

A comparative analysis of *Borrelia burgdorferi* and *Babesia microti*: Potential coactions in transmission and infection

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1 Problem Statement

Lyme disease and Human babesiosis are two common diseases in the United States caused by ticks. They are caused by two distinct pathogens: *Borrelia burgdorferi* and *Babesia microti* re-spectively. These pathogens occur in overlapping areas of the United States[1] and are primarily transmitted through a tick vector known as *Ixodes Scapularis*[1, 2, 3]. In this project, we aim to compare and analyze the genetics of these causative pathogens in order to determine the reason for their shared mode of transmission. By analyzing the genetics of these pathogens, we can understand the reason behind their shared mode of transmission and the overlap in the affected geographical areas of the United States.

2 Data

The genome data to be used for this project can be procured from the NCBI data-base. The reference genomes are as follows[4]:

1. *Borrelia burgdorferi*:
 - RefSeq: GCF₀00181575.2
2. *Babesia microti*