Source of *Cryptosporidium* in a rural watershed

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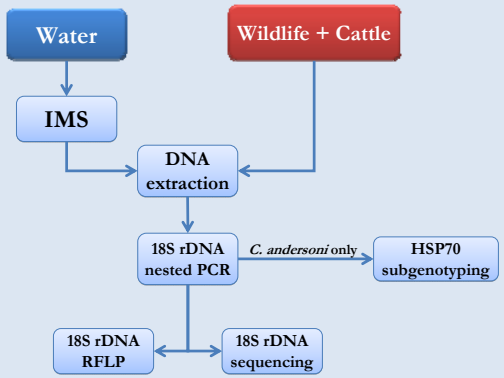
INTRODUCTION

Cryptosporidium is a significant cause of waterborne outbreaks in the U.S. Oocysts of this parasite may remain viable in water for months and are difficult to eliminate by conventional disinfection. Although the occurrence of *Cryptosporidium* in surface water is common, our understanding of the source and public health significance of contamination is poor. Major sources of surface water contamination by *Cryptosporidium* are livestock, humans and wildlife. Advances in molecular typing have made it possible to determine the source and public health significance of contamination by exploiting the host adapted nature of *Cryptosporidium* species and genotypes. In this study, we determined sources of *Cryptosporidium* in a rural river by identifying and genotyping isolates from the river, and from wildlife and cattle in the watershed.

MATERIALS AND METHODS

An area of the Buffalo River watershed in Minnesota, which has both cattle and wildlife, was selected for the study (Figure 1). Nine fecal samples were obtained from cattle. Forty small, wild mammals were captured in traps along the river both upstream and downstream of where cattle were located. Water samples were collected upstream and downstream of the cattle location. *Cryptosporidium* species and genotypes were identified using the methods outline below.



RESULTS

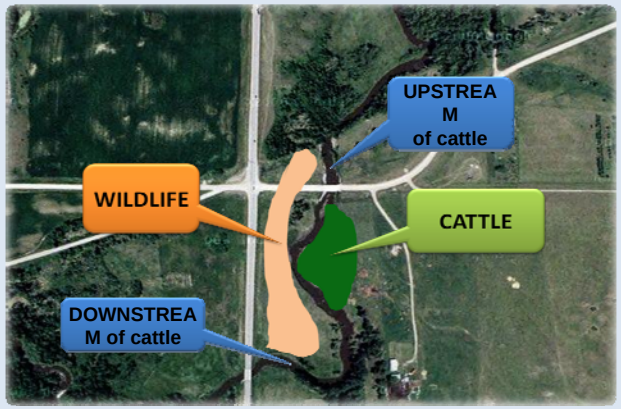


Figure 1. Buffalo River study site

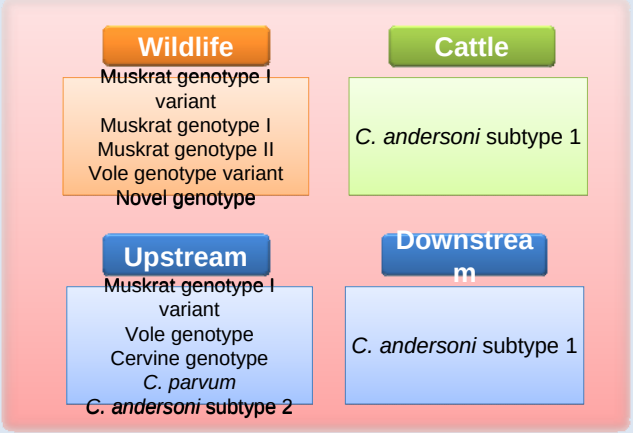


Figure 2. Species and genotypes detected in water, small mammals and cattle

KEY FINDINGS

- **Meadow voles**, the most abundant small mammal, were infected with muskrat genotype I variant, muskrat genotype I, muskrat genotype II, vole genotype variant, and a novel genotype.
- **White footed-mice** were infected with the deer mouse genotype.
- **Northern short-tailed shrew** were infected with muskrat genotype I variant.
- **Southern red-backed voles** were infected with muskrat genotype I variant.
- The vole genotype and muskrat genotype I were found in both meadow voles and water.
- *C. parvum* and the cervine genotype were identified in an upstream water sample.
- The same *C. andersoni* subgenotype (subtype 1) was identified in cattle and in water samples downstream.
- A different *C. andersoni* subgenotype (subtype 2) was identified in upstream water samples.

SIGNIFICANCE OF KEY FINDINGS

•Both cattle and wildlife contribute to water contamination in the Buffalo River.

•Deer may be a source of pathogenic cryptosporidia in the Buffalo River.

C. parvum and the cervine genotype (both human pathogens), which were identified in an upstream water sample, have been identified in deer from the region (unpublished data).

•*C. andersoni* isolated upstream is not likely to be from the sampled cattle as it has a different HSP70 subtype to cattle isolates.

•HSP70 subtyping can be used to differentiate *C. andersoni* isolates from different sources.

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