., 1993). This bacterium displays phenotypic heterogeneity. Because a Dam MTase has been identified in its genome sequence, we investigated its role in the life-cycle of *P. luminescens*.
Methylome analysis revealed that 99% of GATC sites in the genome are methylated in all tested growth conditions. Overexpressing Dam methylates most of the unmethylated sites and causes a decrease in motility and pathogenicity of the bacteria whereas it increases biofilms formation. It does not impair the bacterial ability to perform a mutualistic association with the nematode. Transcriptomic analysis revealed that the observed phenotypes are related to differences at the transcriptional level. Coupling phenotypic, transcriptomic and methylomic analysis provides clues to identify genes transcriptionally regulated by DNA methylation and to understand Dam DNA methylation involvement in *P. luminescens* life-cycle.

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Casadesús, Josep, and David Low. 2006. *Microbiology and Molecular Biology Reviews: MMBR* 70 (3): 830–56.
Casadesús, Josep, and David Low. 2013. *The Journal of Biological Chemistry* 288 (20): 13929-13935