Crystal structure of the \textit{BcZBP}, a zinc-binding protein from \textit{Bacillus cereus}

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\textit{Bacillus cereus} is an opportunistic pathogenic bacterium closely related to \textit{Bacillus anthracis}, the causative agent of anthrax in mammals. A significant portion of the \textit{B. cereus} chromosomal genes are common to \textit{B. anthracis}, although \textit{B. cereus} is not associated with anthrax. \textit{B. cereus} provides thus a convenient model organism for studying the corresponding proteins of the highly infectious \textit{B. anthracis}. The \textit{BcZBP} protein of \textit{B. cereus}, is encoded from the \textit{bc1534} gene which has three homologues to \textit{B. anthracis}. The protein exhibits deacetylase activity with the N-acetyl moiety of the N-acetylglucosamine and the di- and tri-acetylchitobiose. However, neither the specific substrate of the \textit{BcZBP} nor the biochemical pathway have been conclusively identified. We have determined the crystal structure of \textit{BcZBP} at 1.8 Å resolution. The N-terminal part of the 234 amino acid protein adopts a Rossmann fold while the C-terminal part consists of two $\beta$-strands and two $\alpha$-helices. In the crystal the protein forms a compact hexamer, in agreement with solution data. A zinc binding site and a potential active site have been identified in each monomer. These sites have extensive similarities to those found in two known zinc-dependent hydrolases with deacetylase activity, MshB and LpxC, despite a low degree of amino acid sequence identity. Functional implications and a possible catalytic mechanism can be deduced from the crystal structure.

Figure 1: Structure of the \textit{BcZBP} hexamer

References