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Prevalence and molecular characterisation of *Cryptosporidium* from dairy cattle in five farms in Kuantan (Article)

Yusof, A.M.^{ab} [✉](#), Isa, M.L.M.^{ab} [🔍](#)^aDepartment of Basic Medical Sciences, Kulliyah of Nursing, International Islamic University of Malaysia, Jalan Sultan Ahmad Shah, Bandar Indera Mahkota, Kuantan, Pahang, Malaysia^bIntegrated Cellular and Molecular Biology Cluster (iMolec), Integrated Centre for Research Animal Care and Use, International Islamic University Malaysia, Jalan Sultan Ahmad Shah, Bandar Indera Mahkota, Kuantan, Pahang, Malaysia

Abstract

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Cryptosporidium spp. are ubiquitous enteric protozoan parasites that cause diarrhoeal disease known as cryptosporidiosis. This research was conducted to find the prevalence of *Cryptosporidium* from dairy cattle in Kuantan, Pahang, Malaysia and to identify the genotype of *Cryptosporidium* by using 18S rRNA gene. Besides, this study aims to investigate the association between *Cryptosporidium* infection and the age of dairy cattle. A total of 375 stool specimens of dairy cattle were collected and concentrated with formal-ether concentration technique. The *Cryptosporidium* oocysts were detected with modified Ziehl Neelsen staining. *Cryptosporidium* species was identified by nested PCR amplification of 18S rRNA gene. Based on microscopic examination, 16.3% (61/375) dairy cattle were positive for *Cryptosporidium* infection. This research has shown that the highest prevalence of *Cryptosporidium* was recorded in calves with the percentage of 17.4% (12/69), followed by adult cattle and yearling with the percentage of 16.1% (29/180) and 15.9% (20/126), respectively. The findings demonstrated that there was no significant difference ($p > 0.05$) in *Cryptosporidium* infection rates by age. Molecular characterisation revealed that the species of *Cryptosporidium* found in dairy cattle was *Cryptosporidium* ryanae. The present study suggested that proper hygiene practices must be practiced by farmers in order to control the *Cryptosporidium* infection. © 2017, Malaysian Society of Applied Biology. All rights reserved.

Author keywords

18S rRNA Age *Cryptosporidium* Dairy cattle Prevalence

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🔍 Yusof, A.M.; Department of Basic Medical Sciences, Kulliyah of Nursing, International Islamic University of Malaysia, Jalan Sultan Ahmad Shah, Bandar Indera Mahkota, Kuantan, Pahang, Malaysia; email:afzan@iiium.edu.my

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