

Molecular functional analysis of RadA/Sms: A RecA-like protein

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Homologous recombination (HR) is one of the most important processes in various biological phenomena. HR contributes to maintain the genetic information through DNA repair, such as double-strand break repair and interstrand-crosslink repair. On the other hand, HR generates genetic variation and is thought to be one of the driving forces of evolution through horizontal-gene transfer or intrachromosomal recombination. Because of these contradictory properties, numerous proteins engage in and control each reaction of HR system. In bacteria, RecA protein is one of the most important proteins involved in HR. RecA searches for a homologous DNA sequence and catalyzes strand exchange reaction. Interestingly, most bacteria have another RecA-like protein, RadA/Sms. RadA/Sms is a multidomain protein consisting of three putative functional regions (Fig. 1). Zinc-finger motif, RecA-like ATPase domain, and Lon_C (Lon protease C-terminal) domain are located at N-terminal, center, and C-terminal regions, respectively. Genetic studies have indicated that *radA/sms* gene is involved in HR. However, RadA/Sms-mediated reaction and its molecular function in HR system have been unknown. To investigate the molecular function of RadA/Sms, we analyzed RadA/Sms protein from *Thermus thermophilus*, which is suitable for this study because of its simple but sufficient HR system as well as its high protein stability (Fig. 2). Here, we report DNA substrate specificity of RadA/Sms and relationships between its DNA binding and ATPase activities. We also report the molecular properties of purified RadA/Sms protein, such as its oligomeric state and stability. Finally, we propose a model of RadA/Sms function in HR system.

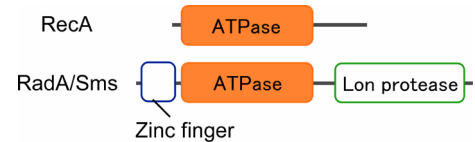


Fig. 1. Domain structures of RecA and RadA/Sms.

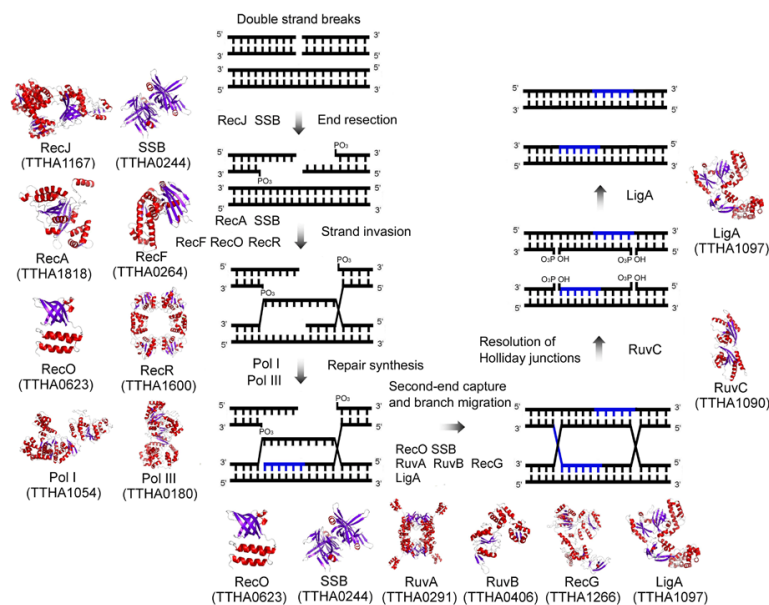


Fig. 2. A schematic representation of a model for homologous recombination (DNA double-strand break repair) pathway in *T. thermophilus*.