IN BRIEF

AGEING

Longevity by design

Sagi and Kim used genome engineering to explore how lifespan could be enhanced in *Caenorhabditis elegans*. As expected, the individual overexpression of known *C. elegans* longevity-related genes increased lifespan. Importantly, this was also achieved by zebrafish transgenes that provide biochemical functions not found in *C. elegans*, such as an antibacterial lysozyme and a mitochondrial uncoupling protein. Combining up to four manipulations resulted in lifespan increases of up to 130%. The authors also characterized physiological features of long-lived strains, such as overexpression of superoxide dismutase 3 (SOD-3), as a possible rapid readout for longevity.

ORIGINAL RESEARCH PAPER Sagi, D. & Kim, S. K. An engineering approach to extending lifespan in *C. elegans*. *PLoS Genet.* **8**, e1002780 (2012)

GENE EXPRESSION

Transcriptional roles for DNA repair factors

The xeroderma pigmentosum factors XPG and XPF are DNA repair endonucleases; however, various roles in transcription have also been proposed. Le May *et al.* investigated further by knocking down xeroderma pigmentosum factors in HeLa cells and studying the effects on the induction of the *RARB* gene (which is induced by retinoic acid) and on various molecular features at the *RARB* locus. They found that XPG and XPF are required for optimal *RARB* transcription by a complex mechanism involving single-strand DNA break generation, DNA demethylation, CTCF transcription factor recruitment and chromosomal looping to bring the promoter and terminator sequences into proximity.

ORIGINAL RESEARCH PAPER Le May, N. *et al.* XPG and XPF endonucleases trigger chromatin looping and DNA demethylation for accurate expression of activated genes. *Mol. Cell* 5 Jul 2012 (doi:10.1016/j.molcel.2012.05.050)

PATHOGEN GENOMICS

Within-host sequencing of malaria parasites

Deep sequencing was used to analyse *Plasmodium falciparum* DNA using blood samples from patients with malaria across Africa, Asia and Oceania. These data were used to develop a measurement of within-host parasite diversity that relates to the level of inbreeding and that is an important factor in the evolution of drug resistance. The data from this study are publicly available as a part of the ongoing MalariaGEN project, which aims to monitor evolutionary changes in this important pathogen.

ORIGINAL RESEARCH PAPER Manske, M. *et al.* Analysis of *Plasmodium falciparum* diversity in natural infections by deep sequencing. *Nature* 13 June 2012 (doi:10.1038/nature11174)

EVOLUTIONARY GENOMICS

The genomic landscape of maize

Genomic analysis from large-scale resequencing of diverse maize varieties is reported in three new papers. Together, these studies reveal insights into genomic diversity, phenotypic associations, selection and evolution of maize, which has been a staple food crop since it was first domesticated 10,000 years ago. This detailed characterization of maize genomes will provide targets for future breeding efforts.

ORIGINAL RESEARCH PAPERS Chia, J.-M. *et al.* Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genet.* **44**, 803–807 (2012) | Hufford, M. B. *et al.* Comparative population genomics of maize domestication and improvement. *Nature Genet.* **44**, 808–811 (2012) | Jiao, Y. *et al.* Genome-wide genetic changes during modern breeding of maize. *Nature Genet.* **44**, 812–815 (2012)