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Health workers swab a pigeon in a market in Changsha, China.

VIROLOGY

Flu genomes trace H7N9 evolution

But surveillance of avian influenza viruses is patchy and slow.

BY DECLAN BUTLER

No one knows the pandemic potential of the H7N9 avian influenza that has infected more than 560 people in China and killed 204 since it was first detected in March 2013. But the largest-ever genomic survey of the virus in poultry now provides a more detailed picture of its evolution and spread.

Such information can help to target control efforts, and to monitor the evolution of the virus. But an analysis of sequences submitted to the GenBank repository in the past 15 years suggests that genetic surveillance of avian flu viruses in birds is patchy and less than prompt.

For now, H7N9 flu does not spread easily among people. But as with many bird-flu

viruses, a concern is that it could evolve to do so.

In a paper published on *Nature's* website this week (T. T.-Y. Lam *et al.* *Nature* <http://dx.doi.org/10.1038/nature14348>; 2015), an international team of researchers describes how it tracked the virus from October 2013 to July 2014 by taking swabs from poultry at live-bird markets in 15 cities over 5 provinces in eastern China. The group detected the virus in markets in seven cities and in 3% of samples on average.

The team then sequenced the genomes of 438 viral isolates and found that as the virus spread south, it evolved into three main branches, with multiple sub-branches.

Such diversification is expected, but tracking it can help to identify the main trade routes and markets that fuel a virus's spread. "The extent of

viral transmission among chickens was largely unclear until our paper showed that the virus had diverged into regional lineages," says Yi Guan, a co-author of the paper and a virologist at the State Key Laboratory of Emerging Infectious Diseases in Shenzhen, China. "Eastern China remains as a reservoir and 'distribution centre' for this virus," he says.

Despite such insights, relatively few sequences of H7N9 have been collected. Sequences from only eight H7N9 viral isolates collected from birds in 2014 have been deposited in GenBank. That is not enough for geographical mapping of the virus over time, says Marius Gilbert, an avian-flu epidemiologist and ecologist at the French-speaking Free University of Brussels.

Nor is the latest paper up to date. A new winter wave of H7N9 is under way, and probably has different patterns of spread.

In 2012, *Nature's* news team reported that genetic surveillance of animal-flu viruses is patchy globally: most genomes are sequenced months or years after collection (see *Nature* **483**, 520–522; 2012). Current GenBank data suggest that this is still true. Far more flu sequences are being deposited in GenBank, but many are from samples collected some time ago.

Guan agrees that timely monitoring is important. But surveillance and viral sequencing are costly and time-consuming, and for H7N9 require access to a biosafety-level-3 lab. Given the complications, Guan thinks that the number of recent H7N9 sequences is not grossly low.

Adding to the time lag, public authorities and researchers who sequence flu strains sometimes make the data public only when, or if, they publish — so sequences can languish. The authors of the latest study have sent sequences to GenBank and had already shared the data with the World Health Organization and other bodies.

Guan and his co-authors warn that H7N9 "should be considered as a major candidate to emerge as a pandemic strain". But predicting pandemic potential is an embryonic science. Last year, a prominent international group of researchers argued that there is little evidence that flu viruses that cause sporadic human infections are a greater pandemic threat than viruses that have not yet infected humans (C. A. Russell *et al.* *eLife* **3**, e03883; 2014). But Guan says that given the vast number of flu viruses, it is necessary to prioritize targets for control and vaccine development — and that H7N9 should be high on that list. ■