

IN BRIEF

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URLs

➤ GENOMICS

The medaka draft genome and insights into vertebrate genome evolution.

Kasahara, M. *et al. Nature* **447**, 714–719 (2007)

The medaka fish has become an important model organism. A high-quality draft sequence of its ~700 Mb genome, containing some 20,000 predicted genes, has now been published. A comparison of the medaka, zebrafish, pufferfish and human genomes provided interesting insights into early vertebrate genome evolution — the zebrafish and medaka genomes appear to have undergone eight major interchromosomal rearrangements in ~50 million years following the whole-genome duplication event in the common ancestor of the bony fish. For the next ~300 million years, medaka's karyotype appears to have been preserved.

➤ CHROMOSOME BIOLOGY

Positional stability of single double-strand breaks in mammalian cells.

Soutoglou, E. *et al. Nature Cell Biol.* **9**, 675–682 (2007)

Incorrectly repaired double-strand breaks can result in chromosomal translocations. Two models have been proposed for how broken chromosome ends find their translocation partners: broken ends scan the nucleus for potential partners; alternatively, translocations occur only between neighbours. Having developed a cell-based system in which double-strand breaks are induced at a defined genomic site and their fate followed in real time, the authors show that broken ends are unable to roam the nucleus and that their immobilization requires the DNA-end-binding protein Ku80, but not DNA repair factors.

➤ HUMAN EVOLUTION

Localizing recent adaptive evolution in the human genome.

Williamson, S. H. *et al. PLoS Genet.* **3**, e90 (2007)

This genome-wide search for regions that have undergone selection in the human genome uses a new method that is not biased by variation in recombination rate and SNP frequency. Unlike previous methods, it can detect complete selective sweeps, in which no polymorphism is left in the population. Genes for components of the dystrophin complex, pigmentation proteins and centromeric regions were particularly likely to have been selected. Stronger signals of selection in non-African populations might represent adaptation to novel environments since the migration out of Africa.

➤ NETWORK BIOLOGY

MicroRNA-mediated feedback and feedforward loops are recurrent network motifs in mammals.

Tsang, J., Zhu, J. & van Oudenaarden, A. *Mol. Cell* **26**, 753–767 (2007)

Gene regulatory networks in bacteria and yeast are made up of recurring motifs that resemble the components of electrical circuits. This paper shows that similar motifs exist in the microRNA-mediated circuits of mammals. Genome-wide expression data shows that the expression of mRNAs tends to be highly correlated, either positively or negatively, with that of the microRNAs that regulate them. Positive correlation might represent a feedback control mechanism, whereas negative correlation implies that the microRNAs provide an extra level of control to ensure robustness of gene expression.