Francisco, and her colleagues. They call the gene *happyhour* and have found, through a series of genetic manipulations in flies, that the normal happyhour protein seems to work by inhibiting the activity of the extracellular growth factor receptor pathway. This is conserved in flies and mammals, and is a target of some cancer drugs.

One such drug, erlotinib, made lightweights of flies and mice, enhancing their sensitivity to ethanol, and reduced alcohol consumption in rats that had become accustomed to a tipple. The authors suggest the results might point to therapeutic avenues for people with drinking problems.

OCEANOGRAPHY

Arctic freshening

Geophys. Res. Lett. doi:10.1029/2009GL037525 (2009)
An inventory carried out during the International Polar Year 2007–2008 reveals substantial increases in fresh water in parts of the Arctic Ocean.

Matthew Alkire of Oregon State University in Corvallis and his colleagues found that in March and April 2008 the freshwater content in the Canada and Makarov basins had increased by around 8,500 cubic kilometres, or 26%, compared with average freshwater content in winters past. Other areas saw small decreases.

Chemical analysis suggests that precipitation and increased river runoff, as well as Pacific water, are dominant freshwater sources; accelerated sea-ice melting also has a role. Prevailing anti-cyclonic wind patterns seem to have favoured freshwater redistribution towards the western Arctic basin.

ANIMAL BEHAVIOUR

Singing in the rain

Curr. Biol. doi:10.1016/j.cub.2009.04.061 (2009)
Mockingbird songs are more elaborate in species that live in more variable climates.

Carlos Botero of Cornell University in Ithaca, New York, and his colleagues analysed almost 100 separate recordings spanning 29 species of mockingbird collected from across the New World. Places where precipitation and temperature were more variable and less predictable had birds that sang more consistently, had a broader repertoire and were better at copying the calls of other species.

The researchers suspect that the correlation relates to a sexual display of fitness, either spurred by increased competition for limited resources and females in variable climes, or tracking with neurological adaptations needed to survive in an unpredictable world.

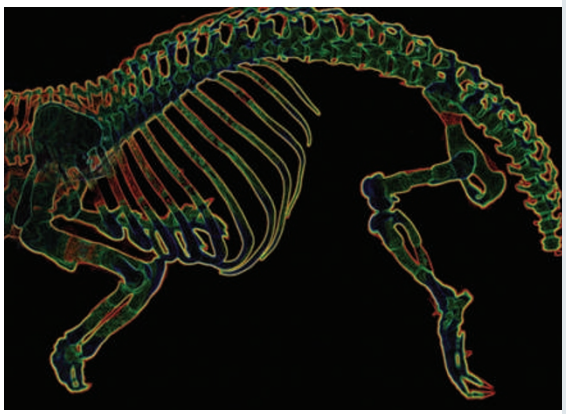
MICROBIOLOGY

Bacterial break-in

J. Clin. Invest. doi:10.1172/JCI36759 (2009)
Many have wondered how pathogens that cause bacterial meningitis slip through the tight defences of the blood–brain barrier.

Dlawer Ala'Aldeen at the University of Nottingham, UK, Elaine Tuomanen at St Jude Children's Research Hospital in Memphis, Tennessee, and their collaborators used murine and human cells and live mice to show that *Streptococcus pneumoniae*, *Neisseria meningitidis* and *Haemophilus influenzae* all use the same means of entry. These bacteria recognize and attach to a specific target on laminin receptors on the inner surface of the brain's many blood vessels.

The team isolated the proteins used by the pathogens to bind to this receptor. These could be used in the design of a broadly protective meningitis vaccine.



ELSEVIER

DEVELOPMENTAL BIOLOGY

Use it or lose it

Dev. Cell **16,** 734–743 (2009)
Embryos need to flex their growing muscles if developing cells are to give rise to joints, says a team led by Elazar Zelzer at the Weizmann Institute of Science in Rehovot, Israel.

They found that mutant mouse embryos with defective muscles fail to form various joints, including elbows, shoulders and hips (a normal embryo is pictured above). Without muscle contraction, the cells that generate joint tissues do not activate a key regulatory pathway controlled by the protein β-catenin, and the progenitors switch fate to form cartilage instead.

One idea put forward by the authors is that the mechanical stress created by developing muscles might inform the cells of where they are and what cell type they should generate. The study could be relevant to rare human cases in which babies whose movement is restricted *in utero* develop abnormal joints.

JOURNAL CLUB

Maite Huarte
Broad Institute, Cambridge, Massachusetts

A biologist looks at new functions for non-coding RNAs.

The increasing study of small and large RNA molecules that do not encode protein — non-coding RNAs — is widening our view of their relevance, and of their roles in important developmental mechanisms such as gene silencing and X-chromosome inactivation. Nevertheless, our knowledge covers only a fraction of the non-coding transcripts produced from the mammalian genome.

Much of the non-coding RNA transcribed is associated with protein-coding genes: for example, the transcripts that are complementary or 'antisense' to the gene sequence. These can be created by 'bidirectional' transcription from either DNA strand. Kevin Morris of the Scripps Research Institute in La Jolla, California, and his colleagues have now shed light on the function of this type of transcription (K. V. Morris *et al. PLoS Genet.* **4,** e1000258; 2008).

They focused on the gene encoding the tumour suppressor p21, transcription of which must be finely tuned, and show that an endogenous antisense transcript of p21 controls the amount of p21 mRNA made by silencing its promoter. This transcriptional suppression is dependent on Argonaute-1, a protein implicated in RNA-mediated gene silencing. Suppression correlates with bidirectional transcription within p21's promoter.

This observation is not limited to p21: a similar regulatory mechanism controls gene expression of the protein E-cadherin, suggesting that this balancing of sense and antisense transcription might be a common mechanism of transcriptional regulation.

The next challenge is to understand how RNAs can induce transcriptional gene silencing; information that will probably reveal just how much power RNA wields in the control of gene expression.

Discuss this paper at **http://blogs.nature.com/nature/journalclub**