Microbial Source Tracking

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Water Quality Quote

Of all our natural resources, water has become the most precious…In an age where man has forgotten his origins and is blind even to his most essential needs for survival, water along with other resources has become the victim of his indifference'.

Rachel Carson, Silent Spring.

What is the source of bacterial contamination ?

Bacterial Contamination

Maintenance of the microbiological quality and safety of water systems used for drinking, for recreating, and in the harvesting of seafood is imperative, as contamination of these systems can exact high risks to human health as well as result in significant economic losses due to closures of beaches.

Waters contaminated with human feces are generally regarded as a greater risk to human health, as they are more likely to contain human-specific enteric pathogens

Name of the organism of group	Major disease	Major reservoirs and primary sources
BACTERIA		
Salmonella typhi	Typhoid fever	Human feces
Salmonella Paratyphi	Paratyphoid fever	Human feces
Other salmonella	Salmonellosis	Human and animal faces
Shigella	Bacillary dysentery	Human faces
Vibro cholerae	Cholera	Human faces
Enteropathogenic E. coli	Gastroenteritis	Human faces
Yersinia enterocolitica	Gastroenteritis	Human and animal faces
Campylobacter jejuni	Gastroenteritis	Human and animal (?) faces
Legionell pneumophila and related bacteria	Acute respiratory illness (legionellosis)	Thermally enriched waters
Mycobacterium tuberculosis	tuberculosis	Human respiratory exudates
Other (atypical) mycobacteria	Pulmonary illness	Soil and water
Opportunistic bacteria	Variable	Natural waters

Name of the organism of group	Major disease	Major reservoirs and primary sources
Protozoon's		
Acanthanmoeba castellani	Amoebic meningoencephalitis	Soil and water
Balantidium coli	Balantidosis (dysentery)	Human faces
Cryptosporidium	Cryptosporidiosis	Human and animal faces
Entamoeba histolytica	Amoebic dysentery	Human faces
Giardia lamblia	Giardiasis (gastroenteritis)	Human and animal faces
Naegleria fowleri	Primary amoebic meningoencephalitis	Soil and Water
Anabaena flos-aquae	Gastroenteritis	Natural waters
Microcystis aeruginosa	Gastroenteritis	Natural waters
Alphanizomnon flos aquae	Gastroenteritis	Natural waters
Schizothrix calciola	Gastroenteritis	Natural waters

Enteric Viruses

Name of the organism of group	Major disease	Major reservoirs and primary sources
Enteroviruses		
Polioviruses	Poliomyelitis	Human faces
Coxsackieviruses A	Aseptic meningitis	Human faces
Coxsackieviruses B	Aseptic meningitis	Human faces
Echoviruses	Aseptic meningitis	Human faces
Other enteroviruses	Encephalitis	Human faces
Reoviruses	Mild upper respiratory and gastrointestinal illness	Human and animal faces
Rotaviruses	Gastroenteritis	Human faces
Adenoviruses	Upper respiratory and gastrointestinal illness	Human faces
Hepatitis A virus	Infectious hepatitis	Human faces
Norwalk and related GI viruses	Gastroenteritis	Human faces

WHAT IS MICROBIAL SOURCE TRACKING (MST)?

Track the source of bacterial contamination

Match microbes from a polluted site and an different sources to suggest the origin of the fecal pollution

MICROBIAL SOURCE TRACKING

Method Classification

Library Dependant

Relies on building a collection of microorganisms from different potential sources as well as from the watershed under study. This poses time as well as geographic limitations.

THIS IS LABORIOUS, EXPENSIVE AND TIME CONSUMING

Library Independent

No time and space restraints. They are based on nucleic acid techniques arising from the field of molecular ecology, such as developing host-specific strains that can be characterized to identify host-specific markers.

THIS IS MUCH FASTER AND LESS TEDIOUS

Library Dependent

Host specific *E. coli* isolates (library) are needed

The method is cumbersome

Requires expertise in *E.coli* isolation

Lot of Geographical variation

Match with the library

E. Coli isolates from the water body

Library Dependent MST

Library Dependant

EXAMPLES:

- **ARA (Antibiotic Resistance Analysis)**
- **CUP (Carbon Utilization Profile)**
- **RFLP (Restricted Fragment Length Polymorphism)**
- **AFLP (Amplified Fragment Length Polymorphism)**
- **Rep-PCR (repetitive extragenic palindromic - PCR)**

Library Independent MST

Molecular biomarker

Molecular biomarker

Molecular biomarker

Molecular biomarker

Extract DNA

PCR

Determine the source & quantify

Library Independent

Because of many drawbacks of library dependent methods

Library independent methods are under development

For example *Bacteriodes* oriented method can easily differentiate between human and non human sources

Emigration creek MST

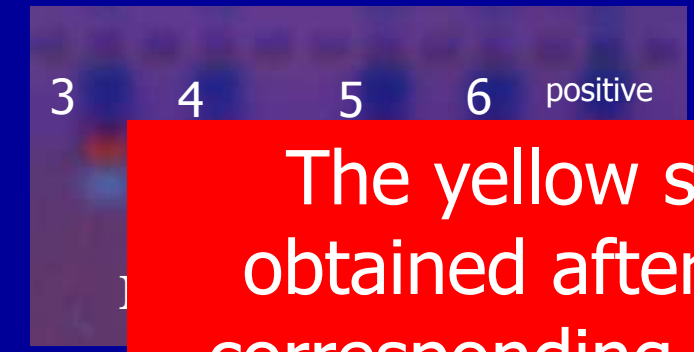
We used *Bacteriodes specific polymerase chain reaction (PCR) to find out human contamination*

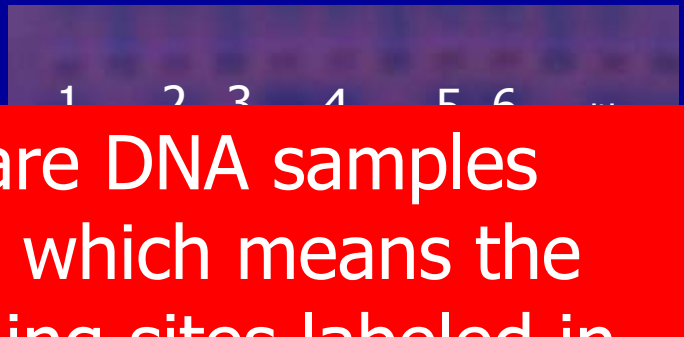
The procedure involved DNA extraction and PCR using human specific biomarkers for Bacteriodes

The study was qualitative rather quantitative

Quantitative study can be done easily

PCR positive signal from Emigration creek water samples





The yellow spots are DNA samples obtained after PCR, which means the corresponding sampling sites labeled in the pictures showed contamination from human origin

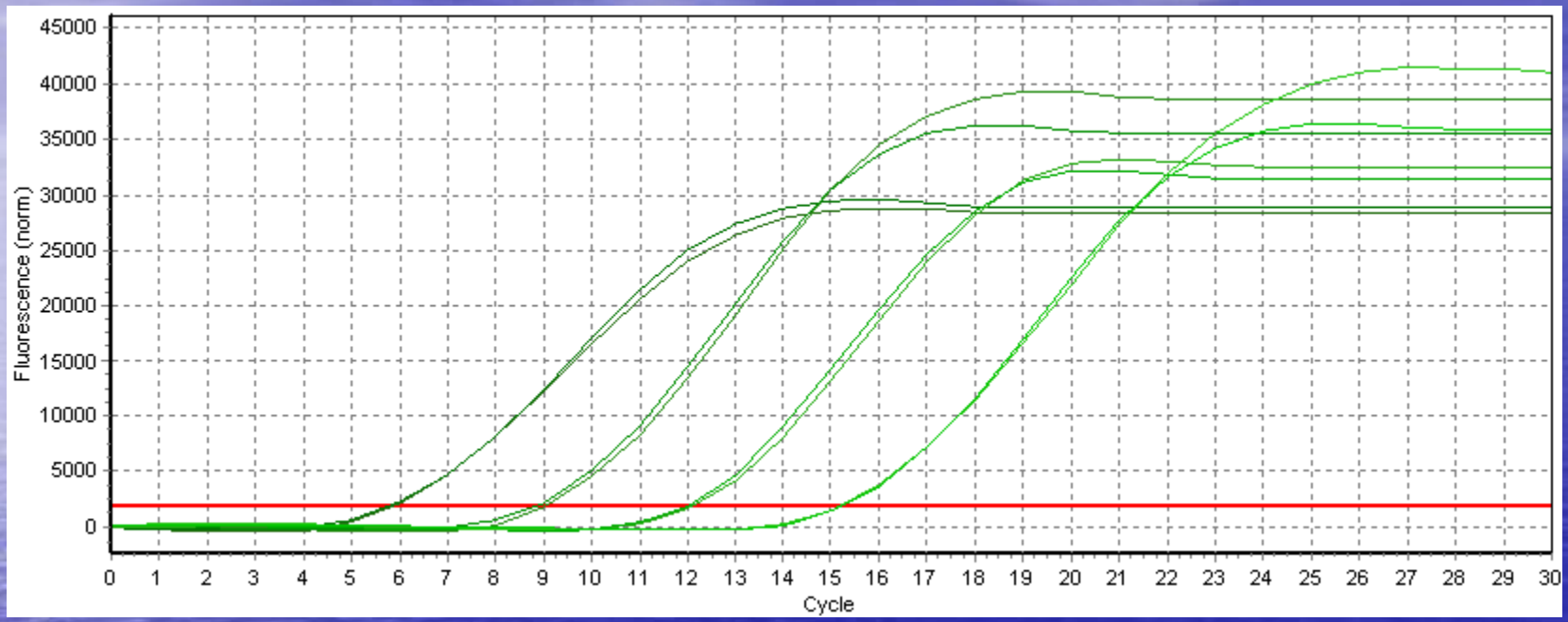
MST for samples from Zion National Park

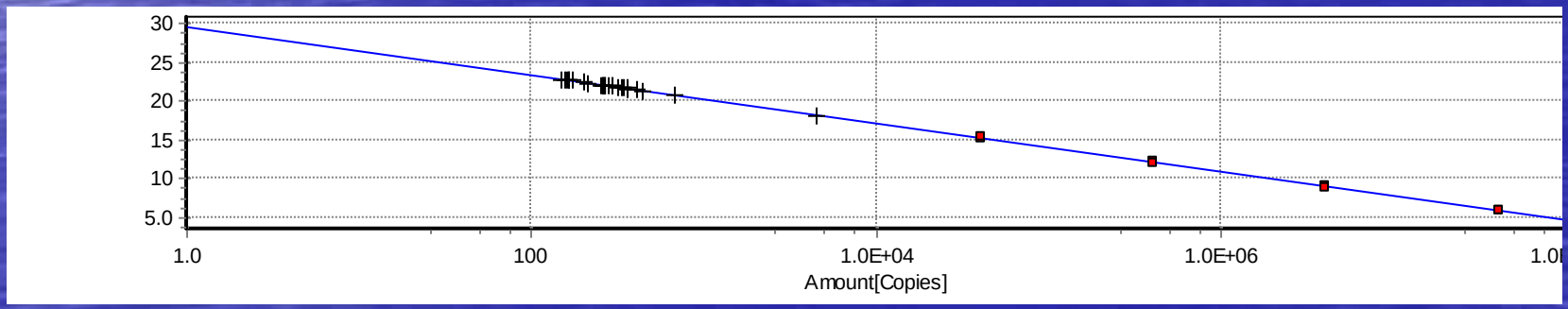
The MST work for Emigration Creek was qualitative- presence or absence

For Zion's water samples, we employed an advanced PCR method to identify and quantify source contribution

The method is called quantitative PCR

Quantitative PCR





MST for ZION

MST for water samples from Zions in June

Label	Sample Name	Label	Sample Name
1-1	Blank-1	1-2	Blank-1
2-1	Temple-1	2-2	Temple-1
3-1	NFK Bridge-1	3-2	NFK Bridge-1
4-1	Bulloch-1	4-2	Bulloch-1
5-1	Ab Stevens-1	5-2	Ab Stevens-1
6-1	Return Flow-1	6-2	Return Flow-1
7-1	WSA Broadway-1	7-2	WSA Broadway-1

For sample labeled as **Temple**, 70-73% of all *Baceteriodes* were deduced to be from the Human origin and 5-7% were from Bovine origin. The remaining may be from other sources

For samples labeled as **Bulloch**, 45-47% of all *Baceteriodes* were concluded to be from the human origin and 5% were from the Bovine sources.

QUESTIONS