

Study finds TB strains in Russia becoming both more resistant to drugs and faster evolving

January 27 2014, by Bob Yirka



M. tuberculosis bacterial colonies. Credit: Centers for Disease Control and Prevention.

(Medical Xpress)—An international team of researchers has found that bacteria responsible for Tuberculosis (TB) are becoming more resistant to drugs in Russia than are strains in other parts of the world. In their paper published in the journal *Nature Genetics*, the team describes how they collected TB isolates from 2,348 people and sequenced the genomes of 1000 of them. In so doing they discovered that not only are many of the strains becoming resistant to drugs meant to disable them, but they have evolved in a way that allows them to overcome antibacterial agents' tendency to cause a slowdown in cell division.

The breakup of the Soviet Union had a lot of political and economic impact on the world, and more and more scientists are finding it also had an impact on the spread of TB—second only to HIV as a leading cause of death from an infectious disease. As the Union fell apart, so too did part of the medical establishment, which led to many patients with TB not getting full treatment—partial treatment oftentimes leads to an increase in resistance as bacteria that are not sufficiently impacted produce stronger offspring. Prior research has suggested that [drug](#) resistant strains have become prevalent in Russia, and now this new study suggests how serious the problem has become. The researchers found nearly half of all isolates tested were resistant to many antibacterial agents—they suffered no harm from at least two of the so-called first line types of drugs. Worse perhaps, they also found that 16 percent of that group was also impervious to so-called second line types of drugs. Treating such patients is both difficult and expensive, and presents a challenge to other nations as people travel to other places.

Drugs for stopping TB don't necessarily kill the bacteria, instead, they disrupt how they function, making it impossible for them to move around, for example, or to reproduce—most cause them to divide more slowly as well. Sadly, the researchers found that several strains in Russia have evolved to overcome this problem as well, and are now able to divide as fast as ever after exposure to antibacterial agents.

Overall, it appears the researchers report, that TB strains in Russia are developing resistance to [antibacterial agents](#) in general and are evolving into whole new strains that are becoming increasingly difficult to control. Fortunately, all is not lost, they add, noting that as Russia's health system gains strength, so too will the effectiveness of treatment, slowing resistance trends and reducing infection rates, bringing them back into line with most other developed countries.

More information: Evolution and transmission of drug-resistant

tuberculosis in a Russian population, *Nature Genetics* (2014) [DOI: 10.1038/ng.2878](https://doi.org/10.1038/ng.2878)

Abstract

The molecular mechanisms determining the transmissibility and prevalence of drug-resistant tuberculosis in a population were investigated through whole-genome sequencing of 1,000 prospectively obtained patient isolates from Russia. Two-thirds belonged to the Beijing lineage, which was dominated by two homogeneous clades. Multidrug-resistant (MDR) genotypes were found in 48% of isolates overall and in 87% of the major clades. The most common *rpoB* mutation was associated with fitness-compensatory mutations in *rpoA* or *rpoC*, and a new intragenic compensatory substitution was identified. The proportion of MDR cases with extensively drug-resistant (XDR) tuberculosis was 16% overall, with 65% of MDR isolates harboring *eis* mutations, selected by kanamycin therapy, which may drive the expansion of strains with enhanced virulence. The combination of drug resistance and compensatory mutations displayed by the major clades confers clinical resistance without compromising fitness and transmissibility, showing that, in addition to weaknesses in the tuberculosis control program, biological factors drive the persistence and spread of MDR and XDR tuberculosis in Russia and beyond.

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Citation: Study finds TB strains in Russia becoming both more resistant to drugs and faster evolving (2014, January 27) retrieved 22 September 2024 from <https://medicalxpress.com/news/2014-01-tb-strains-russia-resistant-drugs.html>

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