

Random amplified polymorphic DNA (RAPD) and internal transcribed spacer 2 (ITS2) rDNA study of some paramphistome isolates from Southern Africa

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Paramphistomes are parasites of both domestic and wild ruminants whose effects still remain underestimated. Limited studies in Africa have been done using molecular techniques to resolve problems associated with taxonomical groupings and epidemiology of these parasites. In this study, the genetic variability of nine representative paramphistome isolates collected from different geographical locations in Southern Africa (namely South Africa, Botswana, Zambia and Zimbabwe) was assessed using RAPD data analysis and ITS2 rDNA sequence data. All isolates were sectioned for morphological characterization and for molecular analyses; DNA was extracted, amplified and purified. Sagittal sections revealed three species of paramphistomes belonging to three different sub-families: one *Stephanopharynx compactus* isolate, a member of the Stephanopharyngidae sub-family, one *Carmyerius dollfusi* isolate, a member of the Gastrothylacidae sub-family and seven *Calicophoron microbothrium* isolates belonging to the Paramphistomidae sub-family. The ITS2 rDNA sequences were submitted to Genbank and were assigned accession numbers (KP639630-KP639638). Two isolates *S. compactus* (KP639630) and *C. dollfusi* (KP639636) were first reported in this study. Phylogenetic reconstruction of the paramphistome isolates based on the ITS2 rDNA sequence data obtained using Mega 6, separated them into three clades representing the three species. However, the clade with all the *C. microbothrium* isolates is the only one that was supported by a higher bootstrap value of 92% although there was no differentiation of these isolates according to geographical locations. The low divergence values on the ITS2 sequences of the *C. microbothrium* isolates indicate that ITS rDNA sequence data can be used as a molecular tool to infer knowledge for resolving taxonomic groupings. RAPD data analysis using Popgene 32 clustered the paramphistome isolates according to their geographic origin in spite of the differences in species of the isolates. There was significant variability between the isolates with an average genetic distance value of 0.4381. These results show that RAPDs can be used as a molecular marker for epidemiological studies of *C. microbothrium* and could possibly show that cross fertilization between species does occur.

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Burden of intestinal helminth infections among children of the Kashmir valley, India

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In any geographical area, surveys of the prevalence of intestinal helminths are necessary to suggest appropriate control measures. The aim of this study was to determine the prevalence of intestinal helminth infections in children of the Kashmir valley and to identify the risk factors. Stool samples were collected from 2256 children from rural as well as urban areas of the Kashmir valley. The samples were examined by simple smear and zinc sulfate concentration methods. Intensity of the infection was quantified by Stoll's egg-counting technique. Infection by at least one intestinal helminth was found in 71.18% of the sampled population. The prevalence of *Ascaris lumbricoides* was highest (68.30%), followed by *Trichuris trichiura* (27.92%), *Enterobius vermicularis* (12.67%) and *Taenia saginata* (4.60%). Light (57.1%) to moderate (42.8%) intensity of infection was observed for *A. lumbricoides*, while the majority of the infected children (92.3%) harbored a light intensity of infection for *T. trichiura*. The age group, rural or urban residence, type of water source, boiled or unboiled water, type of defecation site, level of personal hygiene and maternal education were associated with helminth infection. Adequate control measures are urgently needed to combat the high prevalence of intestinal helminths and risk factors in the children of Kashmir valley.

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