

Genomics reveals evolutionary history of drug resistant tuberculosis

From the dawn of agriculture to the fall of the Soviet Union, major events in human history have left marks in the DNA of the bacterium that causes tuberculosis (TB). A study of nearly 5,000 samples of *Mycobacterium tuberculosis* from around the world shows how a lineage of the bacterium that emerged thousands of years ago in Asia has since become a global killer that is widely resistant to antibiotic drugs.

First identified in greater Beijing in the mid-1990s, the 'Beijing lineage' now circulates throughout the world and many strains are resistant to drugs that vanquish other types of TB.

Travel along the Silk Road, which connected China with the Middle East, probably helped to spread the lineage beyond East Asia, the researchers say.

Global upheavals also propelled the rise of the Beijing lineage. The team used the whole-genome sequences to model how its population changed over time and showed that numbers of the bacterium (and, therefore, people infected) shot up in the early nineteenth century, possibly because of the rise of urban populations during the Industrial Revolution. It spiked again in the early twentieth century, which Wirth says could be related to further urbanization after the First World War and exacerbated by influenza pandemics at the time, which made people more susceptible to TB.

The increasing availability of antibiotics in the 1960s, meanwhile, coincides with a fall in the numbers of the bacterium.

Read full, original story: [Tuberculosis genomes track human history](#)