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A DISSERTATION SUBMITTED IN FULL FULFILLMENT OF THE REQUIREMENTS

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BY

LIMPOPO PROVINCE

AND ANIMAL SICKNESS IN THE VETERINARY AND MOPANI REGIONS OF

MOLECULAR CHARACTERIZATION OF CRYPTOSPORIDIUM FROM HUMAN
The CYP96 gene failed to produce any desired amplicons probably due to lack of sensitivity. Using 18S rRNA as the target sequences, 14% of C. anisporum, 4% of C. galili, and 15% of C. scortorum were found. From the 13.3% prevalence in animal and plant samples, we found 7.4% of C. parvum, 33.3% of C. albicans, and 8.5% of C. pyrosporum. In humans, by PCR using HSP-70 as the target gene, 10.3% of samples were confirmed to be C. hominis. Among the animals, by Ziehl-Neelsen microscopy, from the 10.2% found by microscopy, the present study reports a Cyp96 prevalence of 10.5% among the humans and 31.2% among the animals.

Bacterial and phylogenetic trees were computed using MEGA7. Sequences were aligned using ClustalW and phylogenetic trees were computed using the Neighbor-Joining method.

C. albicans was isolated from animal and plant samples by PCR using HSP18 rRNA, HSP70, and Cyp96 as target genes. PCR amplicons were used to further verify the results obtained by CLP, and Ziehl-Neelsen was used to verify the results obtained by CLP. The samples were screened for C. albicans and C. parvum. The samples were collected from the Viburnum and Myrtaceae regions of Limnos province. The samples were collected from the Viburnum and Myrtaceae regions of Limnos province. The samples were collected from the Viburnum and Myrtaceae regions of Limnos province.

In the present study, a total of 33 animal and 31 human samples were collected from the Viburnum and Myrtaceae regions, and 50 positive samples were obtained. The prevalence of C. albicans and C. parvum was found to be 10.5% in humans and 31.2% in animals. The prevalence of C. albicans and C. parvum was determined by PCR using HSP18 rRNA, HSP70, and Cyp96 as target genes. The prevalence of C. albicans and C. parvum was determined by PCR using HSP18 rRNA, HSP70, and Cyp96 as target genes. The prevalence of C. albicans and C. parvum was determined by PCR using HSP18 rRNA, HSP70, and Cyp96 as target genes. The prevalence of C. albicans and C. parvum was determined by PCR using HSP18 rRNA, HSP70, and Cyp96 as target genes. The prevalence of C. albicans and C. parvum was determined by PCR using HSP18 rRNA, HSP70, and Cyp96 as target genes.

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

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