Prevalence of *Anaplasma phagocytophilum* and its coinfection with *Borrelia afzelii* in *Ixodes ricinus* and *Ixodes persulcatus* ticks inhabiting Tver Province (Russia) – a sympatric region for both tick species

Toshiyuki Masuzawa,1 Igor G. Kharitonenkov,2 Yoshihiro Okamoto,1 Takashi Fukui1 and Norio Ohashi3

**Correspondence**

Toshiyuki Masuzawa
masuzawat@cis.ac.jp

1Laboratory of Microbiology and Immunology, Faculty of Pharmacy, Chiba Institute of Science (CIS), Choshi 288-0025, Japan

2Faculty of Basic Medicine, Moscow Lomonosov State University, Lomonosovsky Prospect 31, Korpus 5, 117192 Moscow, Russia

3Laboratory of Environmental Microbiology, Institute for Environmental Sciences, University of Shizuoka and Global COE Program, Shizuoka 422-8526, Japan

Received 26 October 2007
Accepted 26 March 2008

**INTRODUCTION**

Human granulocytic anaplasmosis (HGA) and Lyme borreliosis (LB) are tick-borne infectious diseases caused by *Anaplasma phagocytophilum* and *Borrelia burgdorferi sensu lato* species, respectively. In this study, p44/msp2 paralogues specific to *A. phagocytophilum* and 5S–23S rRNA gene-intergenic spacers specific to *B. burgdorferi sensu lato* species were detected by PCR in ticks collected in two regions, Tver (Kalinin) and Konakovo, of the Tver (Kalinin) Province located 150 km north-west of Moscow. The PCR amplicons obtained were further characterized by sequencing and RFLP analysis. In the total of 199 ticks collected, 8.8% (7/80) and 33.8% (27/80) of *Ixodes ricinus*, and 2.5% (3/119) and 45.4% (54/119) of *Ixodes persulcatus*, were found to be infected with *A. phagocytophilum* and *B. burgdorferi sensu lato* spp., respectively. Of those 199 ticks, 5 (2.5%) were coinfected with *A. phagocytophilum* and *Borrelia afzelii*. Phylogenetic analysis revealed unique p44/msp2 paralogous genes in *A. phagocytophilum*-infected Russian ticks. The sequence similarities with those of *A. phagocytophilum* in the United States, UK and Japan ranged from 42% to 80.4%, and there were no sequences showing more than 90% similarity with those sequences from the other countries. The results showed that the p44/msp2 sequence similarity groups may provide an index of adaptation of *A. phagocytophilum* strains to specific vector ticks or reservoir hosts in different countries and areas. These findings suggest that there is a public health threat from HGA and LB in Tver Province surrounding Moscow.
sensu lato, are classified into at least 13 species. Among them, *Borrelia burgdorferi sensu stricto*, *Borrelia garinii* (Eurasian type), *Borrelia afzelii*, *Borrelia lusitaniae*, *Borrelia valaisiana* and *Borrelia spielmanii* are found to infect *Ixodes ricinus* ticks in Europe. Since both pathogens are transmitted by *Ixodes* tick species, human cases coinfected with both LB and HGA pathogens have been reported (Ahkee & Ramirez, 1996; Bakken et al., 1996; Lebech et al., 1998).

Prevalence rates of *A. phagocytophilum* in *I. ricinus* were found to be different among European countries (Blanco & Oteo, 2002). In Russia, *A. phagocytophilum* were detected from *I. ricinus* ticks collected in the Baltic region (Alekseev et al., 2005) and from *Ixodes persulcatus* ticks collected in Vologda Province (Eremeeva et al., 2006), in Western Siberia (Rar et al., 2001) and from the Urals to the Far East of Russia (Shpynov et al., 2006).

We previously showed the prevalence rate of *B. burgdorferi sensu lato* species by their isolation from *I. ricinus* and *I. persulcatus* collected in Moscow Province (Masuzawa et al., 2005). Moscow and its suburbs are unique ecosystems with respect to tick habitat. *I. ricinus* ticks, which primarily inhabit the Western part of Eurasia, and *I. persulcatus* ticks, which primarily inhabit Eastern part of Eurasia, overlap around the Moscow region. However, little information is available regarding the epidemiological features and the prevalence rate of *A. phagocytophilum* in the area surrounding Moscow. The aim of this study was to determine the prevalence of *A. phagocytophilum* and the possibility of coinfection with LB *Borrelia* species and *A. phagocytophilum* in *I. persulcatus* and *I. ricinus* in Tver Province near Moscow.

**METHODS**

**Survey area and tick sampling.** During the summer of 2002, unfed adult ticks (*I. persulcatus* and *I. ricinus*) were collected from vegetation by a dragging method using 1 m² flannel flags, in the Tver (Kalinin) and Konakovo regions of the Tver Province, which are located 110–150 km north-west from Moscow. Vegetation in the survey area consists of Russian plain and forest (aspen, firs and birches) with bushes. The areas are mostly forest with limited human attendance and no livestock. Konakovo is located on the bank of a large reservoir (Ivankovskoe reservoir on the Volga river); other environmental features are similar for the two regions.

**DNA preparation and qualification of tick DNA.** After collection, the ticks were placed in a refrigerator, where they were naturally killed and dried in test tubes under low moisture conditions. Dry ticks were kept at 4 °C for 6 months prior to analysis.

The dried tick samples were disrupted for 30 s with 3 mm tungsten carbide beads in 1.5 ml tubes by TissueLyser (Qiagen). Total DNA was isolated from whole tick tissues by using the QuickGene-800 Nucleic-acid Isolation System with the QuickGene DNA tissue kit (both Fuji film). Quality of the extracted DNA was evaluated by PCR targeting the tick rDNA internal transcribed spacer 2 (ITS2) with primers 5.8S F3/1 (5′-GGG TCG ATG AAG AAC GCC GGC AGC-3′) and 28S R1/1 (5′-TTG AGG GGG TGG TCT CGC CTG ATG-3′), according to the method described by Fukunaga et al. (2000). Briefly, PCRs were performed with denaturation at 94 °C for 5 min, followed by 35 cycles consisting of denaturation at 94 °C for 1 min, annealing at 60 °C for 1 min and extension at 72 °C for 2 min with a T-gradient thermocycler (BioMetra). The PCR products were electrophoresed on a 1% agarose gel, stained with ethidium bromide and visualized under UV light. After confirmation of the tick DNA quality by the PCR, the tick DNA was used as a template for the following experiments.

To prevent carryover of amplified DNA, the PCR reaction mix before and after PCR was handled in a safety cabinet which was UV illuminated before and after use to degrade contaminated DNA. Electrophoresis was done in a separate room. To detect carryover caused by amplified or contaminated DNA in the PCR, one negative control tube was prepared for each seven samples. All PCRs were repeated at least three times to confirm results.

**Detection of *A. phagocytophilum*-specific p44/msp2 DNA by PCR.** To detect *A. phagocytophilum*, a nested-PCR was conducted using primers p3726F (5′-GCT AAG TTA GCT TAT GA-3′), p3761F (5′-CTG CTC TCT [T/G] CCA [A/G/A] CCT C-3′), p4183R (5′-AAG TAG T[C/T]F TAG GTA GTA ACC-3′) and p4257R (5′-AGA AGA TCA TAA CAA GCA GTG-3′) (Ohashi et al., 2005; Lin et al., 2002; Zhi et al., 1999), which were previously designed based on the highly conserved region of p44/msp2 paralogues. Briefly, the PCR conditions were 1 cycle of denaturation at 94 °C for 5 min, followed by 35 cycles consisting of denaturation at 94 °C for 30 s, 1 min of annealing at 58 °C and 1 min of extension at 72 °C. The second-step PCR was conducted with 1 μl of the first-step PCR product as template DNA under the same conditions. The ~300–400 bp nested-PCR products of p44/msp2 obtained from 10 PCR-positive samples were cloned into the pCR2.1 vector using TA Cloning kit (Invitrogen) and introduced into *Escherichia coli* DH5α; *E. coli* containing recombinant plasmids were identified by PCR targeted to p44/msp2 genes.

**DNA sequencing and phylogenetic analysis.** For sequencing, recombinant *E. coli* clones were randomly selected and the plasmid DNA was amplified by using the Illustra Templiphi DNA amplification kit (GE Healthcare) at 30 °C for 18 h according to the manufacturer’s protocol. Sequencing was carried out by using BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems) with an ABI 3130-Avant Genetic Analyzer (Applied Biosystems). A phylogenetic tree was constructed based on the alignment of Russian p44/msp2 sequences and the previously published sequences by CLUSTAL W algorithm using sequence analysis software, MEGA6 (DNASTAR Inc., Madison, WI, USA) followed by the neighbour-joining method with 1000 bootstrap resamplings. All DNA sequences determined in this study were deposited in DDBJ/EMBL/GenBank under the following accession numbers. Sequences (accession numbers given in parentheses) derived from seven *I. ricinus* ticks were R10-13 clones a, b and d (AB262195, AB262196 and AB262219), R10-14 clones a, c and d (AB262199, AB262201 and AB262202), R13-10 clones a, b and c (AB262207 to AB262209), R18-8 clones a to d (AB262211 to AB262214), R17-3 clones a to d (AB262215 to AB262218), R18-9 clones a to d (AB262219 to AB262222) and R7-10 clones a to d (AB262229 to AB262232). The sequences derived from three *I. persulcatus* ticks were R10-16 clones a to d (AB262203 to AB262206), R29-6 clones a, b and d (AB262223, AB262224 and AB262226) and R29-9 clones a and b (AB262227 and AB262228).

**Detection and genotyping of *Borrelia* spp.** For detection of *B. burgdorferi sensu lato* species, the 55–235 rDNA intergenic spacer was amplified with primers RIS1 corresponding to the 3′ end of 3S rDNA (rfr) (5′-CTG CCA GTT CCG GCC AGA-3′) and RIS2 corresponding to the 5′ end of 23S rDNA (rfl) (5′-TCC TAG CTA ACC ATG AA-3′) (Postic et al., 1994) in the first-step PCR. For the nested
PCR, inner primer sets, RIS3 (5'-GGA GAG TAG TTG ATT GCC AGG-3') and RIS4 (5'-GAC TCT TAT TAC TTT GAC C-3') were used, which amplified about 200 bp DNA. The initial amplification consisted of 45 cycles, each consisting of 30 s at 95 °C, 30 s at 50 °C and 30 s at 72 °C. To perform the second-step PCR, 1 µl of the product from the first-step PCR was used for amplification in a 25 µl reaction mixture. The amplification was carried out under the same condition as the first-step PCR. The products amplified were electrophoresed in 1 % agarose gels stained with ethidium bromide. To identify B. burgdorferi sensu lato species that were infecting the ticks, the PCR products were digested with MseI and DraI, and the digested DNA was electrophoresed through 10–20 % gradient polyacrylamide gels (Atto) as described previously (Masuzawa et al., 1996). The DNA bands were visualized by ethidium bromide staining and the RFLP pattern of these amplicons was compared with those of the reference strains: B. burgdorferi B31, B. garinii 20047, B. afzelii PfGau, B. lusitaniae PotiB2, B. valaisiana V5116 and B. spielmani PSigII.

RESULTS AND DISCUSSION

A total of 199 unfed adult Ixodes ticks (119 I. persulcatus and 80 I. ricinus) were collected in the Tver region and the Konakovo region of Tver Province, Russia, during the summer of 2002. The ITS2-PCR specific to tick DNA was positive in all of the extracted DNA samples (data not shown) and the DNAs extracted from the ticks were analysed for the presence of A. phagocytophilum and B. burgdorferi sensu lato species genes. By PCR of p44/msp2, we found that 8.8 % of I. ricinus ticks (7/80) and 2.5 % of I. persulcatus ticks (3/119) were infected with A. phagocytophilum, while by PCR of the 55–235 rDNA spacer, 33.8 % of I. ricinus ticks (27/80) and 45.4 % of I. persulcatus ticks (54/119) were infected with B. burgdorferi sensu lato species. Among 100 male and 99 female ticks, five ticks of each sex were infected with A. phagocytophilum. No differences between prevalence rate for male and female ticks were found. In Konakovo region, 10 % of I. ricinus (7/70) and 4.3 % of I. persulcatus (3/70) were infected with A. phagocytophilum. We believe that this is the first record showing ticks infected with A. phagocytophilum in the region. However, A. phagocytophilum-infected ticks were not found in the Tver region located to the north-west of the Konakovo region. The prevalence rates were similar to those previously reported in other European countries (Blanco & Oteo, 2002) and other regions in Russia (Alekseev et al., 2001; Ermeeva et al., 2006; Rar et al., 2005; Shypynov et al., 2006). This finding indicates that both I. ricinus and I. persulcatus maintain this pathogen, and leads us to speculate that the infected ticks are distributed in a limited area in the region. However, further study is necessary to reach this conclusion.

The p44/msp2 amplicons obtained from ten A. phagocytophilum-infected ticks (three I. persulcatus and seven I. ricinus) were cloned, and a total of 38 randomly selected clones (two to four per tick) were sequenced, yielding 34 different sequences (accession numbers AB262195 to AB262232). A phylogenetic tree was constructed based on the p44/msp2 sequences derived from Russian ticks in this study and the previously published sequences from the United States, UK and Japan (Fig. 1). p44/msp2 sequences derived from I. ricinus (Ir) and I. persulcatus (Ip) clustered together on the phylogenetic tree (Fig. 1), indicating that there are no differences between p44 genes detected from I. ricinus and I. persulcatus. All p44/msp2 gene sequences detected from the Russian ticks showed some similarity to the sequences from the United States, UK and Japan, which ranged from 46.2 % to 73.2 %, 46.6 % to 80.4 %, and 42 % to 78.1 %, respectively. Among the Russian sequences, 25 out of 34 sequences which were grouped into seven clusters had more than 90 % similarity as shown in Fig. 1, whereas

![Fig. 1. Phylogenetic tree of A. phagocytophilum p44/msp2 gene sequences in Russia, the United States, UK and Japan. The phylogenetic tree was constructed based on the alignment of p44/ msp2 sequences by CLUSTAL W algorithm and followed by the neighbour-joining method with 1000 bootstrap resamplings. The sequences obtained from Russian ticks are indicated in bold type. J, US and UK indicate Japan, the United States and UK, respectively. Ip and Ir indicate tick species and the origin of the sequence, I. persulcatus and I. ricinus, respectively. Bar, sequence divergence of 5 %.

Downloaded from www.microbiologyresearch.org by IP: 54.70.40.11 On: Thu, 27 Dec 2018 02:48:51
Table 1. Prevalence of *A. phagocytophilum* and *B. burgdorferi sensu lato* in ticks collected in two regions of Tver Province in Russia in 2002

<table>
<thead>
<tr>
<th>Place</th>
<th>Tick species</th>
<th>No. of ticks examined</th>
<th>No. of PCR-positive ticks (%)</th>
<th>No. of ticks infected with one <em>Borrelia</em> species</th>
<th>No. of ticks dually infected with different <em>Borrelia</em> species and/or <em>A. phagocytophilum</em></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Ap</td>
<td>Bbsl</td>
<td>Bbs</td>
</tr>
<tr>
<td>Tver (Kalinin) region</td>
<td><em>I. ricinus</em></td>
<td>10</td>
<td>0 (20)</td>
<td></td>
<td>0</td>
</tr>
<tr>
<td></td>
<td><em>I. persulcatus</em></td>
<td>49</td>
<td>0 (22 (44.9))</td>
<td>22 (44.9)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td><em>I. ricinus</em></td>
<td>70</td>
<td>7 (10)</td>
<td>25 (35.7)</td>
<td>0</td>
</tr>
<tr>
<td>Konakovo region</td>
<td><em>I. persulcatus</em></td>
<td>70</td>
<td>3 (4.3)</td>
<td>32 (45.7)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td><em>I. ricinus</em></td>
<td>80</td>
<td>7 (8.8)</td>
<td>27 (33.8)</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td><em>I. persulcatus</em></td>
<td>119</td>
<td>3 (2.5)</td>
<td>54 (45.4)</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td><em>I. ricinus</em></td>
<td>199</td>
<td>10 (5)</td>
<td>81 (40.7)</td>
<td>1</td>
</tr>
</tbody>
</table>

Ap, *A. phagocytophilum*; Bbsl, *B. burgdorferi sensu lato*; Bbs, *B. burgdorferi sensu stricto*; Baf, *B. afzelii*; Bg(A), *B. garinii* Asia (NT29 type); Bg(E), *B. garinii* Eurasia (20047 type).
Clethrionomys

I. ricinus

2002). We previously detected et al.

Borrelia
genus

philum

phagocytophilum,

These facts suggest that are reservoir hosts for B. garinii

while the majority of B. burgdorferi sensu stricto

are infected via blood feeding from an animal reservoir infected with B. burgdorferi sensu stricto transmitted from I. ricinus ticks. Since the vector potential and competence of I. persulcatus for B. burgdorferi sensu stricto have not been fully understood, further study of experimental transmission is necessary to prove this theory. No

competence of mental transmission is necessary to prove this theory. No B. valaisiana-infected tick was detected in this study whereas one (of 72) I. ricinus infected with B. valaisiana was isolated in our previous study (Masuzawa et al., 2005). These facts suggest that B. valaisiana is sparsely distributed in the survey area.

Among ticks infected with B. burgdorferi sensu lato or A. phagocytophilum, five were coinfected with A. phagocyto-philum and B. afzelii, but not with the other species of the genus Borrelia (Table 1). It has been reported that rodents are reservoir hosts for B. afzelii and some types of B. garinii, while the majority of B. garinii types and B. valaisiana appear to be associated with birds (Kurtenbach et al., 2002). We previously detected B. afzelii and B. garinii (type 20047, Eurasia) from the wild mammals Clethrionomys glareolus and Apodemus flavicollis in Russia (Masuzawa et al., 2005). Reservoirs for A. phagocytophilum are likely to comprise some ruminants, rodents, and perhaps other small and intermediate-size mammals (Dumler et al., 2005). However, to determine the reservoir host for A. phagocytophilum in the survey area, further study is needed.

Coinfection with both pathogens has been reported in humans (Ahkee & Ramirez, 1996; Bakken et al., 1996; Lebec et al., 1998), Ixodes ticks (Daniels et al., 1997; Pancholi et al., 1995; Telford et al., 1996) and wild rodents (Levin et al., 1999). In experimentally infected mice, the coinfection of A. phagocytophilum and B. burgdorferi sensu stricto resulted in increased levels of both pathogens and more severe Lyme arthritis compared with those in mice experimentally infected with B. burgdorferi sensu stricto alone (Thomas et al., 2001; Grab et al., 2007). It was suggested that the severity of disease was associated with diminished interleukin-12, gamma interferon and tumour necrosis factor alpha levels, and elevation of interleukin-6 levels; it was also suggested that coinfection induced the modulation of host immune responses, resulting in increased severity of the diseases.

In conclusion, we demonstrated that LB and HGA agents infected I. persulcatus and I. ricinus ticks in Tver Province.

ACKNOWLEDGEMENTS

This study was supported in part by Grants for Scientific Research and Education from Chiba Institute of Science and by Grant E0249/942 from the Russian Federal Program ‘Integracija’. We thank Valentina V. Matjushkova and Olga V. Esaulenko (Tver Sanitary and Epidemiology Center) and Vladimir B. Vibornov (Konakovo Sanitary and Epidemiology Station) for their help with tick collection in 2002.

REFERENCES


Borrelia burgdorferi ribosomal DNA spacer, internal transcribed spacer 2, sequences.