

ITS2領域の塩基配列によるマダニ属の系統解析

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Molecular phylogenetic analysis of ixodid ticks based on the ribosomal DNA spacer, internal transcribed spacer 2, sequences

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ABSTRACT: An internal transcribed spacer (ITS2) sequence between the 5.8S and 28S rRNA genes was used to estimate the phyletic relationships among *Ixodes* spp. tick vectors of Lyme disease-causing *Borrelia* spirochetes. Analysis indicates that *Borrelia burgdorferi* sensu lato species associated with Lyme disease are found mainly in ticks of the *Ixodes ricinus* species complex. Other closely related tick species are not known to transmit the *Borrelia*-that cause Lyme disease in humans, but they appear to have a specific association with other closely related *Borrelia* species. There is a high degree of concordance in the phylogenetics of *Borrelia* taxa and the phylogenetic relationships among *Ixodes* ticks.

抄録 ライム病ボレリア媒介マダニの系統解析に5.8Sと28SRNA間のITS2領域を用いた。*Borrelia burgdorferi sensu lato species*は主に*Ixodes ricinus* species complexが保有する。他の近縁なダニはライム病ボレリアを保有することが知られていないが、ボレリア種と特別な関係を持っているらしい。ボレリアの系統分化と寄生マダニのそれには高度な一致が見られた。

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