

Abstractions



SECOND AUTHOR

Michael Studinger and his colleagues have discovered four subglacial lakes in East Antarctica (page 904), to add to the two they found last year. Located two miles

beneath the ice surface in the catchment area of the Recovery Glacier, the new lakes are comparable in total size to Lake Vostok, a 15,690 km² lake buried in Antarctica's interior. But it is their location that makes the lakes noteworthy. Subglacial lakes can drain catastrophically, and the newly discovered lakes are positioned precariously near fast-flowing ice streams on the eastern coast. Studinger, a researcher at the Lamont-Doherty Earth Observatory of Columbia University in Palisades, New York, explains why the Recovery lakes could be a potential hazard.

Why haven't they been found before?

The Recovery lakes region has remained virtually terra incognita because it's out of range of research aircraft. Essentially all we had were data collected on a ground expedition in 1964. Most satellite maps have gaps around the poles because satellite orbits are typically inclined below 80° north and south. The new Ice, Cloud and Land Elevation Satellite orbits have been pushed to 86°, enabling us to determine the elevation of ice surface in this area for the first time.

How can subglacial lakes pose a threat?

These lakes are located at the onset of fast-flowing ice streams. If they drained rapidly this could trigger a faster flow of ice and eventually affect the stability of a significant part of the East Antarctic ice sheet. We have to think about the impacts that such a large influx of fresh water would have on ocean circulation and climate.

What is the most impressive documented lake drain?

Multiple floods have come from subglacial lakes the size of Lake Vostok. These occurred between 12 million and 14 million years ago.

Can you tell whether a catastrophic flooding event is likely soon?

We have only just discovered these lakes and their location. To answer this question we need a more detailed understanding of them. Our current analyses are based on ice-surface data collected from satellites that provide virtually no information on what's underneath. We need to map these new lakes from aircraft equipped with ice-penetrating radar systems. Such data should allow us to understand their dynamic history, their hydrological setting, and their potential for catastrophic change. ■

MAKING THE PAPER

Mark Achtman

A gut bacterium throws light on ancient human migrations.

When modern humans migrated out of Africa they were already carrying the bacterium that causes gastric and duodenal ulcers. In a paper on page 915, molecular biologist Mark Achtman and his colleagues show that *Helicobacter pylori* has hitchhiked along in the gut of *Homo sapiens* for more than 58,000 years.

To track down the evolutionary history of the microbe has taken nearly a decade and the combined efforts of an international multidisciplinary team ranging from gastroenterologists and medical microbiologists to statisticians and population geneticists. The current paper is the culmination of research begun by Achtman and his colleagues at the Max Planck Institute of Infection Biology in Berlin, Germany, in the late 1990s.

Investigations into the genetic differences between *H. pylori* strains from different parts of the world revealed that there were genetic differences between bacteria from Asia and Europe, as is the case in humans. This suggested that the geographical spread of *H. pylori* might parallel ancient human migrations.

Phase two, says Achtman, was inspired by Jared Diamond's book *Guns, Germs, and Steel*. "That book floored me," says Achtman, adding that it led to exciting brainstorming sessions with his collaborators, in particular Sebastian Suerbaum. The notion that *H. pylori* had moved along with humans was supported by the subsequent larger study. To track the bacterium's evolution, the team developed new statistical methods that could cluster bacterial strains on population genetic criteria.

They found that differences between *H. pylori* strains on different continents were consistent with its movement along with human migrations for at least the past few thousand years. Achtman and his team then asked a provocative



question. Are these correlations good enough to use the bacterium to elucidate ancient patterns of human migration rather than vice versa?

Even when this question had been answered in the affirmative, the question of how long *H. pylori* had been continuously associated with humans remained open. To address this quantitative question, more strains were collected and analysed from key populations in the Basque region of Europe, central and southern Asia, and Africa. But the raw data still didn't provide the vital quantitative correlation between the geographic diversity of humans and that of *H. pylori* that would establish how long the association had existed.

Co-author François Balloux, a population geneticist at the University of Oxford, UK, helped to make the breakthrough. He and his colleagues recognized that the data were very 'noisy' as a result of recent migrations, such as those associated with the slave trade in the Americas, which mixed up ethnic groups. This noise obscured the deeper, older, genetic patterns. After excluding obvious recent migrants, the numbers added up. The bacterium could indeed be used to track human population migrations right back to the time that anatomically modern human left Africa.

The intellectual and scientific journey has been incredibly rewarding, says Achtman. "All of us have learned from each other," he says. "Although we are experts in different areas, the discussions have been via the common language of population genetics." ■

KEY COLLABORATORS

It took the combined skills of 21 researchers to tease out four new risk factors for type 2 diabetes mellitus.

A team led by Phillipe Froguel at the Pasteur Institute in Paris, France, provided the samples, phenotypes and assistance with data analysis, while researchers at McGill University in Montreal, Canada, handled the genotyping and data analysis.

Essential to that task was Rob Sladek, who has both an MD

and an engineering degree. "He's very good with machines and with calculations," says co-author Constantin Polychronakos at McGill. "He was instrumental in setting up the technology and the bioinformatics." High-density bead-based microarrays enabled the team to analyse 400,000 single-nucleotide polymorphisms from 1,300 individuals.

Polychronakos decided to exclude people with the known

risk factor of obesity from the study. "I wanted to see what else is there that makes people diabetic." The all-important statistical advice was provided by David Balding, at Imperial College, London, UK.

Four genes were identified as new risk factors for type 2 diabetes and a known association was confirmed (see page 881). Further study of these genes may help explain how the disease works. ■