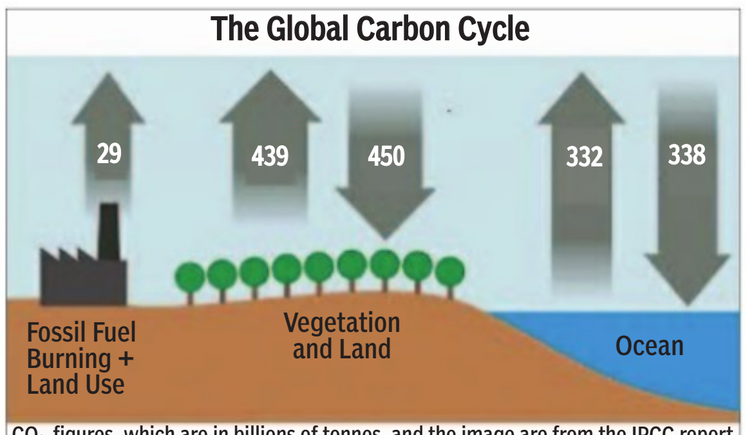
Turning foe to friend

FINDING A USE FOR CO_2 MAY BLUNT THE EDGE OF CARBON EMISSIONS, WRITES **S ANANTHANARAYANAN**

The earth's atmosphere weighs about five million billion tones and the weight of the CO_2 component, with a carbon dioxide content of 400 volume parts per million, comes to about eight billion tonnes. This is the residue, on balance, after an annual emission of over nearly 800 billion tonnes, mostly by natural processes, but also by manmade causes, and then the absorption of nearly as much by vegetation and by the sea. But the manmade contribution, which is a fraction of the total, has been pushing up the atmospheric load, which we urgently need to reduce.

While the rate of emission may not see a fall for some years, it is a priority to find ways to sequester, or prevent some of the CO_2 that we emit from entering the atmosphere. Methods of physical containment of emissions, in natural, underground cavities as a gas or in solution, are limited by cost and technology. But Aanindeeta Banerjee, Graham R Dick, Tatsuhiko Yoshino and Matthew W Kanan, from Stanford University, report in the journal *Nature* a way to do one better — to new make use of CO_2 to produce raw material for products that we need.

The difficulty of using CO_2 in this way is that the gas is already at the lower energy end of processes like burning, which release energy. Carbon dioxide is thus relatively inert and does not react readily, except in conditions that take energy to create. Photosynthesis, by which plants create sugars from CO_2 with the help of the sun's energy, is a way to separate the carbon atom from its low energy bond with oxygen atoms and create bonds with other carbon atoms. Ways to harness the process artificially and create energy from sunlight are hence being worked on *(The Statesman*, 22 April 2015). More modest conversion of CO_2 into chemicals that could be used in other processes have also been devised and used in industry, albeit sparingly, as they were generally not energy efficient.

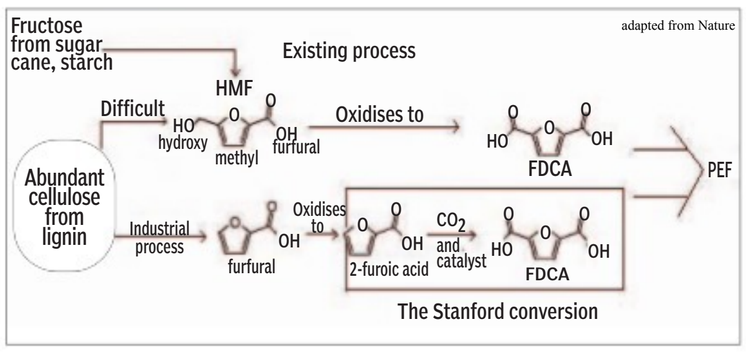


CO_2 figures, which are in billions of tonnes, and the image are from the IPCC report published in 2007. The human caused emissions were nearly 35 billions tonnes by 2011 and are rising

Commercially viable methods have been mostly with the help of catalysts, or special substances that provide an intermediate platform as a way around the need for a high-energy route to create specific chemicals. The Stanford group adds a new instance that emulates the process in photosynthesis, of creating a useful chemical building block with CO_2 as a starting point.

Nature's way

In the action of plants and photosynthesis, energy from sunlight is first converted into a chemically available form, in the form of molecules called *ATP* and *NADPH*, which store and transport energy. In the next stage, in the presence of an enzyme, *RuBisCO*, which catalyses or enables and accelerates the reaction, each carbon atom, which is attached to two oxygen atoms in CO_2, forms bonds with carbon atoms in five-carbon-atom intermediary, to form chains of three-carbon atoms. As a next stage, the five-carbon intermediary is regenerated, leaving a carbon atom ready to combine, and repeated cycles lead to a six-carbon molecule, like glucose or even other carbohydrates like starch or cellulose.



The Stanford team notes that the basic enabler of the sequence is that RuBisCO promotes a carbon-hydrogen bond in the five-carbon intermediate to separate and then form a bond with the carbon atom in CO_2. The team then seeks to recreate these conditions and they find that caesium carbonate is a material that enables the separation of carbon-hydrogen bonds and reaction with the carbon atoms in CO_2. As an application of this function, the team demonstrates that a substance called furoic acid can take up CO_2 and form a derivative called FDCA, which has industrial utility.

FDCA is a material manufactured from sugars like fructose that, so far, can be processed into the polymer, polyethylene furandicarboxylate (PEF), which could take the place of polyethylene terephthalate (PET), a widely use plastic packaging material that is manufactured with petroleum-based terephthalic acid. The manufacture of PEF, which is now from fructose, would emit 50 per cent less CO_2 emissions than PET, of which the annual production is 50 million tonnes, the Stanford paper says. The problem, however, is that producing FDCA from fructose is not scalable. On the other hand, production from a cellulose base, which is abundant in non-edible biomass (corn husk, sawdust, etc), and which is being processed on a large scale to a related compound, Furfural, would be economical, except that in this route as well, the last stage in conversion of bio-mass to FDCA is not efficient. This is where the principle of catalysing the conversion of FC to FDCA, to enable the use of bio-mass for the manufacture of PEF, with the consumption of CO_2 along the way, could be a double winner. While the process needs to be refined and studied to demonstrate the economics, the team also finds the possibility of producing terephthalic acid, for the production of PET, using CO_2, like in the case of PEF. This would again lead to a sizeable "sink" for sequestering CO_2 and still getting some value out of it.

"Our results demonstrate a very simple strategy for engaging CO_2 in C-C bond formation… the ability to make use of the carbon-hydrogen in this way opens up the possibility of using this approach to prepare numerous high-volume targets… synthesis of multi-carbon alcohols and hydrocarbons using CO_2 and renewable hydrogen," the authors of the paper say.

THE WRITER CAN BE CONTACTED AT
response@simplescience.in


Aanindeta Banerjee, Graham R Dick, Tatsuhiko Yoshino and Matthew W Kanan

PLUS POINTS

Horse-sized dinosaur

The discovery of a new species of horse-sized dinosaur has shed fresh light on the evolution of Tyrannosaurus rex, suggesting that the famous predators had to "get smart before they got big", according to newly published research. The dinosaur species unearthed in northern Uzbekistan, from which T. rex later evolved, had highly developed brains and sharp senses but much smaller bodies than their more famous descendants, a study by a team of Scottish scientists has found. The discovery is significant because the remains, which were found in the Kyzylkum desert, fill a 20-million year gap in the fossil record of tyrannosaurs.

The species, *Timurlengia euotica*, lived about 90 million years ago and was about the size of a horse, according to the study published in the journal *Proceedings of the National Academy of Sciences*. The dinosaurs had long legs, a skull studded with sharp teeth and were probably fast runners. The fact that the species was still small around 80 million years after tyrannosaurs first appeared suggests that they only became large at the end of their evolutionary history, when they dominated the top of the prehistoric food chain, according to a team of palaeontologists led by researchers at the University of Edinburgh.

"The ancestors of T. rex would have looked a whole lot like Timurlengia, a horse-sized hunter with a big brain and keen hearing that would put us to shame," said Dr Steve Brusatte of the university's School of GeoSciences, who led the study. "Only after these ancestral tyrannosaurs evolved their clever brains and sharp senses did they grow into the colossal sizes of T. rex. Tyrannosaurs had to get smart before they got big."

CHRIS GREEN/THE INDEPENDENT

CHROMOSOMAL FUNCTIONS

TAPAN KUMAR MAITRA EXPLAINS THE UNIQUE FEATURES OF MEIOSIS

The evolutionary establishment of the complex chromosomes of higher organisms has been accompanied by new patterns of chromosomal behaviour called Meiosis. The processes of synapsis, segregation and crossing over, are evolutionary innovations associated with and probably, arising out of, the molecular architecture of these chromosomes — neither are they displayed by genes as such nor by the relatively simple chromosomes of viruses and bacteria.

Let's address the phenomenon of synapsis first. There is no known mechanism whereby double DNA helices can be brought into homologous alignment with each other. This can only be accomplished at the molecular level with single polynucleotide strands, as demonstrated through annealing experiments to give DNA-DNA or DNA-RNA hybrid structures.

When viewed in meiotic cells at the highest resolution of the light microscope, synapsis appears to be a most exact process, dependent upon sequential homologies but the exactness of homologous recognition at this level of resolution is a chromosomal event. The chromosomes prior to synapsis are visible in the light microscope and hence partially condensed, and since synapsis follows replication and the formation of chromatids, the units of homologous recognition are at least two DNA helices thick. It may be that further understanding of the "synaptinemal complex" as described by experts, will shed new light on this problem, but at the moment synapsis has not been explained by known physical forces or chemical attractions. It is, therefore, a property of complex chromosomes functioning as organelles and at a supragenic level of behaviour.

The products of replication of viral and bacterial chromosomes are separated into their respective particles or cells by mechanisms different from, but as effective as, the process of segregation taking place in higher cells. Like synapsis, segregation is a property of complex chromosomes which has its origin in the fact that a portion of each chromosome (whole in some species) is differentiated into a unit of movement called the centromere. This structure acts in conjunction with another organelle peculiar to higher cells — the spindle. These two organelles make biological sense only when both are present and functioning.

It is possible to imagine equipping each10^5 or 10^6 genes with independent centromeres capable of making connections with an equal number of spindle fibres, but in terms of biological economy the argument is not particularly defensible. Segregation must, therefore, be viewed as behaviour acquired through differentiation of both chromosome and cell, and only after genes were assembled into linear arrays.

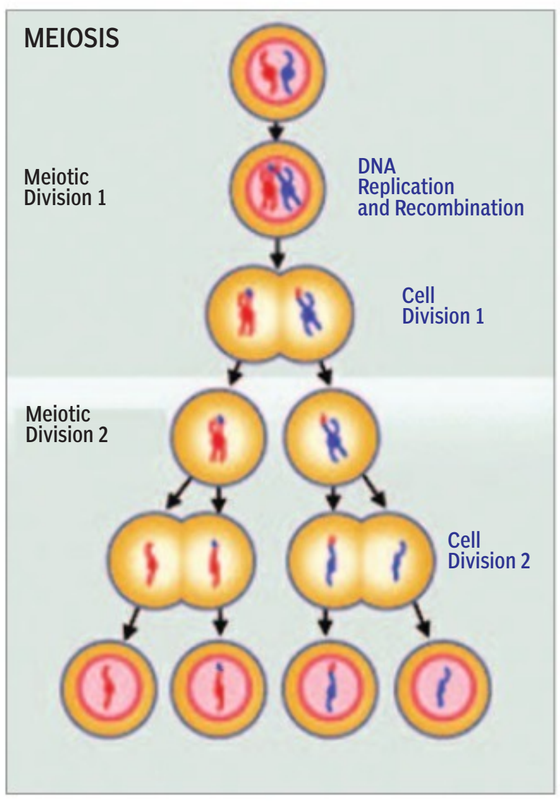
The same may be said of crossing over as it is an acquired property of complex chromosomes. A parallel phenomenon is displayed by viral and bacterial chromosomes but that is mainly in the recombination of genes, not necessarily in terms of how it is attained. A number of schemes for recombination in viruses and bacteria have been proposed with the exchange of genes generally considered to take place between single polynucleotide strands. In higher forms of organisms, all genetic evidence points to recombination taking place between chromatids.

Yet an open mind as to the mechanism must be maintained if only for the reason that while an exchange may occur at a seemingly structural level, it is minutely exact at the molecular level — gains or losses of nucleotides do not normally occur as the result of crossing over. Of more immediate interest is the fact that, regardless of the mechanism of recombination or perhaps, more likely. because of it, the rates of recombination per physical unit of DNA vary widely in different organisms.

When examining the data in the picture, it needs to be kept in mind that a map unit in microbial systems (those above the dividing line) is not determined with the same degree of ease as a map unit in higher organisms. The property of high negative interference, characteristic of these systems, means that the reliable construction of a genetic map can be based only on very small intervals. Making use of computer techniques, however, they have shown that phage T4 has a map distance of about 2,500 units and that there is a good correspondence between map distance and physical length of the chromosome.

When a comparison is made between the genetic maps of higher organisms the correspondence with physical distance measured in number of nucleotide pairs is not a clear one. The genetic maps of mice, maize, and humans are approximately the same as that of *E. coli* and T4 yet contain more than 1,000 times more DNA than the former and 10,000 times more than the latter.

In general, therefore, chromosomes that are structurally simple recombine much more freely than those that are complexed with RNA and proteins, a factor that suggests that linkage in higher forms has cytogenetic meaning that transcends the mechanics of segregation.



During Meiosis, diploid cells undergo two cell divisions that result in haploid cells. In meiosis I, homologous chromosomes pair up along the cell equator and are divided into separate cells. In meiosis II, sister chromatids are divided into separate cells, making a total of four haploid cells that are genetically unique.

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

Full of hidden patterns

PI MIGHT LOOK RANDOM BUT THE FURTHER YOU GO THROUGH ITS ENDLESS SERIES OF DIGITS THE MORE INTERESTING THE NUMBER BECOMES, WRITES **STEVE HUMBLE**

After thousands of years of trying, mathematicians are still working out the number known as pi or "?". We typically think of pi as approximately 3.14 but the most successful attempt to calculate it more precisely worked out its value to over 13 trillion digits after the decimal point. We have known since the 18th century that we will never be able to calculate all the digits of pi because it is an irrational number, one that continues forever without any repeating pattern.

In 1888, logician John Venn, who also invented the Venn diagram, attempted to visually show that the digits of pi were random by drawing a graph showing the first 707 decimal places. He assigned a compass point to the digits 0 to 7 and then drew lines to show the path indicated by each digit. Venn did this work using pen and paper but this is still used today with modern technology to create even more detailed and beautiful patterns.

But, despite the endless string of unpredictable digits that make up pi, it's not what we call a truly random number. And it actually contains all sorts of surprising patterns. The reason we can't call pi random is because the digits it comprises are precisely determined and fixed. For example, the second decimal place in pi is always 4. So you can't ask what the probability would be of a different number taking this position. It isn't randomly positioned.

But we can ask the related question, "Is pi a normal number?" A decimal number is said to be normal when every sequence of possible digits is equally likely to appear in it, making the numbers look random even if they technically aren't. By looking at the digits of pi and applying statistical tests you can try to determine if it is normal. From the tests performed so far, it is still an open question whether pi is normal or not.

For example in 2003, Yasumasa Kanada published the distribution of the number of times different digits appear in the first trillion digits of pi:

Digit	Occurrences
0	99,999,485,134
1	99,999,945,664
2	100,000,480,057
3	99,999,787,805
4	100,000,357,857
5	99,999,671,008
6	99,999,807,503
7	99,999,818,723
8	100,000,791,469
9	99,999,854,780
Total	1,000,000,000,000

His results imply that these digits seem to be fairly evenly distributed, but it is not enough to prove that all of pi would be normal.

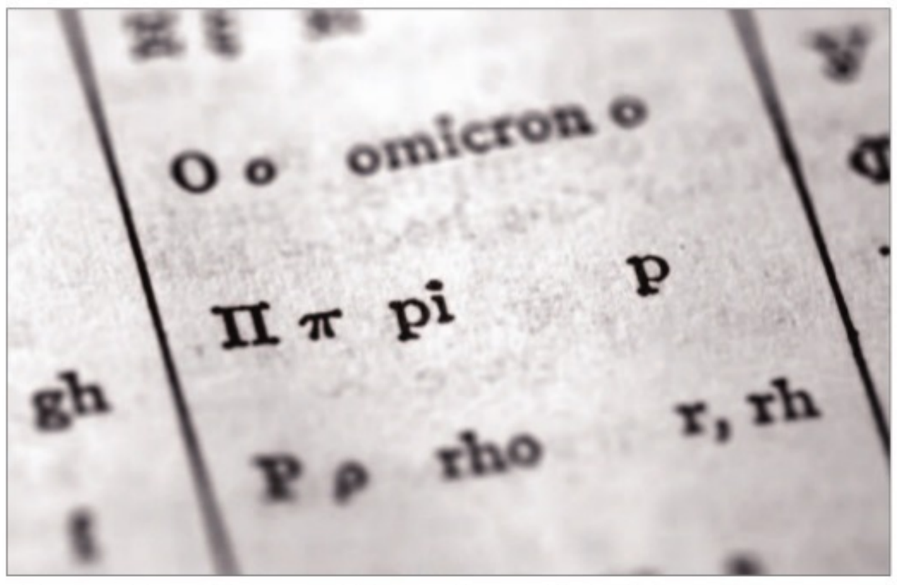
We need to remember the surprising fact that if pi was normal then any finite sequence of digits you could name could be found in it. For example, at position 768 in the pi digits there are six 9s in succession. The chance of this happening if pi is normal and every sequence of *n* digits is equally likely to occur, is 0.08 per cent.

This block of nines is famously called the "Feynman Point" after Nobel Prize-winner Richard Feynman. He once jokingly claimed that if he had to recite pi digits he would name them up to this point and then say "and so on".

Other interesting sequences of digits have also been found. At position 17,387,594,880 you find the sequence 0123456789, and surprisingly earlier at position 60 you find these 10 digits in a scrambled order.

Pi-hunters search for dates of birth and other significant personal numbers in pi asking the question, "Where do I occur in the pi digits?" If you want to test to see where your own special numbers are in pi, then you can do so by using the free online software called Pi birthdays.

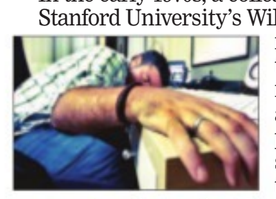
THE INDEPENDENT



"If pi was normal then any finite sequence of digits you could name could be found in it"

Seeking shut-eye

In the early 1970s, a colleague of Stanford University's William Dement remarked on the resemblance of a narcolepsy patient's symptoms to those of a recent canine patient he had read about. The similarity of the symptoms — excessive daytime sleepiness, sudden switch from an awake state to Rapid Eye Movement sleep, sleep paralysis and muscle weakness called cataplexy — prompted psychiatrists to track down a narcoleptic dog of their own to study, and then to gather a kennel full of such dogs to figure out what caused the disease. When Dement bred two affected Doberman pinschers in 1976, he found that their narcolepsy was genetic; many of the puppies had episodes of muscle cataplexy and would collapse into sudden sleep, especially when excited.



In 1986, Emmanuel Mignot went to Stanford to work with the narcoleptic dogs, first to evaluate the effects of different narcolepsy drugs and then to tease out the molecular basis of the disorder. More than a decade later he discovered an autosomal recessive mutation in the orexin receptor in the dogs' brains that was responsible for the disorder. Although orexin receptor mutations have not been found in humans with narcolepsy, patients with the disorder do have reduced levels of orexin (also called hypocretin), a neuropeptide that regulates wakefulness.

"The biological basis for orexin mediating wakefulness was pretty strong," says Joseph Herring, neuroscientist and executive director of the clinical neuroscience programme at Merck Research Laboratories.

ANNA AZVOLINSKY/THE SCIENTIST

Cholera threat

The ongoing El Niño event may be spreading cholera and other diseases caused by *Vibrio* bacteria from Asia to South America, researchers suggest. This is because the bacteria, which are typically found in salty water, could "piggyback" on zooplankton that travel to Peru and Chile with the warm easterly and southerly Pacific currents associated with El Niño, according to a comment published in *Nature Microbiology* last month.

Vibrio bacteria cause severe diarrhoea when people eat raw, contaminated molluscs such as oysters, clams and mussels. Such outbreaks have been linked to previous El Niño episodes. The ongoing El Niño — dubbed El Niño Godzilla because of its intensity — may be the strongest on record. It is developing similarly to an episode in 1977, during which a diarrhoea epidemic broke out in Peru. In that year, *Vibrio parahaemolyticus* bacteria caused an estimated 10,000 cases of severe gastroenteritis along the South American coastline.

SCI DEV.NET