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Structural study on toxin-antitoxin systems in Pathogenic Bacteria: a target for developing antimicrobial agents

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The bacterial toxin–antitoxin (TA) system is a module that may play a role in cell survival under stress conditions. Generally, toxin molecules act as negative regulators in cell survival and antitoxin molecules as positive regulators. Thus, the expression levels and interactions between toxins and antitoxins should be systematically harmonized so that bacteria can escape from such harmful conditions. Since TA systems are able to control the fate of bacteria, they are considered as potent targets for the development of new antimicrobial agents. TA systems are widely prevalent with a variety of systems existing in bacteria: there are three types of bacterial TA systems depending on the property of the antitoxin which binds either the protein toxin or mRNA coding the toxin protein. Moreover, the multiplicity of TA genes has been observed even in species of bacteria. Therefore, knowledge on TA systems such as the individual characteristics of TA systems, integrative working mechanisms of various TA systems in bacteria, interactions between toxin molecules and cellular targets, and so on is currently limited due to their complexity. In this regard, it would be helpful to know the structural characteristics of TA modules for understanding TA systems in bacteria. Here, we present the structural information of TA systems by using NMR & X-ray crystallography and suggest antibiotics candidates which inhibit the interaction between Toxin and Antitoxin proteins from pathogenic bacteria, especially focusing on the TA modules of *Mycobacterium Tuberculosis* and *Streptococcus pneumoniae*.