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Partial characterisation of ATP-binding cassette protein encoding genes in *Cryptosporidium parvum*

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Cryptosporidium parvum, the etiological agent for cryptosporidiosis, is notoriously known as one of the most common pathogens causing human diarrhoea disease worldwide. *C. parvum* is intrinsically resistant to an array of drugs that is generally effective against similar organisms, therefore, there is no consistently efficacious therapy for eradicating cryptosporidiosis. The present study aims to explore the possible mechanisms underlying the multidrug resistance characteristic of *C. parvum* by detecting the presence of ATP-binding Cassette (ABC) protein encoding genes, especially one that shows high similarity to members belonging to the Multidrug resistance protein (MDR) and Multidrug resistance associated protein (MRP) subfamilies which have been associated with multidrug resistance phenomenon in human cancer cells and various human pathogens. PCR using ABC-specific degenerate primers successfully amplified two unique fragments, designated Cpnbd1 and Cpnbd2, from *C. parvum* genomic DNA. Cpnbd1 exhibited high degree of homology (99-100%) with the nucleotide-binding domains (NBDs) at the NH₂-terminal halves of two previously reported ABC proteins (CpABC and CpABC1) of human and bovine *C. parvum* isolates. It is likely that CpABC, CpABC1 and Cpnbd1 were encoded by homologous genes of a type of ABC transporter protein found in different *C. parvum* isolates. However, Cpnbd2 showed moderate levels of similarities (28-49%) to the NBDs of four ABC proteins characterised in *C. parvum* to date. Therefore, Cpnbd2 could be a novel member of an ABC superfamily of proteins in *C. parvum*. On the other hand, similarity analyses on a list of ABC transporters known to associate with MDR phenotype has significantly related Cpnbd1 and Cpnbd2 to these transporters, thus suggesting that Cpnbd1 and Cpnbd2 proteins may contribute to the intrinsic multidrug resistance phenotype of *C. parvum*.