

## News in focus

the original boundaries.”

He says that for the 90-million to 70-million-year-old ecosystems he studies from the Cretaceous period, “there’s nowhere else better on Earth” for fieldwork than Grand Staircase–Escalante. Fossils of relatives of *Tyrannosaurus rex* found here recently bolstered evidence that the animals hunted in packs (A. L. Titus *et al.* *PeerJ* 9, e11013; 2021), and around 20 new species of dinosaur in total have come from here and Bears Ears, Sertich says.

Bears Ears preserves swathes of “critically important” fossil history from the Triassic period (252 million to 201 million years ago) and Cretaceous period (145 million to 66 million years ago) that is exposed in rocks nowhere else, adds Jessica Theodor, president of the Society of Vertebrate Paleontology (SVP), which is based in McLean, Virginia, and represents some 2,000 palaeontologists globally.

This is why researchers were alarmed when Trump cleaved a total of more than 8,000 square kilometres from the monuments in late 2017, shrinking Bears Ears by 85% and Grand Staircase–Escalante by almost half. This led the SVP to join a coalition of Native American and conservation groups to sue the Trump administration. A judgment is yet to be made on the lawsuit, but might no longer be necessary if the cuts to the monuments are reversed.

### Fossil poaching risk

Trump’s move opened up public land, which was previously protected by its national monument status, to ranching and resource extraction, including coal and uranium mining. The decision also removed certain protections that had been afforded to fossils, exposing invertebrate and plant fossils to the risk of ‘casual collection’, according to one report.

The rangers and resources afforded to national monuments make the sites better equipped than most public lands to safeguard fossil beds, and by removing land from the monuments, Trump made some sites vulnerable to looting. In 2018, *The Washington Post* reported that “extremely rare” vertebrate fossils from the Triassic period had been removed from a fossil bed now outside Bears Ears’ boundaries.

Kevin Madalena, an independent geologist who works on Indigenous land issues in the region, met with Haaland during her visit in April. He says that looting of cultural and fossil sites is an ongoing problem in the region, and that areas excised from the monuments are at greater risk than those still protected by national monument status. Given that fossils of dinosaurs such as *T. rex* routinely sell at auction for millions of dollars, scientists are concerned that, without adequate protection, important specimens could be lost to science.

Shrinking the monuments has also had other effects. Sertich, who has worked on fossil digs at Grand Staircase–Escalante

for 17 years, says that he hasn’t seen direct evidence of increased looting or vandalism, but has noticed more four-wheel-drive traffic.

Madalena, who is Jemez Pueblo, one of the tribes with cultural ties to the region, says the biggest threat could be from resource extraction. Mining and oil-drilling leases were expedited during the Trump administration, he says. “I was kind of staggered. It seemed like flame stacks doubled overnight.”

### Irreplaceable data on prehistory

But not all researchers agree that monument status is essential for protecting or advancing scientific research on public land. “We already have laws protecting fossils on federal lands,” says Brooks Britt, a palaeontologist at Brigham Young University in Provo, Utah, and a member of the Bears Ears National Monument Advisory Committee. “If things get too locked down, it can be difficult to do science,” he notes.

Speaking outside his capacity as a council

member, Britt says that research on public lands can be hindered by onerous restrictions and requirements for government permits, and that national monument status is not always necessary to safeguard fossil resources.

However, Theodor argues that the number of palaeontologists not in favour of restoring Bears Ears and Grand Staircase–Escalante to Obama-era boundaries are “vanishingly small”.

Researchers aren’t sure what the recommendations from Haaland – who is Laguna Pueblo, another tribe with ties here – will look like, but most expect that the review will call for at least a partial enlargement of the monument boundaries.

Former SVP president David Polly, a palaeontologist at Indiana University Bloomington, says he thinks it’s a “logical conclusion” for Grand Staircase–Escalante. Madalena is also hopeful, adding “there’s irreplaceable data from past environments that needs to be preserved”.

# A COMPLETE HUMAN GENOME IS CLOSE: HOW THE GAPS WERE FILLED

## Researchers added 200 million DNA base pairs and 115 genes – but they’ve yet to finish the Y chromosome.

By Sara Reardon

**W**hen the sequencing of the human genome was announced two decades ago by the Human Genome Project and biotech firm Celera Genomics, the sequence was not truly complete. About 15% was missing; technological limitations left researchers unable to work out how certain stretches of DNA fitted together, especially those where there were many repeating letters (or base pairs). Scientists solved some of the puzzle over time, but the most recent human genome, which geneticists have used as a reference since 2013, still lacks 8% of the full sequence (see ‘Completing the human genome’).

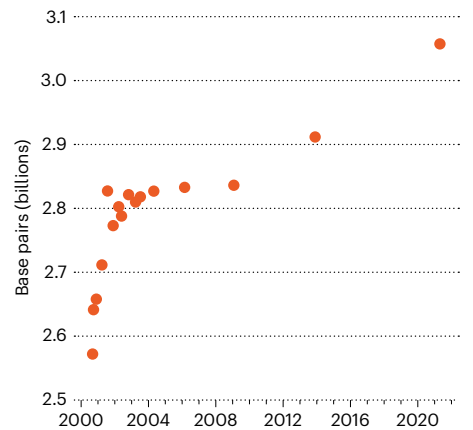
Now, researchers in the Telomere-to-Telomere (T2T) Consortium, comprising 30 institutions, have filled in the gaps. In a 27 May preprint entitled ‘The complete sequence of a human genome’, genomics researcher Karen Miga at the University of California, Santa Cruz, and her colleagues report that they’ve sequenced the remainder, discovering about 115 new genes that code for proteins, for a total of 19,969 (S. Nurk *et al.* Preprint at bioRxiv <https://doi.org/gj8jk3>; 2021).

“It’s exciting to have some resolution to the problem areas,” says Kim Pruitt, a bioinformatician at the US National Center for Biotechnology Information in Bethesda, Maryland, who calls the result a “significant milestone”.

The newly sequenced genome – dubbed

### COMPLETING THE HUMAN GENOME

Researchers have been filling in incompletely sequenced parts of the human reference genome for 20 years, and have now almost finished it, with 3.05 billion DNA base pairs.



0.3% of sequence might still have errors. Includes X but not Y chromosome. Count excludes mitochondrial DNA.

SOURCE: ADAM PHILLIPPY

T2T-CHM13 – adds nearly 200 million base pairs to the 2013 version of the human genome sequence.

This time, instead of taking DNA from a living person, the researchers used a cell line derived from a complete hydatidiform mole, a type of tissue that forms in humans when a sperm inseminates an egg with no nucleus. The resulting cell contains chromosomes only from the father, so the researchers don't have to distinguish between two sets of chromosomes from different people.

Miga says the feat probably wouldn't have been possible without new sequencing technology from Pacific Biosciences in Menlo Park, California, which uses lasers to scan long stretches of DNA isolated from cells – up to 20,000 base pairs at a time. Conventional sequencing methods read DNA in chunks of only a few hundred base pairs at a time, and researchers reassemble these stretches like puzzle pieces. The larger pieces are much easier to put together, because they are more likely to contain sequences that overlap.

T2T-CHM13 is not the last word on the human genome, however. The team had trouble resolving a few regions and estimates that about 0.3% of the genome might contain errors. There are no gaps, but Miga says quality-control checks have proved difficult in those areas. And the sperm cell that formed the hydatidiform mole carried an X chromosome, so the researchers have not yet sequenced a Y chromosome, which typically triggers male biological development.

T2T-CHM13 represents only one person's genome. But the T2T Consortium has teamed up with a group called the Human Pangenome Reference Consortium, which aims over the next 3 years to sequence more than 300 genomes from people all over the world. Miga says that the teams will be able to use T2T-CHM13 as a reference to understand which parts of the genome tend to differ between individuals. They also plan to sequence an entire genome that contains chromosomes from both parents, and Miga's group has been working on sequencing the Y chromosome, using the same new methods to help fill in gaps.

Miga expects that genetics researchers will quickly find out the whether newly sequenced areas and possible genes are associated with human diseases. "When the human genome came out, we didn't have the tools poised and ready to go," she says, but information about the function of the newly sequenced genes should come much faster now, because "we've built up a ton of resources".

She hopes that future human genome sequences will cover everything, including the newly sequenced sections – not just the parts that are easy to read. This should be easier now that the reference genome has been completed. "We need to reach a new standard in genomics where this isn't special, but routine," she says.



A university investigation found that Geoffrey Marcy had infringed sexual-harassment policies.

## US SCIENCE ACADEMY EXPELS MEMBER OVER HARASSMENT COMPLAINT

Astronomer Geoffrey Marcy is first to be kicked out for violating elite group's amended code of conduct.

By Nidhi Subbaraman

**T**he US National Academy of Sciences (NAS) has terminated astronomer Geoffrey Marcy's membership, in light of sexual-harassment complaints – the first time the respected group has expelled a member.

The action comes two years after the NAS introduced a code of conduct that would allow the organization to expel members "for the most egregious violations ... including for proven cases of sexual harassment".

The 158-year-old academy changed its by-laws following pressure from the scientific community and after the #MeToo movement, which highlighted pervasive workplace harassment and institutional failures to prevent it. In 2018, a report by the US National Academies of Sciences, Engineering, and Medicine warned that sexual harassment is widespread in academic science.

Marcy, an exoplanet researcher, resigned from his tenured position at the University of California, Berkeley, in 2015, after BuzzFeed News reported that a university investigation had found that he had infringed sexual-harassment policies in several cases over nearly a decade, until 2010.

Responding to his NAS expulsion, Marcy

told *ScienceInsider* that he has been "completely out of organized academia for over 5 years", and that he "always supported equal opportunity and success for women in academia and science".

"My engaging and empathic style could surely be misinterpreted, which is my fault for poor communication," he said. "I would never intentionally hurt anyone nor cause distress." (Marcy did not respond to *Nature's* request for comment.)

Last September, *Nature* reported that, despite the NAS's by-law amendment, the organization was yet to expel any harassers, even though there were public reports of investigations and findings involving current members. NAS president Marcia McNutt told *Nature* at the time that the organization requires that a complaint be filed before it can adjudicate on a member's status, and that no complaints had been filed.

That report prompted François-Xavier Coudert, a chemist at the French national research agency CNRS in Paris, to e-mail the organization and file complaints about four scientists, including Marcy, citing findings of inappropriate behaviour that had been reported in the press. "I found it was ridiculous as an argument for the academy to say, 'We have a policy, but no one is filing a complaint,'"