IN BRIEF

GENETIC DISEASE

Virus-plus-susceptibility gene interaction determines Crohn's disease gene *Atg16L1* phenotypes in intestine

Cadwell, K. *et al. Cell* **141**, 1135–1145 (2010)

Although over 30 genes have been associated with susceptibility to Crohn's disease, each variant confers only a modest risk. The authors show that in mice, the pathological features of Crohn's disease are seen in hypomorphs for the susceptibility gene *Atg16L1* (an autophagy gene) only if the mice are also infected with a specific strain of an enteric virus, murine norovirus (MNV). The abnormalities that result from this virus-by-genotype interaction depend on the cytokines tumour necrosis factor-α and interferon-γ as well as commensal bacteria.

TRANSCRIPTOMICS

Global analysis of *trans*-splicing in *Drosophila*

McManus, C. J., Duff, M. O., Eipper-Mains, J. & Graveley, B. R. *Proc. Natl Acad. Sci. USA* 1 Jul 2010 (doi:10.1073/pnas.1007586107)

According to this study, *trans*-splicing — the joining of exons from different mRNAs — might be important for the expression of genes with complex structures. The authors used paired-end mRNA deep sequencing to identify *trans*-splicing events in *Drosophila melanogaster*. They found little evidence for *trans*-splicing between genes at distant locations, but identified 80 genes for which *trans*-splicing takes place between homologous alleles. These genes had either alternative first or 3′ terminal exons or contained very large introns.

COMPLEX TRAITS

Functionally defective germline variants of sialic acid acetylesterase in autoimmunity

Surolia, I. *et al. Nature* 16 Jun 2010 (doi:10.1038/nature09115)

This study highlights the importance of rare variants in common disease. The authors investigated the gene that encodes sialic acid acetylesterase (which negatively regulates antigen signalling by B cells) to see whether rare, loss-of-function variants in *SIAE* contribute to autoimmune disease. Resequencing of *SIAE* exons in 900 patients with autoimmunity and over 600 controls showed that rare germline variants are overrepresented in individuals who are susceptible to several common autoimmune disorders.

SMALL RNAS

Loss of individual microRNAs causes mutant phenotypes in sensitized genetic backgrounds in *C. elegans*

Brenner, J. L., Jasiewicz, K. L., Fahley, A. F., Kemp, B. J. & Abbott, A. L. *Curr. Biol.* 24 Jun 2010 (doi:10.1016/j.cub.2010.05.062)

Although microRNAs (miRNAs) are essential for animal development, most mutations in miRNA genes cause no detectable phenotype. These authors studied mutations in *Caenorhabditis elegans* miRNA genes in two types of genetically sensitized background: one with reduced levels of processing or function of all miRNAs, and another with decreased expression of chromatin regulatory genes that function widely in development. In these backgrounds, mutant phenotypes were identified for 35 out of 31 miRNAs, providing new insights into the roles of individual miRNAs.