

Insight into Bridging and Condensing DNA for Chromosome Partitioning

In the ParABS (partition system of ParA, ParB and *parS*) bacterial chromosome-partitioning system, ParB spreads along the chromosomal DNA by binding at specific *parS* and non-specific DNA sites to form a high-order partition complex.^{1–3} This partition complex is required for the loading of SMC onto the chromosomal DNA. In addition, ParB can interact with ParA and stimulate its ATPase activity.⁴ This nucleoid-adaptor complex, ParA-ParB-*parS*, is used to promote chromosome segregation.⁵ In the *Helicobacter pylori*, ParABS system consists of *HpSoj* (ParA), *HpSpo0J* (ParB) and *parS* DNA.⁶ In 2015, a research team of Yuh-Ju Sun (National Tsing Hua University) solved a new crystal structure of the Ct-*HpSpo0J-parS* complex. The team reported that Ct-*HpSpo0J* folds into an elongated structure that includes a flexible N-terminal domain for ParB spreading and a conserved DNA-binding domain for specific *parS* binding. Importantly, Ct-*HpSpo0J* undertakes multiple protein-protein interactions with neighboring molecules through the N-terminal domain and forms an oligomer.

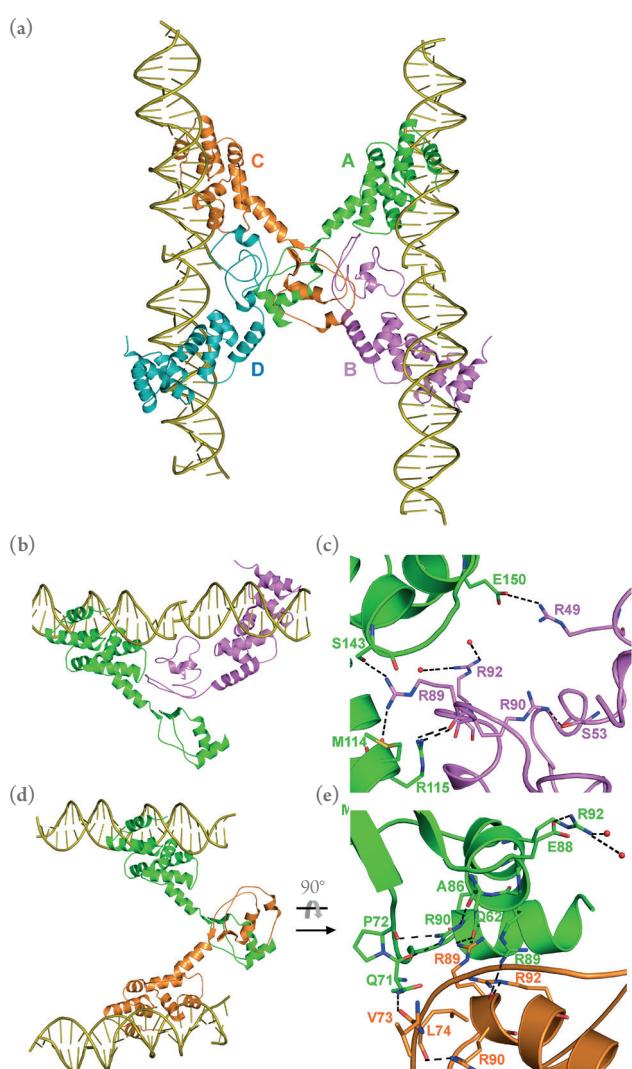


Fig. 1: (a) Ct-*HpSpo0J-parS* complex. Four Ct-*HpSpo0J* molecules (A/green, B/magenta, C/orange, and D/cyan) and four *parS* DNA (yellow) form as a tetramer. (b) Adjacent interactions at the AB dimer. (c) Key residue interactions (⁸⁹RRLR⁹²) at the AB dimer. (d) Transverse interactions at the AC dimer. (e) Key residue interactions (⁸⁹RRLR⁹²) at the AC dimer. [Reproduced from Ref. 7]

According to previous reports,^{1–6} the ParB spreading was studied with biochemical data, but the detailed mechanism is still unclear. To realize the molecular-level story, that team used techniques of biological crystallography, including X-ray diffraction at BL13B1, BL13C1 and BL15A1, and small-angle X-ray scattering (SAXS) at BL23A1. In their work, a Ct-*HpSpo0J-parS* complex crystal was grown from a precipitant solution (PEG 8000 14–16 % and Li₂SO₄ 450–525 mM) within 3–7 days. The X-ray diffraction data of the Ct-*HpSpo0J-parS* complex crystal were collected to resolution 3.1 Å. The SAXS data for the full-length *HpSpo0J* (3 mg mL⁻¹) were collected at 20 °C. The primary data were reduced with an in-house program at BL23A1 and the processed data were analyzed using the ATSAS package software.

According to this work,⁷ shown in Fig. 1, the oligomeric structure of the Ct-*HpSpo0J-parS* complex is formed by four Ct-*HpSpo0J* molecules (chains A, B, C and D) binding with four *parS* molecules (Fig. 1(a)). This oligomer might mimic a high-order complex in the ParABS system to promote ParB spreading. In the Ct-*HpSpo0J-parS* complex, molecules A and B form a crosswise dimer using adjacent molecular interactions via N-terminal domain residues (Fig. 1(b)). At the residue level, they found that residues of α3 and α4 in molecules A interact with Arg89 of chain B. There are also several hydrogen bonds formed between Met114/Arg115 (α3) and Ser143 (α4) of molecule A and Arg89 of molecule B (Fig. 1(c)). Glu150 (α5) of molecule A forms a salt bridge with conserved Arg49 of molecule B. These hydrophilic interactions might be essential for the formation of the AB dimer. This team found that molecules A and C use transverse molecular interactions in their N-terminal domains to form a bridging dimer (Fig. 1(d)). At the residue level, they observed that a hydrogen bond forms between the side chain and main chain of Arg89 in molecules A and C, respectively. Gln62 (α1) of molecule A interacts with Arg89 of molecule C; molecule A Gln71 (loop α1-β1) interacts with chain C Val73 (Fig. 1(e)). They observed that the ParB dimers interact with adjacent and transverse interactions through the N-terminal domain to spread along and to bridge the chromosomal DNA.

As shown in Fig. 2, they utilized SAXS to investigate further the full-length *HpSpo0J*. From the SAXS data, a low-resolution non-globular molecular envelope of *HpSpo0J* was determined with calculations *ab initio*. After fitting the C-terminal domain of P1 ParB (gray) into the Y-shaped envelope, the *HpSpo0J* (green and purple) were fitted into the two arms. The Y-shaped full-length *HpSpo0J* utilizes its N-terminal domain for neighboring molecular interactions and to dimerize via its C-terminal domains to stabilize this structure.

According to their crystal structure and SAXS solution data, they proposed a ParB spreading model (Fig. 3). In this model, all three domains of the ParB take part cooperatively for molecular spreading. The DNA-binding domain binds to a specific *parS* site at a chromosome. The C-terminal domain of ParB dimerizes with a vicinage to maintain the ParB-*parS* complex. The flexible N-terminal domain provides diverse protein-protein interactions. The ParB dimers interact by adjacent and transverse interactions through the N-terminal domain to spread along and to bridge the chromosomal DNA, horizontally and vertically.

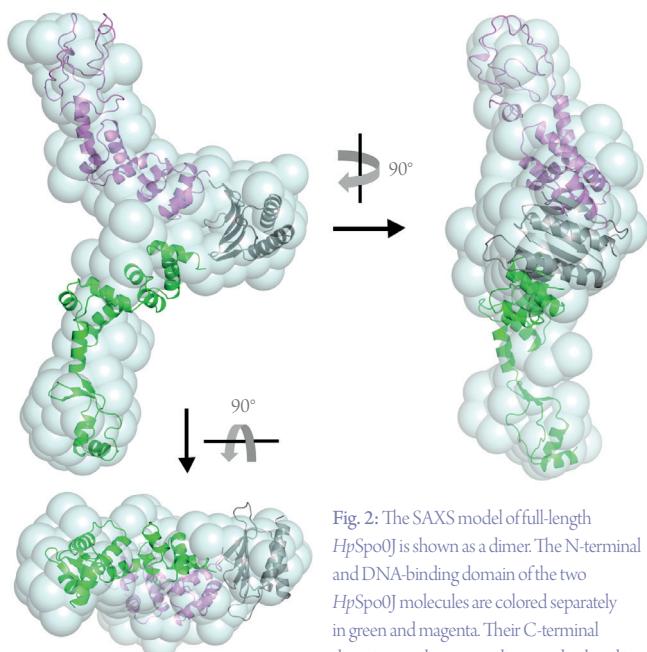


Fig. 2: The SAXS model of full-length *HpspoJ* is shown as a dimer. The N-terminal and DNA-binding domain of the two *HpspoJ* molecules are colored separately in green and magenta. Their C-terminal domains are shown as a dimer and colored in grey. [Reproduced from Ref. 7]

This work showed the structural details of the complex and combined with results from SAXS to provide a mechanism to mimic ParB spreading in the chromosome partition system. This significant work not only provides structural evidence how ParB spreads along the chromosomal DNA by *parS* binding in the bacterial chromosome partitioning system but also renews our knowledge about how ParB bridges DNA to condense the chromosome during the chromosome segregation. (Reported by Chun-Jung Chen)

*This report features the work of Yuh-Ju Sun, Bo-Wei Chen and their co-workers published in Proc. Natl. Acad. Sci. USA **112**, 6613 (2015).*

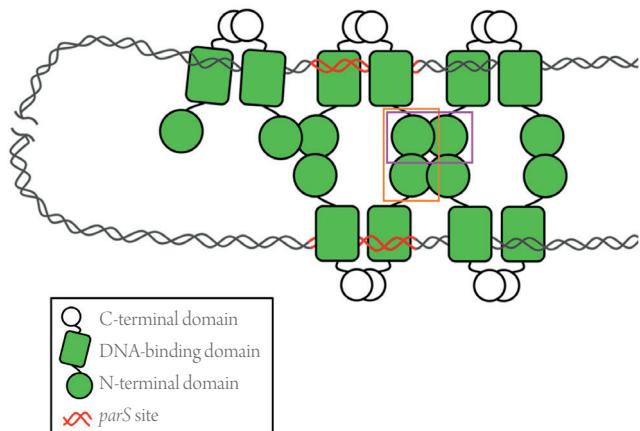


Fig. 3: The C-terminal dimerization (in white spheres), the DNA-binding (in green rectangles) and the flexible N-terminal domains (in green spheres) of ParB are shown. ParB binds chromosomal DNA at specific *parS* sites (in red) or non-specific sites (in gray). Multiple ParB molecules spread along the chromosomal DNA through the N-terminal domain by adjacent interactions (boxed in magenta) and transverse interactions (boxed in orange). [Reproduced from Ref. 7]

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Complicated Designs of Dinosaur Teeth: Functions and Protective Mechanisms

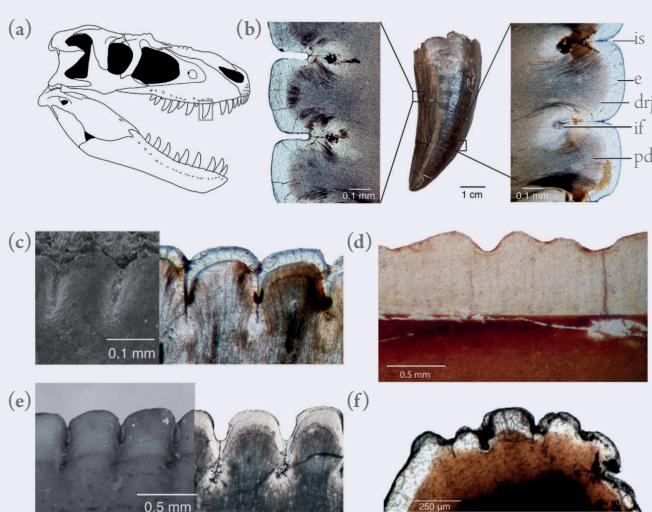


Fig. 1: Microanatomy of ziphodont teeth with (a, b, c, e) and without (d and f) deep folds. (a) Drawing of a skull of a carnivorous dinosaur. (b) Sagittal thin sections through distal (left) and mesial (right) carinae. (c and e) Denticles of ziphodont teeth of an indeterminate phytosaur (c) and *Carcharodontosaurus saharicus* (e), under SEM (left) and in thin section (right). (d) Structure of a carina, lacking denticles, on a tooth of *Smilodon* sp. (f) Denticles of *Hadrosaurid*. Abbreviations: dej, dentine-enamel junction; e, enamel; if, interdental fold; is, interdental sulcus; pd, primary dentine. [Reproduced from Ref. 1]

From the evolutionary point of view, the relationship between dietary habits and tooth morphology was thought to be strongly correlated. The dinosaur fossil teeth could be a suitable tissue fossil for investigation of mechanical functions and evolutionary progresses of dinosaur teeth, and it could provide novel information on the feeding habits, possible habitats and living environments of dinosaurs.

Two papers based wholly and partly on experimental and simulation results from the NSRRC reported on the evolution, function and self-protection of dinosaur teeth based on the analysis of the native components and nanostructures of the teeth of dinosaurs using scanning electron microscopy (SEM), synchrotron-based Fourier transform infrared spectroscopy,¹ and synchrotron-based transmission X-ray microscopy² at the BL14A1 and BL01B1 beamlines.

The drawing of a skull and sections of a tooth shown in Figs. 1(a) and 1(b) belong to a typical archosaur. When magnified manyfold, one can see that the tooth features serrated edges (also called ziphodonty) along different carinae (keel-