Investigating *Rickettsia africae* infection in *Amblyomma hebraeum* ticks in Mnisi, Bushbuckridge Municipality, South Africa

E Mazhetese, Z Lukanj, L Neves, D Morar-Leather

Vector and Vector-borne Diseases Research Programme, Department of Veterinary Tropical Diseases, Faculty of Veterinary Science University of Pretoria, Onderstepoort, South Africa.

Introduction

*Rickettsia africae* is an intracellular gram-negative bacteria which belongs to the Spotted Fever Group (SFG). It is transmitted by *Amblyomma hebraeum* ticks in Southern Africa and *Amblyomma variegatum* in West, Central and Eastern Africa (Kelly et al., 1992). It causes African Tick Bite Fever (ATBF) in humans and has mostly been reported in tourists who visit Southern Africa (Raoult et al., 2001). Transovarial and transtadial transmission of *R. africae* in *A. hebraeum* ticks has been proved (Kelly & Mason, 1991).

Aim

The aim of the study was to investigate *R. africae* infection in *A. hebraeum* ticks in Mnisi.

Objectives

To determine *R. africae* infection rates at different developmental stages (larvae, nymphs, and adults) of the ticks.

To determine the efficiency of transovarial transmission of *R. africae* in *A. hebraeum* ticks.

Materials and Methods

Study area

This cross-sectional study was performed in the Mnisi Community, Mpumalanga province, South Africa. Two diptanks, Utah and Welverdiend, were selected for the collection of samples.

Sample collection and processing

The calculated sample size (n) was 106 for all stages. Adult ticks and engorged female ticks were collected from cattle. Larvae were collected by dragging at the selected dip tanks. Engorged females were incubated under laboratory conditions, until they oviposited and egg masses were collected.

DNA was extracted from all the samples and were screened by real-time PCR (qPCR) targeting the gltA gene which is *Rickettsia* genus specific. OmpA gene, belonging to the SFG was amplified from the gltA gene positive samples using conventional PCR (cPCR). The amplified products were sent for sequencing to Inqaba Biotech.

Results

PCR results from DNA of adult ticks:

From Utah, out of the 96.23% (n=106) gltA gene positive samples, 14.71% (n=102) were positive for the gltA gene. From Welverdiend, out of the 95.28% (n=106) samples that tested positive for the gltA gene, 14.85% (n=101) were positive for the ompA gene. Resulting sequences were 99.98% identical to *R. africae*.

Table 1: PCR results from larvae:

<table>
<thead>
<tr>
<th>Dip tanks</th>
<th>Utah</th>
<th>Utah</th>
<th>Welverdiend</th>
<th>Welverdiend</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reaction</td>
<td>qPCR</td>
<td>cPCR</td>
<td>qPCR</td>
<td>cPCR</td>
</tr>
<tr>
<td>Positive</td>
<td>73</td>
<td>18</td>
<td>49</td>
<td>10</td>
</tr>
<tr>
<td>Negative</td>
<td>33</td>
<td>55</td>
<td>57</td>
<td>39</td>
</tr>
<tr>
<td>Minimum Infection Rate % (MIR)</td>
<td>68.67</td>
<td>16.96</td>
<td>46.23</td>
<td>9.43</td>
</tr>
</tbody>
</table>

Transovarial transmission efficiency

The transmission efficiency of *R. africae* in *A. hebraeum* engorged ticks collected from Utah was 100% and 71% in the engorged females collected from the cattle in Welverdiend.

Discussion and Conclusion

The results indicate a substantial percentage of *A. hebraeum* ticks from the study area are infected by *R. africae*. There are no notable differences in the infection rates in ticks even though the selected dip tanks have different vegetation and they are in different geographical locations. The dip tank in Welverdiend is in the proximity of human dwellings and the dip tank in Utah is close to game parks. This shows that the *Rickettsia* is evenly distributed in ticks from these areas. Transovarial transmission is high and could mean that the tick vector also acts as a reservoir for this pathogen. The presence of the pathogen in the tick vectors from this area poses a risk to the human population.

References


Acknowledgments

Institute of Tropical Medicine (ITM) for the FA4 grant that funded the project, the Mnisi community program team for assistance with sampling logistics (Jeannette Wentzel, Ilana van Wyk and environmental monitors), Ilse Vorster, Charles Byaruhanga and Anna-Mari Bosman from DVTD for technical support.