

IN BRIEF

 **EPIGENETICS**

Small RNA-directed epigenetic natural variation in *Arabidopsis thaliana*.

Zhai, J. *et al. PLoS Genet.* **4**, e1000056 (2008)

This paper suggests that small interfering RNAs (siRNAs) have a widespread role in directing variation in DNA methylation patterns in *Arabidopsis thaliana*. In one ecotype, a set of highly expressed siRNAs direct DNA methylation at a specific locus, whereas another ecotype generates a different set of low abundance siRNAs that do not direct DNA methylation at this locus. A genome-wide comparison identified a total of 68 loci at which siRNAs of ~24 nucleotides were expressed only in one ecotype; in most cases their expression again correlated with differences in methylation.

 **GLOBAL CHALLENGES**

Special issue on plant genomes.

Science **320**, 465–497 (2008)

This special issue of *Science* features editorial, news and perspective articles, and a multimedia feature, that explore our increasing knowledge of plant genomes and how it can be applied. In terms of basic biology, there are articles on plant genome structure and evolution, plant metabolism, epigenetics, and population and ecosystem genetics. The news articles focus on the current status of crop genetic modification for agricultural and industrial applications, highlighting both successes and ongoing challenges, the latter of which include the continuing problem of lack of acceptance of genetically modified crops in some countries.

 **EVOLUTION**

Null mutations in human and mouse orthologs frequently result in different phenotypes.

Liao, B.-Y. & Zhang J. *Proc. Natl Acad. Sci.* 5 May 2008 (doi:10.1073/pnas.0800387105)

An assumption of comparative genomics studies is that orthologous genes have similar functions and phenotypes across organisms. In their systematic survey of null mutant phenotypes, the authors have found that over 20% of essential human genes have non-essential mouse orthologues, and that the change in function has been caused by adaptations in the protein-coding sequence rather than in gene expression. The study might have implications for comparative studies of more divergent species.

 **DISEASE MODELS**

A role for sex chromosome complement in the female bias in autoimmune disease.

Smith-Bouvier, D. L. *et al. J. Exp. Med.* 28 Apr 2008 (doi:10.1084/jem.20070850)

Most autoimmune diseases are more common in females than in males, a feature that is reproduced in animal models. To distinguish genetic from hormonal influences on sex bias, models of two autoimmune diseases — experimental autoimmune encephalomyelitis and pristane-induced lupus — were generated in which XY or XX mice could be examined in the hormonal background of either sex. The female bias persisted, showing that the greater susceptibility is conferred by female sex-chromosome complement.