

IN BRIEF

BACTERIAL TRANSCRIPTION**The right place at the right time**

The positioning of bacterial genes within the cell had previously been proposed to depend on the function of the proteins that they encode — for example, genes encoding membrane proteins would be positioned close to the membrane. This study tests this hypothesis in *Escherichia coli*, examining the dynamics of two loci carrying genes encoding membrane proteins. The authors found that both the *lac* (lactose metabolism) locus and an inducible locus carrying the tetracycline efflux pump TetA fused to mCherry (*tetA-mCherry*) shifted towards the membrane following induction. This relocalization was rapid, occurring within 1–3 minutes of induction for *tetA-mCherry*, and required ongoing transcription and translation. Moreover, the authors detected repositioning of loci that were 90 kb away from *tetA-mCherry*, indicating that large regions of the genome relocalize during gene expression. It is therefore likely that membrane protein expression has an integral role in determining the conformation of the bacterial chromosome.

ORIGINAL RESEARCH PAPER Libby, E. A. et al. Membrane protein expression triggers chromosomal locus repositioning in bacteria. *Proc. Natl Acad. Sci. USA* 23 Apr 2012 (doi:10.1073/pnas.1109479109)

BACTERIAL EVOLUTION**Rewriting the evolutionary rule book**

Mutation in the genome of any organism is thought to occur in a random manner, and selection for beneficial mutations determines whether or not they become fixed in a population. However, in theory the rate of mutation could itself be subject to selection such that, within a single genome, it would be possible to have more mutations in regions where they would be beneficial and fewer mutations in regions where they would be deleterious. Luscombe and colleagues combined phylogenetic and population genetics approaches to analyse 120,000 single nucleotide polymorphisms across 2,659 genes from 34 strains of *Escherichia coli*. They found nonrandom variation in the neutral mutation rate, with mutational hot spots and cold spots that inversely correlate to the degree of purifying selection acting on that particular region of the genome. Thus, it seems that the mutation rate itself is subject to selective pressures, although the mechanisms underlying this surprising observation remain to be determined.

ORIGINAL RESEARCH PAPER Martincorena, I. et al. Evidence of non-random mutation rates suggests an evolutionary risk management strategy. *Nature* 22 Apr 2012 (doi:10.1038/nature10995)

ENVIRONMENTAL MICROBIOLOGY**Dinner for two**

Bacteriophages and predatory bacteria that target the same bacterial prey species had been assumed to compete with each other for infection of an individual cell. However, in a microcosm experiment in which the prey bacterium, *Vibrio vulnificus*, was incubated with both bacteriophage CK-2 and predatory bacterial strains from cluster IX of the *Bacteriovorax* genus, electron microscopy of the prey cells has now revealed that both predators can infect and replicate within a single cell. This is the first time that a co-infection by a bacteriophage and a predatory bacterium has been reported and has important implications for our understanding of microbial predator–prey interactions in the environment.

ORIGINAL RESEARCH PAPER Chen, A. N. et al. Sharing of prey: coinfection of a bacterium by a virus and a prokaryotic predator. *mBio* 3, e00051-12 (2012)