**A locus widely distributed in the *B. cereus* group with functionality in biofilm formation**

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*Bacillus cereus* is a human pathogen responsible of a series of food poisoning due to the consumption of contaminated vegetables or processed foods. The production of spores and the organization in communities called biofilms, are two key factors in the food contamination, transmission to the pathogen and the production of harmful toxins to the consumer. During its life cycle, *B. cereus* can survive as saprophyte as well as in association with a wide range of host: humans, plants and insects.

The formation of bacterial communities or biofilms is thought to be an essential stage for the bacterial survival and adhesion to surfaces. We have previously identified two proteins TasA and CalY as components of the extracellular matrix and thus involved in the formation of biofilm in *B. cereus*. Furthermore, this genomic region contains the locus BC\_1280 which is widely distributed in the *B. cereus* group and related species, but absent in *B. subtilis* and close relatives. In a previous transcriptomic and quantitative proteomic analysis we found BC\_1280 overexpressed in biofilm associated cells compared to planktonic, as *tasA* or *calY*. According to this expression pattern, knock-out mutants in two different strains of *B. cereus*, an emetic and other diarrheic, were severely impaired in biofilm formation. The locus is annotated to codify a hypothetical protein, and indeed, we have failed in finding any identity in our bioinformatic analysis. Interestingly the hypothetical protein possesses several repetitions in the C-terminal region, and the number is variable depending on the strain. Repetitive domains have been demonstrated in other bacteria species to mediate cell-to cell interaction or interaction with the host. Consistent to this idea, auto-aggregation experiments confirmed that definite contribution of this locus to bacterial cell aggregation. Given the relevance of this protein in biofilm formation and apparently cell aggregation, along with the well conserved distribution in the *B. cereus* groups are reasons that lead us to characterize and to study in detail the functionality of this locus in *B. cereus* multicellularity and interaction with hosts.

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