

Sequencing of hundreds of bacteria samples from Lyme disease patients helps explain symptom differences

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Dark field microscopy of *Borrelia burgdorferi*. Credit: Jacob Lemieux, CC BY 4.0, creativecommons.org/licenses/by/4.0/)

A large team of medical researchers affiliated with several institutions in the U.S., working with pair of colleagues from the University of Ljubljana, in Slovenia, has sequenced the genomes of several hundred samples of *Borrelia burgdorferi*, the bacterium that causes Lyme disease.

In their paper published in *PLOS Pathogens*, the group describes differences they found in different strains of the bacteria, and features of its proteins that appear to be related to different symptoms experienced by patients.

Lyme disease is caused by a bacterial infection (*B. burgdorferi*) and is the most common vector-borne disease in both North America and Europe. It is quite commonly characterized by the bulls-eye shaped rings around the site of infection, which is typically a tick bite. Symptoms vary widely between patients depending on which parts of the body are infected. In this new effort, the research team sought to better understand why different body parts become targets for the bacteria and why reactions to infections differ so markedly between patients.

To learn more about *B. burgdorferi* in general, the research team collected [tissue samples](#) from the site of the bite on 299 patients. The team then studied the genes of each sample, looking for [genetic differences](#) between them. Differences were then correlated with symptoms, particularly those that were most severe.

In so doing, they found differences that appeared to be more prevalent in people with more severe symptoms. They also found differences in bacterial proteins that were produced by different strains of *B. burgdorferi*. Such differences, they noted, tended to be in proteins on the surface of the bacteria that were related to the bacteria's ability to spread to different parts of the body.

The team notes that such spreading has typically been associated with more [severe symptoms](#), such as when the bacteria make their way to the [nervous system](#), or the joints, via the bloodstream.

The researchers suggest that they consider their work a stepping stone to a much larger study of Lyme disease—one that will hopefully lead to a better understanding of why the [immune system](#) is so easily overcome by the bacteria in so many patients and why symptoms persist in some patients for months or even years.

More information: Jacob E. Lemieux et al, Whole genome sequencing of human *Borrelia burgdorferi* isolates reveals linked blocks of accessory genome elements located on plasmids and associated with human dissemination, *PLOS Pathogens* (2023). [DOI: 10.1371/journal.ppat.1011243](#)

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