of South Florida in Tampa and his colleagues studied four families in which some members had unusually high amounts of herpesvirus-6 DNA in their blood. The researchers found that the viral genome had inserted into caps called telomeres at the ends of chromosomes.

The viral genomes in parents and their children were identical, suggesting that the DNA is heritable. Treating cells from these families with compounds that stimulate latent herpesviruses also allowed the viruses to infect other cells in culture.

CONSERVATION

Heavy metal history

Environ. Sci. Technol. doi:10.1021/es903176w (2010)

Endangered California condors (*Gymnogyps californianus*; pictured) are heavily affected by lead poisoning, but current biannual testing detects only a fraction of their exposure.

ALL CANADA PHOTOS/ALAMY

Myra Finkelstein at the University of California, Santa Cruz, and her colleagues report that analysis of sequential segments of condor feathers can provide a history of lead exposure over the 2–4 months of feather growth.

By measuring lead concentration and isotope composition in feather and blood samples, the researchers identified lead-exposure events that would have been missed by blood monitoring alone. Their technique, they say, may also be applicable to other bird species.

ARCHAEOLOGY

Adoption or migration?

J. Archaeol. Sci. **37,** 866–870 (2010)

The origin of farming in Britain is hotly debated: did the indigenous population adopt farming practices through trade and exchange with continental Europe or did migrants bring farming from the mainland?

Mark Collard from Canada's Simon Fraser University in Burnaby, British Columbia, and his colleagues used radiocarbon dates to estimate prehistoric population changes in Britain. They found that about 6,000 years ago, population density increased sharply and cultivated plants occurred at around this time.

The best explanation for this is that groups of migrant farmers from mainland Europe established colonies in England and Scotland. Farming would have supported higher population densities than hunting and gathering. And if the indigenous hunter-gatherers had adopted farming from the mainland, they would have taken longer to learn it, resulting in a slower growth in population than is indicated by the data.

NEUROSCIENCE

Memory reading

Curr. Biol. doi:10.1016/j.cub.2010.01.053 (2010)

By decoding patterns of brain activity, researchers can tell which in a list of events a person is recalling.

Eleanor Maguire and her colleagues at University College London, UK, showed ten volunteers short films depicting three different actions such as drinking coffee. The researchers then asked them to remember each action individually while scanning their brains using functional magnetic resonance imaging (fMRI). They found that unique fMRI patterns in the hippocampus corresponded with the recall of specific memories.

These patterns were stable over 24 hours and allowed the scientists to predict which memory participants chose to recall.

GENOMICS

We are family

Science doi:10.1126/science.1186802 (2010)

The human mutation rate is lower than previously thought, according to researchers who sequenced the entire genomes of four family members — two siblings with rare genetic disorders, and their parents.

David Galas and Leroy Hood at the Institute for Systems Biology in Seattle, Washington, and their colleagues estimate that roughly 70 new mutations arise per genome between generations. This is lower than earlier estimates based on genomic comparisons between humans and their closest living relatives, chimpanzees.

The team also pinpointed four genes likely to underlie the siblings' two disorders — Miller syndrome and primary ciliary dyskinesia. The four genes are a subset of those reported in previous studies.

For a longer story on this research, see go.nature.com/Owe9CD

JOURNAL CLUB

Eran Segal
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A computational biologist looks at how identical cells come to differ.

My main interest is in understanding how complex biological behaviours are encoded by DNA. An example of such behaviour is the ability of genetically identical cells to generate diversity in their phenotypes, or observable traits, by changing how genes are expressed from one cell to the next. How expression variability occurs over short timescales (for example, during a cell cycle) has been well studied; much less is known about it over longer timescales.

So I was excited by work from Narendra Maheshri of the Massachusetts Institute of Technology in Cambridge and his colleagues. They demonstrate that slow expression fluctuations of a yeast gene are regulated locally, or in *cis*, by that gene's promoter — a nearby stretch of DNA that regulates the gene's expression (L. M. Octavio *et al. PLoS Genet.* **5,** e1000673; 2009).

They studied the yeast protein FLO11, placing two copies of the protein's promoter in the same cell, each in front of an engineered fluorescent 'reporter' gene. The reporters switched expression slowly and independently, implying that the expression fluctuations were locally encoded. The authors further identified global, or *trans*, regulators that affect the fast and slow expression fluctuations of FLO11. The type of expression effect that a regulator exerts seems to depend on several factors, including the location of the regulator relative to the site at which transcription, or reading of the DNA, begins, and relative to sites for other regulators.

Although the mechanistic details of this encoding are still unclear, applying similar approaches to many more promoters should bring us closer to understanding how other complex phenomena are encoded by DNA. This will hopefully allow us to one day predict the phenotypic effects of human genetic variation.

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