1067-92-930 **Mariel Vazquez*** (mariel@math.sfsu.edu), Mathematics Department, San Francisco State University, 1600 holloway Avenue, San Francisco, CA 94116. *The XerCD-FtsK system unlinks replication catenanes in a stepwise manner.*

Replication of circular chromosomes requires unwinding of the DNA and results in the formation of DNA links. In Escherichia coli, error-free unlinking is required to ensure proper segregation at cell division, thus highlighting the importance to characterize the topological mechanism of DNA unlinking. The site-specific recombination system XerCD mediates sister chromosome unlinking in TopoIV deficient cells. This reaction is activated by FtsK, a powerful DNA translocase, which coordinates the last stages of chromosome segregation.

We here study the topological mechanism of DNA unlinking by the XerCD-FtsK system using knot theory and computer simulations. We use the tangle method to find possible topological pathways of DNA unknotting and unlinking by site-specific recombination on small substrates. When assuming that the enzymes systematically reduce the topological complexity of the substrates, we provide rigorous proof that there is only one possible unlinking pathway. For example the XerCD-FtsK system unlinks 6-crossing catenanes in a stepwise manner, converting the 6-cat into a 5-knot, into a 4-cat, into a 3-knot etc... until reaching the unlinked state. This is joint work with Koya Shimokawa, Kai Ishihara, Ian Grainge, David J.Sherratt. (Received September 16, 2010)