2015 KIAS Workshop on Anomalous Dynamics in Biological Systems

Dynamic Regulation of Mismatch Excision in DNA Mismatch Repair



Physics & IBIO

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During DNA Replication



(Part et al. unpublished)

Error rate ~ 10⁻⁷ /bp

Deficient DNA mismatch repair function



• Error rate of DNA polymerase: I error per 10⁷ bp



DNA mismatch repair increases the fidelity of DNA replication up to 1,000 times.

Error rate ~ 10⁻¹⁰/bp

DNA Mismatch Repair



by UvrD/Exo and DNA Polymerase

MutS

• ATP binding sites EcMutS (Homodimer) HsMsh2-HsMsh6 (Heterodimer) 90° 90° Msh2 Msh6 G/T Mismatched DNA G/T Mismatched DNA 4 nm 9 X 7 X I2 nm

Footprint: 24 bp

Lamers et al. Nature (2001) Warren et al. Mol Cell (2007)

Searching MutS (No ATP)



Polarization of Cy3-MutS







Footprint of MutS: ~ 24 bp

Searching a mismatch by facilitated diffusion



Helical Diffusion along DNA backbone

In the presence of ATP (ATP γ S)



30 bp matched DNA



30 bp mismatched DNA





- ✓ MutS scans duplex DNA in a continuous contact with the DNA backbone to find a mismatch.
- \checkmark ATP-bound MutS moves away from the mismatch in a non-helical diffusion.

Crystal Structure of E. coli ATP-bound MutS



Groothuiaen et al. eLife 2015



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