

## GENETIC CHARACTERIZATION OF *CRYPTOSPORIDIUM* SPP.

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The sporozoan parasites *Cryptosporidium* spp. are now recognized as significant pathogens of vertebrate hosts; primarily involving diarrhoea in mammals, diarrhoea and/or respiratory signs in birds, and gastritis in reptiles and fish. Most infections have been associated with acute transient disease (usually in neonates) but persistent infections may develop causing severe chronic disease (especially in reptiles and immuno-compromised mammals). Six parasite species are currently regarded as valid on the basis of differences in parasite morphology (oocyst size and shape) and host specificity (for individual vertebrate classes).

Comparative morphometric, cross-transmission and isoenzyme electrophoretic studies were performed on *Cryptosporidium* spp. oocysts recovered from mammals (16 human patients, 3 calves and 1 goat), birds (4 quail) and reptiles (1 dugite and 1 taipan). Morphometric analyses revealed significant differences in oocyst size and shape only between isolates from different vertebrate classes. Cross-transmission studies revealed that isolates were only infective to hosts belonging to the same vertebrate class. Mammalian isolates were infective to mice (but not chickens), avian isolates were infective to chickens (but not mice) and reptilian isolates were not infective to mice or chickens. Soluble oocyst extracts were examined by isoenzyme electrophoresis on cellulose acetate gels and good reactivity was observed for 17 of the 55 enzymes screened. Fixed allelic differences were detected not only between isolates from different vertebrate classes but also between isolates from the same vertebrate class (and even the same host species). Two groups of human isolates were found to differ at 2 of 17 loci (12%); one group contained the majority of isolates collected throughout south and central Australia and the other contained a single isolate from an intermediate rural area. Both groups differed from bovine, caprine and reptilian isolates at 5-7 loci (29-41%). Bovine and caprine isolates differed at one locus (6%). The two reptilian isolates differed at one locus (6%) and both differed from bovine and caprine isolates at 1-3 loci (6-18%). Avian isolates differed from bovine, caprine and reptilian isolates at 2-3 loci (12-18%). These genetic characterization studies have revealed considerably greater parasite variation between *Cryptosporidium* isolates than suggested by conventional morphological and cross-transmission studies.