

THOMAS PETER/REUTERS

to stay on the plant. Breeders rushed to incorporate the 'jointless' trait into their tomatoes.

But this trait came with a downside. When it was crossed into existing tomato breeds, the resulting plants had flower-bearing branches that produced many extra branches and looked like a broom, terminating in a host of flowers. The flowers were a drain on the plant's resources, diminishing the number of fruit it produced. Breeders selected for other genetic variants that overrode this defect. But decades later, Lippman's team went looking for the genes behind this phenomenon.

TWO RIGHTS THAT MAKE A WRONG

The researchers had previously screened a collection of 4,193 varieties of tomato, looking for those with unusual branching patterns (Z. B. Lippman *et al.* *PLoS Biol.* **6**, e288; 2008). From that collection, they tracked down variants of two genes that, together, caused extreme branching similar to what plant breeders had seen. One of the two genes, the team reports in a paper published online in *Cell* on 18 May, is responsible for the jointless trait (S. Soyk *et al.* *Cell* <http://doi.org/b7gp>; 2017).

The other gene favours the formation of a large green cap of leaf-like structures on top of the fruit — a trait that was selected for thousands of years ago, in the early days of tomato domestication. The benefits of this trait are unclear, Lippman says, but it may have helped to support heavier fruit.

With these genes uncovered, his team used CRISPR–Cas9 editing to eliminate their activity, as well as that of a third gene that also affects flower number, in various combinations. This generated a range of plant architectures, from long, spindly flower-bearing branches to bushy, cauliflower-like bunches of flowers. Some of the plants had improved yields.

The findings should help to quell lingering doubts among plant breeders that negative interactions between desirable genetic traits are a force to be reckoned with, says Andrew Paterson, a plant breeder at the University of Georgia in Athens. The idea has been controversial, he says, because the effects have been difficult to detect statistically.

Lippman's team is now working with plant breeders to use gene editing to develop tomatoes with branches and flowers optimized for the size of the fruit. Plants with larger fruit, for example, may have better yields if they have fewer flowering branches than those with smaller fruit.

"We really are tapping into basic knowledge and applying it to agriculture," says Lippman. "And ironically, it happens to be in the crop that I least liked harvesting on the farm." ■



China has boosted its security presence in the Xinjiang region, home to a large Uighur population.

HUMAN RIGHTS

China set to expand DNA database

Purchase of sequencers feeds fears about nation's intentions.

BY DAVID CYRANOSKI

Police in the northwestern region of Xinjiang, China, have been collecting DNA samples from citizens and are now ramping up their capacity to analyse that genetic cache, according to evidence compiled by activists and details gathered by *Nature*.

The advocacy group Human Rights Watch reported last month that Xinjiang authorities intend to accelerate efforts to gather blood samples from the region's large population of Muslim Uighur people. China's government has cracked down on Xinjiang's separatist movement in recent years, so the prospect of a DNA database there has stoked fears that authorities could use it as a political weapon.

"Our concern is that there is widespread collection of DNA without legal protection and without telling people," says Maya Wang, a researcher for Human Rights Watch in Hong Kong and the author of the report.

In its report, the organization said that Xinjiang's police had ordered 12 DNA sequencers. *Nature* has confirmed the order and learned, from documents and interviews with those involved in the transaction, that the police have purchased enough machines to process

up to 2,000 DNA samples per day. The police department hung up when *Nature* rang to ask about the reason for the purchase.

That capacity goes well beyond what would be needed for routine forensics, says Sumio Sugano, a genomics researcher at the University of Tokyo. "It's definitely the kind of capacity that can be used to build a database," says a source familiar with the equipping of forensics laboratories in China, who did not want to be identified. "They are building a laboratory," he suggested after being shown the full purchase order for the sequencing equipment.

According to a sales officer at a firm involved in the procurement, Xinjiang police have purchased eight sequencers produced by Thermo Fisher Scientific in Waltham, Massachusetts. The machines can be used to look at short stretches of DNA that tend to vary between individuals and are typically used in forensic DNA fingerprinting to match samples collected from a crime scene with individuals listed in a database (or even their close relatives). The police also purchased four domestically produced sequencers made for the same purpose.

Nature has learned that Xinjiang officials have also bought a 'next generation' ▶

► DNA sequencer, which could be used to determine ancestry, eye colour and other physical characteristics from genetic samples.

The report also gives details of a nationwide database that began in the early 2000s and has accrued 44 million entries from 40 million individuals, including 1.5 million from samples, such as cigarette butts, found at crime scenes. China's police have said that the database is for solving crimes. But Human Rights Watch says it has found evidence of “campaigns to amass biometrics from ordinary citizens”.

Many countries use DNA fingerprinting to solve crimes, reunite kidnapped children with their parents and identify bodies, and some

researchers say that the boost in Xinjiang's DNA-analysis capacity does not, by itself, stand out. “Expansion of police surveillance is expected by any civilized nation,” says Sara Katsanis, who researches the applications of genetic testing at Duke University in Durham, North Carolina.

Still, Katsanis and others worry about how DNA is being collected in China and especially in Xinjiang. Last year, Human Rights Watch reported that citizens in Xinjiang were required to give a blood sample to get a passport. And in March, Chinese state media detailed the conclusion of a 4-month programme during which 17.5 million people — who were predominantly

Uighurs — were given health checks, including blood tests. Last week, reports emerged that many of the people who underwent these examinations had been forced to do so.

Megan Allyse, a biomedical-ethics researcher at Mayo Clinic in Rochester, Minnesota, says that DNA profiling is especially fraught in China, because there seems to be no clear framework governing how the samples can be collected, transferred or stored, or when they are allowed to be used in court, and other matters. She hopes that countries can work together to use the data justly. “We need broad, international consensus on the appropriate use of DNA in national-security collections,” she says. ■

PUBLIC HEALTH

Decline in Zika throws trials into doubt

Large studies to assess the risks of Zika are in jeopardy as scientists struggle to find cases.

BY DECLAN BUTLER

Studies of thousands of pregnant women that were set up to probe the link between Zika and birth defects may not provide definitive answers because of a sharp drop in the number of new cases, researchers have warned. The unexpected development is making the disease harder to study, and threatens to hamper trials of experimental vaccines that might protect pregnant women in future outbreaks.

“We’re seeing few, if any, cases, particularly in southern Brazil, which we thought might be

the next big area to be hit this year,” says Oliver Brady, an epidemiologist at the London School of Hygiene and Tropical Medicine.

Seventy countries have reported mosquito-borne Zika virus transmission since 2015, with the most intense epidemics sweeping South America and the Caribbean. Phylogenetic research suggests that the virus first entered Brazil in late 2013 or early 2014 (see <http://dx.doi.org/10.1038/nature22495>), although it was not detected until mid-2015. The virus has been linked with a range of birth defects, including microcephaly, in the fetuses and newborns of

women infected during pregnancy — a pattern of abnormalities known as congenital Zika syndrome. But reliable data on the absolute risks are lacking, and gathering such information is one of the objectives of the affected studies.

The two largest studies each intend to recruit 10,000 or more pregnant women. The Zika in Infants and Pregnancy (ZIP) study was launched last June by the US National Institutes of Health (NIH) and the Fundação Oswaldo Cruz-Fiocruz (Fiocruz), a national scientific agency in Brazil, and has so far recruited almost 3,000 women. The other study is just beginning to recruit. It is being carried out by the ZIKAlliance, a multidisciplinary consortium of 53 research centres that launched in December with €12 million (\$13.5 million) from the European Union. Both trials are taking place across multiple sites in South America and the Caribbean.

But with the drop in new cases (see ‘Decline and fall’), the ZIKAlliance is now reconsidering its plan. “We are going to be pragmatic, we are going to try, but if there are not enough infected cases, then there is little point,” says the consortium’s scientific coordinator Xavier de Lamballerie, a virologist at Aix-Marseille University and French national biomedical agency INSERM.

The ZIKAlliance intends to capture what cases it can at its sites, and is considering focusing resources in sites where Zika has been rarer, such as Bolivia, where future flare-ups might be more likely. “We will track cases there where they are,” he says, “It’s a race against the clock.”

The ZIP study is similarly faced with low



Zika infection in pregnancy can cause birth defects, but a fall in cases means risks may not be understood.

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