# Industrialisation, WWI helped fuel TB spread, study says

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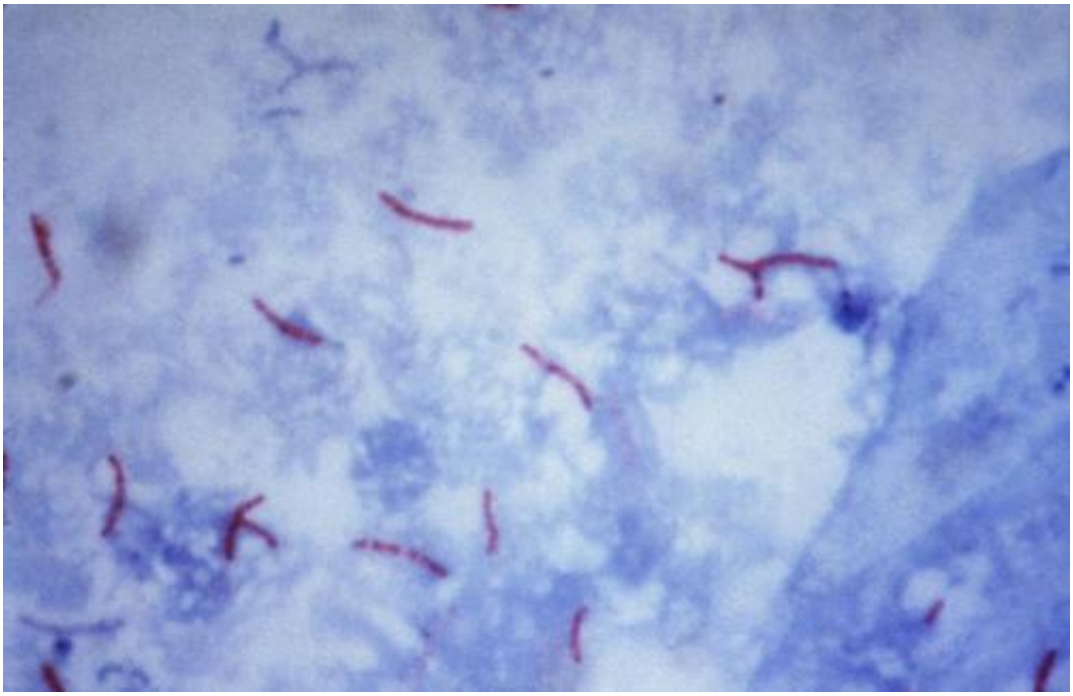

This photomicrograph reveals Mycobacterium tuberculosis bacteria using acid-fast Ziehl-Neelsen stain; Magnified 1000 X. The acid-fast stains depend on the ability of mycobacteria to retain dye when treated with mineral acid or an acid-alcohol solution such as the Ziehl-Neelsen, or the Kinyoun stains that are carbolfuchsin methods specific for M. tuberculosis. Credit: public domain

A virulent group of tuberculosis germs spread from East Asia in waves propelled by industrialisation, World War I and Soviet collapse to yield some of the drug-resistant strains plaguing the world today, a study said

Monday.

Researchers' massive trawl through nearly 5,000 TB samples from 99 countries pinpointed changes in the DNA code to draw a partial family tree of the germ Mycobacterium tuberculosis.

A branch of that tree known as the "Beijing lineage" begins in a region around northeast China, Korea and Japan some 6,600 years ago, said a study published in the journal *Nature Genetics*.

It evolved into several sub-lineages and strains, spreading eastward to Micronesia and Polynesia and westward to central Asia, Russia and eastern Europe.

The migration waves have become more pronounced over the past two centuries, spurred by industrialisation and urbanisation, as well as episodes of widespread deprivation like World War I that brought infected and vulnerable people close together.

Among the toughest modern-day versions—two multi-drug resistant (MDR) clones, started spreading through eastern Europe and Asia on an epidemic scale about 20-30 years ago, "coinciding with the collapse of the public health system of the former Soviet Union," study co-author Thierry Wirth of France's National History Museum told AFP.

There was a single decrease visible on a chart plotting the global spread of the "Beijing lineage" from the year 1500 to 2000. It coincided with a rise in antibiotic use in the 1960s and ended with the HIV epidemic from the 1980s.

TB itself is theorised to be about 40,000 years old.

Unravelling the disease's genetic history may offer pointers for tackling

its spread.

MDR strains, which do not respond to frontline antibiotics, are a major concern as they are much more costly and difficult to treat.

In 2013, there were nine million new cases of TB and 1.5 million deaths worldwide, including 360,000 people who were also infected with HIV, the World Health Organization (WHO) said in its latest TB report.

## 200 million malaria cases

In a separate paper published in the same journal, scientists said they had identified a genetic mechanism by which the malaria parasite, Plasmodium falciparum, develops resistance to the main drug artemisinin.

An analysis of 1,612 samples from 15 locations in southeast Asia and Africa found 20 mutation in a gene called kelch13, they reported.

These appeared to work in concert with mutations in four other genes to support the development of artemisinin resistance in the parasite transferred by mosquitoes.

Monitoring for such mutations can serve as an early warning system to identify areas at risk for artemisinin resistance—a fast-growing problem in southeast Asia, said the study authors.

The team found that kelch13 mutations were rare in Africa, and not linked to artemisinin resistance.

"At present, artemisinin resistance appears to be largely confined to southeast Asia, but the situation might change as the parasite population continues to evolve," said study co-author Dominic Kwiatkowski, a

genomics professor at Oxford University.

There were nearly 200 million cases of malaria worldwide in 2013 and some 584,000 deaths, according to the WHO. Ninety percent of malaria deaths occur in Africa.

**More information:** *Nature Genetics*, nature.com/articles/DOI: 10.1038/ng.3195