IN BRIEF

CIRCADIAN GENETICS

Association of the length polymorphism in the human *Per3* gene with the delayed sleep-phase syndrome: does latitude have an influence on it?

Pereira, D. S. *et al. Sleep* **28**, 29–32 (2005)

Obesity and metabolic syndrome in circadian *Clock* mutant mice.

Turek, F. W. *et al. Science* 21 April 2005 (doi:10.1126/science.1108750)

These papers highlight intriguing aspects of the role of circadian genetics in disease. Pereira *et al.* investigated the role of *PER3*, a circadian gene, in human delayed sleep-phase syndrome (DSPS). The association of a specific *PER3* polymorphism with the syndrome was found to vary with latitude, indicating that the same circadian genotype responds differently to the distinct environmental cues provided at different geographical locations. Turek and colleagues showed that mice that are mutant for *Clock*, another circadian gene, develop obesity and a metabolic-syndrome phenotype. Levels of neurotransmitters involved in regulating energy balance were altered in these mice, indicating a direct link between the circadian system and metabolism.

EVOLUTIONARY GENETICS

Genetic variance in female condition predicts indirect genetic variance in male sexual display traits.

Petfield, D. *et al. Proc. Natl Acad. Sci. USA* **102**, 6045–6050 (2005)

Indirect genetic effects (IGEs) occur when the genotype of one individual affects the phenotype of another. Although IGEs between related individuals are well studied, less is known about their importance in interactions between unrelated individuals. Using *Drosophila serrata* as a model, these authors demonstrated that the production of male pheromones, a sexual display trait, varies in response to genetic variance in the condition of unrelated females. IGEs might therefore have an important impact on sexual selection.

GENE EXPRESSION

Interchromosomal associations between alternatively expressed loci.

Spilianakis, C. G. *et al. Nature* 8 May 2005 (doi:10.1038/nature03574)

Recent work described how the T-helper-cell 2 (T_H2) locus control region (LCR) co-ordinately regulates T_H2 cytokine genes, which are spread over 120 kb, through interchromosomal interactions between the LCR and the cytokine loci in question. Spillanakis *et al.* used a chromosome-conformation capture technique to show that interactions between loci on different chromosomes (in this case, mouse chromosomes 10 and 11) also occur. This phenomenon might function in coordinating gene expression, and might also apply to other genes, such as those that encode olfactory receptors and globin proteins.