IN BRIEF

EPIGENETICS

Argonaute slicing is required for heterochromatic silencing and spreading.

Irvine, D. V. *et al. Science* **313**, 1134–1137 (2006)

It has been proposed that small interfering RNA (siRNA)-guided histone H3 dimethylation on lysine 9 (H3K9me2) might be caused by an interaction of siRNA with DNA and the recruitment of modified histones by the RITS complex. Alternatively, siRNAs might guide histone modification by base-pairing with RNA. Working in fission yeast, Irvine *et al.* provide support for the second mechanism. They show that the endonucleolytic cleavage motif of Argonaute is required for heterochromatic silencing and for 'slicing' mRNAs that are complementary to siRNAs. They also show that spreading of silencing requires read-through transcription, as well as slicing.

TECHNOLOGY

Trans-kingdom transposition of the maize *Dissociation* element.

Emelyanov, A. *et al. Genetics* 1 September 2006 (doi:10.1534/genetics.106.061184)

Transposons are useful tools for genetic manipulation, but the range of hosts for any given transposon system is restricted. These authors report that the maize *Dissociation* (*Ds*) element transposes in zebrafish, yielding high germline transmission rates, and in mammalian cells, in which it can carry large inserts and still transpose accurately and at high frequency. This is the first example of a mobile element that can transpose in hosts from both the plant and animal kingdoms, making *Ds* a versatile genetic tool.

POPULATION GENETICS

Global genetic change tracks global climate warming in *Drosophila subobscura*.

Balanyá, J. *et al. Science* 31 August 2006 (doi:10.1126/science.1131002)

Global warming over the last 2–3 decades has altered gene frequencies in the fruitfly *Drosophila subobscura*. The frequency of a chromosomal inversion in this species varies clinally with latitude because of temperature differences. The authors compared data sets that had been collected, on average, 24 years apart from North American, South American and European populations. They found that in most populations the frequency distribution had shifted in favour of the low-latitude, warm-climate genotype, and that the average shift was 70 miles closer to the equator.

DEVELOPMENT

The dwarf phenotype of the *Arabidopsis acl5* mutant is suppressed by a mutation in an upstream ORF of a *bHLH* gene.

Imai, A. *et al. Development* **133**, 3575–3585 (2006)

This study reveals a role for upstream open reading frames (uORFs) in plant development. Loss-of-function mutations in the *Arabidopsis thaliana ACL5* gene cause dwarfism. Imai and colleagues show that a mutation in *SAC51* suppresses the *ACL5* mutant phenotype. The *SAC51* mutation causes premature termination of a short uORF, which results in increased translation of the main ORF. The authors provide evidence that wild-type *ACL5* functions by overcoming the inhibition of translation of *SAC51* mRNA that is mediated by its uORF.

HUMAN GENETICS

INDELible markers

Over 10 million unique SNPs, some of which influence human traits and disease susceptibilities, have been identified in the human genome. Now, another type of natural genetic variation, which involves insertion and deletion polymorphisms (indels), has been systematically studied and mapped for the first time.

Understanding more about indels is important because they are known to contribute to human disease. A common mutation that causes cystic fibrosis involves a 3 bp deletion that eliminates a single amino acid. A number of diseases such as fragile X syndrome are caused by DNA insertions that result from the expansion of short trinucleotide repeat units. The insertion of transposable genetic elements into genomes has also been implicated in haemophilia, neurofibromatosis, muscular dystrophy and cancer.

Mills *et al.* used a novel computational approach to analyse independent sets of previously generated DNA sequence traces that were derived from several individuals. The sequence traces were mapped to unique locations in a reference human genome and then aligned with the reference DNA sequence to identify indels that ranged in size from 1 bp to 10,000 bp. The analysis identified over 400,000 non-redundant indels, of which more than 280,000 were validated by comparison with other human or chimpanzee genomes.

Several types of indel polymorphism were identified. Insertions and deletions of single base pairs comprised about 30% of the total. Another ~30% consisted of expansions of either monomeric base-pair repeats or multi-base repeats. Approximately 40% of indels included insertions of apparently random DNA sequences. Transposons accounted for only a small proportion (less than 1%) of the polymorphisms that were identified.

Indels were spread throughout the genome at an average density of one polymorphism every 7.2 kb and their distribution was similar for all chromosomes, although hot spots of indel variation were also detected. Over 148,000 indels were found in known human genes, of which more than 5,000 were located within the promoters or exons. Of the 262 indels that were identified within the protein-coding regions of genes, only 34 had been previously described.

The authors estimate that the total number of indels in the human genome is approximately 1.5 million. Given the potential effects of indels on gene function, it will be important to extend this systematic analysis to more of the known genomic DNA sequences. A more complete genomic map of genetic polymorphisms of all types should facilitate the identification of the specific variations that are relevant to human disease.

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ORIGINAL RESEARCH PAPER Mills, R. E. *et al.* An initial map of insertion and deletion (INDEL) variation in the human genome. *Genome Res.* 10 August 2006 (doi:10.1101/gr.4565806)
FURTHER READING Feuk, L., Carson, A. R. & Scherer, S. W. Structural variation in the human genome. *Nature Rev. Genet.* **7**, 85–97 (2006)

ERRATUM

Evolutionary genetics: High-resolution mutation mapping reveals parallel experimental evolution in yeast.

Nature Reviews Genetics **7**, 665 (2006); doi:10.1038/nrg1958

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