EVIDENCE FOR THE PRESENCE OF *Rhinosporidium seeberi* IN DOMESTIC ANIMALS AND HUMANS IN SRI LANKA

R.P.V.J. Rajapakse, S.N. Arseculeratne and S.D.T.G. Sudasinghe

Division of Parasitology, Department of Pathobiology, Faculty of Veterinary Medicine and Animal Sciences, University of Peradeniya

Introduction

Rhinosporidiosis is an infective disease caused by an aquatic protozoan previously considered to be a fungus. This is a chronic granulomatous infection of the mucous membranes and usually manifests as vascular friable polyps in the nasal mucosa or external structures of the eye. (Herr *et al.*, 1999). The etiologic agent of rhinosporidiosis is *Rhinosporidium seeberi*, which is closely related to several protoctistan fish and amphibian pathogens. Seeber in 1900 described it in an individual from Argentina that was rhinosporidiosis is endemic in India, Sri Lanka, South America and Africa. Many cases from the United States and Southeast Asia, as well as scattered occurrences throughout the world, have been reported. Most cases of rhinosporidiosis are infected in persons from or residing in the Indian subcontinent or Sri Lanka. (Rivard and Hospenthal, 2007). The disease affects humans, horses, dogs, and to a lesser extent cattle, cats, foxes, and birds (Berrocal and López, 2007)

The objectives of this study were to determine the sero epidemiology of *Rhinosporidium* in humans, cattle, buffalos, cats, and dogs and to detect the prevalence of *Rhinosporidium seeberi* in the reservoir water deposits by *Rhinosporidium seeberi* specific PCR.

Materials and Methods

Human (36), cattle (55), buffalo (50) and dog (60) blood samples were collected from different districts of the country and sera were separated by centrifugation. The Immuno dot blot method was used to determine the sero-prevalence in animals. Antibody titer was estimated in all positive samples at 1/25.

Cattle nasal scrapings were collected from Kandy and Colombo municipal council slaughter houses while human nasal swabs were collected from hospitals. Water samples were collected from reservoirs in the dry zone and the sediment of each water sample was subjected to DNA extraction to detect *Rhinosporidium seeber* DNA. Extracted DNA was amplified by Polymerase Chain Reaction and the PCR products were run on a Gel Electrophorosis System and visualized using a Gel documentation system.

Results

Of the 36 human samples titrated to determine the sero- prevalence of the disease, 33 samples was found to be positive at a titer of 1/25. Fifty five out of 63 cattle, 12/60 dog, 25/50 buffalo samples were found to be positive at 1/25. The titer of all the human and animal positive samples were also determined.

Table 1. IgG titres of different species

Type of species	Maximum Titre Value	No. of Animals
Cattle (Anuradhapura)	1/1600	3
Buffalo (Bandarawela)	1/800	3
Dog (Veterinary Teaching hospital Peradeniya)	1/1600	3
Human (Kandy General hospital)	1/1600	4

Twelve cattle nasal scrapings and four suspected human samples were amplified by PCR. Out of the 12 samples, five showed positive bands. Of the 4 human samples two showed *Rhinosporidium seeberi* positive bands. Human and cattle positive bands appeared at the same levels (377 bp region). Of the water deposits that were amplified, all samples tested were found to be negative.

Discussion

Animal Rhinosporidiosis has been reported from many countries. In this study many animals showed high titres of *Rhinosporidium seeberi* IgG. This may have resulted from sub clinical exposure to *Rhinosporidium seebei,* probably found in ground water.

Conclusion

Rhinosporidium seeberi infection on animals has not been reported in Sri Lanka. The present study showed the existence of subclinical infection with appreciable level of *Rhinosporidium seeberi IgG* in the blood.

Acknowledgement

We like to thank the National Science Foundation for funding this research study.

References

Alexis Berrocal and Alfonso López (March 2007), Nasal rhinosporidiosis in a mule, *Can Vet J.* 48 (3): 305–306

Herr R. A. *et al.* (1999) Phylogenetic analysis of *Rhinosporidium seeberi*'s 18S small subunit ribosomal DNA groups this pathogen among members of the Protoctistan *Mesomycetozoa* Clade. J. Clin. Micro. (Sept) 2750-2754.

http://emedicine.medscape.com/infectious_diseases#heent