



UNIVEN LIBRARY
Library Item : 20161801

APRIL 2016

CO-SUPERVISOR: PROF. P.A. MBATI

SUPERVISOR: PROF. A. SAMIE

UNIVERSITY OF VENDA

SCHOOL OF MATHEMATICAL AND NATURAL SCIENCES

THE DEPARTMENT OF MICROBIOLOGY

TO

FOR AWARD OF THE DEGREE OF MASTER OF SCIENCE

A DISSERTATION SUBMITTED IN FULFILMENT OF THE REQUIREMENTS

MOGANE LAZARUS KATLEGO (11565419)

By

LIMPOPO PROVINCE

AND ANIMAL STOOLS IN THE VHEMBE AND MOPANI REGIONS OF

MOLECULAR CHARACTERIZATION OF *CRYPTOSPORIDIUM* FROM HUMAN



Cryptosporidium species are important causes of diarrhoea especially in developing countries. The epidemiology of *Cryptosporidium* has been dynamically changing over the past decade from that of a largely asymptomatic infection to an acute enteric disease of animals and humans. *Cryptosporidium parvum* has been reported in both animals and humans. This study sought to determine the prevalence of *Cryptosporidium* in animals and humans, to identify the prevalent genotype and to determine the zoonotic threat of *Cryptosporidium* in the Vhembe and Mopani regions.

In the present study, a total of 333 animal and 313 human stool samples were collected from the Mopani and Vhembe regions of Limpopo province. The samples were screened for *Cryptosporidium* using the modified Ziehl-Neelson acid fast staining. Caesium chloride flotation was used to purify oocysts that were further used to extract genomic DNA. Molecular detection was done by a multilocus PCR using 18S rRNA, HSP-70 and GP60 as target genes. PCR amplicons were further sequenced using the Sanger DNA sequencing method. Sequences were aligned using BioEdit and phylogenetic trees computed using MEGA5.

The present study reports a *Cryptosporidium* prevalence of 10.5% among the humans and 31.3% among the animals by Ziehl-Neelson microscopy. From the 10.5% found positive by microscopy, 85% of these were confirmed *C. hominis* in humans by PCR using HSP-70 as the target gene. From the 31.3% prevalence in animals stool samples, we found 7.4% of *C. parvum*, 33.3% of *C. suis*, 41% of *C. andersoni*, 4% of *C. galli* and 15% of *C. scrofarum* using 18S rRNA as the target gene. The GP60 gene failed to produce any desired amplicons probably due to lack of sensitivity in our region.

ABSTRACT

Keywords: *Cryptosporidium*, human, animal, 18S rRNA, HSP-70

prevalence of *C. andersoni*.

This study can conclude that *Cryptosporidium* is common among inhabitants of the Mopani and Thembe regions and this may account for the persistent diarrhoea commonly observed in the region although this remains to be confirmed. Moreover, cattle are in abundance in these regions and interaction with humans increases the risks of cross transmission. Further, this study reports a rare occurrence of *C. suis* in cattle and a lower prevalence of *C. parvum* in cattle while there was high