

High prevalence of *Cryptosporidium andersoni* in surface water during a major spring flooding event

Pennil, C. C.^a, Clark, M.E.^b, Schneck, B.L.^{a,b}, Giddings, C.W.^a, and McEvoy, J.M.^a

^aDepartment of Veterinary and Microbiological Sciences, North Dakota State University, Fargo, ND, USA

^bDepartment of Biological Sciences, North Dakota State University, Fargo, ND, USA

Background/Objectives

The Red River and its tributaries originate in South Dakota, North Dakota and Minnesota and flow north through agricultural and metropolitan areas before emptying into Lake Winnipeg, Canada. Many of the metropolitan areas, including Fargo-Moorhead (pop. 150,000), Grand Forks, (pop. 59,000), and Winnipeg (pop. 650,000) use the Red River as a municipal source of water. The Red River drainage area is estimated to be 104,000 km² (40,200 mi²). The northern flow of the river combined with the extreme flatness of its gradient leave it susceptible to seasonal flooding.

In March 2009, the Red River in Fargo, North Dakota experienced its worst flooding in recorded history. Following the winter snow melt the river crested on March 28 and April 16 at 22.82 and 16 ft above flood stage, respectively. Our goal was to determine the presence of *Cryptosporidium* in the Red River and its tributaries during peak flooding.



Figure 1a. Red River at 15.5 feet on March 14, 2009. White area is snow covering frozen soil.

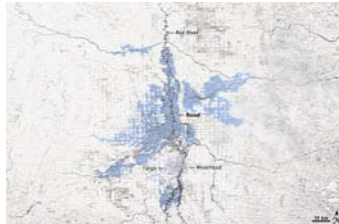


Figure 1b. Red River at 40.82 feet on March 28, 2009. Spring thaw has begun.

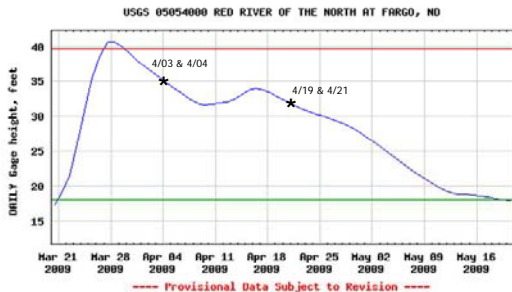


Figure 2. Hydrograph of the Red River. * Denotes sampling dates.

Methods

Thirteen water samples were collected on four occasions in April (two occasions following the flood's first peak and two following the second peak). Twelve samples were from the Red River and its tributaries and one was from a ditch that had been flooded by the Red River. Twenty liter water samples were collected, filtered and analyzed in accordance with EPA Method 1622. DNA was extracted and a fragment of the 18S rRNA gene was amplified using nested PCR. Amplified fragments were cloned and sequenced. Sequences were compared with non-redundant sequences in GenBank to determine the species/genotype.

Results

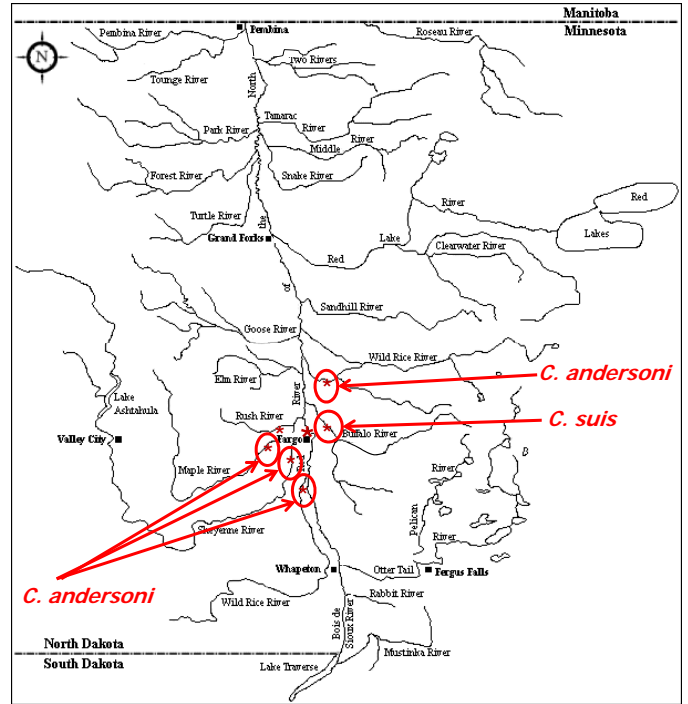


Figure 3. Red River of the North and tributaries. Asterisks show approximate sampling sites.

- ❖ *Cryptosporidium* was detected in 9 of 13 (69%) samples.
- ❖ *Cryptosporidium andersoni* was detected in 7 out of 9 samples from the Red River and its tributaries.
- ❖ *Cryptosporidium suis* was detected in one of the Red River tributaries.
- ❖ Deer mouse genotype III was detected in a ditch that had been flooded by the Red River.

Conclusions

Livestock contributed significantly to *Cryptosporidium* contamination in the Red River during a major spring flood.

Acknowledgements

The authors gratefully acknowledge funding from the USDA National Research initiative (Project # 2008-35102-19260)

Contact information

John.McEvoy@ndsu.edu