the lunar south pole, where it will release the rover Pragyan, which can travel for up to 500 metres. Previous US, Soviet and Chinese missions have landed nearer the equator.

"The Chandrayaan-2 landing site will be in completely new terrain," says Brett Denevi, a planetary scientist at Johns Hopkins University Applied Physics Laboratory in Laurel, Maryland.

The most important reason for choosing the site is the high likelihood of finding water there, says Mylswamy Annadurai, who led the Chandrayaan-2 project before retiring last year.

Ever since Chandrayaan-1 detected signatures of frozen water on the Moon, scientists have been trying to identify deposits and calculate how much is there. This could help them to explain how water came to be on the Moon in the first place. Evidence gathered by Chandrayaan-1 and other spacecraft show there is water ice across the surface of the south pole[1,2], and possibly buried deposits, too[3].

The presence of water at the lunar south pole also makes it an attractive potential outpost for future astronaut missions, as does the fact the area is thought to be rich in minerals such as magnesium, iron, calcium and titanium. NASA is planning to send astronauts to the south pole by 2024. "There is a lot of international interest in the lunar south pole due to the resources it can provide," says Denevi.

Chandrayaan-2 carries 13 instruments from India and one from NASA, which is on the lander and will collect data to more precisely measure the distance from Earth to the Moon. Of the Indian instruments, eight are on the orbiter, which separated from the lander on 2 September and is currently circling the Moon.

Denevi says she's most excited about the orbiter's imaging infrared spectrometer, which will map light reflected off the lunar surface over a wide range of wavelengths. This information can be used to identify and quantify surface water, which absorbs light strongly at certain wavelengths. Although Chandrayaan-1 provided some of the first key evidence for water on the Moon, its wavelength range did not cover the full absorption band, making it difficult to calculate the abundance and distribution of water[4]. "As far as I know, this will be the first time this full wavelength region has been covered," Denevi says.

"The entire world is waiting for our data."

The orbiter is also carrying a radar operating at two frequencies to detect water ice inside permanently shadowed craters, and to map the thickness and electrical conductivity of lunar rocks, says Ryan Watkins, a lunar scientist at the Planetary Science Institute in Tucson, Arizona. This will be the first radar mapper of this type to orbit the Moon, she says.

A probe on Vikram will also measure a strange phenomenon known as 'Moonquakes'. The Moon has become some 50 metres 'skinnier' over the past several hundred million years, and, as it shrinks, its brittle crust breaks and generates quakes. Annadurai says there is much about the Moon's core that is unknown, such as its composition, and Vikram's data could help researchers to better understand it.

Although Vikram, which carries three instruments, and the Pragyan rover, which has two, are designed to last only one lunar day — about 14 Earth days — Sivan says they will be able to collect a wealth of information in that time. "The entire world is waiting for our data," he says. ■

1. Li, S. *et al. Proc. Natl Acad. Sci. USA* **115**, 8907–8912 (2018).
2. Fisher, E. A. *et al. Icarus* **292**, 74–85 (2017).
3. Rubanenko, L., Venkatraman, J. & Paige, D. A. *Nature Geosci.* **12**, 597–601 (2019).
4. Pieters, C. M. *et al. Science* **326**, 568–572 (2009).

HUMAN GENOME

No 'gay gene': study looks at genetic basis of sexuality

Five DNA markers are linked to sexual behaviour — but can't predict a person's preferences.

BY JONATHAN LAMBERT

The largest study yet on the genetic basis of sexuality has revealed five spots on the human genome that are linked to same-sex sexual behaviour — but none of the markers is reliable enough to predict someone's sexuality.

The findings, which were published on 29 August in *Science* and are based on the genomes of nearly 500,000 people, shore up the results of earlier, smaller studies and confirm the suspicions of many scientists: although sexual preferences have a genetic component, no single gene has a large effect on sexual behaviours (A. Ganna *et al. Science* **365**, eaat7693; 2019).

"There is no 'gay gene'," says lead study author Andrea Ganna, a geneticist at the Broad Institute of MIT and Harvard in Cambridge, Massachusetts.

Ganna and his colleagues also used the analysis to estimate that up to 25% of sexual behaviour can be explained by genetics, with the rest influenced by environmental and cultural factors — a figure similar to the findings of smaller studies.

"This is a solid study," says Melinda Mills, a sociologist at the University of Oxford, UK, who studies the genetic basis of reproductive behaviours.

But she cautions that the results might not be representative of the overall population — a limitation that the study authors acknowledge. Most of the genomes come from the UK Biobank research programme and the consumer-genetics company 23andMe, based in Mountain View, California. The people who share their genetic and health information with those databases are mostly of European ancestry and tend to be older. UK Biobank participants were between 40 and 70 years old when their data were collected, and the median age for people in 23andMe's database is 51.

The study authors also point out that they followed convention for genetic analyses by dropping from their study people whose biological sex and self-identified gender didn't match. As a result, the work doesn't include sexual and gender minorities (the LGBTQ community) such as transgender people and intersex people.

Scientists have long thought that a person's genes partly influence their sexual orientation. Research from the 1990s showed that identical twins are more likely to share a sexual orientation than are fraternal twins or adopted siblings (R. C. Pillard and J. M. Bailey *Hum. Biol.* **70**, 347–365; 1998).

But these studies all had very small sample sizes and most focused on men, says Mills. This hampered scientists' ability to detect many variants linked to sexual orientation.

In the latest study, Ganna and his colleagues used a method known as a genome-wide association study (GWAS) to look at the genomes of hundreds of thousands of people for single-letter DNA changes called SNPs. If lots

of people with a trait in common also share certain SNPs, chances are that the SNPs are related in some way to that characteristic.

The researchers split their study participants into two groups — those who reported having had sex with someone of the same sex, and those who didn't. Then the researchers performed two separate analyses. In one, they evaluated more than one million SNPs and looked at whether people who had more SNPs in common with each other also reported similar sexual behaviours. The scientists found that genetics could explain 8–25% of the variation in sexual behaviour.

For their second analysis, Ganna and his colleagues wanted to see which particular SNPs were associated with same-sex sexual behaviours, and found five that were more common among individuals in that group. However, those five SNPs collectively explained less than 1% of the variation in sexual behaviour.

This suggests that there are a lot of genes that influence sexual behaviour, many of which researchers haven't found yet, says Ganna. An even larger sample size could help to identify those missing variants, he says.

But Ganna cautions that these SNPs can't be used to reliably predict sexual preferences in any individual, because no single gene has a large effect on sexual behaviours.

IT'S COMPLICATED

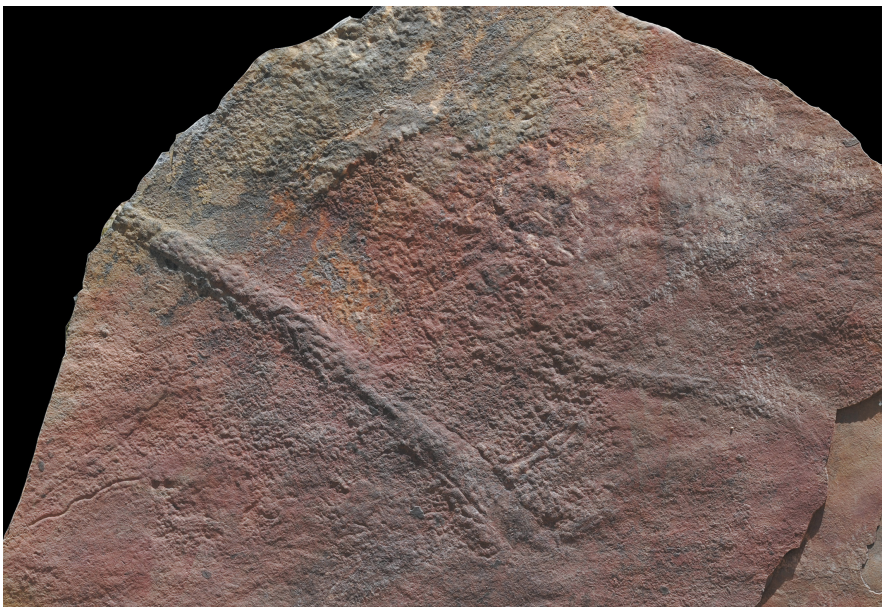
Although the researchers have identified some of the SNPs involved in same-sex sexual behaviour, they aren't sure what the variants do. One is near a gene related to smell, which Ganna says has a role in sexual attraction. Another SNP is associated with male-pattern baldness — a trait influenced by levels of sex hormones, which suggests that these hormones are also linked to same-sex sexual behaviour.

The results demonstrate the complexity of human sexuality, says Ganna. They also presented a challenge to the researchers, who knew that explaining nuanced findings on such a sensitive topic would be tricky.

To ensure that their results are not misinterpreted, the study researchers worked with LGBTQ advocacy groups and science-communication specialists on the best way to convey their findings in the research paper and to the public. Their efforts included the design of a website that lays out the results — and their limitations — to the public, using sensitive, jargon-free language (https://geneticsexbehavior.info/).

Ewan Birney, a geneticist and director of the EMBL European Bioinformatics Institute near Cambridge, UK, applauds that effort.

Although some researchers and LGBTQ advocates might question the wisdom of conducting this kind of research, Birney says that it's important. There has been a lot of sociological research on same-sex sexual behaviour, he says, but this is a complicated topic. It's time to bring a strong, biologically based perspective to the discussion, Birney says. ■



Z. CHEN *ET AL./NATURE*

A fossil of *Yilingia spiciformis* and the track it left as it moved.

EVOLUTION

Worm fossil recasts origins of animal life

Half-a-billion-year-old creature challenges theory that animals burst onto the scene in abrupt event.

BY COLIN BARRAS

More than half a billion years ago, a strange, worm-like creature died as it crawled across a muddy sea floor. Both the organism and the trail it left in its wake lay undisturbed for so long that they fossilized. Now, they are helping us to revise our understanding of when and how animals evolved.

The fossil, which formed some time between 551 million and 539 million years ago, in the Ediacaran period, joins a growing body of evidence that challenges the idea that animal life burst onto the scene in an event known as the Cambrian explosion, which began about 539 million years ago. An analysis of the fossil, which was found in southern China and has been named *Yilingia spiciformis*, is published in *Nature* (Z. Chen *et al. Nature* https://doi.org/10.1038/s41586-019-1522-7; 2019).

"It is just pushing things further and further back into the Ediacaran," says Rachel Wood, a geoscientist at the University of Edinburgh, UK. The Cambrian explosion no longer appears to be such an abrupt event in the history of life on Earth, she says.

The rock record has already revealed that the Ediacaran seas were rich in life, but many fossils from the period have strange anatomical features unlike those seen in modern animals. Palaeontologists have struggled to relate the Ediacaran organisms to the creatures of the Cambrian, which bolstered the idea that the Cambrian explosion represented the dramatic first appearance of familiar animals.

But opinions have begun to shift. Some Ediacaran organisms have been recognized as animals despite their peculiar anatomy, suggesting that animal life began millions of years before the Cambrian explosion (I. Bobrovskiy *et al. Science* **361**, 1246–1249; 2018).

Yilingia spiciformis fits into that picture, and helps push the idea further. The animal grew up to 27 centimetres long and 2.5 centimetres wide. With a segmented body that is symmetrical down its length, it has an anatomy that is more obviously similar to that of Cambrian animals, says Shuhai Xiao, a palaeontologist at Virginia Tech in Blacksburg and a member of the research team that found and analysed the fossils.

"In the past, palaeontologists emphasized the differences between the Ediacaran and Cambrian," says Xiao. "But when you think about it, life had to continue through the boundary. Some lineages had to survive." ■