IN BRIEF

MICROBIAL GENETICS

All by myself — mutation rates in lone bacteria

A new report by Krašovec *et al.* has shown that the rate of mutation in *Escherichia coli* to rifampicin resistance is inversely correlated with population density, and that lowering population density can increase mutation rates by up to threefold. The ability of *E. coli* to sense surrounding population densities is dependent on the *luxS* gene, and bacteria with deletions of this gene show no change in mutation rate even when exposed to variations in surrounding population densities. This study provides insights into how mutation rates are controlled in bacteria and has implications for studies of antibiotic resistance.

ORIGINAL RESEARCH PAPER Krašovec, R. *et al.* Mutation rate plasticity in rifampicin resistance depends on *Escherichia coli* cell–cell interactions. *Nature Commun.* **5**, 3742 (2014)

DNA ELEMENTS

Dinucleotide repeats form an enhancer signature

Using a comparative computational approach, Yáñez-Cuna *et al.* studied thousands of enhancers in three *Drosophila melanogaster* cell lines and determined sequence features of enhancers, including enrichment of dinucleotide repeat sequences. Experimental validation of these dinucleotide repeats showed that they are sufficient to form *de novo* enhancers from non-functional sequences. These results have implications for the identification of novel enhancers and for genome sequencing annotations in general.

ORIGINAL RESEARCH PAPER Yáñez-Cuna, J. O. *et al.* Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features. *Genome Res.* http://dx.doi.org/10.1101/gr.169243.113 (2014)

EPIGENETICS

DNA methylation maps of archaic humans

Neanderthal and Denisovan whole-genome DNA methylation maps have been constructed using a method that analyses the degradation of methylated and unmethylated cytosine modifications, and these maps have been compared to those of modern-day humans. Around 2,000 differentially methylated regions were identified, including changes in regions that are likely to be associated with several diseases, such as neurological and psychiatric disorders. Changes in the HOXD gene cluster were also identified, and the authors propose that these changes might be responsible for anatomical differences between archaic and modern-day humans.

ORIGINAL RESEARCH PAPER Gokhman, D. *et al.* Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. *Science* **344**, 523–527 (2014)

EVOLUTION

Parallel evolution of pathogenic *Yersinia*

Whole-genome sequencing of >200 pathogenic and non-pathogenic species of the *Yersinia* genus of bacteria has revealed that pathogenic members of the genus — including *Yersinia pestis* (which causes bubonic plague) and *Yersinia enterocolitica* (which causes gastroenteritis) — have followed parallel evolutionary paths. Phylogenetic analysis shows that these two species did not share a recent common ancestor, as previously thought, but evolved independently to acquire virulence factors and to lose several metabolic genes on the transitional route to pathogenicity.

ORIGINAL RESEARCH PAPER Reuter, S. *et al.* Parallel independent evolution of pathogenicity within the genus *Yersinia*. *Proc. Natl Acad. Sci. USA* **111**, 6768–6773 (2014)