Nature Reviews Genetics | AOP, published online 12 March 2013

IN BRIEF

REGULATORY RNA

Circular sponges

Two groups have identified a stable circular RNA that acts as a molecular sponge for microRNAs. The RNA is highly expressed in the human and mouse brain and contains ~70 sites for miR-7 binding, thus sequestering the miRNA away from its targets. The circular RNA was also shown to bind Argonaute proteins, which are a part of the RNA-induced silencing complex. The binding of miR-7 prevents translation of the circular RNA, suggesting that its sole function is the titration of small regulatory RNAs. Bioinformatic analysis revealed numerous other circular RNAs, suggesting this could be a widespread mechanism of gene regulation.

ORIGINAL RESEARCH PAPERS Memczak, S. *et al.* Circular RNAs are a large class of animal RNAs with regulatory potency. *Nature* 27 Feb 2013 (doi:10.1038/nature11928) | Hansen, T. B. *et al.* Natural RNA circles function as efficient microRNA sponges. *Nature* 27 Feb 2013 (doi:10.1038/nature11993)

GENE REGULATION

Allosteric effects

In this study, the authors carried out a single-molecule analysis of DNA–protein interactions. They compared the dissociation constant of a protein after binding to naked DNA or to DNA with an adjacent bound protein. This revealed interference between the binding of the two proteins and hence allosteric effects. The authors' data suggest that the deformation of the double helix by the binding of the first protein mediates this interaction. These effects were shown to be relevant to the affinity of a transcription factor for histone-bound DNA and were shown to influence gene expression in bacteria.

ORIGINAL RESEARCH PAPER Kim, S. *et al.* Probing allostery through DNA. *Science* **339**, 816–819 (2013)

EVOLUTION

Tracking down human adaptations

Candidate regions of the human genome that may have been involved in the adaptation of our species can be identified using methods that detect signals of positive selection. However, few human adaptive traits have been characterized because of the difficulties in pinpointing adaptive mutations and characterizing their functions; these challenges are addressed in two recent papers by Pardis Sabeti and colleagues. The study by Grossman *et al.* analysed sequencing data from the 1000 Genomes Project using a previously developed method called the composite of multiple signals (CMS) test. This test leverages several population genetic statistics to reduce the number of candidate causal variants in a candidate region identified as being under positive selection. The authors present a catalogue of annotated candidate causal variants that will provide a valuable resource for functional follow-up. In an elegant example of such functional analysis of a candidate adaptive variant, Kamberov *et al.* used a mouse model to identify the phenotypic effects of a variant in the ectodysplasin A receptor (*EDAR*) gene. A specific variant in this gene has previously been shown to associate with hair thickness and incisor tooth shape in East Asian populations. The authors knocked the variant into a mouse model and showed that it increased hair thickness; they also found new effects of the mutation, which they subsequently analysed in an association study in humans.

ORIGINAL RESEARCH PAPERS Grossman, S. R. *et al.* Identifying recent adaptations in large-scale genomic data. *Cell* **152**, 703–713 (2013) | Kamberov, Y. G. *et al.* Modeling recent human evolution in mice by expression of a selected EDAR variant. *Cell* **152**, 691–702 (2013)