Cryptosporidium genotypes in Midwestern mammals

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Empirical evidence supports host adaptation and a limited host range for most *Cryptosporidium* species and genotypes. This knowledge has been used to track sources of water contamination and characterize human health risk; however, the factors affecting host range remain unclear. We are using small mammals as a model to study the effect of factors such as host population density, diversity and behavior on the host range of *Cryptosporidium* genotypes. We report preliminary findings of the prevalence of *Cryptosporidium* genotypes in Midwestern mammals. We live-trapped mammals in the North Dakota region. We identified species, collected a fecal sample and then released more than 60 captured individuals. DNA was extracted from fecal samples and a fragment of the 18S rRNA gene was amplified using nested *Cryptosporidium* specific primers. PCR products of the expected size were purified, cloned, and sequenced. Sequences were aligned and a phylogenetic tree was constructed. Thirteen small mammal species were identified and sampled. *Cryptosporidium* genotypes, including Muskrat I and II, deer mouse I, II and III, shrew, and novel genotypes were identified in 32/67 (47.6%) mammals. Some genotypes were identified in multiple host species. These data show that *Cryptosporidium* is ubiquitous in small North American mammals with multiple genotypes present.