

Scientists sequence genomes of lyme disease bacteria

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Scientists supported by the National Institutes of Health (NIH) have determined the complete genetic blueprints for 13 different strains of *Borrelia burgdorferi*, the bacteria that cause Lyme disease.

The achievement should lead to a better understanding of how genetic variations among strains may result in different courses of illness in people with [Lyme disease](#), the most common tickborne disease in North America. The wealth of new genetic data will also help scientists develop improved ways to diagnose, treat and prevent Lyme disease.

The first genome of a strain of *B. burgdorferi* was sequenced more than 10 years ago. The 13 newly sequenced strains include ones isolated from humans and ticks and represent a range of geographic origins. Together, the genomes provide a more complete picture of scope of natural variations in the microbe and the disease it causes.

The sequencing and analysis was led by Claire M. Fraser-Liggett, Ph.D., of the University of Maryland School of Medicine, and was performed at a Microbial Sequencing Center funded by the NIH's National Institute of Allergy and Infectious Diseases (NIAID). The research project was initiated by Steven E. Schutzer, M.D., of the University of Medicine and Dentistry of New Jersey-New Jersey Medical School, an NIAID grantee.

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More information: SE Schutzer et al. Whole genome sequences of thirteen isolates of *Borrelia burgdorferi*. *J. Bacteriology*
[DOI:10.1128/JB.01158-01](https://doi.org/10.1128/JB.01158-01) (2010).

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