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Molecular methods routinely used to detect Coxiella burnetii in ticks cross-react with Coxiella-like bacteria

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Background: Q fever is a widespread zoonotic disease caused by Coxiella burnetii. Ticks may act as vectors, and many epidemiological studies aim to assess C. burnetii prevalence in ticks. Because ticks may also be infected with Coxiella-like bacteria, screening tools that differentiate between C. burnetii and Coxiella-like bacteria are essential.

Methods: In this study, we screened tick specimens from 10 species (Ornithodoros rostratus, O. peruvianus, O. capensis, Ixodes ricinus, Rhipicephalus annulatus, R. decoloratus, R. geigy, O. sonrai, O. occidentalis, and Amblyomma cajennense) known to harbor specific Coxiella-like bacteria, by using quantitative PCR primers usually considered to be specific for C. burnetii and targeting, respectively, the IS1111, icd, scvA, p1, and GroELHttpB genes.

Results: We found that some Coxiella-like bacteria, belonging to clades A and C, yield positive PCR results when screened with primers initially believed to be C. burnetii-specific.

Conclusions: These results suggest that PCR-based surveys that aim to detect C. burnetii in ticks by using currently available methods must be interpreted with caution if the amplified products cannot be sequenced. Future molecular methods that aim at detecting C. burnetii need to take into account the possibility that cross-reactions may exist with Coxiella-like bacteria.

Keywords: Q fever; tick-borne diseases; tick endosymbiont; false positive; surveillance; PCR primers

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with their arthropod hosts (16–19). To date, there has been no indication that these tick-carried Coxella-like bacteria are transmitted to vertebrates, although Coxella-like bacteria have sporadically been detected in pet birds (19, 20). Recent investigations based on multilocus phylogenetic analyses and whole genome sequencing data revealed that all known C. burnetii strains originate within the vast group of Coxella-like endosymbionts and are the descendants of a Coxella-like progenitor hosted by ticks (17).

Because epidemiologic studies that aim at assessing C. burnetii prevalence in ticks frequently rely on DNA detection by polymerase chain reaction (PCR), it is important to make sure that these screening methods are specific for C. burnetii. The objective of this study was to determine whether five molecular methods frequently used to detect or characterize C. burnetii cross-react with Coxella-like bacteria present in ticks.

Materials and methods

Selection of a panel of 20 ticks infected with specific Coxella-like bacteria

Ten tick species, previously shown to harbor specific Coxella-like bacteria (17), were investigated.

They were selected with the aim to represent the four clades (A–D) currently described for the Coxella genus (17) (Fig. 1): clade A (Ornithodoros rostratus, O. peruvianus, O. capensis), clade B (Ixodes ricinus), clade C (Rhipicephalus annulatus, R. decoloratus, R. geigi, O. sonrai, O. occidentalis), and clade D (Amblyomma cajennense). This panel included three tick species from which C. burnetii had previously been reported, namely O. sonrai (12), I. ricinus (21–23), and R. annulatus (24).

Two tick specimens were examined for each species. They were either obtained from breeding colonies or sampled from their host species or habitats and they were processed as previously described (17). Briefly, the ticks were first washed with sterile water to avoid external bacterial contamination. Then, DNA was individually extracted using the DNeasy Blood & Tissue Kit (Qiagen) following manufacturer’s instructions. DNA template quality was verified via PCR amplification of 18S ribosomal RNA or cytochrome oxidase 1 arthropod primers. Nested PCR assays were conducted using primers designed to amplify bacteria from the Coxiellaceae family (i.e. Coxella and its sister genus Rickettsiella) and to target the rpoB (DNA-directed RNA polymerase beta) gene and the GroEL/htpB (60 kDa chaperone heat shock protein B) gene as described elsewhere (17, 25). Sequencing of the PCR products obtained showed that each tick species was infected by a specific Coxella-like bacterium that was genetically related to, but distinct from, C. burnetii. None of these tick DNA templates was found infected with C. burnetii on the basis of multilocus DNA sequencing (17).

Selection of qPCR primers thought to be specific for C. burnetii

The 20 tick specimens were tested using quantitative PCR (qPCR) methods using primers that are usually considered to be specific for C. burnetii (Table 1). We used TaqMan

Fig. 1. Genetic relatedness of the 10 tick species used in this study using as reference the phylogenetic network published by Duron et al. (17) with concatenated 16S rRNA, 23S rRNA, GroELhtpB, rpoB, and dnaK sequences for 71 tick-borne Coxella strains, 15 C. burnetii reference strains, and several bacterial outgroups.
<table>
<thead>
<tr>
<th>Gene</th>
<th>Function</th>
<th>Primer designation</th>
<th>Primers and probe sequences (5′–3′)</th>
<th>Fragment length (bp)</th>
<th>% covering with the endosymbiont of R. turanicus&lt;sup&gt;b&lt;/sup&gt;</th>
<th>% covering with the endosymbiont of A. americanum&lt;sup&gt;c&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>IS1111</td>
<td>Insertion sequence</td>
<td>Forward primer</td>
<td>Confidential&lt;sup&gt;a&lt;/sup&gt;</td>
<td>76</td>
<td>58</td>
<td>63&lt;sup&gt;d&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Reverse primer</td>
<td>Confidential&lt;sup&gt;a&lt;/sup&gt;</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe</td>
<td>Confidential&lt;sup&gt;a&lt;/sup&gt;</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>icd</td>
<td>Isocitrate dehydrogenase</td>
<td>Forward primer</td>
<td>GACCGACCCATTATTCCCT</td>
<td>139</td>
<td>84</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Reverse primer</td>
<td>CGGCCTAGATCTCCATCCA</td>
<td></td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe</td>
<td>CGCCCGTATGAAAAACGTGGTC</td>
<td></td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>p1</td>
<td>Porine</td>
<td>Qp1-F</td>
<td>CGGCATTGGGCTTTTC</td>
<td>68</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Qp1-R</td>
<td>GGTTCGCGTAAATGCCTAAGTAA</td>
<td></td>
<td>12&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe</td>
<td>AACGTTCAAAATCCGAAACCGAGTCGCA</td>
<td></td>
<td>50&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>scvA</td>
<td>Chromatin condensation</td>
<td>QscvA-F</td>
<td>TGGAAAGACAAAATGCTCACCACCA</td>
<td>69</td>
<td>52&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>QscvA-R</td>
<td>GGTTGAAGCACCAGCTG</td>
<td></td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe</td>
<td>ACGTGGAAGACGACAAAGCG</td>
<td></td>
<td>67&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>GroEL/htpB</td>
<td>Heat shock protein</td>
<td>HtpB-1</td>
<td>TGGCTCAAGCGATTTTGGTT</td>
<td>82</td>
<td>65&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>HtpB-2</td>
<td>TTATCAATCCCGTGTTGTC</td>
<td></td>
<td>92&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe</td>
<td>AAACGCGTATTGCTGAAATGACCCCG</td>
<td></td>
<td>70&lt;sup&gt;d&lt;/sup&gt;</td>
<td>0</td>
</tr>
</tbody>
</table>

<sup>a</sup>The detailed protocol used for the amplification of IS1111 will be soon published by Sidi-Boumedine et al. (in preparation) and remains meanwhile confidential; <sup>b</sup>GenBank accession number: CP011126; <sup>c</sup>GenBank accession number: CP007541; <sup>d</sup>sequence positions are distant from each other on the endosymbiont complete genome.
Universal PCR Master Mix (UMM 2×) following the amplification protocol: 1 cycle at 50°C for 2 min and 1 cycle at 95°C for 10 min, followed by 40 PCR cycles of 95°C for 15 s and 60°C for 1 min. Two of the targeted markers – the multiplex IS1111 insertion sequence (26, 27) and the icd (isocitrate dehydrogenase) housekeeping gene (26) – are frequently used in surveys that aim to estimate the prevalence of C. burnetii infection in ticks (16). The following genes were also targeted: scvA (small-cell-variant protein A), which is likely involved in chromatin condensation when the bacterium is ‘sporulating’, and porine p1, which encodes an outer membrane protein (28). Finally, we focused on a specific region of the GroEL/htpB, distinct from the region targeted to amplify the genome of Coxiella-like bacteria (17) and considered to be specific to C. burnetii (29). Nine Mile phase II genomic DNA (RSA 493 isolate) was used as a reference. In silico comparisons of the primers and probes with currently published sequences of R. turanicus (GenBank accession number: CP011126) and A. americanum (GenBank accession number: CP007541) suggested that mismatches with these symbionts were unlikely (Table 1).

Results

We found that some Coxiella-like bacteria, belonging to clades A and C, yield positive PCR results when screened with primers initially believed to be C. burnetii-specific (Table 2). Overall, DNA was amplified for at least one marker in 6 of the 10 tick species studied. The most frequently amplified marker was IS1111, which was detected in five different species, whereas GroEL/htpB and scvA were amplified from three species. Porine p1 was solely amplified from a R. geigyi specimen, which was also positive for htpB, scvA, and IS1111, and displayed a particularly low C1 value (C1 = 33) for IS1111. Conversely, icd was not detected in any of our samples. Interestingly, we observed intraspecific variation: one of the Coxiella-like endosymbiont from R. decoloratus was positive for IS1111, whereas the other was positive for scvA. Unfortunately, because all PCR products were poorly concentrated, sequencing was unsuccessful.

Discussion

The marker we most frequently detected in ticks infected with Coxiella-like endosymbionts was the IS1111 transposable element, which is routinely targeted during epidemiological surveys examining C. burnetii prevalence in ticks (16). We thus showed that C. burnetii detection assays based only on IS1111 may lead to misidentification with Coxiella-like endosymbionts. The recent work of Duron (30) corroborates this finding: several genetically divergent IS1111 copies were found widespread in many Coxiella-like endosymbionts, therefore showing that IS1111 can no longer be considered specific to C. burnetii. These findings may explain why surveys based on IS1111 screening occasionally report prevalence levels >10% (23, 31–33).

Our results also showed that the use of a combination of primers targeting different markers, as performed in some studies (11, 21, 34–36), is not sufficient to guarantee the specificity of C. burnetii detection. Indeed, up to four of our markers were detected in a same Coxiella-like endosymbiont. Interestingly, icd, which is frequently used as a PCR target in epidemiological studies (16, 34), was not amplified from our panel of Coxiella-like infected ticks. However, Reeves et al. (37) were able to amplify a 612-bp icd fragment, displaying 93% homology with C. burnetii, from a Coxiella-like bacterium that infects ticks from the O. capensis complex in South Carolina, USA. This result contrasts with our observation that icd was not amplified from the endosymbiont of O. capensis ticks sampled from Cape Verde and highlights the fact that the amplification of a specific genetic marker strongly depends on the PCR method (PCR, nested PCR, or qPCR) and the primer sequences used.

Table 2. C1 values obtained using qPCR for both specimens of the 10 tick species tested

<table>
<thead>
<tr>
<th>Coxiella-like clade</th>
<th>Tick species</th>
<th>IS1111</th>
<th>icd</th>
<th>GroEL/htpB</th>
<th>p1</th>
<th>scvA</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>O. rostratus</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td></td>
<td>O. peruvianus</td>
<td>39/37</td>
<td>–/–</td>
<td>30/31</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td></td>
<td>O. capensis</td>
<td>–/–</td>
<td>–/–</td>
<td>35/35</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td>B</td>
<td>L. ricinus</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td>C</td>
<td>R. annulatus</td>
<td>37/38</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td></td>
<td>R. decoloratus</td>
<td>–/36</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/39</td>
</tr>
<tr>
<td></td>
<td>R. geigyi</td>
<td>37/33</td>
<td>–/–</td>
<td>–/38</td>
<td>–/35</td>
<td>–/38</td>
</tr>
<tr>
<td></td>
<td>O. sonrai</td>
<td>39/36</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td></td>
<td>O. occidentalis</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
</tr>
<tr>
<td>D</td>
<td>A. cajennense</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
<td>–/–</td>
</tr>
</tbody>
</table>

The sign ‘/’ is used to separate the results obtained for the first and the second tick specimen; ‘–/–’ indicates that no amplification was observed.

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More generally, negative results may be due to low detection sensitivity, which is supported by high detection thresholds for most of the genes. In particular, intraspecific variation may be due to the individual ticks having a low bacterial burden, sex- or stage-specific differences, and the presence of PCR inhibitors. In our study, it is possible that the IS1111-based PCR method was the most sensitive of the tests used, because several copies of this gene are likely present in the genome of Coxiella-like bacteria, as is the case for C. burnetii. This hypothesis is supported by the observation that GroELIhspB, porine p1, and svCA were detected in the endosymbiont of a R. geigyi specimen that displayed a low C\textsubscript{j} value for IS1111.

Standardizing methodology across laboratories is essential to allow comparisons among studies. Although remarkable progress has recently been made in designing new PCR-based techniques to detect C. burnetii, these advances have overlooked that an important genetic diversity actually exists within the Coxiella genus (16). In this context, it may not be surprising that the PCR primers routinely used to target C. burnetii actually cross-react with Coxiella-like bacteria. Therefore, in the future, molecular methods aiming at detecting C. burnetii should make sure that no cross-reaction exists not only with other abortive agents but also with Coxiella-like organisms. Recent full-genome sequencing data indeed not only highlighted obvious genetic similarities of C. burnetii with Coxiella-like bacteria but also revealed some mutations specific to Coxiella-like bacteria (18, 38). This pattern likely explains why PCR cross-reactions with Coxiella-like bacteria are partial and variable between markers. Interestingly, identical IS1111 copies were found in C. burnetii and some Coxiella-like bacteria (30), suggesting that the risk of detecting Coxiella-like bacteria with IS1111 primers designed to detect C. burnetii is very high and must not be underestimated.

PCR-based surveys that aim to detect C. burnetii in ticks must be interpreted with caution if the amplified DNA products are not sequenced. Unfortunately, the ratio of bacterial DNA to tick DNA is frequently low, which makes it challenging to obtain PCR products concentrated enough for direct sequencing via conventional PCR. Additionally, currently available qPCR methods, such as those used in this study, often yield very short DNA fragments that are difficult to concentrate for sequencing purposes and that correspond to rather uninformative sequences. Therefore, there is an urgent need to develop a multiplex qPCR or microchip method that would make it possible to directly differentiate Coxiella-like bacteria from C. burnetii in tick samples and to detect co-infections. Pending development of such a test, useful alternative methods include the sequencing of the 16S rRNA, rpoB, and GroEL genes of Coxiella bacteria, after amplification by nested PCR, as previously described (17, 25).

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