

Dating chimpanzees

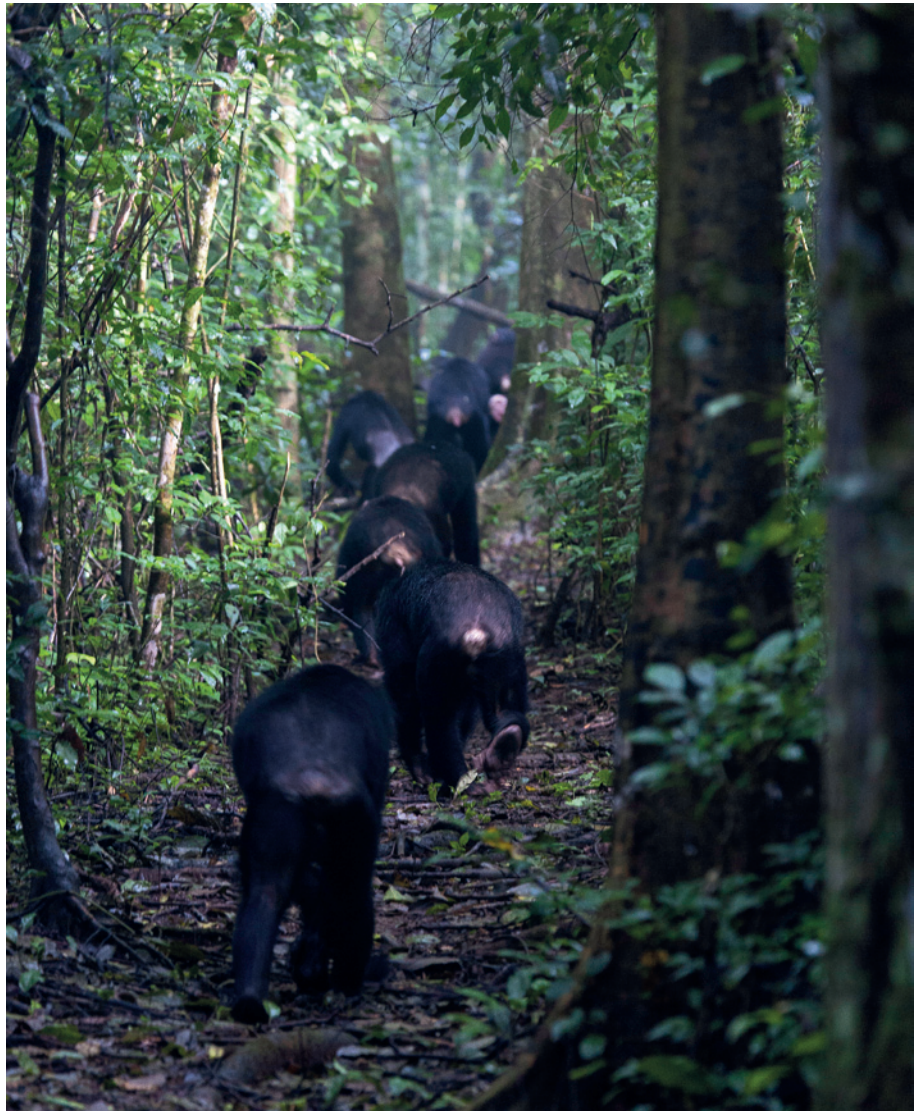
Genetic research has tracked lineages of male chimpanzees thousands of years into the past, opening the door to the study of long-term behavioural evolution in our close primate relatives.

MICHAEL HASLAM

To a casual observer, one chimpanzee can seem much the same as another. Yet there are four distinct subspecies of chimpanzee living across Africa today, each of which is made up of many discrete communities. Within these groups, specific behavioural characteristics are shared from one generation to the next, resulting in a patchwork of behaviours that bears the hallmarks of cultural transmission¹. Recent studies have shown how such transmission may occur, in both experimental² and wild³ groups. But one crucial factor was missing: time. Now, writing in the *Journal of Human Evolution*, Langergraber *et al.*⁴ show that some modern chimpanzee communities have probably existed for hundreds or even thousands of years. By providing a chronological scaffold for chimpanzee behaviour, this research offers a rare opportunity to examine the tempo of chimpanzee cultural evolution.

Langergraber and colleagues used genetic markers on the Y chromosome, which are passed only from father to son, to examine the relationships between eight communities of East African chimpanzees (*Pan troglodytes schweinfurthii*) in Uganda (Fig. 1). Chimpanzees are male philopatric, which means that males tend to stay in the territory in which they were born and adolescent females emigrate to a new community. The stable core of a group is therefore composed of related males — an unusual pattern among primates, and a potential contributor to high levels of male aggression between chimpanzee groups⁵. Y chromosomes accumulate mutations over time, resulting in the build-up of community-specific shared mutations known as haplotypes. Combined with an estimate of the rate of mutation, haplotype variations allow calculation of the time that has elapsed since any pair of individuals shared a common ancestor.

Large-scale genetic comparisons among the great apes have suggested that chimpanzees probably split from bonobos around 2 million years ago⁶. Concentrating on much finer timescales, Langergraber *et al.* estimate a time to the most recent common ancestor (TMRCA) ranging between 125 and 2,625 years for their eight chimpanzee communities. Because chimpanzee groups are



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Figure 1 | Stable communities. The Sonso group of East African chimpanzees (*Pan troglodytes schweinfurthii*), from the Budongo Forest in Uganda, is estimated to be the oldest of the eight chimpanzee communities studied by Langergraber and colleagues⁴.

likely to be founded by small numbers of individuals splitting from larger communities, the authors argue that the TMRCA estimates are close to the time that those groups were established. They even uncovered evidence for a likely fission event: two neighbouring communities, the Ngogo and Kanyantale groups in Kibale National Park, share a haplotype and a

TMRCA of about 450–500 years ago, suggesting that these two groups may have split from one another around this time. Future work will be necessary to refine the wide confidence intervals surrounding these estimates.

The findings clearly show that East African chimpanzee groups display great stability and longevity. For example, the founding of the

oldest sampled community, the Sonso group in the Budongo Forest, at more than 2,500 years ago, may pre-date the Roman Empire, the Classic Maya and the Chinese Han Dynasty. On this evidence, the Sonso chimpanzees could be considered to have one of the world's oldest continuous cultures. However, the techniques and results presented by Langergraber *et al.* offer significant potential beyond simply estimating the time of community-founding events.

Chimpanzee cultural differences are maintained through social learning, in which group members conform to observed behaviour, either during their juvenile development³ or as newly immigrant females⁷. Although females act as an important cultural vector, bringing new behaviours into a group when they arrive, it is possible that the resident males act as a brake on the speed at which cultural variation accrues. Without such a conservative mechanism, cultural differences between groups would be eroded with each passing generation, and the pattern we observe today would not have emerged. A similar mechanism was probably in place among early human ancestors, if stasis in the development of flaked-stone technology over its first million years is a guide⁸.

Hypothetically, in the absence of a conservative tendency, longer-lived groups should accrue more cultural idiosyncrasies. But the new genetic data cast doubt on that hypothesis. For example, the Kanyawara and Ngogo groups in Kibale National Park are located less than 20 kilometres apart, and have similar numbers of observed cultural variants, yet the TMRCA estimates are more than 1,700 years for the former and close to 450 years for the latter. Once similar genetic data are available for other sites and subspecies, it will be possible to assess more clearly whether there is a pattern to how quickly a new community reaches a certain level of cultural complexity. We may also be able to estimate age ranges for the origin of behaviours shared by communities in a specific region, such as stone-tool use by West African chimpanzees⁹.

The availability of dated communities also allows us to look more closely at the reasons for their founding. For example, fluctuation in African forest sizes through time probably influences chimpanzee community dynamics¹⁰. Keeping error margins in mind, it is interesting that for the five chimpanzee groups with a TMRCA of less than 1,000 years, these dates all coincide with periods of East African drought¹¹. Do droughts promote chimpanzee group fission, as forests fragment and food scarcity increases? The same factors might also negatively affect the retention of cultural knowledge related to the exploitation of particular insect or nut species, creating a complex temporal link between genetic and cultural evolution.

Genetic dates such as those provided by Langergraber *et al.* open up a complementary

perspective to that provided by the past 50 years of field observations of wild chimpanzees. They also demonstrate that the array of approaches used to reconstruct human evolution is applicable to chimpanzees, aiding the study of primate archaeology¹². Clearly, the process of exploring the fine-grained history of non-human animal behaviour has only just begun. ■

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GENETICS

Up and down in Down's syndrome

A comparison of identical human twins, only one of whom has Down's syndrome, reveals a genome-wide flattening of gene-expression levels in the affected individual. SEE ARTICLE P.345

BENJAMIN D. POPE & DAVID M. GILBERT

Down's syndrome occurs when humans have an extra copy of chromosome 21 (ref. 1), a situation referred to as trisomy 21. Because each chromosome contains a distinct set of genes that serve as blueprints for the expression of cellular components, it has been presumed for decades that the condition is mainly caused by an overabundance of the products of chromosome 21 genes. But on page 345 of this issue, Letourneau *et al.*² report a case of Down's syndrome that is associated with altered gene expression across every chromosome, not just chromosome 21. This observation implies that the expression of any number of genes on any chromosome may contribute to Down's

syndrome, and raises the possibility that an extra copy of any chromosome can disrupt general gene regulation.

The discovery was made possible by an elegantly controlled experiment that compared a set of twins derived from the same fertilized egg (monozygotic, or 'identical', twins) in which one twin had an extra chromosome 21 and the other did not, owing to chromosome-segregation errors that occurred before the twinning event³. This unusual circumstance allowed the effects of the extra chromosome 21 to be studied in isolation. Although gene expression has been extensively studied in individuals with Down's syndrome, the genome-wide effect discovered by Letourneau *et al.* had gone undetected because, as they show, natural variation among individuals

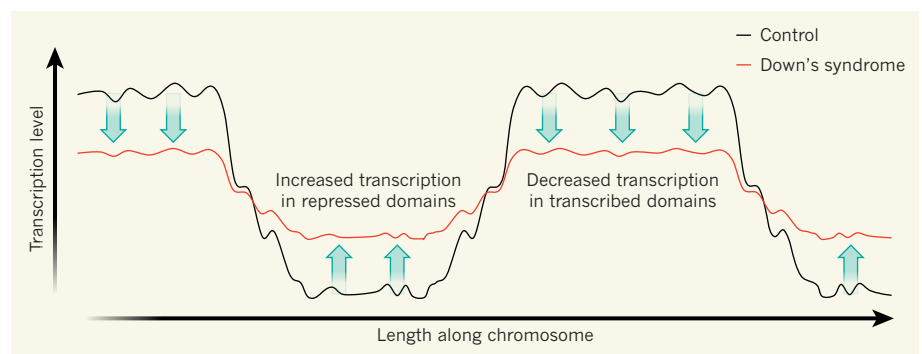


Figure 1 | Flattened gene expression. Letourneau *et al.*² show that genomic domains that are normally associated with low or high levels of gene expression are respectively up- or downregulated in a person with Down's syndrome, compared with their identical twin who does not have the condition. The result is a genome-wide flattening of gene expression.