(초청강연)

Crystal structure of mismatch repair protein MutS and its complex with a substrate DNA

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Mismatches in a DNA duplex are mainly due to DNA duplication errors that are generated by improper function of DNA polymerase. MutS, MutL and MutH are crucial proteins for the initiation of the methyl-directed mismatch repairing in bacteria. MutS has an ATPase activity and recognize the mismatched or unpaired bases on DNA. After binding to a mismatch, MutS recruits MutL to mediate the activation of MutH an endonuclease, which cleaves the 5' site of d(GATC) on the un-methylated strand. Both MutL and MutS also have essential roles in the subsequent removal and re-synthesis of the daughter strand. We have determined the crystal structures of either intact or active fragments of each of these proteins, both alone and complexed with ligands (DNA, ADP and ATP). The biochemical and mutagenesis studies based on the detailed 3-D structures led to new insights into the role of the ATPase activity of MutS in the mismatch recognition and directions for future investigation of mismatch repair.