

## IN BRIEF

**RNA INTERFERENCE****Antiviral immunity in *Drosophila* requires systemic RNA interference spread**

Saleh, M.-C. *et al. Nature* 8 Feb 2009 (doi:10.1038/nature07712)

Insects can mount a local antiviral RNAi defence; however, it has now been shown that *Drosophila melanogaster* can also generate a systemic RNAi response. Inoculation of flies with dsRNA corresponding to regions of the Sindbis and *Drosophila C* viral genomes led to a sequence-specific systemic immune response, which required a recently defined dsRNA uptake pathway. This study suggests that immunity in vertebrates and invertebrates may be more highly conserved than previously believed.

**DEVELOPMENT****Nodal points and complexity of Notch–Ras signal integration**

Hurlbut, G. D. *et al. Proc. Natl Acad. Sci. USA* 26 Jan 2009 (doi:10.1073/pnas.0812024106)

Although it is known that signalling pathways interact during development, how signals are integrated remains unexplored. By examining the genome-wide, common transcriptional targets of two pathways — Notch and receptor tyrosine kinase (RTK) — in transgenic fly embryos, the authors reveal extensive crosstalk between the two pathways, identify the integration points (which were validated through genetic interaction analysis) and suggest that Notch increases the output specificity of RTK signalling.

**GENOME EVOLUTION****Cryptic variation in the human mutation rate**

Hodgkinson, A. *et al. PLoS Biol.* **7**, e1000027 (2009)

**Hotspots of biased nucleostide substitution in human genes**

Berglund, J. *et al. PLoS Biol.* **7**, e1000026 (2009)

These two papers examine factors affecting the rate of mutation in the human genome. Hodgkinson and colleagues identified nucleotide positions with rapid mutation rates as those that have SNPs in both humans and chimpanzees. Substantially increased mutation rate at these sites was not due to CpG dinucleotides or neighbouring nucleotides, but was influenced by sequence context in a complex and previously undetected way. A bias towards AT-to-GC substitutions in genes with accelerated substitutions in humans, detected by comparison with primate genomes, suggested to Berglund and colleagues that increased mutation in these genes is influenced by recombination rather than positive selection.

**CANCER GENETICS****The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer**

Fernandez, A. F. *et al. Genome Res.* 10 Feb 2009 (doi:10.1101/gr.083550.108)

This paper suggests that the progression of viral-linked cancers might be caused by epigenetic changes in the viral DNA. The authors created a methylation map of three oncogenic viruses — Epstein–Barr virus, human papilloma virus and hepatitis B virus — and show that these genomes become progressively methylated during disease progression. Methylation, which might shield viruses from the immune system, could therefore be used as a biomarker for disease.