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]
[a]Department of Veterinary and Microbiological Sciences, North Dakota State University, Fargo, ND, USA
[b]Department of Biological Sciences, North Dakota State University, Fargo, ND, USA

In March 2009, the Red River in Fargo, ND experienced its worst flooding in recorded history. Flooding of the Red River follows winter snow melt; however, on this occasion the river attained a record crest more than 7 m above flood stage. Our goal was to determine the prevalence of *Cryptosporidium* in the Red River and its tributaries during peak flooding. Fourteen 20-L water samples were collected from the Red River and five large tributaries (Buffalo, Maple, Rush, Sheyenne and Wild Rice Rivers). Samples were processed in accordance with EPA Method 1622. DNA was extracted from IMS purified oocysts and a fragment of the18S rRNA gene was amplified, cloned, and sequenced. Sequences were aligned and compared with the non-redundant Genbank database to determine the species/genotype of *Cryptosporidium* present. Nine out of fourteen (64%) water samples tested positive for *Cryptosporidium* with *Cryptosporidium andersoni* and the deer mouse genotype III identified in 7/9 and 1/9 samples, respectively. These data suggest that cattle were a significant source of water contamination during this major spring flooding event.