

Structural and functional studies of ParB protein from *H. pylori* (HpSpo0J) in chromosome segregation system, ParABS

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Abstract

Chromosome segregation system, ParABS, is an important biological functional system to drive the initial gene replication and chromosome segregation in several species of bacteria. ParABS system contains three components: ParA (an ATPase), ParB (a *parS* binding protein) and *parS* (a centromere-like DNA). The homology of ParA and ParB are *HpSoj* and *HpSpo0J* in *H. pylori*. Recently, the CTP binding was identified in ParB and it is reported as an important cofactor for ParB translocation in DNA spreading, but the molecular mechanism of DNA spreading is still unclear. A crystal structure of the homology ParB protein from *B. subtilis*, *BsSpo0J*, and CDP complex was solved. Comparing the crystal structure of Ct-*HpSpo0J-parS* complex and *BsSpo0J*-CDP complex, a N terminal domain swapping was observed in *BsSpo0J*-CDP complex. For speculation, the important regulation role of CTP for ParB during chromosome segregation, we conduct the biochemical analysis and crystallization experiments. In order to increase the purity of *HpSpo0J-parS* complex, the difference length *parS* DNA were incubated with *HpSpo0J* and then applied to size exclusion chromatography. The gel filtration result showed that when *HpSpo0J* interacts with different length of *parS* DNA, the different conformation complex might be formed. The EMSA result showed that the *parS* DNA binding ability of *HpSpo0J* decreased when CTP is participated. In contrast to CTP, there is no effect to the interaction between *HpSpo0J* and *parS* when CDP is involved. Up to now, we obtained the micro crystal of *HpSpo0J-parS*-CDP complex and we still try to improve the quality of crystal for X-ray diffraction data collection.

Reference:

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- [2] Chu, C.H., et al., *Crystal structures of HpSoj–DNA complexes and the nucleoid-adaptor complex formation in chromosome segregation*. Nucleic Acids Research, 2019.