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# Mechanisms for the Spread of Antibiotic Resistance in Tuberculosis

Julie Allison Spencer

*University of New Mexico - Main Campus, [jaspence@unm.edu](mailto:jaspence@unm.edu)*

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Mechanisms of Horizontal Gene Transfer in Antibiotic Resistant Tuberculosis  
Julie Allison Spencer  
UNM Department of Biology

Tuberculosis (TB) is currently the ninth leading cause of death for humans worldwide, causing 10.4 million new infections in 2016. According to the World Health Organization, of these infections, 600,000 were antibiotic resistant. However, the treatment success rate for resistant TB was only 54%. The potential for emergent epidemics of drug resistant TB highlights the need to understand the mechanisms for the spread of resistance. *Mycobacterium tuberculosis*, the bacterium that causes TB, evolves resistant strains within individuals who are being treated with antibiotics. It has been assumed previously that the resistant characteristics of these strains are spread primarily by the transmission of the strains themselves through the air, by coughing. However, in other bacterial diseases, genes for resistance often spread by horizontal gene transfer, or the movement of DNA between cells. In this study, I asked whether resistant genes in *Mycobacterium tuberculosis* (*Mtb*) could also spread by the same mechanism. One way to show evidence of horizontal transfer is to look for places in the cell's DNA where new DNA has recently been incorporated, or recombined. I analyzed 67 whole genomes of drug resistant *Mtb* for recombination, using the program FastGEAR. I found evidence of ancestral recombination in 3 different places, and of recent recombination in 30 different places. This discovery may lead to new approaches for treating drug resistant tuberculosis.