Biological function and molecular structure of SegA, the chromosome segregation protein in archaea

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Abstract

The replicated genomes segregation is critical for the genetic material retaining. In eukaryotes, the microtubules formed bipolar mitotic spindle is crucial for the chromosome segregation. The microtubules depolymerize result in the movement of centromere at chromatids. The wide-spreading plasmid partition system, ParABS is applied in the most bacterial chromosome segregation. However, the genomes segregation is still unclear in archaea. The first archaea chromosome segregation system SegAB was reported in *Saccharolobus solfataricus* [1]. The SegAB construct by a walker A-type ATPase, SegA, specific DNA-binding protein, SegB, and the specific recognized DNA binding sites. SegA from *S. solfataricus* (*Sso*SegA) reveals a sequence identity of 27-34% to that of ParA in ParABS system and both belong to the walker A-type ATPase. It might imply that chromosome segregation in archaea share a similar functional role with that in bacterium. In this study, we purified the *Sso*SegA and DNA binding ability. In addition, we solved crystal structures of the ADP bound *Sso*SegA and *Sso*SegA-DNA complexes by X-ray diffraction method. *Sso*SegA shows a typical Walker A type ATPase folding with a central eight-stranded β-sheet (β1–β8) and nine helices (α1-α9) around. *Sso*SegA structure contains a highly conserved ATP binding motif in the central core and a large basic DNA binding patch in the C-terminal region. The molecular structure and function of chromosome segregation in archaea, SegAB is progressively developing.

Keywords – SegAB, Archaea chromosome segregation.

References

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