



GENOMICS

Sweet sequencing rewards

When Gregor Mendel finished his work on peas, he focused his attentions on the honey bee — the agricultural importance, social behaviour and cognitive abilities of which certainly make it a compelling genetic model. Now, honey bee genetics has taken a leap forward with the report in *Nature* of the *Apis mellifera* genome sequence by the Honey Bee Genome Sequencing Consortium.

Gazing at this AT-rich, ~240 Mb genome, the authors have uncovered some striking genetic idiosyncrasies, which they hope will lead to the molecular mechanisms of eusociality. For example, they describe novel features of orthologues of genes that, in *Drosophila melanogaster*, are involved in vision, mechanotransduction, learning and memory. They also found that some gene families are much larger than their equivalents in other insects — among the most extreme of these being those that encode the royal jelly proteins, which have roles during the differentiation of social castes. Other gene families are unexpectedly small — such as those that encode detoxifying enzymes, gustatory receptors and, surprisingly, components of innate immunity — and the authors discuss how these might reflect the specialized life history of the honey bee.

Having the genome sequence has already led to the development of new tools for research into the mechanisms and origins of social behaviour. First, it has improved the annotation of ESTs, which the authors have already used to identify candidate genes that are involved

in caste differentiation — their data show that changes in metabolism are important during this process. Second, by comparing European-derived and 'Africanized' honey bees (which have spread across the New World in the last 50 years), the authors identified a large array of SNPs, which will help with the cloning of genes that underlie behavioural and social traits.

These SNPs have also allowed the researchers to revise the phylogenetic and migrational history of the honey bee. Furthermore, sequence comparisons with other insects contradict the prevailing phylogeny of the Hymenoptera (ants, bees and wasps), indicating that the Hymenopteran lineage diverged earlier than previously thought, and that honey bees belong to the oldest lineage of eusocial bees.

The diversity of related papers in this month's issue of *Genome Research* shows how many areas of research will be accelerated by the honey bee genome sequence. Mendel — who, like subsequent geneticists, found genetic studies of this haplodiploid, polyandrous creature difficult — might have been delighted by the researchers' hope that the honey bee will help us understand the molecular basis of social life.

Jenny Bangham

REFERENCES Honey Bee Genome Sequencing Consortium. Insights into social insects from the genome of the honey bee *Apis mellifera*. *Nature* **443**, 931–949 (2006)

FURTHER READING Robinson, G. E. *et al.* Sociogenomics: social life in molecular terms. *Nature Rev. Genet.* **6**, 257–270 (2005) | Special issue: Honey Bee Genomics. *Genome Research* **16**, November Issue (2006)

IN BRIEF

DEVELOPMENT

Cell lineage transport: a mechanism for molecular gradient formation.

Ibañes, M. *et al. Mol. Syst. Biol.* 17 October 2006 (doi:10.1038/msb4100098)

These authors provide a new model for the formation of morphogenetic gradients. Using a mathematical simulation of cell division and growth dynamics, they show how mRNAs and non-secreted proteins can form robust gradients when dividing cells dilute and transport their contents. The biological relevance of this model, which the authors call 'cell lineage transport', was demonstrated by experimental evidence that *Hoxd13* mRNA forms a gradient during vertebrate limb development as a result of such a mechanism.

RNA WORLD

A two-hit trigger for siRNA biogenesis in plants.

Axtell, M. J. *et al. Cell* **127**, 565–577 (2006)

In some of their targets, plant microRNAs (miRNAs) direct cleavage to define one end of RNAs that are further processed to produce phased small interfering RNAs (siRNAs). In a search for other features that are required for this type of siRNA production, Axtell and colleagues showed that the presence of two cleavage sites for moss miR390 results in such an outcome. In an *Arabidopsis thaliana* siRNA locus, two miR390 sites are also required for phased siRNA production. However, cleavage is not needed at one of these sites, demonstrating an alternative role for some miRNA target sites.

GENE EXPRESSION

Tandem riboswitch architectures exhibit complex gene control functions.

Sudarsan, N. *et al. Science* **314**, 300–304 (2006)

Bacterial gene expression is often controlled by riboswitches — structured RNAs in the UTRs of an mRNA that repress gene expression when bound to the relevant metabolite. These authors have discovered a new level of complexity in such systems — the *metE* mRNA of *Bacillus clausii* contains two riboswitches that bind two different metabolites, either of which can turn off expression. This Boolean NOR logic is similar to the mechanism that controls *metE* expression in *Escherichia coli*, but, in that species, proteins are used to sense the presence of both metabolites.

EPIGENETICS

Recent assembly of an imprinted domain from non-imprinted components.

Rapkins, R. W. *et al. PLoS Genet.* **2**, e182 (2006)

Mammals are the only animals with imprinted genes, but how and when genomic imprinting arose is unclear. The authors compared the arrangement of genes in placental mammals at the imprinted Prader–Willi/Angelman domain with that in other groups of mammals. In monotremes and marsupials, the components of the domain — genes and regulatory regions — are distributed on different chromosomes, as they are in non-mammals. Expression studies confirmed that this locus is not imprinted in marsupials and monotremes, showing that an imprinted domain was assembled relatively recently from non-imprinted components.