No. 65

Cellular and molecular functional analysis of a bacterial Rad52_Rad22 family protein from *Thermus thermophilus* HB8

Tatsuhiko Inoue[1], Atsuhiro Shimada[2], Noriko Nakagawa[2, 3], Ryoji Masui[2, 3] and Seiki Kuramitsu[1, 2, 3]

([1]Grad. Sch. Frontier Biosci., Osaka Univ., [2]Grad. Sch. Sci., Osaka Univ., [3]RIKEN SPring-8 Center, Harima Inst.)

e-mail: tatsuhiko@bio.sci.osaka-u.ac.jp

All organisms have several kinds of DNA repair systems to maintain the genome integrity. Homologous recombination (HR) is one of the DNA repair systems conserved among a wide range of species. HR is an important pathway to repair very severe DNA damage including DNA double-strand break (Fig. 1). In eukaryotes, Rad52 plays crucial roles in HR by recruiting Rad51 recombinase to DNA and promoting the annealing of complementary single-stranded DNA. In bacteria, RecO plays the same functions as eukaryotic Rad52. Though there is little sequence homology, it is said that bacterial RecO is a functional homolog of eukaryotic Rad52. However, some bacteria have Rad52_Rad22 family proteins, which contain the Rad52_Rad22 domain conserved in eukaryotic Rad52 and its homolog Rad22. Bacterial Rad52_Rad22 family proteins lack the C-terminal region of eukaryotic Rad52 which is known as the interaction region with other proteins such as Rad51 (Fig. 2). Bacterial Rad52_Rad22 family proteins are not well studied and its functions are unclear. To reveal the role of this family protein in the bacterial DNA repair system, we genetically and biochemically characterized the Rad52_Rad22 family protein TTHA0081 from *Thermus thermophilus* HB8. In this poster, we discuss the results of cellular and molecular functional analysis of TTHA0081.

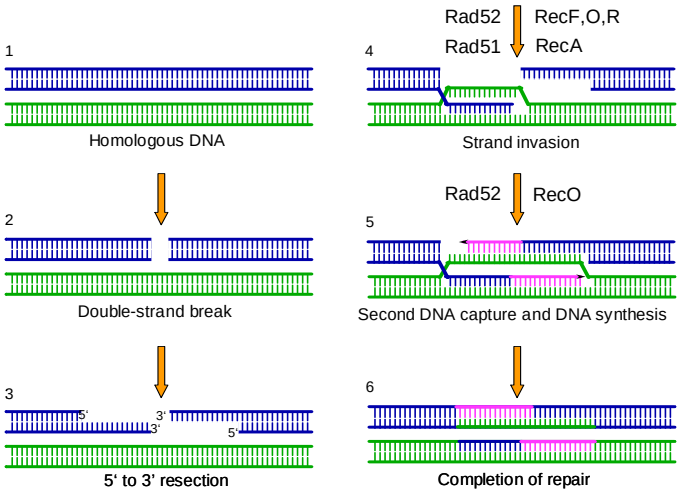

Fig. 1. A model of HR repair

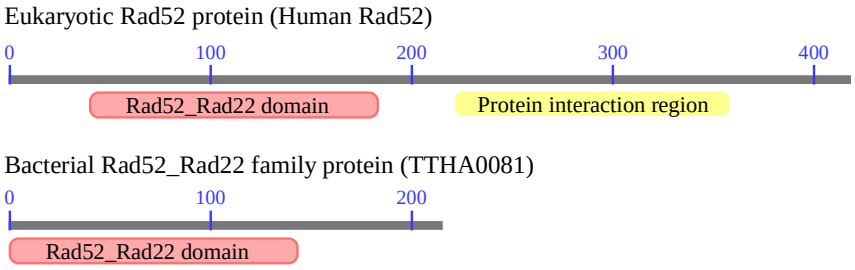

Fig. 2. The domain structures of human Rad52 and TTHA0081