

IN BRIEF

EVOLUTIONARY GENETICS

Birth and adaptive evolution of a hominoid gene that supports high neurotransmitter flux.

Burki, F. & Kaessmann, H. *Nature Genet.* **36**, 1061–1063 (2004)

There are two glutamate dehydrogenase genes in humans: *GLUD1* — a housekeeping gene — and *GLUD2*, which is expressed specifically in neural tissue and testis. The authors show that *GLUD2* originated by retrotransposition from *GLUD1* in our ancestor, 23 Mya. The changes that give *GLUD2* its tissue specific properties are a result of positive selection, following a duplication event. *GLUD2* probably contributed to enhanced brain function in humans and apes, and has also been implicated in late memory formation.

POPULATION GENETICS

Global patterns of human mitochondrial DNA and Y-chromosome structure are not influenced by higher migration rates of females versus males.

Wilder, J. A. *et al.* *Nature Genet.* **36**, 1122–1125 (2004)

Genetic evidence supports demic diffusion of Han culture.

Wen, B. *et al.* *Nature* **431**, 302–305 (2004)

These studies analyse the effects of historical migration on human population structure. Wen *et al.* examined patterns of Y-chromosome and mitochondrial DNA (mtDNA) variation to study the spread of the Han Chinese culture. Their results indicate that this spread followed migration of the Han people, rather than diffusion of the culture through social interchange without genetic mixing, and show that males had a greater role than females in this expansion. Wilder *et al.* tested the theory that population structures have been more strongly influenced by female migration than that of males due to patrilocality, which occurs when females move to the locality of their spouses following marriage. Analysis of genetic variation between ten populations from different global regions showed that this is not the case, at least at the continental and global level, as similar levels of variation for Y-chromosomes and mtDNA indicate roughly equal contributions of male and female migration.

EVOLUTIONARY GENETICS

Regulatory evolution across the protein interaction network.

Lemos, B. *et al.* *Nature Genet.* **36**, 1059–1060 (2004)

These authors showed that, for a specific gene, the number of interactions that its protein product participates in is negatively correlated with the level of variation in gene expression, both within and between species. Furthermore, for pairs of interacting genes, levels of variation in gene expression were more similar than for randomly assigned pairs. These results indicate that protein–protein interactions might have an important role in constraining evolutionary changes in gene regulation.

CONSERVATION GENETICS

Genes feel the heat

A recent study suggests that climate change affects wildlife at the genetic level, with implications for protecting biodiversity in the face of changing weather patterns.

Hadly and colleagues studied historical changes in genetic variation in northern pocket gophers and montane voles. The two species thrive in wet climates, so population numbers of both are expected to decrease during periods of dry weather. But there are also differences between the two species: whereas pocket gophers are home-loving animals and tend not to venture far from the sub-populations they live in, montane voles are more adventurous, with more migration between groups. What impact might these ecological differences have on genetic variation in these species during periods of climate change?

Over the past 2,500 years, two periods of climate change occurred — the Medieval Warm Period (1,150–650 years ago) and the Little Ice Age (650–50 years ago). To investigate the effects of these periods on gopher and vole genetic diversity, the authors took advantage of the abundance of fossils for the two species that have been found in Yellowstone National Park, in the United States. They used mitochondrial DNA from these fossils to estimate effective population sizes and levels of genetic variation at different times over the past ~2,500 years.

In keeping with their preference for damper climes, both species underwent population decreases during the Medieval Warm Period. However, this similarity didn't hold up for genetic variation: whereas the gophers showed reduced genetic diversity during this period, the reverse was true for the voles. This fits in well with the ecological strategies of the two species. The high level of migration between vole sub-populations is expected to contribute to genetic diversity in this species, and a recent study has shown that migration increases at times of low population density. By contrast, as gophers live in closed populations, this means of maintaining variation would not have applied to them. Another explanation is that genetic variation increased in the voles due to stronger selective pressure, a possibility that needs further investigation.

Whatever the case, this study indicates that climate change affects genetic variation, with varying effects on different species. As levels of genetic variation can contribute to the likelihood of extinction, further studies could provide important pointers as to which species are likely to be hit hardest by climate change.

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References and links

ORIGINAL RESEARCH PAPER Hadly, E. A. *et al.* Genetic response to climatic change: insights from ancient DNA and phylogenetics. *PLoS Biol.* **2**, e290 (2004)

WEB SITE Hadly's laboratory: <http://www.stanford.edu/group/hadlylab/index.html>

