Short Report

Detection of ehrlichiae in African ticks by polymerase chain reaction

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the 2 groups. The indoor workers had a prevalence of 24% and outdoor workers 74% (Fisher’s exact test P = 0.002). None of the indoor workers was positive for IgG4 antibody.

Discussion

It is obvious from these results that there was a significant exposure to filarial in the mine workers, resulting in the production of anti-filarial antibodies. In the case of IgG1 it is possible that the antibody response was due to exposure to in-coming infective larvae rather than infection with the adult parasite, as there is an active IgG1 and adult IgG4 response to infective larvae (KURIAWAN-ATMAJID et al., 1998). As previously noted, IgG4 is strongly associated with active filarial infection and it is possible that these subjects who were positive for IgG antibody had an adult worm in situ, but it is difficult to explain why they were filarial antigen negative as IgG4 positivity in indigenous populations is almost invariably associated with antigenemia (TURNER et al., 1993). It is known from a previous work that unlike infected indigenous inhabitants, who have a down-regulated immune system against filarial antigens, expatriates mount a vigorous tissue response against the adult worm (WARTMAN, 1947) and it is possible that the filarial antigen is bound into an infective complex near the site of the worm and not liberated into the blood. It is also possible that the subjects’ immune response killed the worm shortly after it became established and that the filarial antigen had been cleared from the blood before the person was tested. This study suggests that filariasis is a threat to expatriate workers and travellers especially if their work environment and lifestyle constantly expose them to mosquito bites. This possibility should be considered when investigating illness in returnees from filarial-endemic areas. There is no proven prophylaxis against filariasis and the only effective means of control is protection from mosquito bites. A follow-up study which will include testing all returnees from the person was tested.

Acknowledgements

We thank the management and staff of Misima Mines Ltd for their generous support of this project.

References


Received 18 November 1999; revised 11 May 2000; accepted for publication 24 May 2000

Keywords: tick-borne ehrlichioses, ehrlichia, detection, polymerase chain reaction, ticks, Amblyomma variegatum, Boophilus decoloratus, Acanthoma marginale, Mali

In Africa, tick-borne ehrlichioses are considered among the most important livestock diseases (Sonnenshine, 1993). In recent years, useful and rapid molecular tools such as sequence analysis of polymerase chain reaction (PCR) products have been developed for the detection and identification of microorganisms in arthropods (Higgins & Azad, 1993). The aim of this work was (i) to select broad-spectrum specific primers that could amplify, by PCRs, DNA of all the known ehrlichiae, and (ii) to use them to detect ehrlichiae in ticks collected in Mali.

Two oligonucleotide primers EHR16SD (GTTAC CAYCAGGAAAGTCC) and EHR16SR (TAGC

    

Anaplasma marginale nucleic acids were amplified from the negative control of the 16s rRNA sequencing gene of the ehrlichia is a known vector of this microorganism in Africa. No detectable DNA from bacteria was amplified from the positive control (HGE agent DNA) in each test. No DNA amplification appeared to be specific because PCRs did not result in amplification of DNA extracted from bacteria as previously described (PAROLA et al., 1993). In this work, we pair which primers to detect ehrlichiae in ticks. In February 1998, no ticks were removed from cattle in Mali. The DNA of each tick was extracted as previously described (PAROLA et al., 1998) and used in PCR including EHRl 6SR and EHRl 6SD primers, as described above. No DNA amplification appeared to be specific because PCRs did not result in amplification of DNA extracted from bacteria as previously described (PAROLA et al., 1998) and performed with a PCR procedure was carried out with DNA from all DNA extracted from bacteria as previously described (PAROLA et al., 1998) to detect serial dilution of HGE DNA by PCR.

We aimed to test the usefulness of our broad-spectrum primers to detect ehrlichiae in ticks, primers were group mining sequences of ehrlichiae available in Genbank and previously to detect ehrlichiae in ticks, primers were group mining sequences of ehrlichiae available in Genbank and previously described (PAROLA et al., 1998) and used in PCR including EHRl 6SR and EHRl 6SD primers. The 345-bp DNA fragment was consistently amplified when the ehrlichiae isolates available in Genbank were selected after alignment of the corresponding sequences of the amplified fragments. This allowed us to find sequences of ehrlichiae available in Genbank as previously described (PAROLA et al., 1998) and used in PCR including EHRl 6SR and EHRl 6SD primers. A similar fragment was amplified from the DNA sequence available in Genbank. This allowed us to find sequences of ehrlichiae available in Genbank as previously described (PAROLA et al., 1996) and perform PCR amplification produced a fragment of the expected size.

Ehrlichia sennetsu, E. phagocytophila, and the agent of the human granulocytic ehrlichiosis (HGE) were selected after alignment of the corresponding sequences of the amplified fragments. This allowed us to find sequences of ehrlichiae available in Genbank as previously described (PAROLA et al., 1998) and use them in PCR including EHRl 6SR and EHRl 6SD primers. The 345-bp DNA fragment was consistently amplified when the ehrlichiae isolates available in Genbank were selected after alignment of the corresponding sequences of the amplified fragments. This allowed us to find sequences of ehrlichiae available in Genbank as previously described (PAROLA et al., 1996) and perform PCR amplification produced a fragment of the expected size.
Transactions of the
Royal Society of Tropical Medicine and Hygiene