

## IN BRIEF

**PATHOGEN GENETICS****Origin and transmission of Ebola virus outbreak**

In response to the recent large-scale outbreak of Ebola virus disease, a team of researchers used high-throughput sequencing to study diversity among 99 Ebola virus genomes from 78 patients in Sierra Leone. Comparison with previous outbreak strains revealed that the viruses in this epidemic are likely to have spread from Middle Africa within the past decade, followed by human-to-human transmission during the outbreak. Moreover, they found 395 mutations that are distinct to this current lineage, including 50 fixed non-synonymous mutations, which might represent possible determinants of pathogenicity and therapeutic avenues for this epidemic.

**ORIGINAL RESEARCH PAPER** Gire, S. K. *et al.* Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. *Science* <http://dx.doi.org/10.1126/science.1259657> (2014)

**NON-CODING RNA****Interrogating miRNA–target interactions *in vivo***

Bioinformatic algorithms have predicted many microRNA (miRNA) targets known as miRNA response elements (MREs), but studying their relevance *in vivo* remains challenging. Bassett *et al.* used genome editing to disrupt endogenous MREs, which allowed them to characterize specific miRNA–target interactions in zebrafish embryos and fruitflies. They also developed a new method to custom-edit MREs in human cell cultures using CRISPR-mediated homology-directed repair with short oligonucleotides.

**ORIGINAL RESEARCH PAPER** Bassett, A. R. *et al.* Understanding functional miRNA–target interactions *in vivo* by site-specific genome engineering. *Nature Commun.* **5**, 4640 (2014)

**POPULATION GENOMICS****Determinants of genetic diversity**

Romiguier *et al.* sequenced the transcriptomes of 2–10 individuals from each of 76 non-model animal species to quantify the population genetic diversity, followed by analyses of ecological, biological or geographical features that correlate with the level of diversity. They found that strong parental investment in raising offspring was the best predictor of low genetic diversity. Populations of these low-diversity species, including numerous invertebrates, might be the least able to recover following environmental perturbation.

**ORIGINAL RESEARCH PAPER** Romiguier, J. *et al.* Comparative population genomics in animals uncovers the determinants of genetic diversity. *Nature* <http://dx.doi.org/10.1038/nature13685> (2014)

**SIGNALLING****Male exosomes affect female behaviour**

In *Drosophila melanogaster*, seminal peptides secreted by the male accessory glands can control post-mating behaviour in females, such as inhibiting remating. As exosomes (a type of secretory vesicle) are known to mediate intercellular signalling in various species, Corrigan *et al.* used a fluorescent exosomal marker to track whether exosomes had a role in this male-to-female communication. Exosomes were observed to be secreted into the accessory gland lumens and were released during mating, when they fused with sperm cells and interacted with the female epithelium. Blocking exosome production reduced the ability of males to modulate female behaviour, thus confirming their functional importance.

**ORIGINAL RESEARCH PAPER** Corrigan, L. *et al.* BMP-regulated exosomes from *Drosophila* male reproductive glands reprogram female behavior. *J. Cell Biol.* **206**, 671–688 (2014)