

common than previously thought, she says. Three in the same family were discovered in animals in the past year: the Mengla virus in Chinese bats and two Ebola-like viruses found in fish in the East China Sea. “It is amazing how many animals are infected with viruses

which are very closely related to very, very dangerous pathogens,” she says.

It remains unknown whether these viruses can infect or harm humans, says Mühlberger. But their diversity is “pretty scary”, she says. “These viruses are everywhere.”

Virologist Ayato Takada at Hokkaido University in Sapporo, Japan, is also excited about being able to study BSL-4 pathogens in animals in Japan. Until now, researchers had to apply for access to BSL-4 labs overseas, which are in high demand. ■

GENOME EDITING

Errors in CRISPR–baby study

Geneticists retract paper that suggested first gene–edited babies might die early.

BY EWEN CALLAWAY

A study that raised questions over the future health of the world’s first gene-edited babies has been retracted because of key errors that undermined its conclusion.

The research, published in June in *Nature Medicine*¹, had suggested that people with two copies of a natural genetic mutation that confers HIV resistance are at an increased risk of dying earlier than other people. It was conducted in the wake of controversial experiments by the Chinese scientist He Jiankui, who had attempted to recreate the effects of this mutation in the gene *CCR5* by using the CRISPR gene-editing technique in human embryos. The twin girls born last year as a result of the work did not end up carrying this exact mutation, but the research attracted attention because of its potential relevance to such experiments.

However, studies^{2–4} that looked anew at the *Nature Medicine* research find no evidence that people with the mutation die early. The erroneous conclusion about *CCR5* was caused by errors in how the mutation was identified in a population-health database.

“I feel I have a responsibility to put the record straight,” says Rasmus Nielsen, a population geneticist at the University of California, Berkeley, who led the study, which the authors retracted on 8 October. Nielsen also co-authored one of the papers rebutting its findings.

Some researchers stress that because the twins did not receive exactly the same mutation that occurs naturally, the original research and its retraction would not necessarily offer insights into their health anyway. But the episode raises questions about how best to assess the safety of future attempts to edit genes in human embryos.

He Jiankui shocked the scientific world when he announced, in November 2018, that his team had used CRISPR to disable the *CCR5* gene in two babies born that month. He, who was at the time a biophysicist at the Southern

University of China in Shenzhen, said he targeted *CCR5* because people with a 32-DNA-letter deletion known as delta-32 in the gene are resistant to HIV but seem not to experience significant related health problems.

He has not published data supporting his work, but his announcement — presented at a scientific meeting — indicated that, for one twin, both copies of *CCR5* were altered, whereas the other twin carried edits in just one of her two copies. None of the changes exactly matched the delta-32 variation.

RESULTS NOT REPLICATED

Research has hinted that the delta-32 mutation, which is relatively common in people of European ancestry, might carry down-

predicted it should — a sign that individuals with two copies were dying earlier, on average, than the population at large, Wei and Nielsen argued. Questions over the conclusion emerged as soon as the paper was published. Sean Harrison, an epidemiologist at the University of Bristol, UK, attempted to replicate the findings that night. He did not have UK Biobank data on the gene variant that Wei and Nielsen used to identify carriers of delta-32, so he analysed genetic variants near it on the genome that should have given the same result (adjacent parts of the genome tend to be inherited together, allowing scientists to infer the presence or absence of a DNA sequence by analysing neighbouring variants). When they didn’t, he described his findings in tweets and a blogpost.

The discrepancy piqued the interest of David Reich, a population geneticist at Harvard Medical School in Boston, Massachusetts, whose lab is studying *CCR5*. Working with Nielsen, his team discovered² that Nielsen and Wei’s method had caused them to underestimate the number of people in the UK Biobank with two copies of the delta-32 mutation, because the probe that measured the variant they were tracking did not always identify its target sequence. This — and not the supposed harmful effects of the mutation — explained the apparent absence of carriers from the UK Biobank database, says Nielsen.

Researchers emphasize that the unravelling of Wei and Nielsen’s results does not mean it is a sound idea to target *CCR5* for gene editing. “It’s very reasonable to expect that it might have a valuable function that we just don’t know how to measure. It seems very unwise to edit it out,” says Reich. ■



A 32-letter deletion in the gene *CCR5* confers resistance to HIV.

sides — one small study⁵ found that carriers were more likely than other people to die from influenza. To tackle the question in larger data sets, Nielsen and his Berkeley colleague Xinzhu Wei looked at the UK Biobank database, which contains genome and health data from 500,000 people.

Their paper¹ reported that people with two copies of the delta-32 mutation were slightly more likely to die by the age of 76 than were those with one or no copies. They also found that the database harboured fewer people with two copies of the mutation than evolutionary theory

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