

New genetic analysis of Lyme disease-causing bacteria could improve diagnosis and treatment

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A genetic analysis of Lyme disease bacteria may pave the way for improved diagnosis, treatment and prevention of the tick-borne ailment.

By mapping the complete genetic makeup of 47 strains of Lyme disease-causing [bacteria](#) from around the world, an international team has created a powerful resource for identifying the specific bacterial strains that infect patients. Researchers said this could enable more accurate diagnostic tests and treatments tailored to the exact type or types of bacteria causing each patient's illness.

"This comprehensive, high-quality sequencing investigation of Lyme disease and related bacteria provides the foundation to propel the field forward," said Steven Schutzer, a Rutgers New Jersey Medical School professor and co-author of the study [published](#) in *mBio*.

"Every modern research project—from clinical to public health to ecology and evolution to bacterial physiology to medical-tool development to host-bacteria interaction—will benefit from this work."

Researchers said the [genetic information](#) uncovered in this study—which explains how the bacteria evolves and spreads and the genes are essential for survival—may help scientists develop more effective vaccines against Lyme disease.

Lyme disease is the most common tick-borne illness in North America and Europe, affecting hundreds of thousands of people a year. The disease arises from bacteria belonging to the *Borrelia burgdorferi sensu lato* group, which infect humans through the bite of infected ticks.

Symptoms can include fever, headache, fatigue and a characteristic skin rash. If left untreated, the infection can spread to joints, the heart and the nervous system, causing more severe complications.

Case numbers are increasing steadily, with 476,000 new cases each year in the US, and may grow faster with climate change, the study authors said.

The research team sequenced the complete genomes of Lyme disease bacteria representing all 23 known species in the group. Most of these hadn't been sequenced before this effort. The project included multiple strains of the bacteria most commonly associated with human infections and species not previously known to cause disease in humans.

By comparing these genomes, the researchers reconstructed the evolutionary history of Lyme disease bacteria, tracing the origins back millions of years. They discovered the bacteria likely originated before the breakup of the ancient supercontinent Pangaea, explaining the current worldwide distribution.

The study also revealed how these bacteria exchange genetic material within and between species. This process, known as recombination, allows the bacteria to evolve rapidly and adapt to new environments. The researchers identified specific hot spots in the bacterial genomes where this genetic exchange occurs most frequently, often involving genes that help the bacteria interact with their tick vectors and animal hosts.

"By understanding how these bacteria evolve and exchange genetic material, we're better equipped to predict and respond to changes in their behavior, including potential shifts in their ability to cause disease in humans," said Weigang Qiu, a professor of biology at City University of New York and senior author of the study.

To facilitate ongoing research, the team has developed web-based software tools (BorreliaBase.org) that allow scientists to compare *Borrelia* genomes and identify determinants of its ability to infect humans.

Looking ahead, the researchers plan to analyze more strains of Lyme disease bacteria, particularly from understudied regions. They also aim to investigate the functions of genes unique to disease-causing strains,

which could reveal new targets for therapeutic interventions.

As factors such as [climate change](#) help Lyme disease expand its geographic range, this research provides valuable tools and insights for combating this rising [public health](#) threat.

"This is a seminal study, a body of work that provides researchers with data and tools going forward to better tailor treatment against all causes of Lyme disease and provides a framework toward similar approaches against other infectious diseases caused by pathogens," said Benjamin Luft, the Edmund D. Pellegrino Professor of Medicine at the Renaissance School of Medicine at Stony Brook University.

Other scientists among the study's 20 authors were Claire Fraser and Emmanuel Mongodin of the University of Maryland School of Medicine and Sherwood Casjens of the University of Utah School of Medicine.

More information: Natural selection and recombination at host-interacting lipoprotein loci drive genome diversification of Lyme disease and related bacteria, *mBio* (2024). [DOI: 10.1128/mbio.01749-24](https://doi.org/10.1128/mbio.01749-24)

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