Newly Emerging *Trypanosoma vivax* in Sudanese Camelsis the Second Leading Cause of Camel Trypanosomosis in Sudan after *Trypanosoma evansi*

Ehab Mossaad[1,2]*, Bashir Salim[3], Keisuke Suganuma[2,4], Peter Musinguzi[2], Mohammed A. Hassan[5], Elamin EA[3], Mohammed GE[1], Amel O. Bakhiet[1], Xuenan Xuan[2,4], Rawan A. Satti[1] and Noboru Inoue[6]

[1]Department of Pathology, Parasitology and Microbiology, College of Veterinary Medicine, Sudan University of Science and Technology, P.O.Box 204, Khartoum, Sudan
[2]National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido 080-8555, Japan
[3]Faculty of Veterinary Medicine, University of Khartoum, P.O Box 32, Khartoum-North, Sudan
[4]Research Center for Global Agromedicine, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido 080-8555, Japan
[5]Tsetse and Trypanosomosis Control Department, Central Veterinary Research Laboratory, Animal Resources Research Corporation. Ministry of Livestock, Fisheries and Rangelands, Khartoum, Sudan
[6]Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido 080-8555, Japan

ABSTRACT

This study was conducted in response to recurring reports from eastern Sudan of camel trypanosomosis that can no longer be treated by currently available trypanocidal drugs. One hundred and eighty-nine blood samples were obtained from camels in different herds and local markets in the western part of Sudan, and a cross-sectional study was carried out between December 2015 and February 2016 to identify the causative agents and possible circulating genotypes. The prevalence of trypanosomes detected using the conventional parasitological techniques of Giemsa-stained blood smears, wet blood smears and the microhematocrit centrifugation technique (MHCT) was 7% (13/189), 11% (21/189) and 19% (36/189), respectively. However, a multi-species KIN-PCR targeting the ITS region revealed that the prevalence of *Trypanosoma evansi*was37% (70/189), while that of *T. vivax* was25% (47/189). Consequently, we used a *T. evansi*-specific PCR (RoTat1.2 VSG gene) to analyse the KIN-PCR-positive samples and a *T. vivax*-specific PCR (Cathepsin L-like gene) to analyse all of the samples. The prevalence of *T. evansi*was 59% (41/70), while the prevalence of *T. vivax* was31% (59/189). Mixed infections were detected in 18% (34/189) of the samples. These results were further confirmed by sequencing and a phylogenetic analysis of the complete internal transcribed spacer (ITS) region of *T. evansi*and the TviCatL gene of *T. vivax*. We conclude that *T. vivax* was newly introduced to the camel population and that *T. evansi* is no longer the single cause of camel trypanosomosis in Sudan.The presence of *T. vivax* in camels detected in this study is a challenge in the choice of diagnostic approaches, particularly serology, and PCRs. However, an analysis of drug resistance should be performed, and the genotypic variation should be verified. To our knowledge, this is the first molecular study on *T. vivax* and mixed-infection with *T. vivax* and *T. evansi* in Sudanese camels.

Keywords: *dromedary camels, Sudan, Trypanosomosis, Trypanosoma evansi, Trypanosom avivax*