Borrelia burgdorferi genotype predicts the capacity for hematogenous dissemination during early Lyme disease

Abstract:

Background. \char64nbsp; Lyme disease, the most common tickborne disease in the United States, is caused exclusively by Borrelia burgdorferi sensu stricto in North America. The present study evaluated the genotypes of >400 clinical isolates of B. burgdorferi recovered from patients from suburban New York City with early Lyme disease associated with erythema migrans; it is the largest number of borrelial strains from North America ever to be investigated. Methods. @nbsp; Genotyping was performed by restriction fragment-length polymorphism polymerase chain reaction analysis of the 16S-23S ribosomal RNA spacer and reverse line blot analysis of the outer surface protein C gene (ospC). For some isolates, DNA sequence analysis was also performed. Results. @nbsp; The findings showed that the 16S-23S ribosomal spacer and ospC are in strong linkage disequilibrium. Most B. burgdorferi genotypes characterized by either typing method were capable of infecting and disseminating in patients. However, a distinct subset of just 4 of the 16 ospC genotypes identified were responsible for >80% of cases of early disseminated Lyme disease. Conclusions. @nbsp; This study identified the B. burgdorferi genotypes that pose the greatest risk of causing hematogenous dissemination in humans. This information should be considered in the future development of diagnostic assays and vaccine preparations.