

# Genetic blueprint of bacteria causing Lyme disease unraveled

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Benjamin Luft, M.D., Professor of Medicine, Stony Brook University Medical Center, and a team of medical researchers have determined the genetic blueprint of 13 strains of the bacteria that cause Lyme disease. The finding is crucial to advancing research on Lyme disease, the most frequent tick-borne infection in North America and Europe, and may lead to better diagnostics and a vaccine. Dr. Luft presented the research results at an October 11 meeting in Washington, D.C., at the Institute of Medicine, an arm of the National Academy of Sciences. The study is reported in the early online edition of the [Journal of Bacteriology](#).

*Borrelia burgdorferi* is the causative agent of [Lyme disease](#). The first complete [genome sequence](#) of one strain of *B. burgdorferi* more than 10 years ago has helped researchers understand the pathogenesis of the disease. However, this understanding was limited with only a single genome sequence on one strain completed. By determining all genome sequences of *B. burgdorferi*, the researchers are providing a foundation for novel detection of Lyme disease, diagnostic approaches and prevention strategies. The timing is critical, as disease occurrence has become widespread over the past decade throughout the United States and part of Europe.

“By characterizing every gene in the Lyme disease agents family, we have a blueprint of every possible characteristic of the organism,” says Dr. Luft, senior author on the study. “This is the building block to developing more accurate and effective diagnostic tests, therapeutic agents and vaccines.

“We are depositing the millions of nucleotides that we have sequenced in the public database so that this valuable information will help to further enhance our research and that of other Lyme disease investigators.”

Dr. Luft and colleagues point out in the study that improved diagnostics are needed because the best clinical sign of Lyme disease, the erythema migrans skin rash, does not always occur in patients. In addition, diagnostic assays and vaccines developed before their blueprint of the entire genome of *B. burgdorferi* have had less than satisfactory results.

“A driving force for doing this project was the observation that certain forms of the [bacteria](#) can be more invasive than others,” adds Dr. Steven E. Schutzer, lead author, and Professor of Medicine, University of Medicine and Dentistry of New Jersey. “We wanted to find out why and how to identify this property.”

Provided by Stony Brook University

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