

Scientists step up hunt for bacterial genes tied to Lyme disease

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Investigators at The University of Texas Health Science Center at Houston (UTHealth) have accelerated the search for the bacterial genes that make the Lyme disease bacterium so invasive and persistent. The discovery could advance the diagnosis and treatment of this disease, which affects an estimated 30,000 Americans each year.

The researchers have developed a new technique that allowed them to test 15 times more bacterial genes than had been evaluated in the previous 30 years to ascertain their roles in infection. Findings appeared Oct. 25 in the journal The Public Library of Science ONE ([PLOS ONE](#)), an international, peer-reviewed, open-access, online publication.

Scientists hope to use this information to unravel the mystery of how the spiral-shaped bacterium *Borrelia burgdorferi* causes Lyme disease. Ticks carry the bacterium and transfer it to animals and humans when the tiny spider-like creatures bite. The Lyme disease microorganism was discovered in 1981.

"We believe that this will be one of the most significant publications in Lyme disease in the next several years. This global approach will help 'move the field forward' and also serve as a model for other pathogens with similar properties," said Steven Norris, Ph.D., the study's senior author and the vice chair for research in the Department of Pathology and Laboratory Medicine at the UTHealth Medical School.

The bacterium can invade almost any tissue in humans or animals and

trigger an infection that lasts from months to years. Its symptoms include a reddish rash that often resembles a bull's eye and flu-like symptoms. The disease can lead to nervous system problems, [joint inflammation](#) and [heart abnormalities](#). Most instances of Lyme disease can be treated with antibiotics.

"Our long-term goals are to screen, identify and characterize the virulence determinants of the [Lyme disease](#) bacterium and thereby dissect the mechanism of pathogenesis in mammals and ticks," said Tao Lin, D.V.M., the study's lead author and assistant professor of pathology and laboratory medicine at the UTHealth Medical School. "With this information, we will have a clearer picture about the virulence determinants and virulence factors for this fascinating microorganism and the mechanism of pathogenesis behind this unique, invasive, persistent pathogen."

Norris, the Robert Greer Professor of Biomedical Sciences at UTHealth, and Lin are running tests on the 1,739 genes in the bacterium to see which genes impact the microorganism's ability to spread disease.

To do this, they mutated the bacterial genes and gauged the impact in a mouse infection model. Overall, 4,479 mutated bacteria were isolated and characterized. Whereas it took researchers about three decades to knock out less than 40 [bacterial genes](#), Norris and Lin knocked out 790 genes in a comparatively short period of time; some genes were "hit" multiple times. A newly developed screening technique, which involves signature-tagged mutagenesis and Luminex®-based high-throughput screening technologies, can also be used to identify infection-related genes in other bacteria.

"This kind of study enables us to better understand the disease pathogenesis at the basic level," said Charles Ericsson, M.D., head of clinical infectious diseases at the UTHealth Medical School. "In time,

such understanding of virulence properties might enable us to develop vaccine candidates, better diagnostic tools and perhaps even targeted drug intervention."

Provided by University of Texas Health Science Center at Houston

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