

Cryptosporidium genotypes in Midwestern mammals

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Background/Objectives

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.

Methods

Sample collection

Animals were live-captured in Sherman Box traps at 4 sites in Minnesota and North Dakota. Fresh fecal samples were collected and in cases where an individual died in the trap, the animal was dissected and material taken from the small and large intestines. A total of 181 animals from 13 species were sampled. Live animals were recorded, weighed and ear tagged, depending on the species.

Species/genotype identification

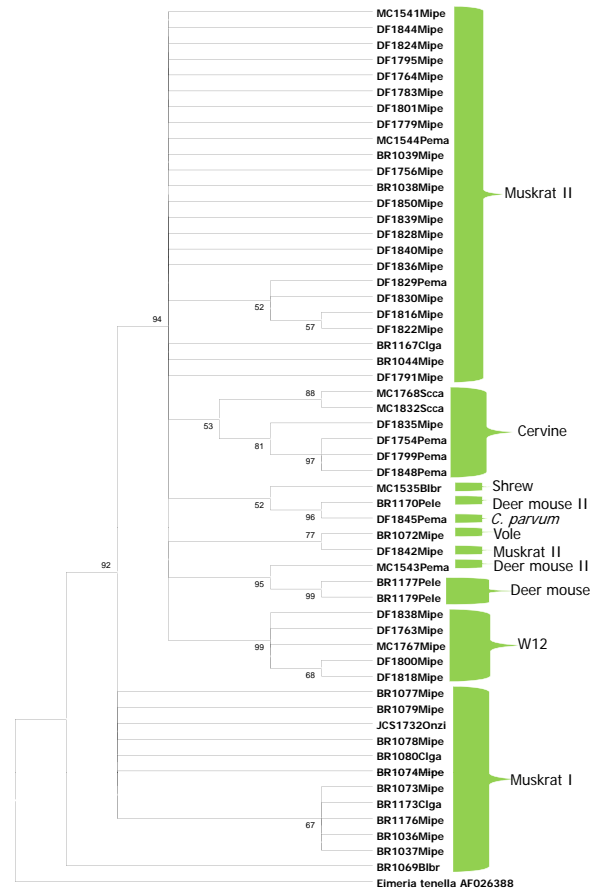
DNA was extracted from feces as previously described (1). A fragment of the 18S rRNA gene was amplified (2), cloned into a pGEM-T Easy vector and sequenced bi-directionally. Sequences were aligned, edited, and compared to non-redundant sequences in GenBank using the BLAST algorithm. A neighbor joining tree was constructed using the Maximum Composite Likelihood model as part of the MEGA 4 bioinformatic software suite (3).

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Results

Figure 1. Evolutionary relationships of wildlife isolates



Sites

DF: Discovery Farms, ND
BR: Buffalo River, MN
JCS: J. Clark Salyer, ND
MC: Moorhead, MN

Wildlife Species

Mipe: *Microtus pennsylvanicus* (Meadow vole)
Pele: *Peromyscus leucopus* (White-footed mouse)
Pema: *Peromyscus maniculatus* (Deer mouse)
Onzi: *Ondatra zibethicus* (Muskrat)
Clga: *Clethrionomys gapperi* (Southern red-backed vole)
Scca: *Sciurus carolinensis* (Eastern gray squirrel)
Blbr: *Blarina brevicauda* (Northern short-tailed shrew)

Figure 2. Prevalence of *Cryptosporidium* in wildlife

Scientific Name	Common Name	No. Sampled	% Positive
<i>Microtus pennsylvanicus</i>	Meadow vole	81	46
<i>Ondatra zibethicus</i>	Muskrat	40	3
<i>Peromyscus maniculatus</i>	Deer mouse	17	41
<i>Peromyscus leucopus</i>	White-footed mouse	10	30
<i>Blarina brevicauda</i>	Northern short-tailed shrew	9	22
<i>Zapus hudsonius</i>	Meadow jumping mouse	5	0
<i>Sciurus carolinensis</i>	Eastern gray squirrel	4	50
<i>Sciurus niger</i>	Eastern fox squirrel	4	0
<i>Procyon lotor</i>	Raccoon	4	0
<i>Clethrionomys gapperi</i>	Southern red-backed vole	3	100
<i>Spermophilus tridecemlineatus</i>	Thirteen-lined ground squirrel	2	0
<i>Tamiasciurus hudsonicus</i>	Red squirrel	1	0
<i>Mustela frenata</i>	Long-tailed weasel	1	0

❖ *Cryptosporidium* was detected in 55/181 (30%) samples

❖ *Cryptosporidium parvum* was isolated from the white footed mouse on 2 occasions. One of the individuals was infected with the cervine genotype.

❖ The Muskrat II was the most prevalent genotype (45%) with 19/25 isolates from a single site (DF).

❖ Muskrat II was found in 22 *Microtus pennsylvanicus*, 1 *Peromyscus maniculatus*, 1 *Clethrionomys gapperi*, and 1 *Blarina brevicauda*.

❖ The Muskrat I genotype was found in 21% of the isolates; 10 of the 12 isolates were from a single site (BR) site.

❖ Muskrat I was found in 8 *Microtus pennsylvanicus*, 2 *Clethrionomys gapperi*, 1 *Ondatra zibethicus*, and 1 *Peromyscus maniculatus*.

Conclusions

Muskrat I and Muskrat II may be misleading genotype names. Both genotypes are more prevalent in voles.

W12, previously identified in surface water, is associated with the meadow vole.

Voles are susceptible to multiple genotypes.

References

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