IN BRIEF

GENE THERAPY

Genome editing in haematopoietic stem cells

Researchers have developed a protocol that enables zinc-finger nuclease-mediated targeted editing of DNA sequences in human long-term repopulating haematopoietic stem cells (HSCs). Genovese *et al.* were able to successfully integrate a corrective complementary DNA downstream of the *IL2RG* (interleukin-2 receptor, gamma) promoter in blood-cell precursors from a patient with X-linked severe combined immunodeficiency syndrome, which is caused by mutations in *IL2RG*. Gene correction occurred in 3–11% of treated cells (depending on primitive versus committed progenitor status).

ORIGINAL RESEARCH PAPER Genovese, P. *et al.* Targeted genome editing in human repopulating haematopoietic stem cells. *Nature* http://dx.doi.org/10.1038/nature13420 (2014)

PLANT GENOMICS

Insights into duplicate gene fate in plants

Polyploidization (that is, whole-genome multiplication) among plants is a pivotal contributor to evolution. US researchers have now developed a statistical learning model to predict whether a duplicate gene is likely to be retained after a polyploidization event on the basis of features identified using comparative genomic analyses of wild radish and three other Brassicaceae species. Retained radish duplicates showed substantial divergence in sequence and expression. They also differed markedly from genes that reverted to singleton states; for example, they have a lower rate of evolution, higher network connectivity, and broader and higher expression.

ORIGINAL RESEARCH PAPER Moghe, G. D. *et al.* Consequences of whole-genome triplication as revealed by comparative genomic analyses of the wild radish *Raphanus raphanistrum* and three other Brassicaceae species. *Plant Cell* http://dx.doi.org/10.1105/tpc.114.124297 (2014)

SYNTHETIC BIOLOGY

Communication from the non-living world

Artificial cells can translate chemical messages to modify the behaviour of bacterial cells and might thus be useful as non-living biological sensors, a new study reports. Lentini *et al.* generated artificial cells that contained a plasmid construct, the transcription–translation machinery and isopropyl-β-D-1-thiogalactopyranoside (IPTG) encapsulated in a phospholipid vesicle. In co-incubation experiments with *Escherichia coli* cells, the artificial cells responded to theophylline treatment through their encoded riboswitch to activate expression of a membrane pore protein that resulted in release of IPTG, which diffused into the *E. coli* cells to modulate transcription.

ORIGINAL RESEARCH PAPER Lentini, R. *et al.* Integrating artificial with natural cells to translate chemical messages that direct *E. coli* behaviour. *Nature Commun.* **5**, 4012 (2014)

EVOLUTION

How the butterfly changed its spots

Serial homologues, such as the eyespots on butterfly wings, are repeated units that occur in different parts of the body. There are two theories on the evolution of eyespots: they could have evolved as a single band that later differentiated into spots or from a single unit that duplicated and spread. Suggestive of the latter theory, a comparative analysis of >400 species of nymphalid butterflies indicates that eyespots arose on the ventral hindwing as a form of protection against predators. They later evolved to spread onto the dorsal and anterior wing surfaces to take on a completely different function in sexual signalling.

ORIGINAL RESEARCH PAPER Oliver, J. C. *et al.* Nymphalid eyespot serial homologues originate as a few individualized modules. *Proc. Biol Sci.* **281**, 20133262 (2014)