s8a.m6.o3 **Bacterial conjugation machinery.** X. Gomis-Rueth[1], G. Moncalian[2], A. Guasch[1], F. de la Cruz[2] & M. Coll[1]. [1]*Institut de Biologia Molecular de Barcelona, CSIC, Jordi Girona 18-26, 08034 Barcelona, Spain.* [2]*Departamento de Biología Molecular, Universidad de Cantabria, Cardenal Herrera Oria s/n, 30911, Santander, Spain.*
Keywords: proteins, nucleic acids.

Conjugation is the unidirectional transfer of DNA between bacteria by cell-to-cell contact. It is the major route for horizontal transfer of genetic information. The process involves two kind of events, DNA processing and DNA transport. Each event is carried out by a set of plasmid-encoded proteins. In the processing step, which involves the cleavage and unwinding of the DNA, a nucleoprotein complex called relaxosome is formed. In simple conjugative systems, like that encoded by the *E. coli* plasmid R388, the DNA processing proteins include the relaxase TrwC, which has both nuclease and helicase activities, the repressor protein TrwA, and the membrane protein TrwB, which is responsible for the coupling of the relaxosome to the transmembrane transport apparatus that transfers the cleaved DNA strand to the recipient cell. We have undertaken the structural study of these three proteins and the crystallographic results will be presented.

s8a.m6.o4 **Crystal structure of the *E. coli* DNA mismatch repair protein MutS in complex with a GT mismatch.** M. Lamers, A. Perrakis, J. Enzlin, H. Winterwerp, N. de Wind and T.K. Sixma. *Dep. of Molecular Carcinogenesis, Netherlands Cancer Institute, Plesmanlaan121, 1066 CX, Amsterdam, The Netherlands.*
Keywords: DNA-mismatch repair, MutS, X-ray crystallography.

DNA mismatch repair (MMR) plays an essential role in the conservation of the genome in prokaryotes and eukaryotes, and in humans has been linked to HNPCC, an hereditary form of colon cancer.

The MMR-protein MutS and its eukaryotic homolog MutSα, recognize mismatched bases and short insertion and deletions (IDLs), and subsequently initiate the repair cascade.

We have recently solved the structure of the *Escherichia coli* MutS protein in complex with a GT-mismatch containing DNA oligo. The structure shows a dimer of MutS with the DNA oligo clamped in between the two monomers. The MutS homodimer behaves like a heterodimer with one ADP-bound monomer recognizing the mismatch, while the second monomer has a substantially different conformation. Mismatch recognition occurs through bending of the DNA by 90 degrees and insertion of a phenylalanine next to the mismatched base. Two long helixes extend from a core domain in both monomers ending in a second aspecific DNA binding domain that locks the DNA into the clamp. The ATPase domains form a large dimerization area located far away from the DNA binding domains, suggesting long-distance cross-talk within the two monomers.