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The development of a molecular-based multiplex method to detect *Blastocystis*, *Cryptosporidium sp* and *Giardia duodenalis*

U. Parkar[1], R. J. Traub[2], N. Hijjawi[3], A. Wayne[4], K. Morris[4], R. C.A. Thompson[1]

[1]*School of Veterinary and Biomedical Sciences, Murdoch University, Perth, WA, Australia*
[2]*School of Veterinary Science, University of Queensland, Brisbane, QLD, Australia*
[3]*Department of Medical Laboratory Sciences, Hashemite University, Zarqa, Jordan*
[4]*Science Division, Department of Environment and Conservation, Perth, WA, Australia*

Blastocystis, Cryptosporidium sp and *Giardia duodenalis* are amongst the most common zoonotic parasites found in humans. This study focuses upon developing a molecular-based multiplex method to simultaneously detect all three pathogens from various hosts. The advantages of this method are that it is cost effective and less time consuming compared to routinely utilized traditional PCRs, which are currently used to detect each of these parasites individually. This method also complements the use of high-throughput sequencing methods, such as pyrosequencing in order to characterize amplified isolates. Hence, this approach would be beneficial for studies involving large sample sizes and could also be useful in a diagnostic laboratory.