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The sequence of the universal bacterial DNA repair protein Mfd dictates the pathogenicity of *Bacillus cereus* strains

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Abstract

The bacterial protein Mfd (mutation frequency decline) is highly conserved among bacteria and has been shown to be involved in bacterial DNA repair. We have recently shown that this protein confers bacterial resistance to the host nitrogen response produced during an infection by the immune system. Indeed, Mfd helps preserving DNA integrity and is involved in the repair following NO-induced DNA damage. Using a large collection of *Bacillus cereus* strains with various pathogenicity, we could further establish a link between Mfd sequences, protein 3D structures and virulence. Protein sequence comparison and 3D modelling were used to determine specific domains involved in the virulence of *B. cereus.* Using an *in vivo* insect model of infection, we show that the *mfd* gene of a pathogenic strain could complement the avirulent phenotype of a non-pathogenic strain. These data strongly suggest that the 3D structure of Mfd plays an essential role in its function and might be a new and interesting way to discriminate pathogenic from harmless *B. cereus* strains.

As Mfd is widely conserved within bacteria, those findings could improve our understanding on the pathogenicity of potentially a large spectrum of bacteria.

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