Fidelity and infidelity in repairing a broken chromosome

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Repair of chromosomal double-strand breaks (DSBs) is crucial for genome stability. Budding yeast use homologous recombination, usually mediated by the Rad51 protein, to identify sequences homologous to the ends of the DSB and then effect repair. The search for homology is intertwined with the 5' to 3' resection of the DSB ends and surprisingly involves the Arp2/3 actin branching complex and type 1 myosins. Even when a suitable donor has been found and new DNA synthesis is initiated, the process is remarkably fragile: mutations arise at 1000 times the rate seen for normal replication and events reflecting the dissociation of a partially-copied repaired strand lead to nonallelic recombination events. There are also changes in the epigenetic marks during repair.