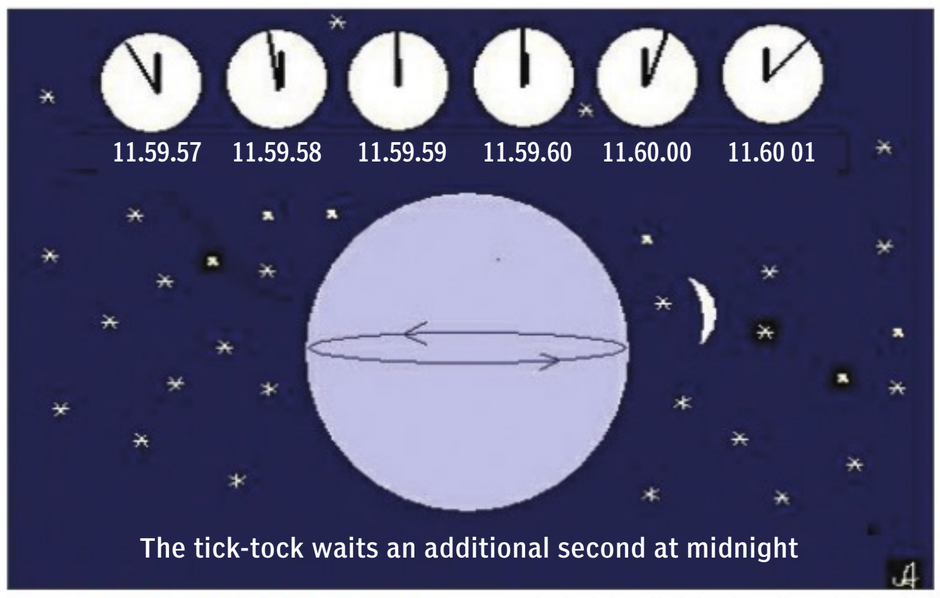
Marking time to stay connected

LATER THIS MONTH THE WORLD'S CLOCKS WILL SOUND ONE EXTRA TICK TO GET IN STEP WITH EARTH'S ROTATION, WRITES S ANANTHANARAYANAN

Our units for measuring time are derived from the constancy of the earth's rotation, but if the planet slows down or speeds up then clocks have to take note and count one second twice so that the earth catches up, or skip one second to catch up with the earth. Although seconds, minutes and hours have their origin in the speed of the earth's movement, the clocks we use work on a more accurate timekeeper and, periodically, when the earth gets nearly a whole second out of step the clocks need to adjust their own count to be in time. This happens about once in two years and such an adjustment is being carried out at midnight on 30 June this year.

A number systems based on the number 60 have been found suitable for dealing with time. Just as the decimal system has become popular, the number 16 was earlier the base for weights and measures and even money — we had 16 ounces to the pound or 16 annas to the rupee, for example. Locations in computer memory, too, are best described by numbers based on 16, the Hexadecimal system. While the base 10 of the decimal system is considered easier to deal with because we have 10 digits, the bases 16 or 12, like 12 pence or 12 inches, also have their merits as the squares, 256 or 144, have more divisors than the number 100. For a simillar reason, that 60 is the smallest number that can be divided by all numbers from one to six, the *sexagesimal* system, or the number system based on 60, came into use in treating time.

This number system was devised by the Sumerians near modern Iraq some 3,000 years ago. The Babylonians who came after the Sumerians also used the system and in 140 AD Greek astronomer Ptolemy divided the length of the day based on 60ths. But it was around 1000 AD that Islamic scholars like Al Biruni divided the day into 24 parts and then divided the hour's length into 60 minutes and then 60 seconds.



The tick-tock waits an additional second at midnight

The modern second is, thus, 1/(24x 60x60) = 1/86,400 of the mean solar day and, in 1874, this was adopted as the unit of time for scientific purposes. But the length of the mean solar day was found to be variable and the base was changed to the length of the day based on the time of revolution of the earth around the sun, first with reference to the constellations and then to the interval between the equinoxes. But even this definition was found inaccurate and, in 1967, the second was defined based on the frequency of radiation from the cesium atom, and this has held so far.

The system of the time of day based on the atomic clock is called the *Coordinated Universal Time* (known as *UTC* — a compromise with the French Temps Universel Coordonné), while standards of mean solar time, like Greenwich Mean Time, are known as *UT1*. As the second based on the atomic clock is quite close to the second based on astronomical time as well as on the average length of the solar day over a long period, UTC does not stray more than a second, over the length of a year, from UT1, and is now the standard for science and also for aviation and other civil uses.

A practical difference of UTC from the systems is that it does not observe *daylight saving time*. However, as the solar day is not exactly 86,400 seconds by the atomic clock, UTC does stray from solar time and needs to be corrected. The year itself, we all know, is not exactly 365 solar days but some six hours longer. We, thus, have the device to adjust the calendar, of adding a day on 29 February every fourth year as a "leap" year. In the same way, the adjustment of one second that needs to be carried out approximately once in two years to keep UTC in step with Mean Solar Time is called a "leap second".

Keeping track of the progress of UTC and IT1, as well as announcing leap seconds, is managed by the International Earth Rotation and Reference Systems Service (known by an earlier acronym, IERS). The adjustment to be carried out on 30 June this year would be that the UTC clock, at midnight, would mark time for one second to slow down to the time kept by the rotation of the earth. Thus, where the clock should have moved from 11.59.59 to 12.00.00, it would first move to 11.59.60 and then to 12.00.00. This is just like February not moving from the 28th to 1st March, but whiling a day away, as the 29th.

Unlike the adjustment for a leap year, which is always to add one day to the calendar, the leap second may be added or taken away. The reason is that the leap second correction is not only for a constant difference factor but for both the increase of reduction of the length of the day due to climatic changes or geological occurrences or even ocean currents, or tides, in the ocean or within the land mass.

East-west movement in the atmosphere would be compensated by corresponding changes in the rotation of the earth. Warming or cooling, which would cause the atmosphere and also the oceans to expand or contract would also have the effect of a spinning ballerina stretching her arms out or drawing them in, and would slow or speed up the earth's rotation.

The 25 corrections since the system of correction started in 1972, however, have all been cases of delaying UTC by one second and none to save a second. This is to say that the solar year has been a little slower than the year according to the atomic clock. Apart from the way the atomic second is defined, it is also a fact that earth's rotation is slowing by a barely perceptible extent for centuries now.

The effects of atmospheric and geological changes have partly compensated, but not in a uniform way. The difference between the two clocks is, hence, not regular and the time taken for the difference between the two to grow to one second has not been the same every time it happens. To have 25 corrections in 43 years works out to one correction in less than every two years. But the last correction was in 2012 and we can see that the 26th, on 30 June, will be well over two years later. In fact, there were no corrections between January 1999 and December 2005, but there were nine corrections in the eight years from 1972 to 1979.

THE WRITER CAN BE CONTACTED AT simplescience@gmail.com

Leap minutes

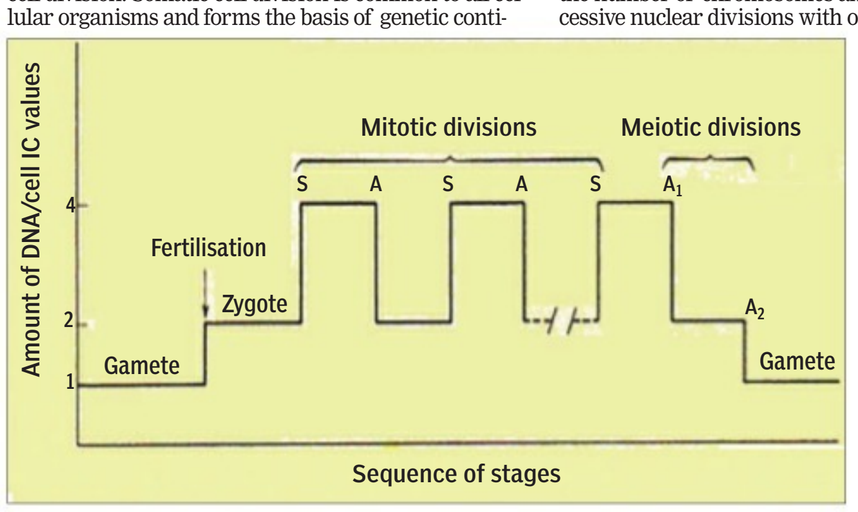
Adding leap seconds, though academically elegant, is not without its problems in the real world. Different processes are aligned either to UTC or UT1 and also different species of local time. Computers, hence, need to take into account the time system followed and make adjustments. In the case of leap years, all calendars are adjusted at the same time and there is no difficulty. But when leap seconds are announced, although this is done six months in advance, there may be problems if all processes do not effect the change together and also with the working of the Internet, which relies on recording the time that data takes to move, to find paths for connections.

There is, hence, some controversy about continuing with leap seconds and alternatives, one being to make adjustments less frequently. If leap minutes were used, for instance, adjustments may need to be made only once in a century. S.A.

FACTORING HEREDITY

TAPAN KUMAR MAITRA EXPLAINS THE PROCESS OF TRANSMISSION AND CONTINUITY

The hereditary behaviour of a sexually propagating organism is such that it allows for the preservation of the species even as it leaves room for the introduction of variation among the offspring. We now know enough about chromosomes and their constituent molecules to realise that our ultimate understanding of heredity will rest, in large part, on our understanding of the behaviour of chromosomes in cell division. Somatic cell division is common to all cellular organisms and forms the basis of genetic continuity. In addition, meiosis is coexistent with functional bisexuality, ensuring intra species (inter-organism) genetic stability. Both of these processes contribute, each in a characteristic fashion, to the transmission and continuity of inherited traits.



The life cycle of a sexually reproducing animal correlate with the changes in the amount of DNA per cell. S, period of synthesis in interphase; mitotic anaphase; A1, first meiotic anaphase; A2, second meiotic anaphase.

The dividing nuclei of a particular species possess a characteristic number of chromosomes. In addition, an essential factor in both plant and animal fertilisation is the fusion of gametic nuclei of paternal and maternal origin. It follows, therefore, that there must be a mechanism that provides for a reduction in chromosome number to compensate for the increase potentially brought about through fertilisation. In 1883-1884, Edouard Van Beneden demonstrated that equal numbers of chromosomes were contributed by parents to offspring at the time of fertilisation. The contribution of each parent, therefore, was a single or haploid set of chromosomes to provide the zygote with a double or diploid set. All cells of the offspring that were subsequently derived from the zygote by normal mitotic division possessed a diploid set of chromosomes, with each chromosome represented twice.

In 1887, August Weismann postulated, without being fully aware of the mechanism involved, that a reduction in chromosome number took place in the germ cells of both plants and animals in such a manner as to separate the diploid chromosomes into two haploid groups. His prediction was long ago fully verified. Reduction division, or meiosis, has been found to exist in those organisms that propagate by sexual means.

There is a parallel between the level of ploidy (haploid, diploid and so on) of a nucleus and the amount of DNA; the two vary directly. In a haploid sperm or egg, a diploid cell such as a zygote or a somatic cell in early interphase would contain a 2C amount of DNA. Note that the *C* value refers to DNA concentration per nucleus and makes no statement about chromosome number, which is expressed by the value of *N*. As the cell prepares to divide, replication of the DNA during the synthesis period of interphase would double the amount to 4C, with the amount again being reduced to 2C per nucleus following anaphase separation of chromatids. Cells in a dividing tissue would show a regular cycle of DNA changes. Meiosis, however, reduces the DNA per nucleus to C during gamete formation.

Meiosis, therefore, is a special kind of cell division and is the antithesis of fertilisation in that it halves the number of chromosomes and consists of two successive nuclear divisions with only a single doubling of the amount of DNA. The first division separates the homologous chromosomes, which had paired with each other in prophase, into two 2C cells. The second division separates the sister chromatids, with the result that four 1C (and 1*N*) nuclei are produced. In animals, meiosis occurs just prior to fertilisation and results in the formation of sexual cells, the sperm and the egg. Their union in fertilisation gives a diploid zygote and, through cleavage and the processes of development and differentiation, a diploid body characteristic of each particular species.

The time relationships between meiosis and fertilisation vary widely in plants. In some algae and fungi, meiosis immediately follows fertilisation and the resultant products, which are haploid asexual spores, germinate to produce a haploid thallus. This structure, the gametophyte, produces gametes by mitosis and the zygote resulting from their union undergoes reduction division without intervening mitotic divisions. There develops, consequently, no diploid body form. Direct phenotypic expression of all genes is possible, so the question of dominance or recessiveness is not normally encountered.

The higher plants, including mosses, ferns and seed plants as well as some of the algae, possess a similar life cycle except that the diploid zygote produces the diploid sporophyte through mitotic division and development. The sporophyte, in turn, develops specialised structures in which meiosis takes place. Thus, a diploid plant body intervenes between fertilisation and meiosis, giving the forms of plant life with which most of us are familiar. In the course of evolution of the higher plants, the gametophyte has become reduced in structural complexity and has lost its independent existence at the same time that the sporophyte has gained in size and dominance, and hence is comparable to the usual condition in animals. The question of dominance and recessiveness appears.

THE WRITER IS ASSOCIATE PROFESSOR, HEAD, DEPARTMENT OF BOTANY, ANANDA MOHAN COLLEGE, KOLKATA, AND ALSO FELLOW, BOTANICAL SOCIETY OF BENGAL, AND CAN BE CONTACTED AT tapanmaitra59@yahoo.co.in

What's old is new again

REVOLUTIONARY NEW METHODS FOR EXTRACTING, PURIFYING AND SEQUENCING EVER MORE ANCIENT DNA HAVE OPENED A WINDOW INTO THE HISTORY OF LIFE ON EARTH, WRITES BOB GRANT

Two researchers sit hunched in front of a fume hood dressed head-to-toe in stark white Tyvek suits, though the yellow-tinted window I'm viewing them through lends the entire scene a sulfurous hue. One of them, Hongjie Li, pipettes tiny volumes of solutions containing decades-old DNA into centrifuge tubes, while the other, PhD student Lu Yao, types information into a laptop. Airlock doors and a sensitive ventilation system minimise the incursion of outside air and the myriad bits of contaminating DNA it carries. Yao, reaching a point when she can take a break, looks up from her work and waves.

This is the ancient-DNA lab at the University of Illinois, Urbana-Champaign, tucked in a corner of the basement at the Carl R Woese Institute for Genomic Biology. Yao has spent hours in this space. Working under the guidance of molecular anthropologist Ripan Malhi, she hopes to answer questions about phylogeny, biogeography and island dwarfism among long-tailed macaques (*Macaca fascicularis*) in Southeast Asia by sequencing decades- and even century-old mitochondrial DNA collected from the dried skulls of monkeys in museum collections. And thanks to recent methodological, computational and conceptual advances in the study of ancient DNA, Yao, Li and other researchers are succeeding in compiling sequences at an unprecedented rate.


Hominin skulls more that 400,000 years old, discovered at the Sima de los Huesos (Pit of Bones) site in Atapuerca, Spain. From a similarly aged femur excavated at the site, researchers extracted and sequenced a full mitochondrial genome.

In just a few decades, the study of ancient DNA has gone from a scientific curiosity to an extremely powerful method for reconstructing past biological phenomena. Malhi recalls that in his own PhD research, which he finished in 2001, he devoted an entire dissertation chapter and a year of lab work to the genetic analysis of 40 ancient samples from Native Americans, zeroing in on a 300-base-pair-long fragment of mitochondrial DNA. "Now, that's something that one of my students can do in a month," he says. "It's pretty amazing."

In addition to greatly condensing the amount of time it takes to extract and sequence old DNA, new techniques are allowing researchers to pluck sequenceable fragments from ever more ancient samples, providing genetic blueprints from long-forgotten epochs of evolution, migration and ancestry.

In 2014 alone, scientists successfully sequenced the mitochondrial genome of a hominin that lived more than 400,000 years ago, exomes from the bones of two Neanderthal individuals more than 40,000 years old and a nearly complete nuclear genome from a 45,000-year-old modern human fossil, to name but a few. In 2013, an international team of researchers led by scientists at the University of Copenhagen published the full genome sequence of an ancestral horse species that roamed the Middle Pleistocene permafrost of North America more than 700,000 years ago — the oldest complete genome sequenced thus far.

For ancient-DNA researchers, these truly are heady times. "The last two or three years have been amazing," says Mattias Jakobsson, a population geneticist at Uppsala University in Sweden who studies ancient DNA as a way to understand human evolutionary history. And the coming years only promise more sequences from more and older specimens, he says. "We're certainly heading to much more data. There's going to be many more studies of many more individuals."

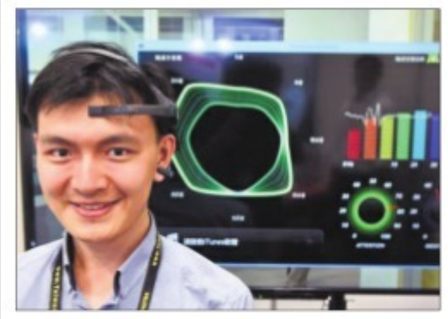
The seeds of ancient DNA research sprouted in 1984, even before Polymerase Chain Reaction became the ubiquitous technique it is today. Researchers at the University of California, Berkeley, successfully cloned and sequenced two fragments of mitochondrial DNA from a 140-year-old museum specimen of a quagga, an extinct relative of the zebra, demonstrating that genetic material could survive and be recovered from the remains of long-dead animals.

THE SCIENTIST

PLUS POINTS

Mind control TV

Remote controls of the physical kind are set to be redundant in the wake of an extraordinary advance, announced by the BBC, which allows people to choose what they want to watch by thought control. And while the appeal to couch potatoes may be obvious, the prospect of not having to move a muscle to operate a TV could have a big benefit for some disabled people, such as those who are completely paralysed.


The "Mind Control TV" prototype works though brain activity signals, which are relayed from an Electroencephalography headset.

A prototype app for an experimental version of the broadcaster's iPlayer, which has been tested on BBC staff, allows viewers to select programmes by simply focusing their thoughts as choices of what to watch appear on screen. The "Mind Control TV" prototype works though brain activity signals, which are relayed from an Electroencephalography that contains two sensors to measure levels of brain activity. It can be operated through concentration or relaxation, depending on whether people choose the "attention" or "meditation" mode.

Commenting on the new app, which has been developed with technology company This Place, Cyrus Saihan, head of business development for the BBC's Digital division, said, "So does it work? In a word, yes."

While it is "very early days" when it comes to controlling TV with your brain, many disabled people could benefit from the new approach. "For example, people affected by motor-neurone disease or locked-in-syndrome may increasingly be able to use brain-computer interfaces to get a better experience of digital and media services than they currently do, potentially opening up the online world of information and experiences that the rest of us now take for granted," said Saihan.

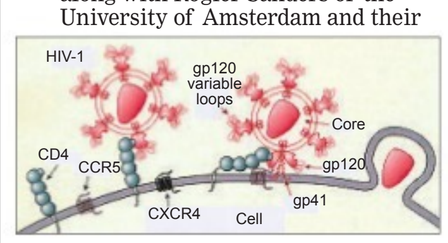
JONATHAN OWEN/THE INDEPENDENT

Neutralising HIV

Three studies published on 18 June advance two different strategies for inducing broadly neutralising antibodies in what amounts to the supreme goal of vaccine development.

HIV is not a single virus but a collection of diverse variants. A practical vaccine, then, would elicit antibodies that recognise a common element among all of them — namely, conserved epitopes of the glycan shield surrounding the virus. The development of immunogens resembling these glycoproteins has been years in the making. Advances in understanding the structure and binding behaviours of various glycoprotein domains of the envelope protein helped Weill Cornell Medical College's John Moore and colleagues to develop a stable, soluble glycoprotein trimer that mimics the native configuration of the viral envelope protein.

To test whether the trimer could spark an immune response, Moore, along with Rogier Sanders of the University of Amsterdam and their collaborators, administered the molecule, called BG505 SOSIP.664, to rabbits and monkeys. "They show there's a real difference," said William Schief, an HIV researcher at the Scripps Research Institute in La Jolla, California, who is an author on all three studies. "When you use their engineered trimer, they're able to induce much higher levels of neutralizing antibodies against a particular strain that you built your trimer from, compared to other previous methods of making trimers."



Although BG505 SOSIP.664 generated potent neutralising antibodies against HIV, it had a narrow range of viral targets, the authors reported in *Science*. "It only neutralises the sequence-matched virus. It doesn't have the breadth," Moore said. Still, without even a narrow response, he added, there would be nothing to build upon. "It demonstrates the capability of the method for future improvement. So it's a recipe for design improvement and strategy improvements that have a reasonable chance of going somewhere."

KERRY GRENS/THE SCIENTIST