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IN BRIEF

COMPLEX TRAITS

Variant associated with phenotypic variability

To date, genome-wide association studies have focused on variants that influence the magnitude of a trait, but evidence from several species suggests that phenotypic variability has some degree of genetic control. A study has now identified the first example of an individual genetic variant associated with variability of a complex trait. Yang *et al.* conducted a meta-analysis of genome-wide association studies for phenotypic variability in body mass index and height and found a SNP at the *FTO* locus that is associated with variability in body mass index. The authors found no SNPs that were associated with variability in height. As this study included ~170,000 samples, it suggests that most SNPs are not associated with phenotypic variability (or that they have very small effects on variability).

ORIGINAL RESEARCH PAPER Yang, J. *et al.* *FTO* genotype is associated with phenotypic variability of body mass index. *Nature* 16 Sep 2012 (doi:10.1038/nature11401)

GENE EXPRESSION

Uncovering sex-biased eQTLs

Dimas *et al.* examined expression quantitative trait loci (eQTLs) in male and female cell lines from four HapMap populations; this is the first investigation of whether sex-specific eQTLs exist in humans. The authors found that 12–15% of eQTLs are sex-biased: they affect expression levels in only one sex. In addition, some eQTLs shared by both sexes have a substantially greater effect in one sex. This work shows that considering the sexes separately is likely to be beneficial in studies of the contribution of genetic variation to disease.

ORIGINAL RESEARCH PAPER Dimas, A. *et al.* Sex-biased genetic effects on gene regulation in humans. *Genome Res.* 7 Sep 2012 (doi:10.1101/gr.134981.111)

EPIGENETICS

Asymmetric complexity of the histone code

Voigt *et al.* developed a mass-spectrometry-based method for studying the histone modifications of single nucleosomes. In various cell types, they found that modifications such as histone H3 lysine methylations occurred both asymmetrically and symmetrically (that is, they were present on either one or both copies of the histone family member in the nucleosomal octamer). These distinctions have biological relevance; for example, methylation of H3K27 by Polycomb-repressive complex 2 (PRC2) was inhibited only when both copies of histone H3 had either H3K4me3 or H3K36me3 modifications. Such symmetry considerations add another layer of complexity to the histone code.

ORIGINAL RESEARCH PAPER Voigt, P. *et al.* Asymmetrically modified nucleosomes. *Cell* **151**, 181–193 (2012)

CANCER

Retrotransposition in colorectal cancer

Insertional mutagenesis has the potential to activate or to inactivate cancer-relevant genes, but how widespread this process is in human cancer is unclear. Solyom *et al.* sequenced DNA adjacent to LINE1 retrotransposons to identify LINE1 locations in colorectal cancer genomes and their normal tissue counterparts. They found evidence of LINE1 mobility (new insertions) in 13 out of 16 tumours but not in normal tissues, and the number of insertions increased with patient age. Although the oncogenic potential of these events awaits functional confirmation, some insertions occurred at known cancer genes.

ORIGINAL RESEARCH PAPER Solyom, S. *et al.* Extensive somatic L1 retrotransposition in colorectal tumors. *Genome Res.* 11 Sep 2012 (doi:10.1101/gr.145235.112)