

**P014** Understanding the interplay between recombinases, helicases and DNA binding proteins during homologous recombination in archaea

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In all kingdoms of life, extensive DNA repair pathways operate to ensure that genomic integrity is maintained prior to cell division. Homologous recombination is the predominant cellular mechanism responsible for resetting blocked or collapsed replication forks. This process is complex, involving an interplay between recombinases, helicases and DNA binding proteins, and is still not fully understood in eukaryotes. Owing to the similarities between DNA replication and repair pathways in archaea and eukaryotes, the archaea are a convenient model system to study these processes. Recently, our laboratory reported the crystal structure of the DNA helicase, Hel308, conserved in metazoa and archaea, which functions during the early stages of homologous recombination following replication fork arrest. There are also several paralogues of the recombinase Rad51 in most archaeal genomes, mirroring the situation in eukarya. We have solved the structures of two of these proteins from *Sulfolobus solfataricus* and shown that, as for eukaryotic Rad51 paralogues, they have divergent activities and functions. We report on the functional insights gained from these structure-function studies, together with unpublished data showing that Hel308 can play a role in remodelling stalled replication forks by displacing bound proteins such as RPA, allowing nucleoprotein filament formation by recombinases. A combination of biophysical techniques, including single-molecule Fluorescence Resonance Energy Transfer (smFRET) and site-directed spin labelling with EPR have been employed to monitor changes in Hel308 during its catalytic cycle.