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IN BRIEF

MOUSE GENETICS

Fruits of the Collaborative Cross

A collection of 15 articles that highlight research carried out using the international Collaborative Cross project has been published in *Genetics* and *G3: Genes, Genomes, Genetics*. In the past decade, the Collaborative Cross project has developed recombinant inbred lines of mice, each containing a different genomic contribution from eight founder strains. Some papers cover the mapping methodology, and others describe the development and successful application of the Collaborative Cross — and of a related 'Diversity Outbred' resource — to studying the effect of sequence variation on many mouse traits. The traits range from blood pressure or glucose levels to the adverse response to drugs.

ORIGINAL RESEARCH PAPERS *Genetics* collection: http://www.genetics.org/site/misc/MouseGeneticResources.xhtml; *G3* collection: http://www.g3journal.org/site/misc/MouseGeneticResources.xhtml.

TECHNOLOGY

High-throughput enhancer screening

The functional effects of genetic variation in enhancer elements are poorly understood. Now, two groups have developed a massively parallel reporter assay for screening such variation. Variants of enhancers are inserted into plasmids linked to transcriptional cassettes that produce a unique sequence tag following activation; tags can be identified by high-throughput sequencing and thus give a readout of the function of each enhancer variant. The assay was shown to be effective in cell lines and *in vivo* in mouse livers.

ORIGINAL RESEARCH PAPERS Melnikov, A. *et al.* Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. *Nature Biotech.* 26 Feb 2012 (doi:10.1038/nbt.2137) | Patwardhan, P. *et al.* Massively parallel functional dissection of mammalian enhancers *in vivo*. *Nature Biotech.* 26 Feb 2012 (doi:10.1038/nbt.2136)

HUMAN DISEASE

Small RNAs in Huntington's disease

Bañez-Coronel *et al.* investigated the pathogenic mechanism of expanded CAG triplet repeats in the huntingtin gene. They focused on repeats of more than 40 triplets that are associated with complete penetrance of the disease. Expression of these repeats corresponded with an increase in 21-nucleotide-long CAG-repeat small RNAs, which are processed in a Dicer-dependent manner and have neurotoxic activity. These RNAs were able to repress the expression of CTG-containing genes that are down-regulated in Huntington's disease.

ORIGINAL RESEARCH PAPER Bañez-Coronel, M. *et al.* A pathogenic mechanism in Huntington's disease involves small CAG-repeated RNAs with neurotoxic activity. *PLoS Genet.* 23 Feb 2012 (doi:10.1371/journal.pgen.1002481)

SMALL RNAs

A new mechanism of microRNA target recognition

Current algorithms for predicting microRNA (miRNA) target sites only partially account for the range of sites that have been experimentally identified. Chi *et al.* analysed the 27% of experimentally determined but non-canonical mouse miR-124 binding sites and found a common motif that requires the bulging of a G nucleotide in the mRNA to bind to the miRNA seed sequence. They showed that this mode of interaction efficiently represses gene expression and could be used by many miRNAs.

ORIGINAL RESEARCH PAPER Chi, S. W., Hannon, G. J. & Darnell, R. B. An alternative mode of microRNA target recognition. *Nature Struct. Mol. Biol.* 12 Feb 2012 (doi:10.1038/nsmb.2230)