Nature Reviews Genetics | AOP, published online 12 April 2012

IN BRIEF

EPIGENETICS

Mapping histone modifications and DNA methylation together

Two papers present approaches for direct identification of the co-occurrence of histone modifications and DNA methylation; the relationship between these marks is usually studied by correlative approaches. In both papers, the authors used chromatin immunoprecipitation to capture the fraction of the genome that is associated with the histone modification of interest — in this case, histone H3 lysine 27 trimethylation — and then performed bisulphite sequencing on the immunoprecipitated material to map DNA methylation at high resolution. This approach should be applicable to other histone marks.

ORIGINAL RESEARCH PAPERS Statham, A. L. *et al.* Bisulphite-sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. *Genome Res.* 30 Mar 2012 (doi:10.1101/gr.132076.111) | Brinkman, A. B. *et al.* Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. *Genome Res.* 30 Mar 2012 (doi:10.1101/gr.133728.111)

EVO-DEVO

Stickleback genomes illuminate adaptive evolution

The threespine stickleback is a valuable organism for studying the molecular basis of adaptive evolution, as populations of these fish have adapted from marine to freshwater environments in many geographic locations. This publication of a reference genome and sequences of multiple marine and freshwater sticklebacks has enabled the genome-wide identification of regions of divergence between the populations; this will be a useful resource for studies of adaptation and ecological speciation. Insights that have already emerged include a substantial contribution of non-coding sequences to the divergent loci.

ORIGINAL RESEARCH PAPER Jones, F. C. *et al.* The genomic basis of adaptive evolution in threespine sticklebacks. *Nature* **484**, 55–61 (2012)

SMALL RNAs

Small RNAs in DNA repair

During repair of an I-SceI endonuclease-triggered double-stranded DNA break (DSB) in *Arabidopsis thaliana*, Wei *et al.* detected small RNAs corresponding to regions surrounding the DSB. The production of these small RNAs and the repair efficiency were attenuated in plants that were deficient for components of the RNAi machinery, suggesting an active role for small RNA processing in the repair; similar results were obtained in human cells. The precise molecular details and relevance for non-I-SceI DNA damage remain to be determined.

ORIGINAL RESEARCH PAPER Wei, W. *et al.* A role for small RNAs in DNA double-strand break repair. *Cell* **149**, 101–112 (2012)

COMPLEX TRAITS

Imprinting meets maternal effects for birth weight control

This study identified a maternal genetic effect that can work together with a maternal epigenetic effect. *PHLDA2* is a maternally expressed imprinted gene that affects birth weight in mammals. Ishida *et al.* identified a *PHLDA2* promoter variant that is associated with lower transcriptional activity in a human cohort and showed that mothers who were homozygous for this variant bore the heaviest babies. This effect was larger than that expected from imprinting alone, indicating that *PHLDA2* exerts its effects through both maternal effects and imprinting.

ORIGINAL RESEARCH PAPER Ishida, M. *et al.* Maternal inheritance of a promoter variant in the imprinted *PHLDA2* gene significantly increases birth weight. *Am. J. Hum. Genet.* 22 Mar 2012 (doi:10.1016/j.ajhg.2012.02.021)