Borrelia burgdorferi Bacteria in Domestic Animals China

Guangyuan Liu1,*, Zhancheng Tian1, Junren Xie1, Jin Luo1, Meiyuan Tian1, Jinfeng Zheng1, Xiaosong Yuan1, Fangfang Wang1, Ronggui Chen2 and Haijun Wang2

1State Key Laboratory of Veterinary Etiological Biology, Key Laboratory of Veterinary Parasitology of Gansu Province, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, Gansu Province 730046, PR China
2ili Center of Animal Disease Control and Diagnosis, ili 835000, China

Abstract

Keywords: Borrelia burgdorferi; Amplicon; Tick-borne zoonotic disease; GenBank

Introduction

Lyme disease (borreliosis) is the most prevalent tick-borne zoonotic disease in Europe, North America, and eastern Asia. Its etiologic agent, Borrelia burgdorferi sensu lato, has been described in China: B. garinii, B. afzelii, B. valaisiana, B. sinica [1,2], B. garinii was the main genotype in China, and it was distributed mainly in northern China. B. afzelii was the second most frequently found species, and it was distributed in both northern and southern China. All B. valaisiana strains were isolated from Guizhou Province [3]. Some B. sinica strains were recently isolated in some regions of the Yangtze River valley [2,3]. But for B. burgdorferi, it seems to be absent from Asia, apart from a report of B. burgdorferi from several different rodents in Taiwan [4]. B. burgdorferi is mainly associated with arthritic forms of Lyme disease. B. garinii is frequently associated with neurological manifestations, and B. afzelii seems to be the exclusive agent of late cutaneous lesions of acrodermatitis chronica atrophicans (Pick- Herxheimer disease) [5]. We determined the prevalence of B. burgdorferi bacteria in domestic animals in the north of Xinjiang Uygur Autonomous Region (XUAR), China.

Methods

99 blood samples were collected from domestic animals in the north of XUAR. Genomic DNA was extracted from individual specimens by using the genomic DNA Purification Kit (Gentra, USA). All DNA samples were amplified by using PCRs specific for 5S-23S rRNA intergenic spacer [6] and flagellin (411bp) gene [7,8].

Randomly selected amplicons for 5S-23S rRNA intergenic spacer (n = 14) and flagellin gene (n = 14) were cloned into the pGEM-T Easy vector (Promega, Shanghai, China) and subjected to bidirectional sequencing (Sangon Biotech, Shanghai, China). All of the unique sequencing data (not including identical sequences) were deposited in GenBank under accession nos. KC262670-KC262675. Bayesian phylogenetic analysis were conducted on the 5S-23S rRNA intergenic spacer and flagellin gene sequences identified a B. burgdorferi-like bacteria, li district (10/72, 13.8%) and Altay district (4/27, 14.8%).

Results: 14 of the 99 specimens (14%) were found to be positive by PCR. Phylogenetic analysis of 5S-23S rRNA intergenic spacer and flagellin gene sequences identified a B. burgdorferi-like bacteria, li district (10/72, 13.8%) and Altay district (4/27, 14.8%).

Conclusions: This study has reported the occurrence of B. burgdorferi-like bacteria in Xinjiang Autonomous Region of China and suggested that B. burgdorferi bacteria encompassed a large area in China. Further studies on the characterization and culture of B. burgdorferi-like bacteria found in domestic animals should be performed to further clarify this. Additionally, the screening of human specimens for borreliosis in this region will define the incidence of infection.

© 2013 Liu G, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.
species, our findings suggest that B. burgdorferi bacteria encompasses a large area in China. However, its vector should be investigated in order to determining the risk factor of infection of human by this species. Further studies on the characterization and culture of B. burgdorferi-like bacteria should be performed.

Acknowledgements

This work was supported, in part, by the National Natural Sciences Foundation of China (No. 31201899) and the Natural Science Foundation of Gansu Province (No. 096RJZA128). The experiments comply with the current laws of the country in which the experiments were performed.

References


Submit your next manuscript and get advantages of OMICS Group submissions

Unique features:

- User friendly/feasible website-translation of your paper to 50 world’s leading languages
- Audio Version of published paper
- Digital articles to share and explore

Special features:

- 250 Open Access Journals
- 20,000 editorial team
- 21 days rapid review process
- Quality and quick editorial, review and publication process
- Indexing of PubMed (partial), Scopus, RBSCQ, Index Copernicus and Google Scholar etc.
- Sharing Option: Social Networking Enabled
- Authors, Reviewers and Editors rewarded with online Scientific Credits
- Better discount for your subsequent articles

Submit your manuscript at: www.omicsonline.org/submission/