IN BRIEF

HUMAN DISEASE

Sequence variants in *SLITRK1* are associated with Tourette's syndrome.

Abelson, J. F. *et al*. *Science* **310**, 317–320 (2005)

Tourette syndrome (TS) has been associated in linkage studies with regions on several human chromosomes, but this paper is the first to study a specific candidate gene. SLIT and NTRK-like 1 (*SLITRK1*) was identified because of its proximity to a chromosomal inversion in a child with TS. In other patients, a frameshift mutation and a microRNA-binding site mutation in *SLITRK1* were found. Expression patterns in the brain of *SLITRK1* and the microRNA, and the ability of wild-type SLITRK1 to promote dendritic growth, further support a role for *SLITRK1* in TS.

MOUSE MODELS

The homeodomain transcription factor Irx5 establishes the mouse cardiac ventricular repolarization gradient.

Costantini, D. L. *et al*. *Cell* **123**, 347–358 (2005)

The rhythmic beating of the heart depends on waves of depolarization and repolarization, with defects in the latter leading to arrhythmia. This study demonstrates that mice that lack the Irx5 transcription factor are susceptible to fatal arrhythmias because they overexpress the $K_v4,2$ potassium channel. Irx5 negatively regulates $K_v4,2$ and is expressed in an opposing gradient. Together these two proteins establish the potassium gradients that ensure repolarization.

RNA WORLD

DICER-LIKE 4 is required for RNAi and produces the 21nt siRNA component of the plant cell-to-cell silencing signal.

Dunoyer, P., Himber, C. & Voinnet, O. *Nature Genet.* 6 November 2005 (doi:10.1038/ng1675)

In plants, the production of 21-nt small interfering RNAs (siRNAs) leads to the degradation of homologous RNAs, and this silencing signal can also move between cells. This paper reports the long-awaited identification of the Dicer protein that is involved in the silencing process. By analysing *Arabidopsis thaliana* mutants that are deficient in cell-to-cell silencing, the authors showed that DICER-LIKE 4 is required to produce the 21-nt siRNAs that mediate this form of RNA interference.

COMPUTATIONAL BIOLOGY

Genomic variability within an organism exposes its cell lineage tree.

Frumkin, D. & Wasserstrom, A. *et al*. *PLoS Comp. Biol*. **1**, e50 (2005)

Reconstructing the cell-lineage tree of *Caenorhabditis elegans* was a tremendous feat, and was made possible by the transparency of the organism and its relatively few cells. The paper shows that it is feasible to accurately determine the cell-lineage trees of complex organisms by analysing the pattern of microsatellite mutations that accumulate during somatic cell divisions. Although the approach is currently only applicable to small cell populations, it might one day be powerful enough to reconstruct the cell-lineage tree of an entire human.