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SMC complexes in bacterial chromosome condensation and segregation

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Abstract

Bacterial chromosomes segregate via a partition apparatus that employs a score of specialized proteins. The SMC complexes play a crucial role in the chromosome partitioning process by organizing bacterial chromosomes through their ATP-dependent chromatin-compacting activity. Recent progress in the composition of these complexes and elucidation of their structural and enzymatic properties has advanced our comprehension of chromosome condensation and segregation mechanics in bacteria.

Keywords

SMC; Condensin; Chromosome condensation; Chromosome segregation

1. Chromosome condensation as a chromatid-partition force in bacteria

Bacterial chromosomes vary greatly in their length, organization, and dynamics (Rocha, 2004), however, many bacterial species share basic principles of genome duplication and partition during cell division (Pogliano et al., 2003; Ryan and Shapiro, 2003; Sherratt, 2003). While the nature of the main force-generating machinery in bacterial chromosome partition is still under investigation (Lewis, 2004), it appears that actin filaments play an important early role in origin separation (Defeu Soufo and Graumann, 2005; Gitai et al., 2005), and tubulin-like filaments are specialized for cell division (Graumann, 2004). Coupling of chromosomes to filaments is mediated by specialized chromosome-partition loci, or ‘centromeres’ (Ben-Yehuda et al., 2005; Kruse et al., 2005; Pogliano et al., 2003; Wu and Errington, 2003). Bacteria may also use some auxiliary forces to achieve final partition of chromatin after the initial separation of replication origins (Defeu Soufo and Graumann, 2005; Gitai, 2005). For example, the force of DNA replication has been implicated in the partition of the sister chromatids (Lau et al., 2003; Sherratt, 2003). The dependence of successful chromosome segregation on the processes coinciding with DNA replication appears to be universal for both Prokaryota and Eukaryota. Even though in the latter case there is a substantial lag between DNA replication and chromosome partition, sister chromatid cohesion is established, and the bulk of protein complexes required for segregation are loaded onto chromosomes during DNA replication.

Bacterial cells also appear to use the forces of chromosome condensation to partition their genetic material (Ben-Yehuda et al., 2005; Long and Faguy, 2004; Volkov et al., 2003). The bulk of chromosome condensation, both in bacteria and eukaryotes, is driven by the structural maintenance of chromosomes (SMC) (Strunnikov et al., 1995) complexes, termed condensins (Hirano, 2005). Condensation activity, albeit visually manifested as a chromatin-compacting

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process, is essentially required to spatially separate sister chromatids (Strunnikov, 2003). Indeed, in all cases where condensin mutants were studied, the chromatin-compacting activity per se appears to be less important (either dispensable (Freeman et al., 2000) or easily compensated by other activities (Hagstrom et al., 2002; Hudson et al., 2003)) compared to the sister chromatid partitioning, which is universally blocked by impaired condensin activity (Bhat et al., 1996; Freeman et al., 2000; Hagstrom et al., 2002; Hudson et al., 2003; Ouspenski et al., 2000).

2. SMC complexes—primordial building blocks of chromatin?

The first protein of the SMC family was described in *Mycoplasma* (Notarnicola et al., 1991), however, it was the functional characterization of the Smc1 protein from *Saccharomyces cerevisiae* that led to recognition of the extensive SMC family in all organisms (Strunnikov et al., 1993). From the early onset, it became clear that SMC proteins are some of the most conserved chromatin components (Cobbe and Heck, 2004). They share a common molecular architecture, as well as substantial conservation of their primary protein structure. Therefore, initially SMC proteins were defined strictly on the basis of amino acid sequences similarity and their ‘head-rod-tail structure’ (partial ATPase domain, coiled-coil one, hinge, coiled-coil two, and another part of ATPase) (Saitoh et al., 1994; Strunnikov et al., 1993) (Fig. 1A). This definition was later substantiated with structural information: bacterial SMC proteins were shown to form symmetrical anti-parallel dimers (Melby et al., 1998), bringing two parts of the ATPase together. This observation was consistent with a simple anti-parallel dimer model (Fig. 1B), where interaction between two SMC molecules is mediated by the coiled-coil domains. However, with the availability of new data, an alternative model, in which the intermolecular interaction of the two hinge domains was responsible for dimer formation, and the coiled-coil domains were stabilizing the intramolecular SMC interactions (Gruber et al., 2003; Hirano et al., 2001; Hirano and Hirano, 2002), has come to dominate the field (Fig. 1C). Thus, SMC proteins form an obligatory dimer in a rather novel manner that is distinct from the majority of long coiled-coil proteins. More recent data suggest that two bacterial SMC proteins in the dimer also interact via their ATP-binding domains, with a potential to form a closed ring-like structure (Anderson et al., 2002; Volkov et al., 2003) (Fig. 1D).

Many proteins that lack a clear homology to SMC (Rad50, MukB, SbcC, designated here as SMC-like) probably share the ‘SMC-type’ of molecular organization, with regards to forming a functional ATP-binding domain from two distant parts of the same molecule by virtue of interacting coiled-coil domains. However, narrowing the SMC definition based on sequence conservation in the globular domains (Fig. 1E) appears to be still valid (Cobbe and Heck, 2004), as it, likely reflects specific biochemical properties of SMC proteins. These particular properties include, for example, a unique ATP-dependent mechanism of SMC intra and intermolecular interaction (de Jager et al., 2004), and a specialized DNA-interaction domain, serving as a cofactor of ATP hydrolysis (Lammens et al., 2004) (see below).

In many gram-negative bacteria, most notably in *Escherichia coli*, the homologs of classic SMC proteins appear to be missing (Soppa, 2001). Instead, a functional analog of the SMC complex has taken over its role in chromosome partitioning: the MukBEF complex appears to compensate functionally for the missing SMC condensin. Remarkably, not only does the MukB protein, the enzymatic core of MukBEF, and share the basic ‘body plan’ (a result of convergent evolution?) with SMC proteins (Melby et al., 1998), but the overall structure of the MukBEF complex is reminiscent of condensin and cohesin SMC complexes (Fennell-Fezzie et al., 2005; Matoba et al., 2005). The wide-spread representation of SMC-like proteins and the apparent reconstruction of SMC-like MukBEF condensin in gram-negative bacteria, both highlight the outstanding uniqueness of SMC ‘molecular design’.

Bacterial SMC complexes represent an especially distinct subset of SMC complexes, for two prominent reasons. First, in bacteria, a single SMC complex probably carries out alone several functions divided between specialized SMC complexes in Eukaryota. Eukaryotic cells commonly have one or two condensin complexes (Smc2/Smc4 dimer as a core), in addition to the Smc1/Smc3 sister-chromatid cohesion complex (cohesin) (Losada and Hirano, 2001) and a large Smc5/Smc6 complex essential for DNA repair and chromosome segregation (Fujioka et al., 2002; Harvey et al., 2004; McDonald et al., 2003; Sergeant et al., 2005; Torres-Rosell et al., 2005; Zhao and Blobel, 2005). An even more specialized version of condensin is involved in the dosage-compensation-driven restructuring of sex chromosomes in *Caenorhabditis elegans* (Csankovszki et al., 2004). The SMC complexes in eukaryotes have multiple non-SMC subunits, in addition to the SMC heterodimer, while in most bacterial species only the SMC homodimer and at least one (often two) non-SMC subunit are present in the complex (Cobbe and Heck, 2004; Soppa, 2001). The second surprising fact is the evident molecular conservation of enzymatic and DNA-binding mechanisms between the bacterial and eukaryotic condensins (Hirano and Hirano, 2004; Strick et al., 2004). While Eukaryota, with a relatively conserved core chromatin composition, developed several specialized SMC complexes, it is noteworthy that prokaryotic species, with chromatin compositions as varied as in Archae and Eubacteria, share essentially one type of SMC condensin. In addition, bacterial SMC complexes must adapt to act in consort with quite diverse chromosome-partition machineries in bacteria. In this light, the evolutionary conservation of SMC complexes among bacteria and in comparison to Eukaryota is even more remarkable. Such conservation demonstrates that this group of proteins is evidently the most persistent structural component of chromosomes through evolution. Thus, SMC complexes carry out one of the most essential nucleic-acid-mediated function, in line with DNA replication, transcription, and protein synthesis.

3. Bacterial SMC machines—both structural proteins and enzymes

The *SMC* genes have been characterized in multiple bacterial species and are involved in chromosome segregation in such diverse bacteria as *Bacillus subtilis*, *Caulobacter crescentus*, and *Methanococcus voltae* (Britton et al., 1998; Graumann et al., 1998; Jensen and Shapiro, 2003; Long and Faguy, 2004; Moriya et al., 1998). However, the detailed functional characterization of the corresponding proteins became possible only after adequate methods of bacterial cell biology were developed (Britton et al., 1998; Graumann et al., 1998; Moriya et al., 1998). Initial genetic characterization of the *SMC* gene in *B. subtilis* (*BsSMC*), has revealed that it is nearly indispensable for cell viability (Britton et al., 1998; Graumann et al., 1998; Moriya et al., 1998) and provided the first example of an SMC protein not being absolutely essential for survival. However, cells lacking the *BsSMC* gene display severely retarded growth with considerable defects in chromosome segregation and condensation. Even though the corresponding condensation defect has never been quantified, the lack of an obvious defect in sister chromatid cohesion has led to the designation of the SMC complex as bacterial condensin (Hirano, 2005), not cohesin.

How do bacterial SMC proteins fulfill their chromosome condensation functions? In the absence of information on the *in vivo* mechanochemical properties of condensin complexes and a significant shortfall of *in vitro* studies on condensin-chromatin interaction, most biochemical data on condensin concern either assembly of the complex or its interaction with naked DNA. Assembly of bacterial condensin has been extensively studied, however, the exact stoichiometry of its subunits and their internal works remain unclear (Mascarenhas et al., 2005). Nevertheless, establishing the fact that, unlike SMC heterodimers in eukaryotic cells, the bacterial SMC is a homodimer (Hirano and Hirano, 2002; Melby et al., 1998), has allowed substantial progress in dissecting its functional domains. For example, genetic and structural analysis of the hinge region in bacterial SMC has established that this region has a crucial role in dimer formation (Haering et al., 2002; Hirano and Hirano, 2002). The globular domains of

the SMC dimer constitute the enzymatic core of bacterial condensin. Indeed, both eukaryotic and prokaryotic SMC proteins are able to bind and/or hydrolyze ATP and their DNA-binding and restructuring activities are dependent on both ATP-binding and ATP hydrolysis (Hirano and Hirano, 1998; Kimura and Hirano, 2000). The nature of this dependence is complicated. While it has been convincingly demonstrated that ATP hydrolysis by eukaryotic condensin is required for its DNA super-coiling activity (Hirano, 2005), the same has not been demonstrated for bacterial condensin. On the other hand, ATP-binding (without hydrolysis) is crucial for assembly of the whole complex (Hirano and Hirano, 2004; Lammens et al., 2004), namely for closing a two-armed clamp with a flexible hinge structure (Fig. 1D) into a 'ring.' The SMC ring is locked by two ATP molecules sandwiched between two globular heads of SMC partners, so that each ATP molecule is shared between two SMC molecules of the dimer (Lammens et al., 2004). Hydrolysis of ATP, in turn, resolves association of the bacterial SMC arms (Hirano and Hirano, 2004), and thus the exact role of this enzymatic activity is not obvious. In addition to ATP-binding, association of SMC arms is apparently promoted by the recently discovered auxiliary subunits of bacterial SMC complex, ScpA and ScpB (Mascarenhas et al., 2002; Soppa et al., 2002), in an ATP-dependent manner (Hirano and Hirano, 2004; Lammens et al., 2004). The similarity of the ScpA protein to the Mcd1/Sccl subunit of eukaryotic cohesin (Mascarenhas et al., 2002; Schleiffer et al., 2003), suggests that by analogy with eukaryotic SMC complexes, ScpA act to physically connect both globular ATP-binding domains, (Anderson et al., 2002; Gruber et al., 2003; Weitzer et al., 2003; Yoshimura et al., 2002). ScpA can bind ScpB in the absence of SMC and the resulting complexes can multimerise thus creating an additional option for supramolecular assembly of bacterial condensin (Mascarenhas et al., 2005). Interaction of the ScpA/ScpB subcomplex with SMC is stimulated by ATP, but can also proceed in its absence (Hirano and Hirano, 2004; Mascarenhas et al., 2005). Thus, bacterial SMC complexes, by and large, manifest themselves as structural proteins, while at the same time are ATP-hydrolases.

4. Mechanisms of DNA–SMC interaction

Investigation of DNA-binding activity of SMC proteins, similarly, has to deal with the inherent duality of SMC complexes (ATPase versus ATP-binding structural protein), as well as with an additional level of complexity: the fact that ATPase activity is stimulated by DNA (Hirano and Hirano, 2004). Initial in vitro analysis of BsSMC suggested that it is able to form aggregates with DNA in an ATP-binding-dependent fashion (Hirano and Hirano, 1998). However, it was not clear how this activity translated into highly ordered and reversible chromatin packaging (Almagro et al., 2004; Kireeva et al., 2004), i.e., the essence of chromosome condensation in vivo. Several recent publications have contributed to a more advanced model of interaction between bacterial condensin and DNA.

At the cornerstone of the current model for interaction between bacterial SMC complex and DNA is the prediction that the condensation-driving DNA-binding activity of SMC subunits is not a sequence-specific interaction, but rather a consequence of architectural (ring-like) make-up of the SMC holocomplex. The latter, however, remains unproven: in the case of condensin some localized and specific DNA–protein interaction cannot be excluded, as indicated by recent findings (Lammens et al., 2004). The ring-like structure of SMC complexes is believed to 'embrace' the DNA strands (Gruber et al., 2003; Stray and Lindsley, 2003; Volkov et al., 2003; Weitzer et al., 2003) and chromatin fibers (Almagro et al., 2004; Kagansky et al., 2004), both of which then get entrapped within the clamp/ring opening. The model is supported by mutational analysis, confirming the predicted analogy between the SMC head domains and ABC transporters (Lammens et al., 2004; Lowe et al., 2001). Thus, the DNA aggregating activity of BsSMC complex can be likened to the ATP-engagement cycle of ABC transporters (Higgins and Linton, 2004). One of the important conclusions from these studies is that ATP-binding itself can bring two SMC head domains together in an engaged

conformation (Fig. 2B), thus allowing either to lock the SMC 'ring' around DNA or to prevent DNA from entering the ring (Hirano and Hirano, 2004). This model also suggests a plausible regulatory role for ATP hydrolysis—to allow passage of DNA strands into the SMC ring embrace. The high-resolution electron-microscopy studies on human condensin suggest, however, that DNA strands are not free to move within the SMC 'ring,' but are instead tightly wrapped around the globular SMC domains, in conjunction with non-SMC subunits (Anderson et al., 2002).

It cannot be excluded that non-SMC subunits of bacterial condensin may also have some biologically relevant DNA-binding activity. However, it seems unlikely that ScpA has DNA-binding activity on its own, outside the context of the SMC complex. Indeed, it has been recently shown that the order of assembly of the bacterial condensin itself plays a significant role in the specificity and size of the DNA-condensin complex (Fig. 2). Particularly, ScpA is important for the stable interaction of SMC dimer with dsDNA: the addition of ScpA to an *in vitro* reaction after DNA results in the formation of a stable aggregation-prone complex (Fig. 2C), while ScpA pre-bound to SMC prevents the complex from binding DNA (Fig. 2D) (Hirano and Hirano, 2004). Aggregation of SMC complexes in the presence of DNA can be probably explained either by multiple embracing complexes on the same DNA molecule or by formation of engaged configuration between the SMC heads from different complexes. Bridging of SMC heads from different complexes by the ScpA/ScpB sub-complex (Fig. 2E) cannot be excluded either. ScpA also plays a regulatory role in the BsSMC ATPase activity: the ScpA-stabilized 'closed' configuration of SMC head inhibits hydrolysis of bound ATP (Hirano and Hirano, 2004). Thus, ScpA serves both as a lock and a key to the SMC DNA-entry gate. The cooperative role of ATP and ScpA in closing the SMC 'ring' might explain the absence of ScpA homologs in some species that nevertheless have SMC proteins (Soppa, 2001). ScpA is also suggested to have some additional roles in DNA repair and transcription, possibly separately from its role in condensation, however these functions are apparently also mediated by the SMC complex as a whole (Dervyn et al., 2004).

While the role of ScpB in the SMC complex architecture is much less clear than the one of ScpA, the ScpB protein may be involved in recognizing hypothetical SMC-targeting motifs in DNA, similarly to accessory subunits SDC-2 and SDC-3 in the *C. elegans* SMC dosage-compensation complex (Hirano, 2005). Indeed, ScpB has a helix–turn–helix domain and was found to be equally important as ScpA and SMC itself for chromosomal binding of bacterial condensin *in vivo*, (Volkov et al., 2003).

The second type of DNA-binding activity displayed by SMC complexes is binding DNA as a cofactor for ATP hydrolysis. A specific site for such DNA-binding has been recently mapped in the globular domain of bacterial SMC (Lammens et al., 2004). The absolute conservation of this motif in the classic SMC proteins may serve as an additional structural signature for the SMC family (Fig. 1E). It is not presently clear, however, whether this domain is part of a DNA-binding interface facilitating the ultimate function of SMC complexes in chromatin compaction.

It should be also noted that a significant gap remains between the data on DNA–SMC interaction and our understanding of the actual process of DNA and chromatin condensation. Although single molecule studies have not been done on bacterial condensin yet, the recent optical-tweezers single-molecule studies shed some light on the kinetic properties of the molecular machine of eukaryotic condensin I. It was demonstrated that condensin I can reversibly bind DNA, independently of ATP, without actually compacting it (Strick et al., 2004). However, DNA compaction was strictly dependent upon ATP hydrolysis and was very efficient at the saturating condensin concentrations. The same study also demonstrated that condensation occurs in discrete variable-length steps, peaking at 60 nm. This length of DNA

is hypothesized to be the elementary unit of condensation and possibly represents the stretch of DNA occupied by the binding of one condensin holocomplex (Strick et al., 2004). Force applied to the ends of DNA molecule is able to reverse this condensin activity with the same step-like pattern (Strick et al., 2004). Both the exact mode of condensin interaction with compacted DNA and the mechanics of chromatin compaction remain unclear even after this promising study. However, this work established a conceptual view of DNA condensation as a gradual and cooperative assembly of a nucleoprotein filament with discrete 'building blocks' corresponding to the elementary condensation events. The above mentioned dualism between the tightly regulated enzymatic core and the cooperatively assembled structural units (SMC complexes) thus falls within an existing archetype of mechanochemical filament (such as microtubules), where DNA serves as a cargo.

5. Insights into activity of bacterial SMC complexes in vivo

While bacterial condensin complexes can be tightly packed into a nucleoprotein filament in vitro, their chromosomal distribution in vivo is not consistent with forming an extensive nucleoprotein filament. For example, the *B. subtilis* condensin complex is localized to several (usually two) foci along the length of the chromosome (Volkov et al., 2003). In *C. crescentus*, the SMC complex is concentrated in two–four foci, with the higher number corresponding to an actively replicating chromosome (Jensen and Shapiro, 2003). The presence of additional structural chromosomal proteins (bacterial chromatin) and the need for the SMC complex to cohabit with other proteins involved in processive reactions (replication, recombination, and repair) with DNA as a template suggest that activity of bacterial SMC complexes in native chromosomes must be notably different from the model systems in vitro. As a result, the bulk of knowledge on bacterial condensin biology in vivo came from the cell biology studies.

Recent high-resolution and time-lapse microscopic analysis of the SMC complex in live cells has confirmed its dynamic positioning in a dividing cell, which was hinted by the earlier indirect immunofluorescence studies (Mascarenhas et al., 2002) and YFP analysis (Britton et al., 1998). In *C. crescentus*, SMC foci are visible in all stages of the cell cycle (Jensen and Shapiro, 2003). However pre-division cells predominately have concentrated polar signals, that subsequently disperse into 3–5 more uniform sites dynamically distributed along chromatin (Jensen and Shapiro, 2003). The cell cycle dynamics of the SMC complex is documented even more comprehensively in *B. subtilis*, where there is compelling evidence of for the dependence of SMC localization on chromosome movement. Early in the cycle, cells have one or two SMC/Scp foci in the middle of the cell, at the nucleoid periphery and flanking the replication origins (Volkov et al., 2003). This localization is dependent upon the presence of DNA. At this stage condensin staining is visibly distinct both from origin positions and from DNA polymerase localization. While the DNA polymerase complex remains in the center of the cell, the origins move to the poles and the SMC/Scp foci also reach polar positions early in the cell cycle. The SMC foci, however, never co-localize with the origins, even though they come very close to each other at the polar sites. After passing the polar sites, the SMC foci continue to move to the center of the cell, further away from the origins.

The fact that the distance between the origins and the SMC/Scp foci constantly changes during cell growth may indicate that the bacterial condensin has a defined chromosomal binding site. This hypothesis is tentatively confirmed by the overexpression of the SMC complex in *B. subtilis*: even in the cells with a significantly higher SMC/Scp dosage the number of foci does not increase (Volkov et al., 2003). At the same time, a clear picture of abnormally highly condensed chromosome was seen in these cells. These two observations have led to a conclusion that chromosome condensation activity is exerted from only one point on the chromosomes, and the magnitude of this cumulative activity is dependent on the condensin

dose. This lends some room to a speculation that bacillar chromosome have a specialized 'condensome,' i.e., a specialized chromosomal domain driving chromatin compaction. In *B. subtilis* slowing the pace of DNA replication can shift the position of SMC-bound site to the mid-cell region (Lindow et al., 2002; Volkov et al., 2003), while a *dnaB-ts* mutation blocks the bipolar distribution of SMC at the nonpermissive temperature (Mascarenhas et al., 2005), again indicating that DNA replication and condensin act in coordination to ensure chromosomal partition. In support of this notion, chromosomal origins in *B. subtilis* can initiate separation without SMC proteins, but they become positioned abnormally in the *smc*(-) cells, indicating that segregation is impaired at later stages. This phenotype is reminiscent of condensin mutants in eukaryotes, and probably is a consequence of a failure to condense and partition the replicated parts of chromatin. The recent study on condensin distribution in yeast also suggests a link between replication dynamics and condensin placement (Wang et al., 2005).

Dynamic changes in superhelical states of DNA may serve as a potential mechanical link between the replication machinery and condensin loading and/or activity. Indeed, in *E. coli* the loss of MukBEF activity can be almost completely compensated by the increase in negative supercoiling of the chromosome (Sawitzke and Austin, 2000). In the case of bacillar condensin, depletion of topoisomerase I (*topA*) suppresses the missegregation phenotype of the *smc* null mutant, while inhibition of DNA gyrase is synthetically lethal with the *smc* deletion (Lindow et al., 2002). A recent study has also established that the position and, more importantly, formation itself of SMC/ScpA foci in vivo is dependent on DNA gyrase activity (Mascarenhas et al., 2005).

Finally, it is necessary to address the apparent condensin-like properties of bacterial SMC complexes, versus it being a cohesin-like complex. It would be reasonable to assume that in bacterial cells, with circular chromosomes and immediate coupling of DNA replication to chromosome-partition, sister chromatid cohesion is probably not essential for successful chromosome segregation. It was noted before that, apparently, the only essential function of eukaryotic cohesin is to establish the bipolar kinetochore attachment (Sjogren and Nasmyth, 2001). The possibility of misdirecting sister chromatid separation in a normal bacterial cell cycle is unlikely to be significant, due to the constitutive chromatid attachment to cytoskeletal elements and to the constant position of the replisome. However, the non-vital function of cohesin in postreplicative repair (Birkenbihl and Subramani, 1992; Kim et al., 2002; Sjogren and Nasmyth, 2001; Unal et al., 2004) could be still a property of bacterial SMC complex, as reported in a recent publication (Dervyn et al., 2004). Discriminating this repair activity from the possible condensin-like involvement in DNA repair (Aono et al., 2002; Huang and Koshland, 2003) would require a more detailed analysis of bacterial SMC complexes.

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Fig. 1.

Generalized models of SMC complex assembly. (A) A block-structure of an SMC protein. 1/2 ATPase represents the complex globular domains (blue to indicate disengaged state), with ATP-binding, DNA-binding, ATPase and dimerization activities. (B) An early model for SMC dimer (Melby et al., 1998; Saitoh et al., 1994). (C) The current model of SMC dimer (Gruber et al., 2003; Hirano and Hirano, 2002). (D) The current view of protein-protein interactions within an SMC condensin holocomplex. (E) Alignment of the ATP-binding motifs of SMC and SMC-like proteins. Red color denotes high similarity within the subgroup. The signature SMC residue (arginine) essential for DNA catalysis of ATP hydrolysis (Lammens et al., 2004) is marked with an asterisk. *S.sp.*, *Synechocystis sp.*; *A.a.*, *Aquifex aeolicus*; *M.j.*, *Methanocaldococcus jannaschii*; *P.h.*, *Pyrococcus horikoshii*; *T.p.*, *Treponema pallidum*; *B.s.*, *Bacillus subtilis*; *H.s.*, *Homo sapiens*; *P.p.*, *Pseudomonas putida*; *H.i.*, *Haemophilus influenzae*; *V.c.*, *Vibrio cholerae*; *S.c.*, *Saccharomyces cerevisiae*; *B.b.*, *Borrelia burgdorferi*.

Fig. 2.

The putative structure–function relationships within a bacterial SMC complex. (A and B) The ATP-binding-driven open and closed states of the SMC complex, respectively. (C and D) Binding of the Scp sub-complex to the SMC head domains can either stabilize or prevent DNA embrace, respectively, depending on the order of assembly. (E) A possible mode of DNA coating by SMC complexes (the ATP role is omitted).