Source tracking of *Cryptosporidium* in the Red River Valley

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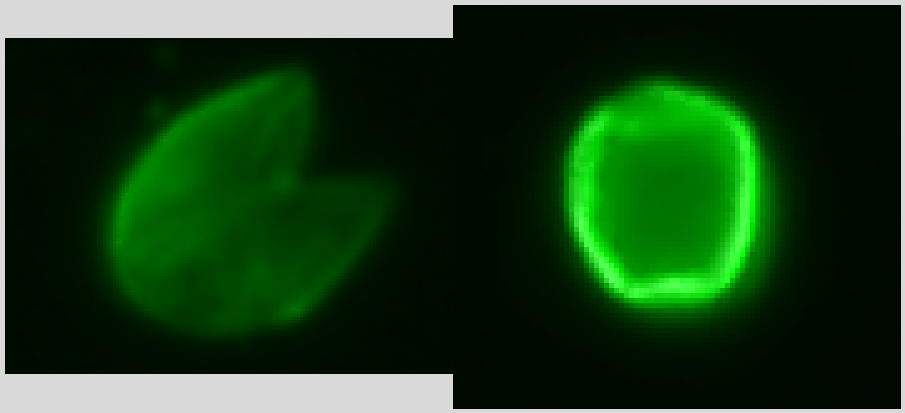
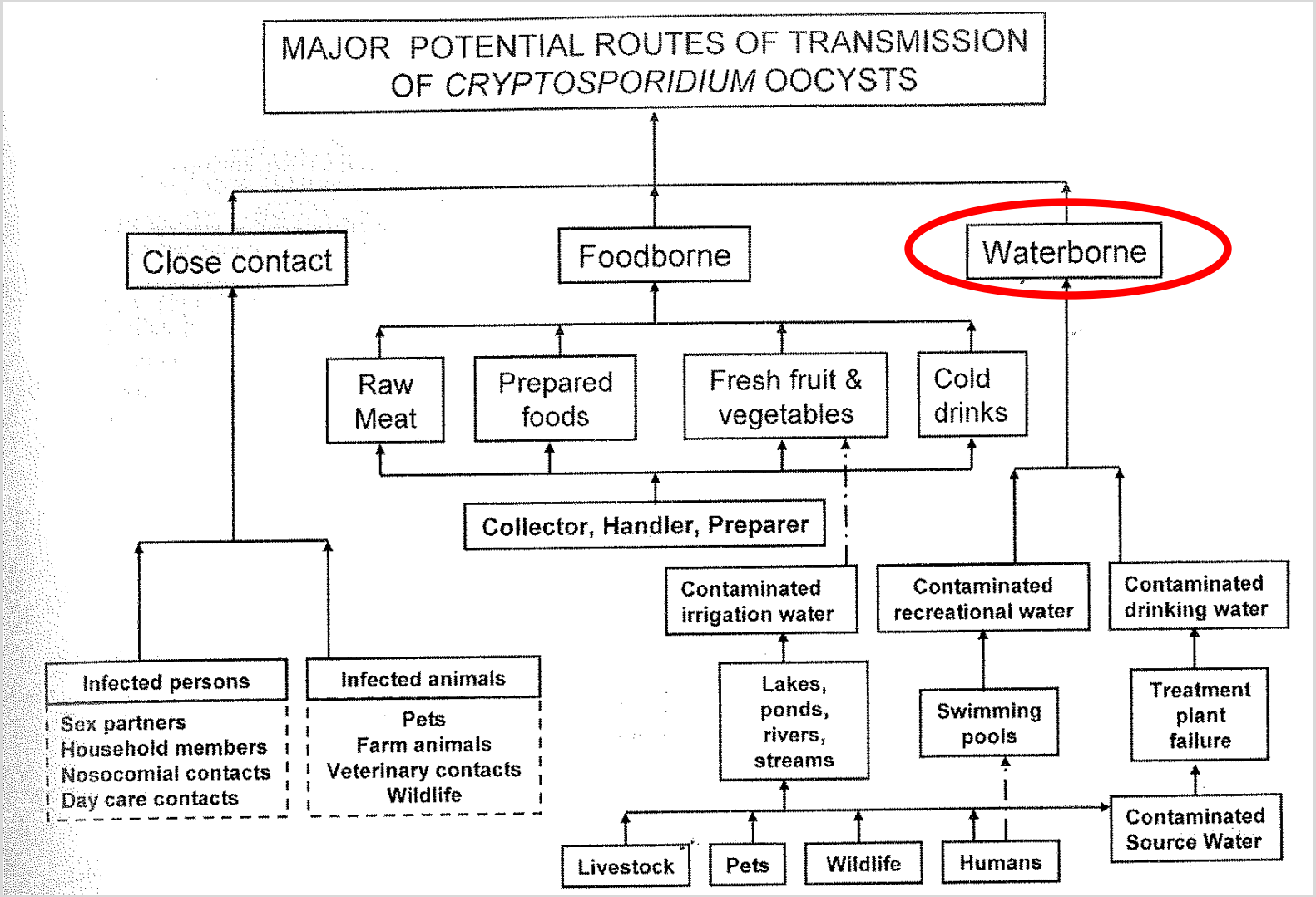
Genus *Cryptosporidium* aka “Crypto”

- 60+ types
- Ubiquitous
  - Humans, livestock, wildlife, water, soil
- May cause Cryptosporidiosis
- Host adaptation
  - *C. andersoni*
- Fecal-oral route



(Xiao & Ryan 2008, Cryptosporidium and Cryptosporidiosis; Fayer 2004, Vet. Paras; Xiao et al. 2004, Int. J. for Paras.)

Transmission



(Fayer 1997, *Cryptopsoridium* and Cryptosporidiosis)

Objectives

- 1. Determine the types of *Cryptosporidium* in the Red River and its tributaries
- 2. Determine which host(s) may contribute to *Cryptosporidium* contamination
- 3. Estimate number of oocysts in flood water

Methods: Animal Samples

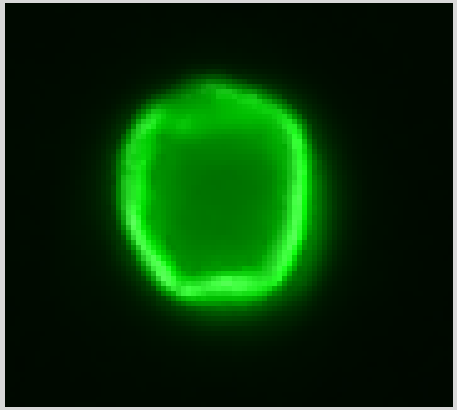
- Live trap small mammals or sample “cow pie”
- Scare the “crap” out of the animals
- Extract DNA from feces

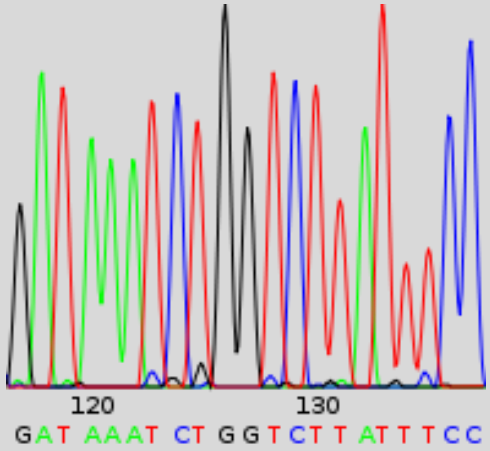
Methods: Water Samples

- 20L water thru Envirochek® HV filters
- Immunomagnetic Separation (IMS)
  - EPA Method 1622/1623
- Slides for counting oocysts
  - Immunofluorescent assay
- Freeze-thaw DNA extraction

Methods

- PCR: 18S rRNA gene
- Sequence to identify the Crypto
- Slides to enumerate oocysts

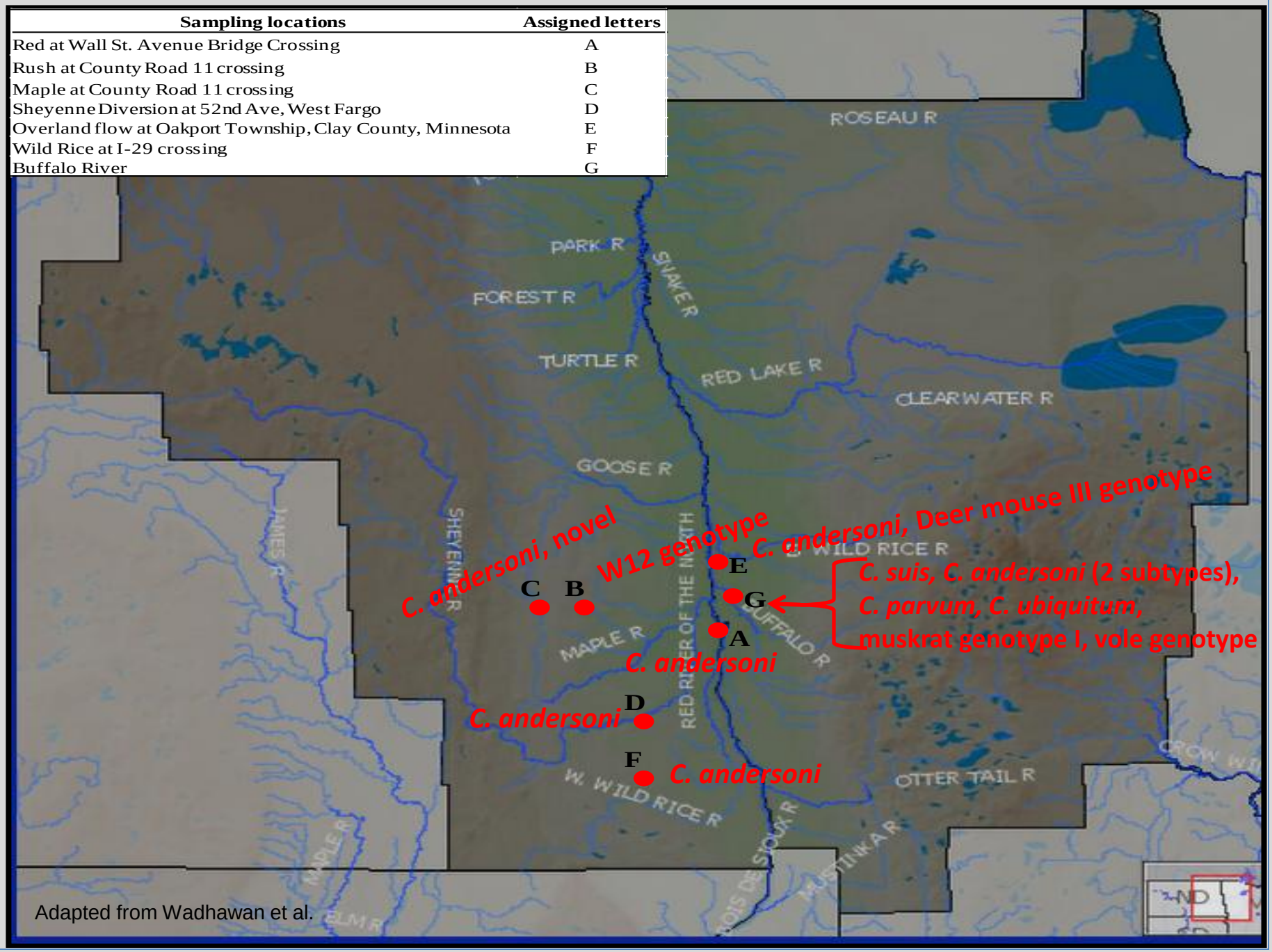




Results

Objective 1: Determine the types of *Cryptosporidium* in the Red River and its tributaries

Sampling locations	Assigned letters
Red at Wall St. Avenue Bridge Crossing	A
Rush at County Road 11 crossing	B
Maple at County Road 11 crossing	C
Sheyenne Diversion at 52nd Ave, West Fargo	D
Overland flow at Oakport Township, Clay County, Minnesota	E
Wild Rice at I-29 crossing	F
Buffalo River	G



Adapted from Wadhawan et al.

Results

Objective 1: Determine the types of *Cryptosporidium* in the Red River and its tributaries

Buffalo River in 2007-08

- 20/28 (71%)
  - –Over half *C. andersoni*
  - –Also *C. ubiquitum, C. parvum*, vole genotype, muskrat I genotype

2009 Flood

- 9/13 (69%)
  - *7 C. andersoni*
  - *1 C. suis*
  - *1. DM genotype III*

2010 Flood

- 14/17 (82%)
  - *1 W12 genotype*
  - *3 C. andersoni*

Results

Objective 2: Determine which host(s) may contribute to *Cryptosporidium* contamination

Host	*Cryptosporidium*
Northern short-tailed shrew	muskrat I genotype, shrew genotype
Southern red-backed vole	muskrat I genotype, muskrat II genotype, fox genotype
Peromyscus spp.	*C. ubiquitum*, *C. parvum*, deer mouse genotype, deer mouse III genotype, muskrat II genotype
Grey squirrel	*C. parvum*, *C. ubiquitum*, skunk genotype, Deer mouse III genotype
Fox squirrel	*C. ubiquitum*
Red squirrel	*C. parvum*, *C. ubiquitum*, skunk genotype
Meadow vole	muskrat I genotype, muskrat II genotype, vole genotype, fox genotype, W12 genotype, *C. parvum*

Results

Objective 2: Determine which host(s) may contribute to *Cryptosporidium* contamination

Small Mammals

- 30/42 (71%) along the Buffalo River
- 60/148 (41%) near the Red River
- 36/108 (33%) along the Red River

Livestock

C. andersoni is host-adapted to cattle

-Calves can be infected with *C. parvum*

C. suis is host-adapted to pigs

Results

Objective 3: Estimate number of oocysts in flood water

2010 Flood

- Estimated the flow of oocysts at 728,000 per second during peak flooding based on an approximate flow of 560,000L per second (USGS)

- Averaged 1.3 oocysts/liter during the crest and .3 oocysts/liter one week after the crest

Take Home

- *Cryptosporidium* is everywhere
  - many different types
- Livestock largely contributed to *Cryptosporidium* in the water systems, but wildlife also played a role
- Generally, the *Cryptosporidium* found in the water are not a concern to human health
  - Caution with *C. parvum* and *C. ubiquitum*

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Questions/Comments

The Onion, 2000