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Dam overexpression impacts motility and virulence of the entomopathogenic bacteria, *Photorhabdus luminescens* TT01

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Abstract

Bacterial DNA methylation is known to play a role in gene expression (Casadesús et al., 2006). Dam is the most described DNA-methyltransferase and is widespread in gamma-proteobacteria. Dam DNA methylation is involved in pathogenicity of several bacteria. *Photorhabdus luminescens* is an entomopathogenic bacterium symbiotically associated with nematodes of the genus *Heterorhabditis*. The nemato-bacterial complex is able to kill insect larvae such as *lepidoptera* by bacterial septicemia (Nielsen-LeRoux et al., 2012). We identified a Dam ortholog in *P. luminescens* genome and we showed that *P. luminescens* *dam* gene is functional by cloning it on a plasmid in an *E. coli* Dam mutant. After overexpression of *dam* in *P. luminescens*, a decrease of about 50% in motility ($p < 0.02$) was observed. In addition, after injection of 1000 CFU in larvae of *Spodoptera littoralis*, the Dam overexpressing strain showed a delayed virulence compared to that of the control strain (harboring an empty plasmid). In contrast, no difference in growth ability was observed in vitro between the two recombinant strains. These results enhance our knowledge about Dam methylation and strengthen the hypothesis that Dam plays a major role for gene expression in proteobacteria. To go further, we plan to identify all DNA methylations in the genome of the two strains using Pacbio sequencing.

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