Tracking Bacteria in the Animas & San Juan Rivers

San Juan Watershed Group
San Juan Soil & Water Conservation District
Animas Watershed Partnership

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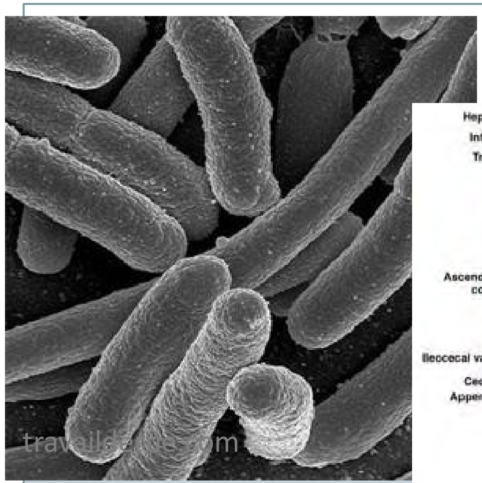
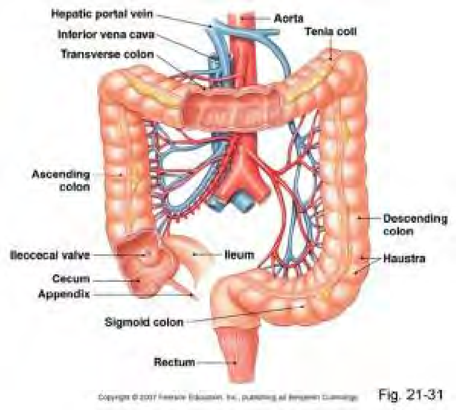
"WHO POOPED IN THE RIVER?"

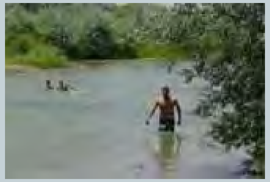
Image courtesy of Source Molecular laboratory

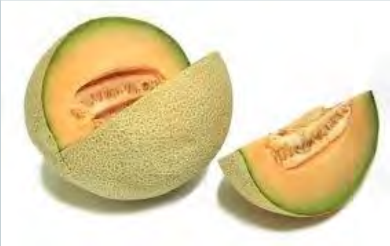




E. coli Bacteria

- Indicator of fecal pollution
  - Pathogenic strains, microorganisms
- Contamination pathways





- Human health risks
  - Diarrhea, infections, severe gastrointestinal illness

Who Cares?

EPA and state water quality criteria

"…designed to protect primary contact recreation, including swimming, bathing, surfing, water skiing, tubing, water play by children, and similar water contact activities where a high degree of bodily contact with the water, immersion and ingestion are likely."

Who Cares?

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→

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DATA GAP → Does primary contact "Recreation" standard protect traditional and ceremonial uses?

DATA GAP → What level of primary contact use is occurring on the San Juan between Farmington and heavily rafted areas in Utah?

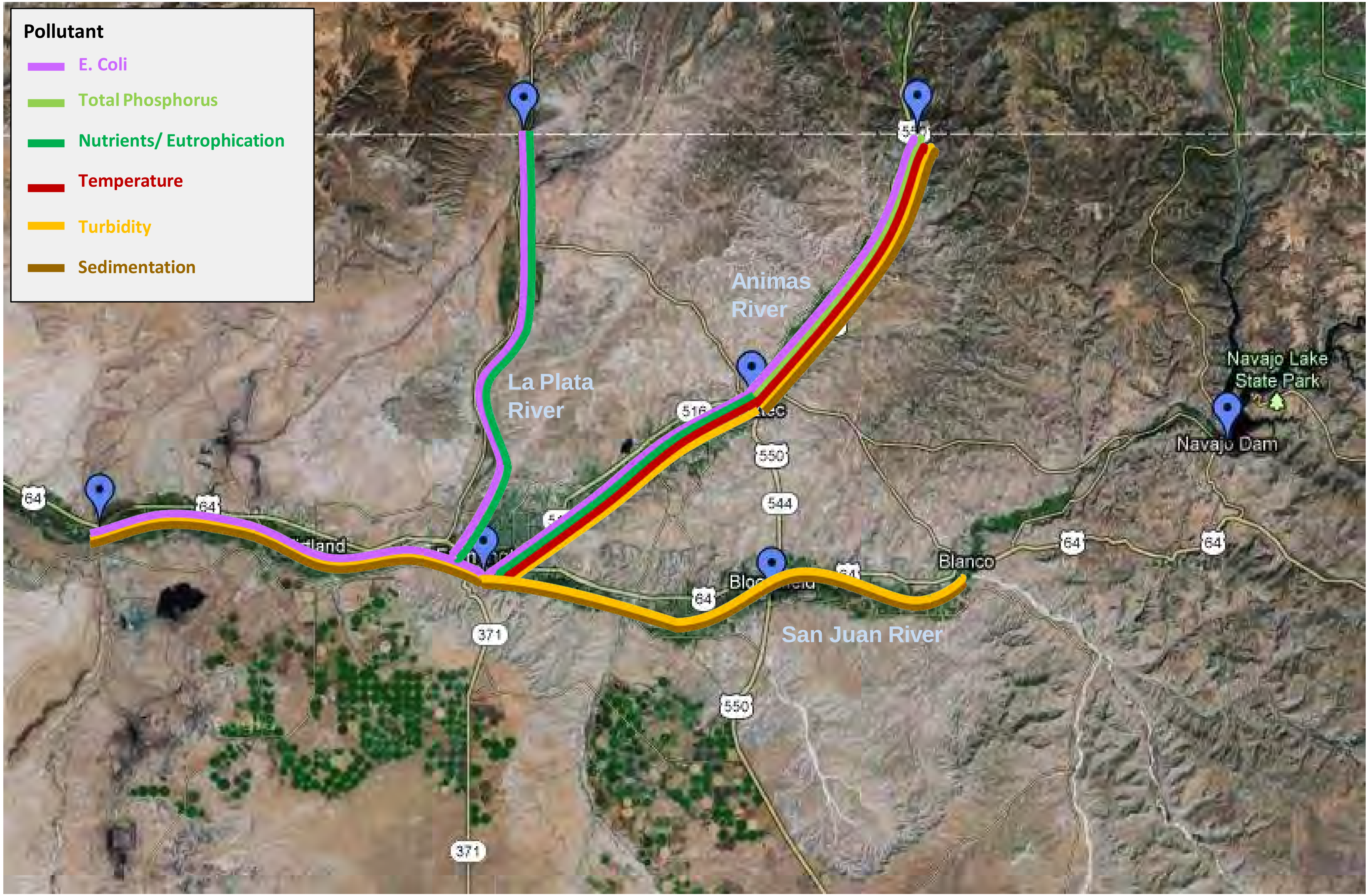
EPA and state water quality criteria → "…designed to protect primary contact recreation, including swimming, bathing, surfing, water skiing, tubing, water play by children, and similar water contact activities where a high degree of bodily contact with the water, immersion and ingestion are likely."

2000-2010 Bacteria identified as a problem in San Juan Watershed

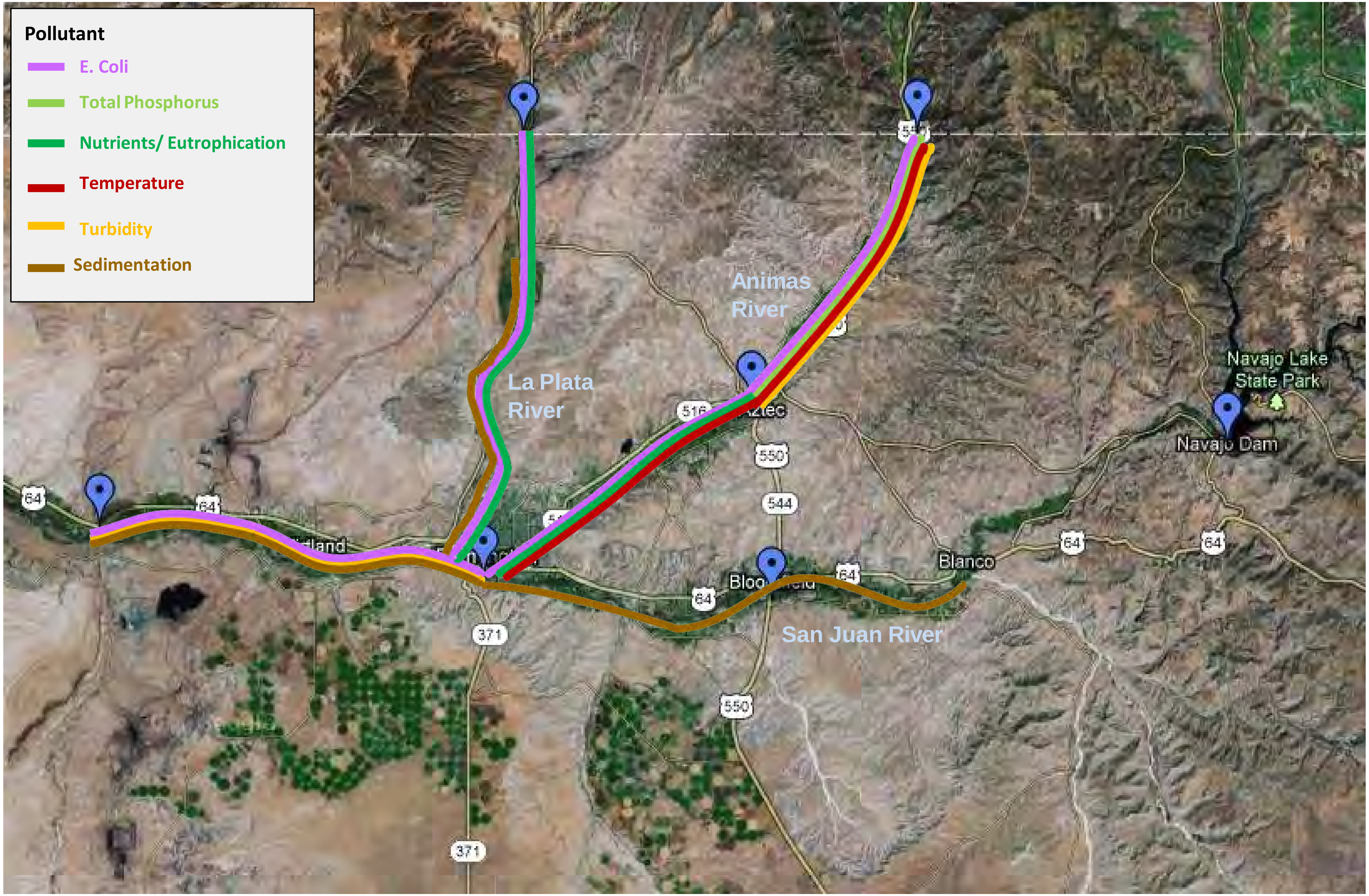
- SJWG formed 2001
- TMDL released by NMED 2010

What is the trend over time?

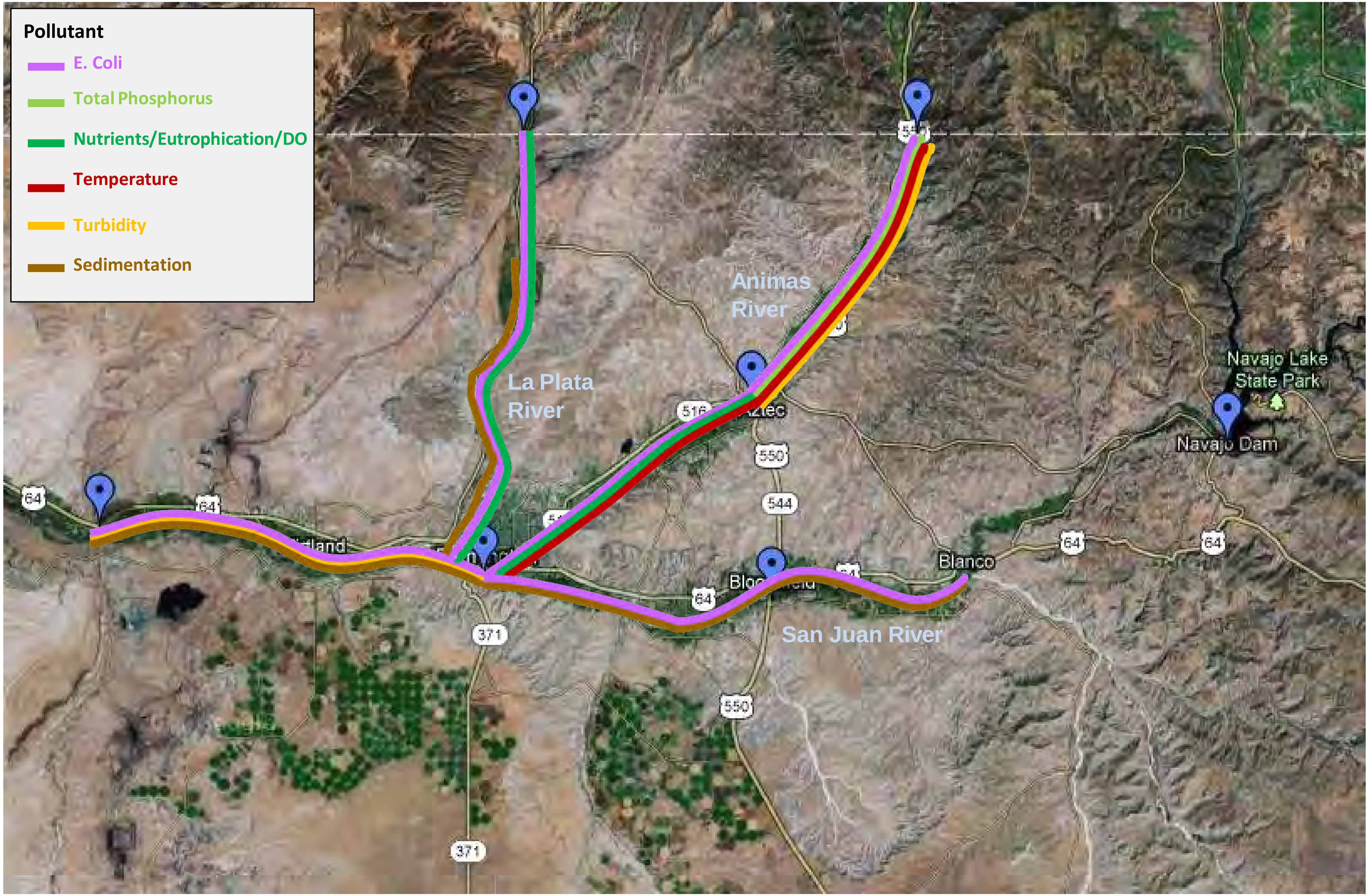
NM Clean Water Act 303(d) List of Water Quality Impairments for 2012



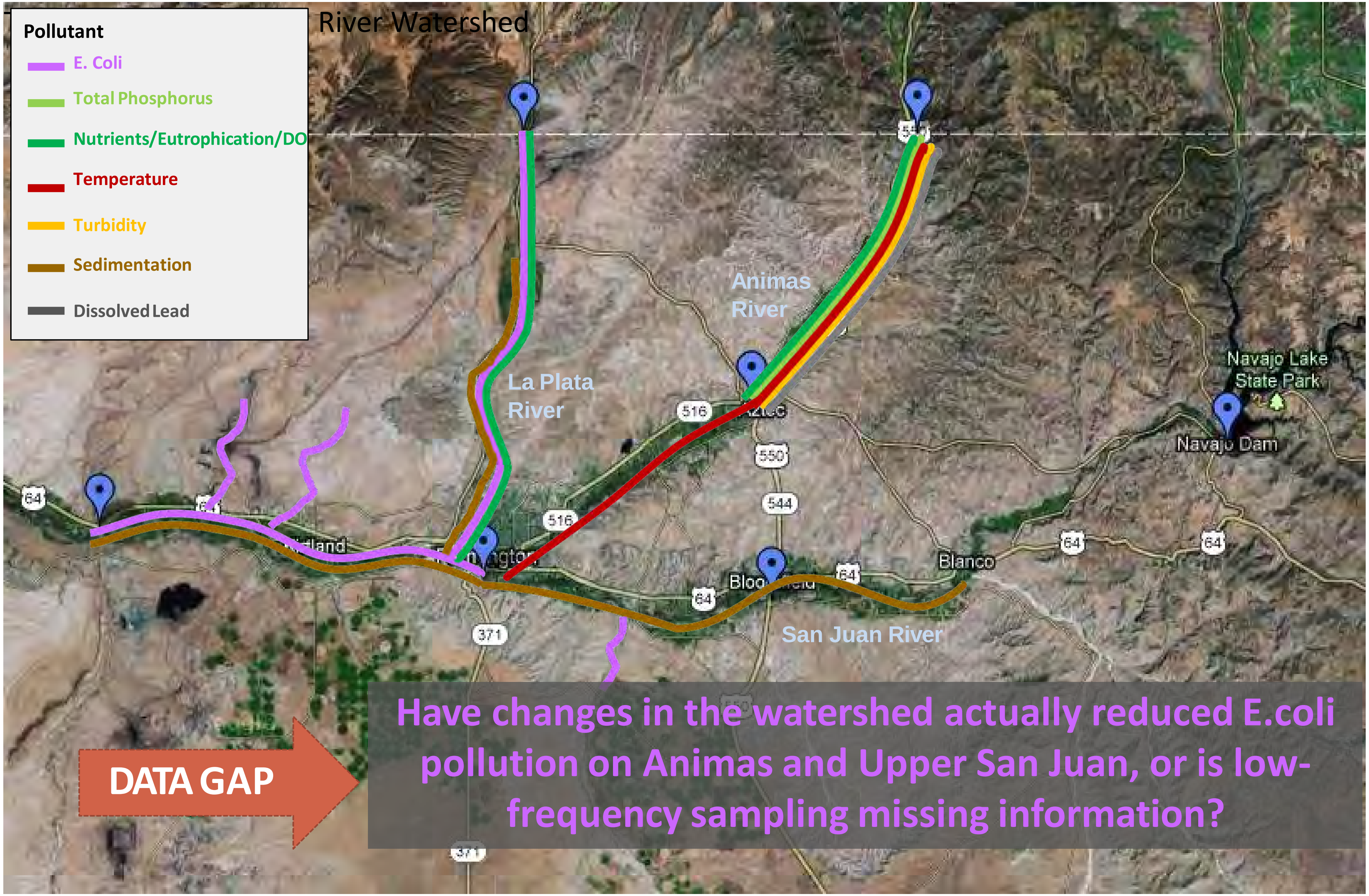
NM Clean Water Act 303(d) List of Water Quality Impairments for 2014-2016



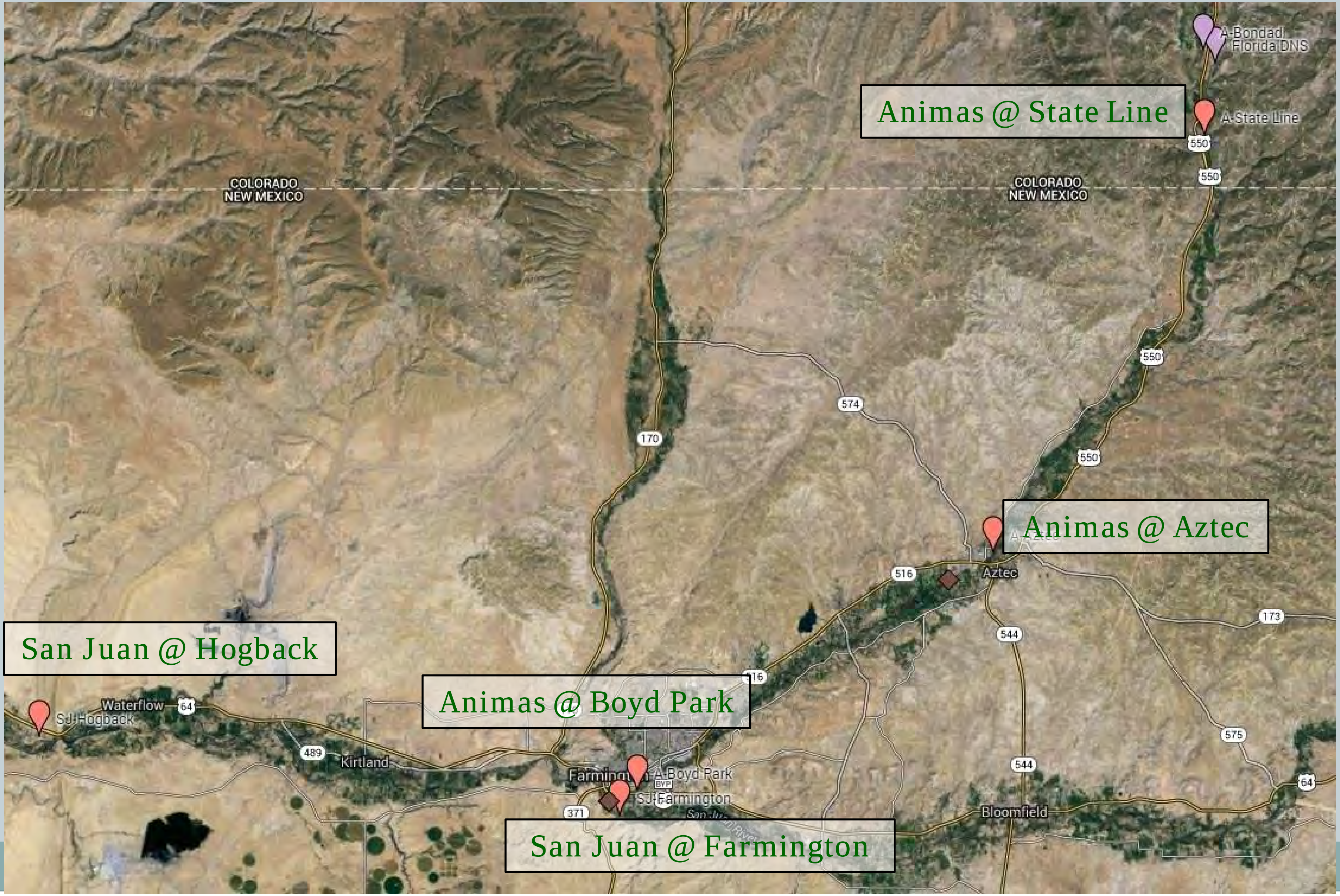
Clean Water Act 303(d) List of Water Quality Impairments for 2016-2018



NM Clean Water Act 303(d) List Proposed Changes to Water Quality Impairments for 2020-2022



Sampling Sites



Sampling Season: April – October 2013 & 2014

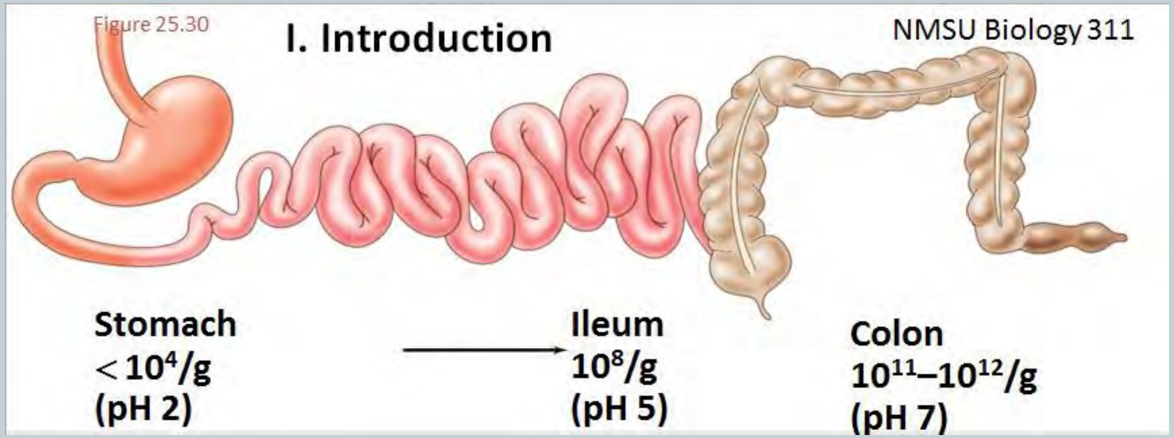
Start of Irrigation

Spring Runoff

Summer Low Flow

Monsoon Runoff

Fecal Indicator Bacteria

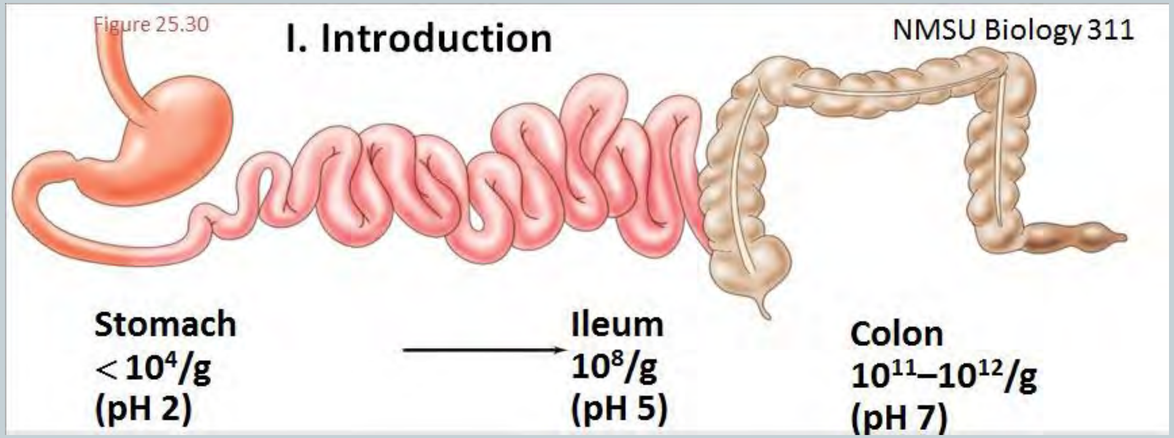


The bacteria *Bacteroides* and *E. coli* are natural inhabitants of warm-blooded animals such as humans, cattle, and birds.

Due to the unique biochemical environment in the G.I. tract of different animals, gut bacteria have become adapted to their animal "host." There are genetic differences in bacteria from different animals.

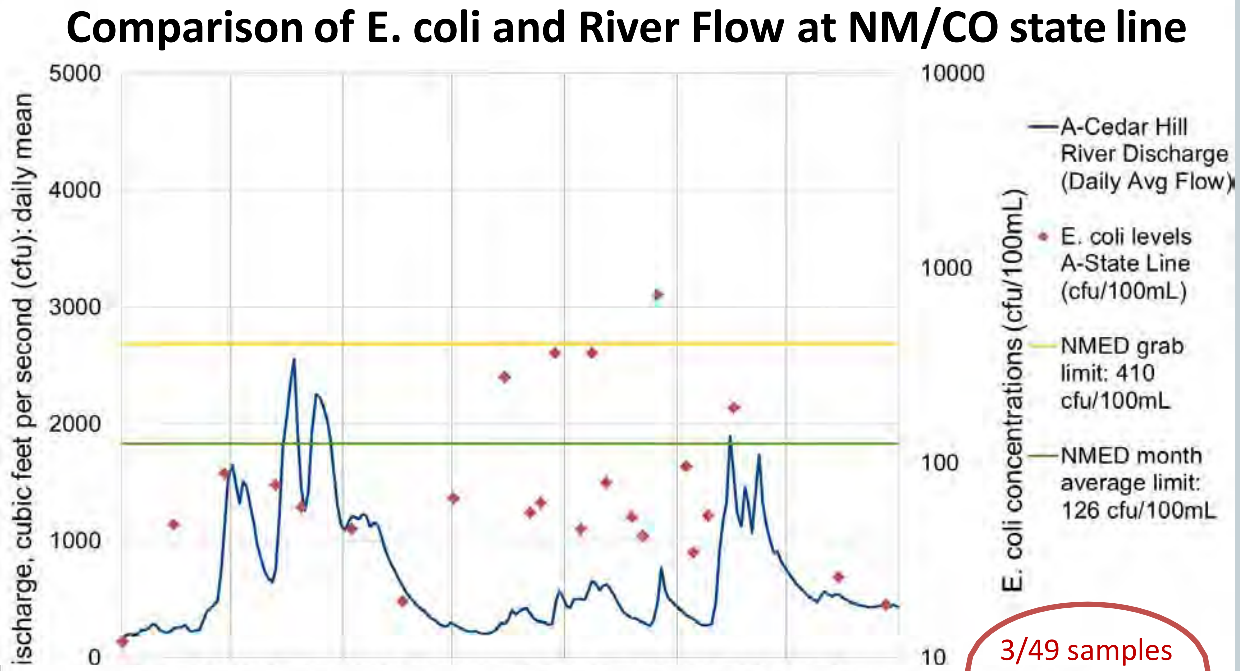
Thus, it is possible to track the source of gut bacteria back to its animal host using genetic analyses.

Fecal Indicator Bacteria

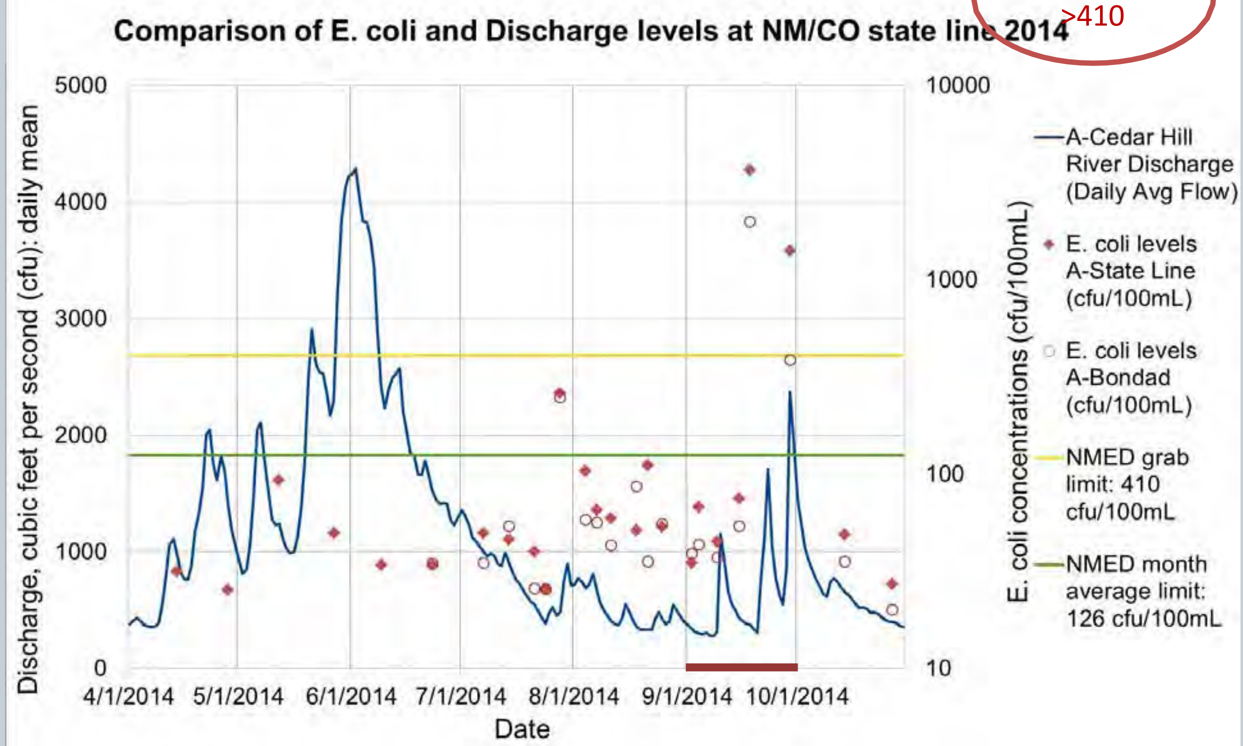


Bacteroides:
Makes up to 20% of the mass in fecal material (E. coli less than 1%). Bacteroides are strict anaerobes so less likely to grow once they exit the intestinal tract. Samples used to ID host sources.

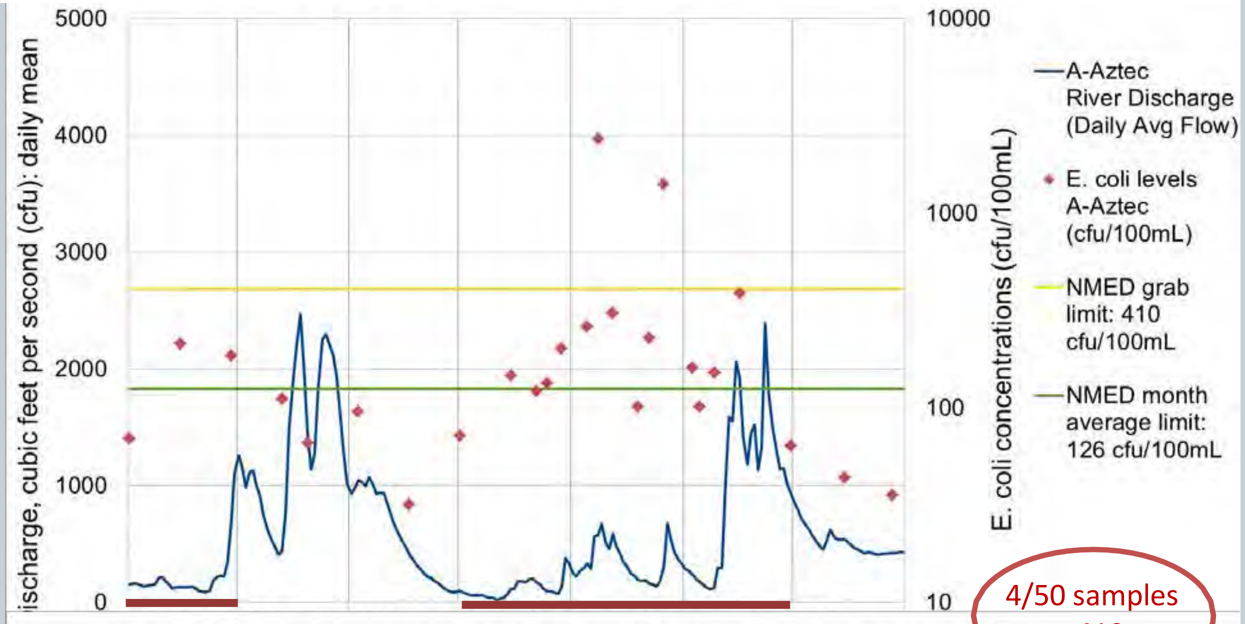
E. coli:
The most widely used fecal indicator bacteria. Infamous O157:H7 strain is virulent, but most strains are harmless. Samples directly comparable with standards used to determine bacteria impairment.

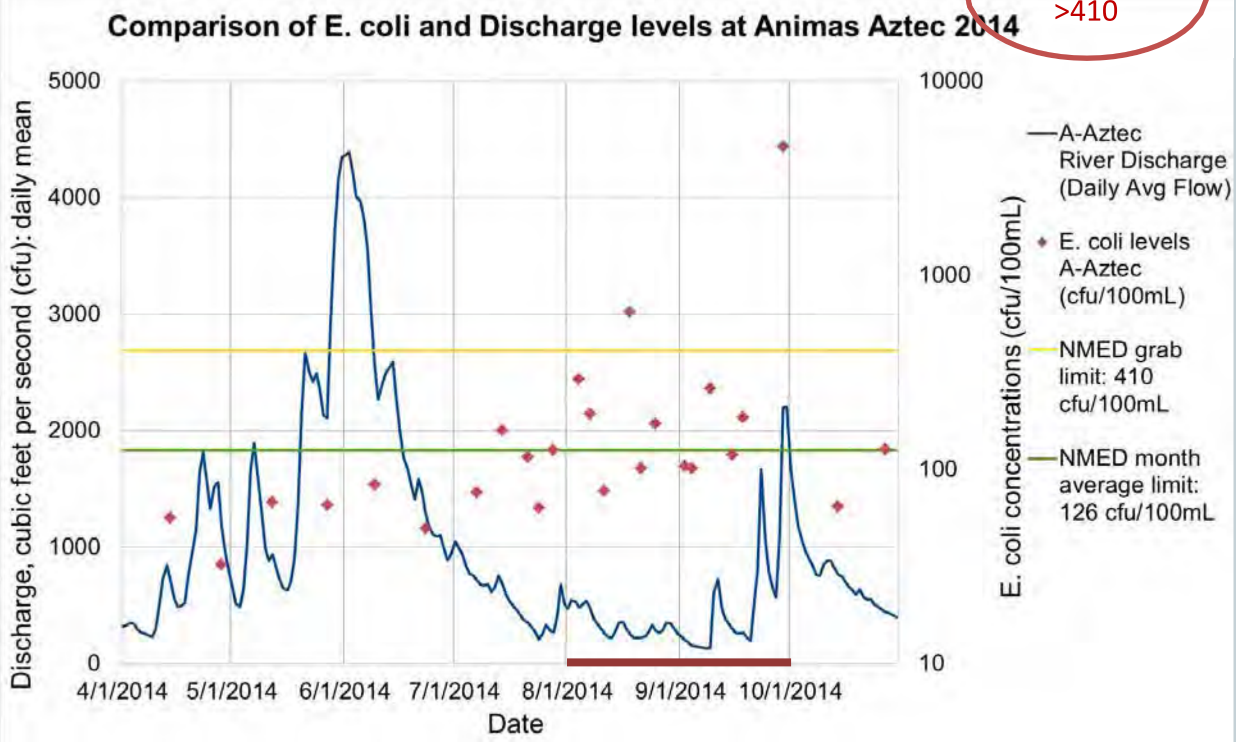


3/49 samples >410

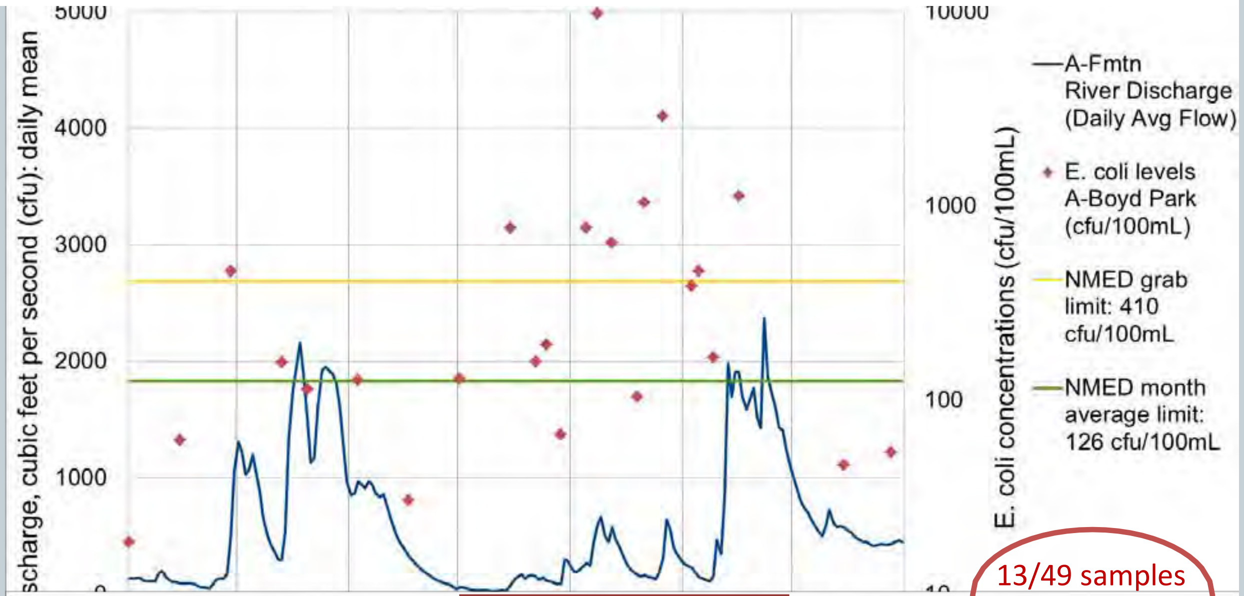


Comparison of E. coli and River Flow in Animas at Aztec

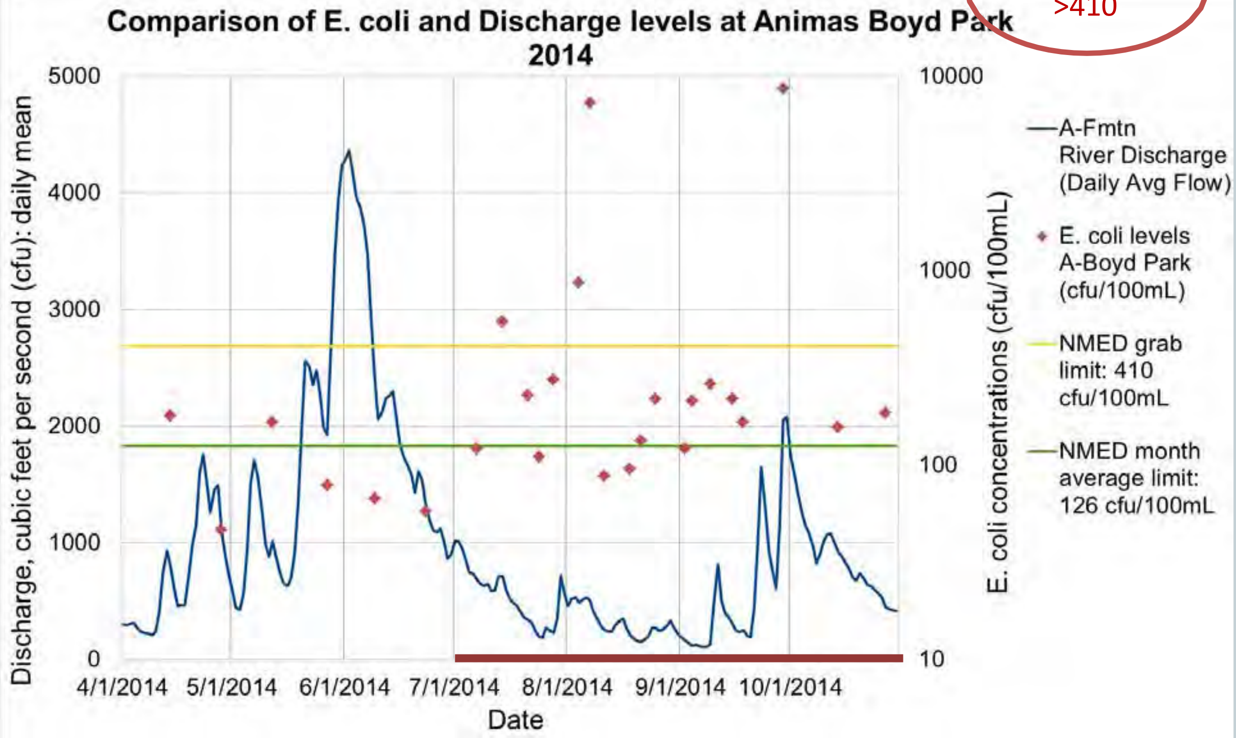




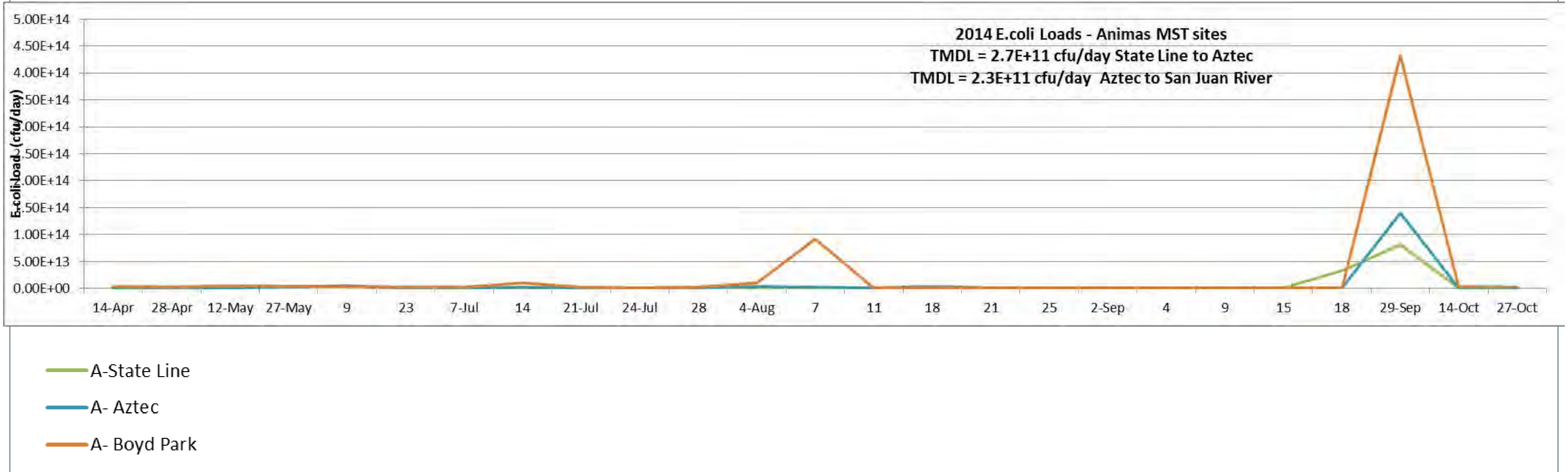
Comparison of E. coli and River Flow in Animas at Boyd Park



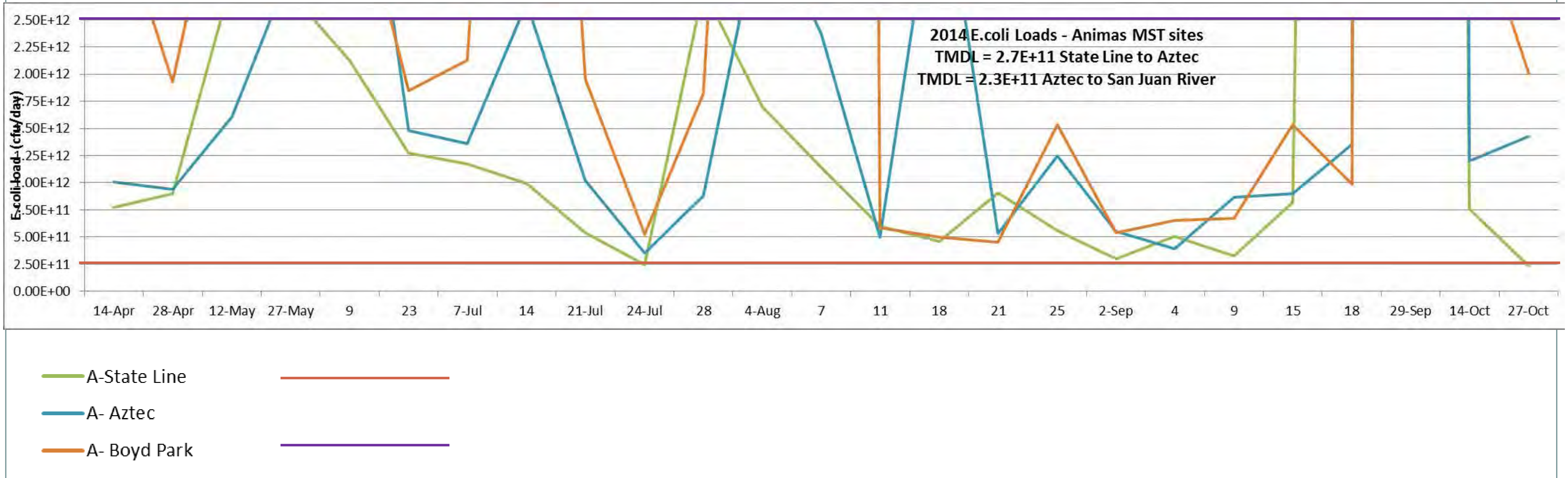
13/49 samples >410



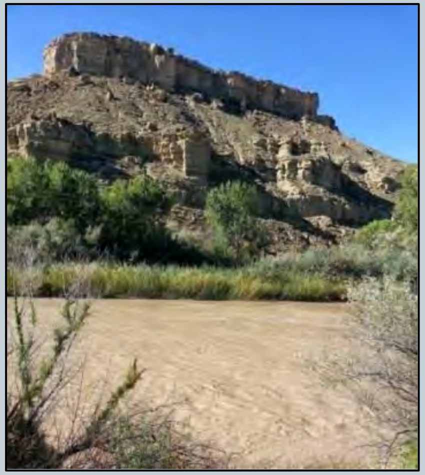
How did 2014 Animas E.coli loads compare to TMDLs?

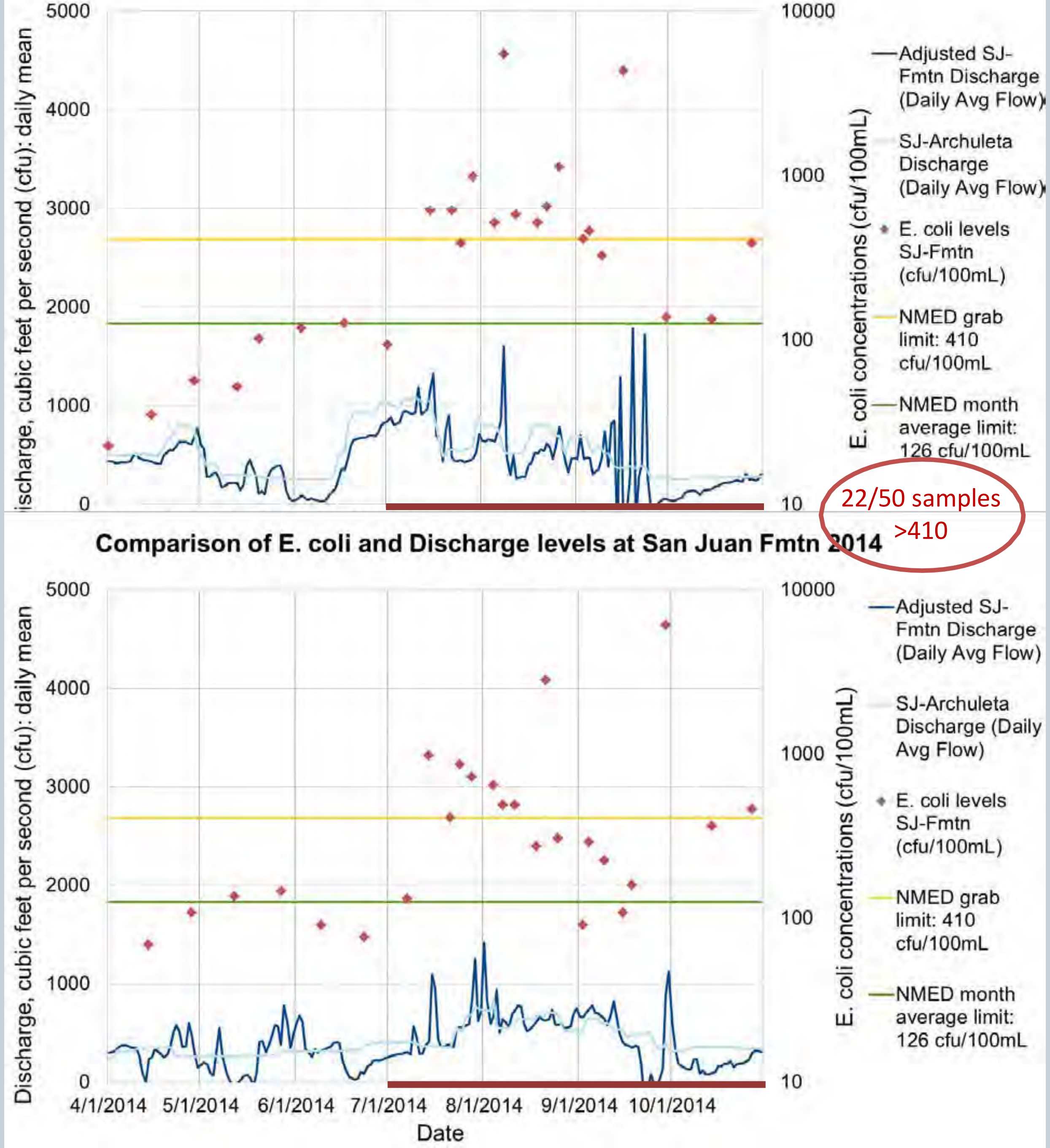


Animas *E.coli* frequently 10 times greater than target loads

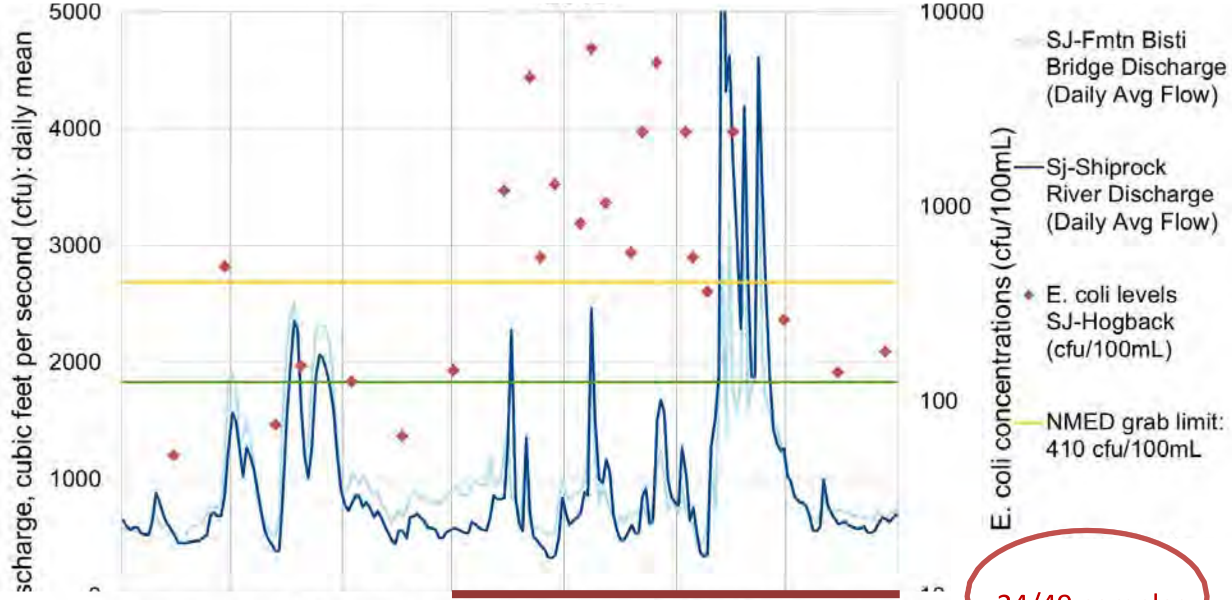


Comparison of E. coli and River Flow in San Juan at Farmington

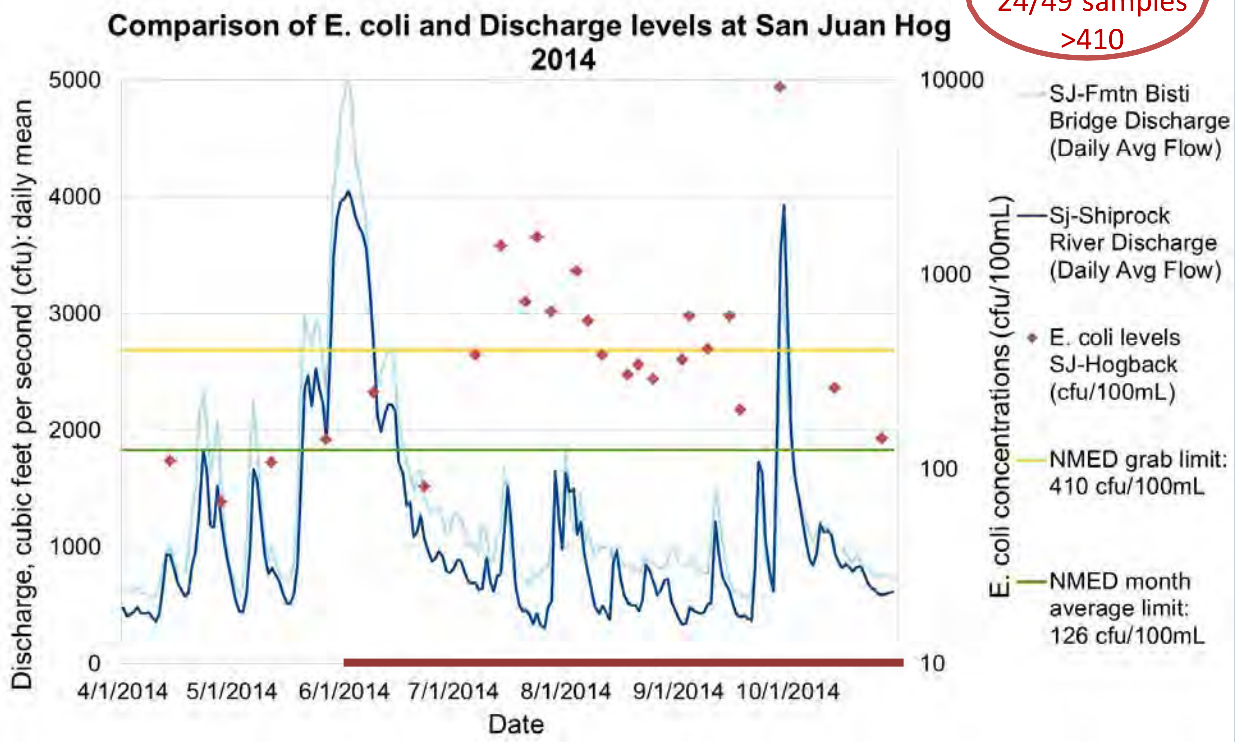




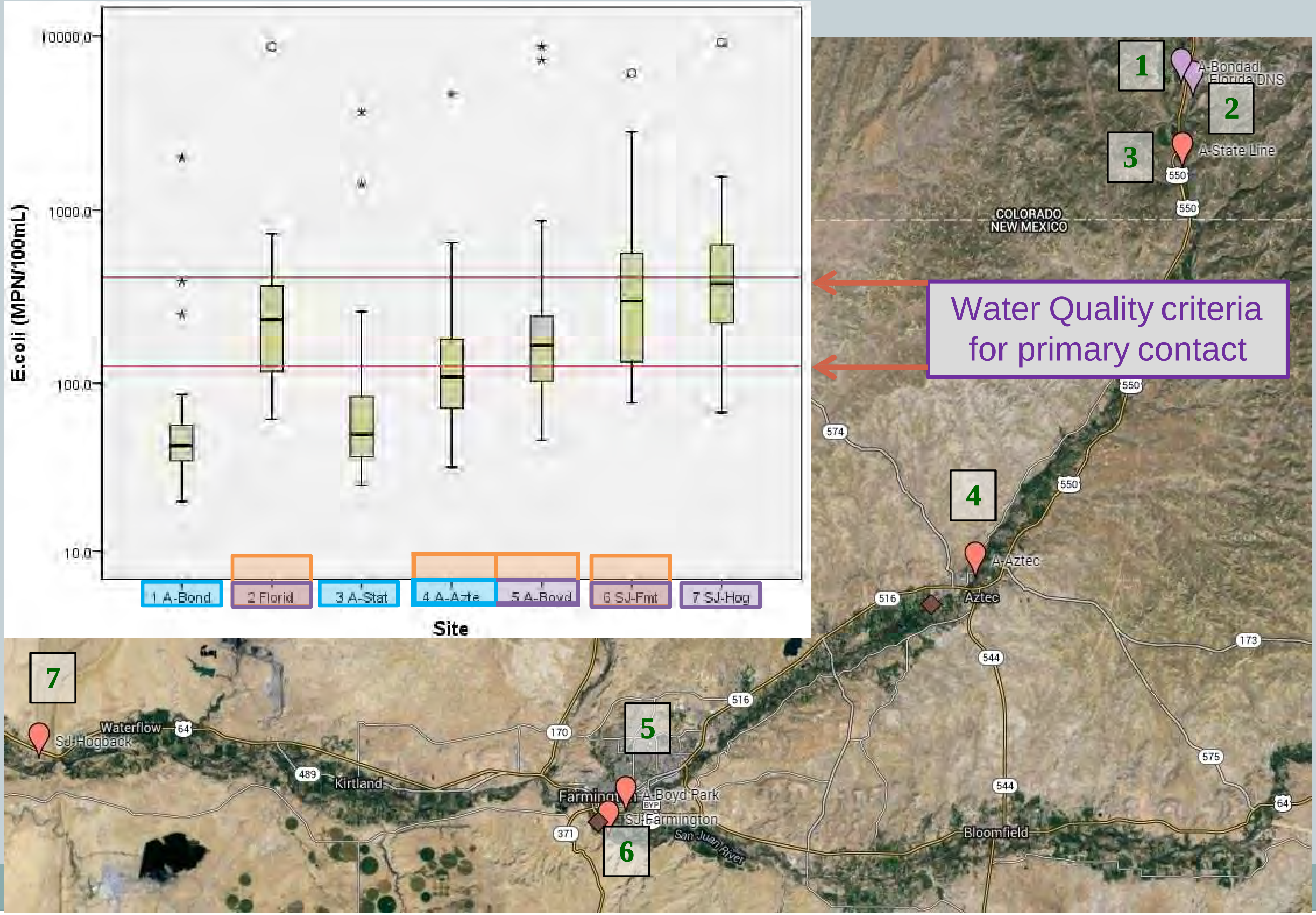
Comparison of E. coli and River Flow in San Juan at Hogback



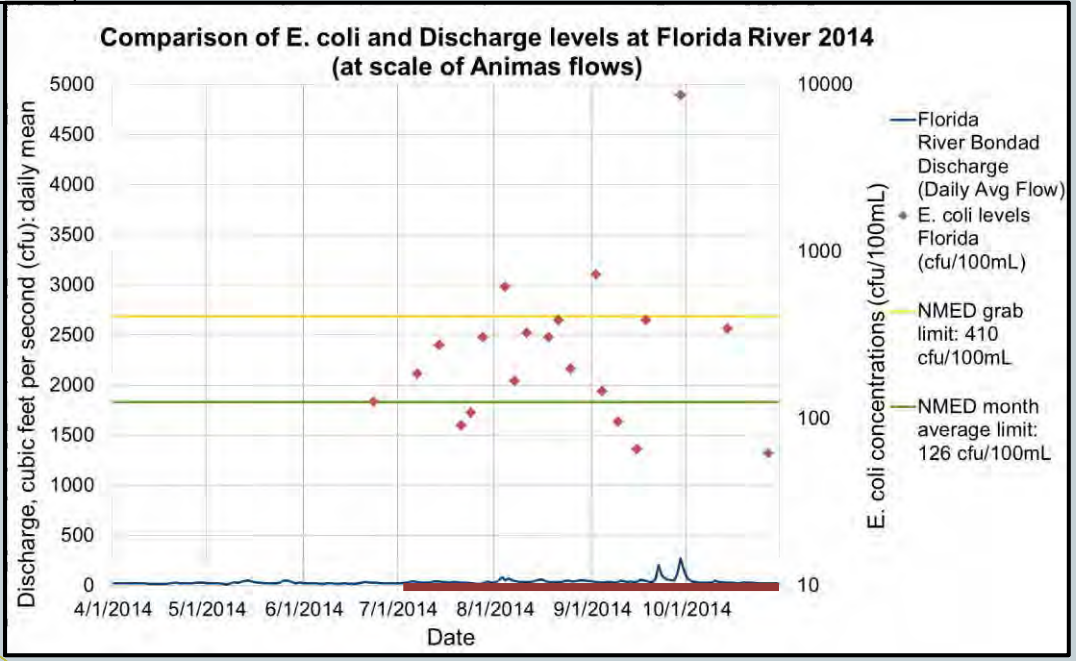
24/49 samples >410



E.coli Quantification



Florida River



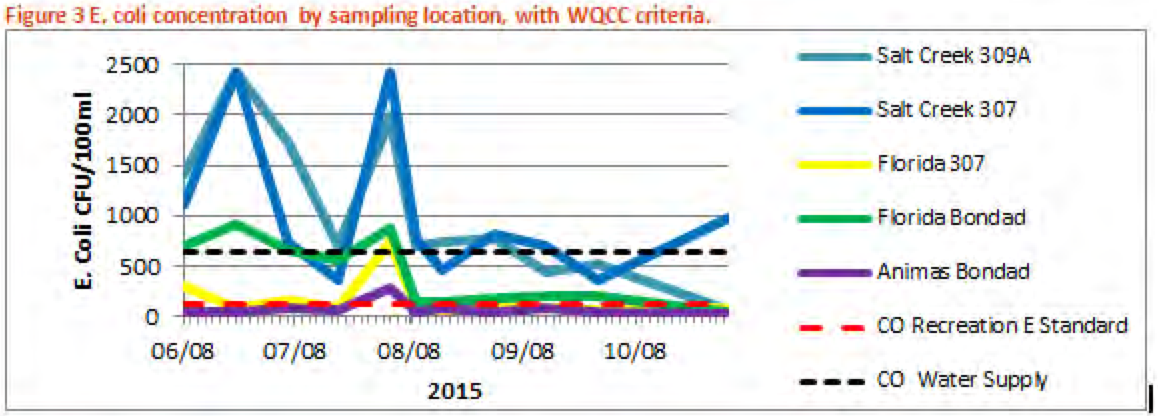
Picture

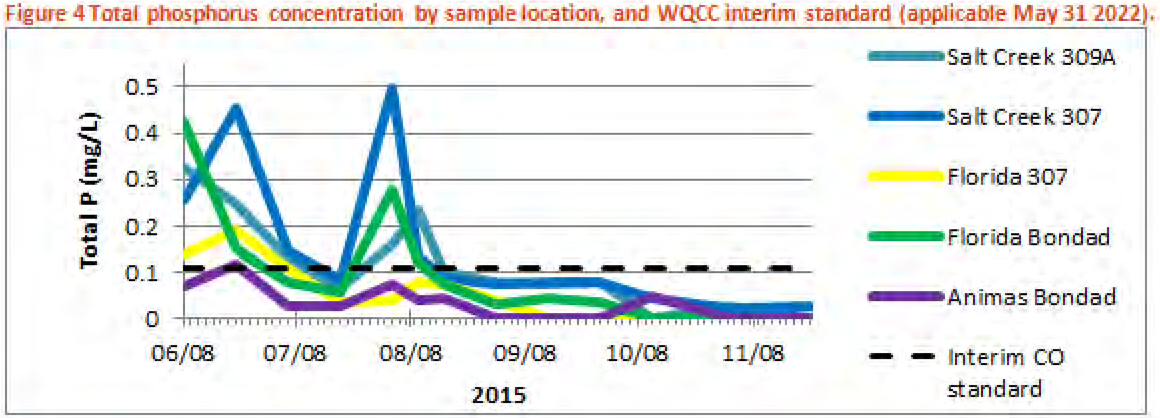
- E.Coli load in the Florida River ranged from 3% - 78% of the E.coli load downstream of the Animas-Florida confluence

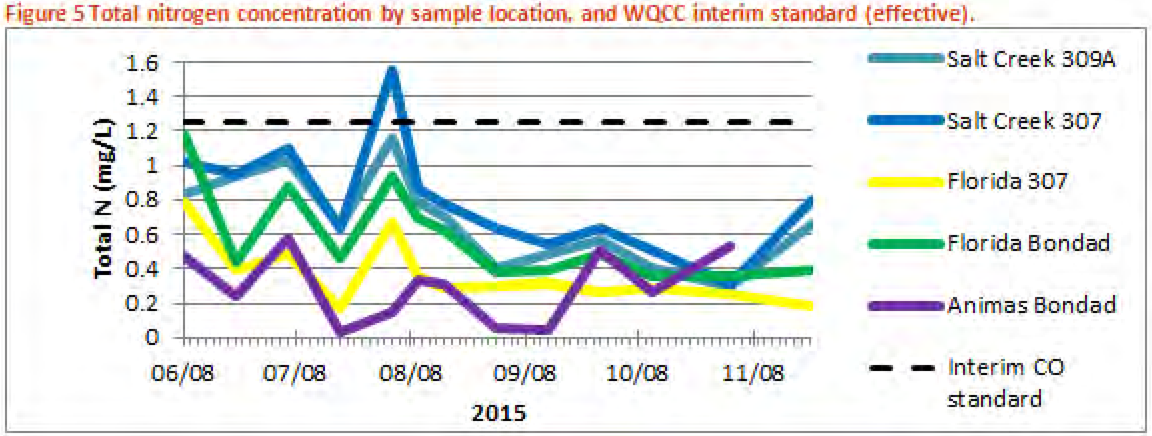
  Average load contribution was 28% despite only contributing an avg. 8% of the flow

Florida River

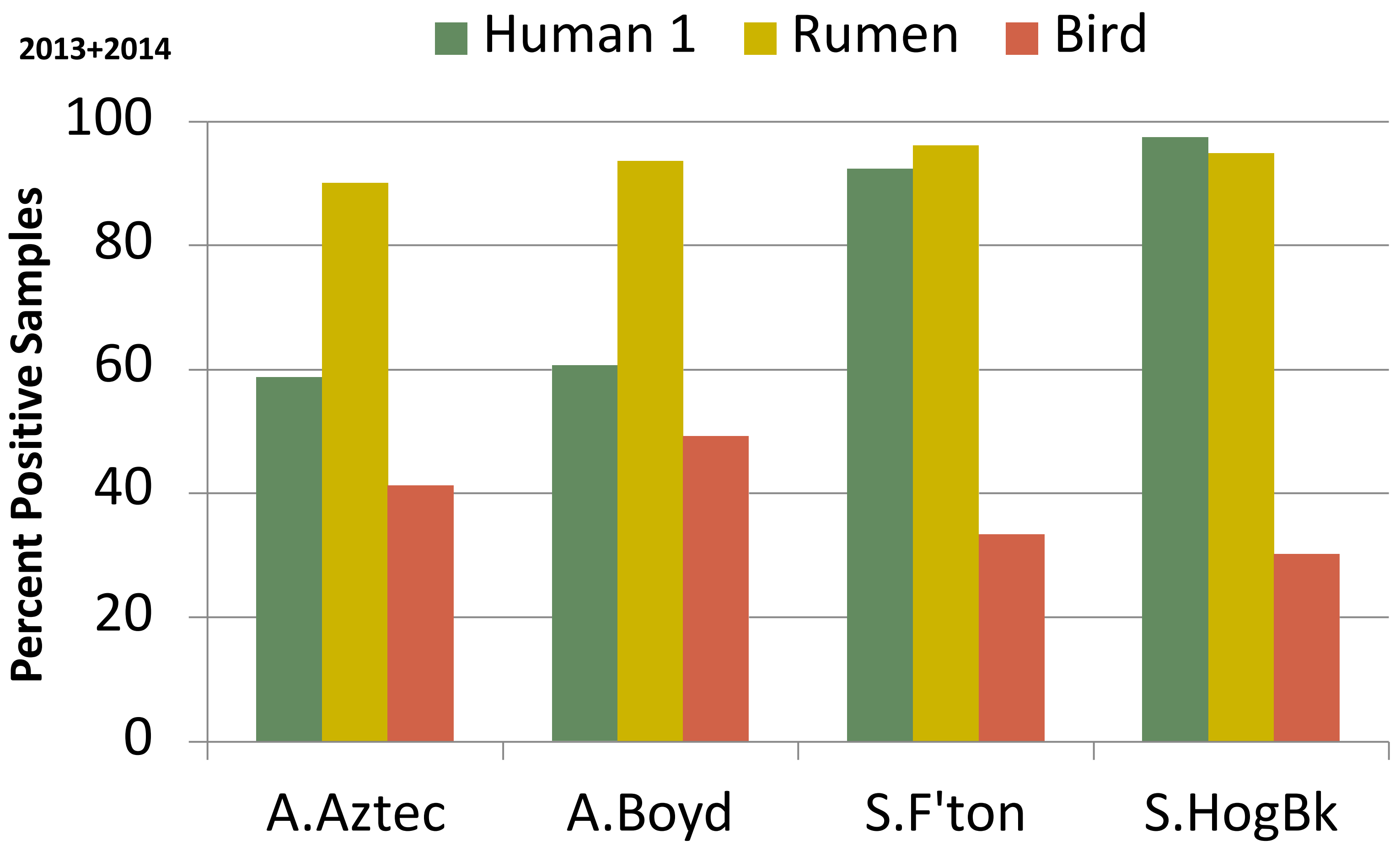
2015 sampling within the Florida drainage indicates Salt Creek as a contributor of *E.coli*, TN, and TP







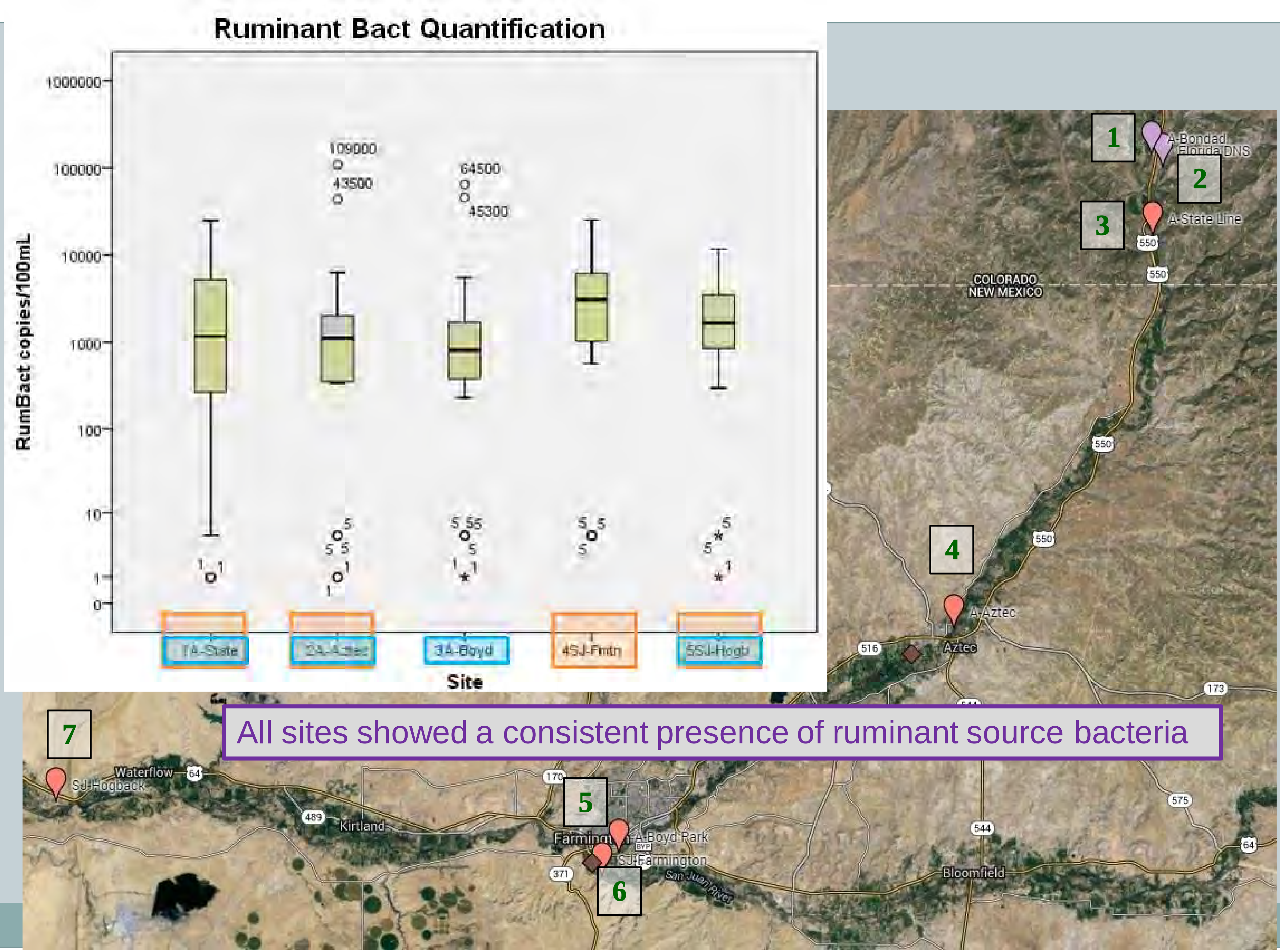
Microbial Source Tracking Two-Year Averages: % of Positive Samples



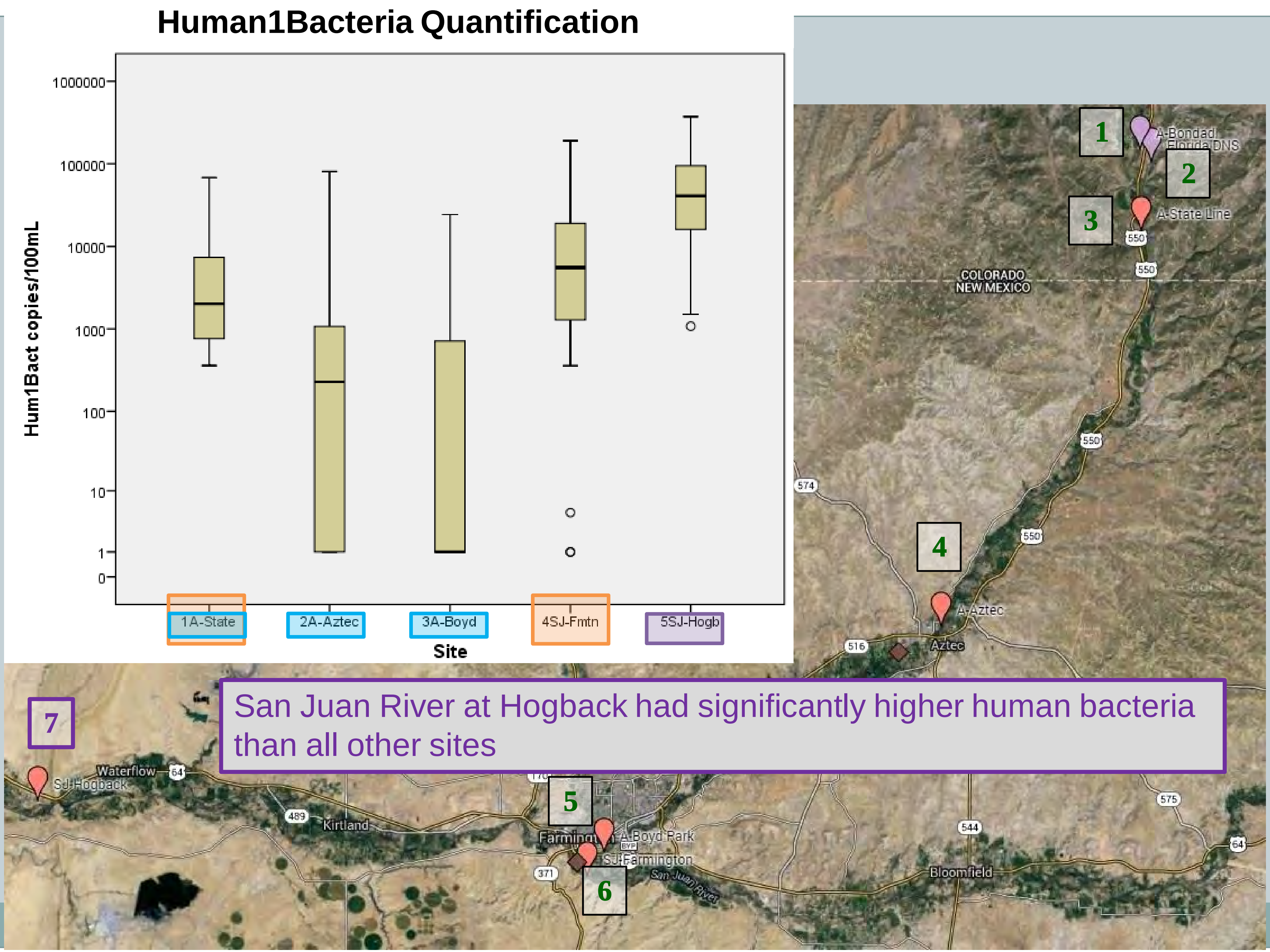
(n = 78 – 80 samples for H1 and Bird, n=54-56 for Rumen)

Bird and Ruminant contamination is similar at all sampling sites

Human contamination more frequent on San Juan River than Animas River



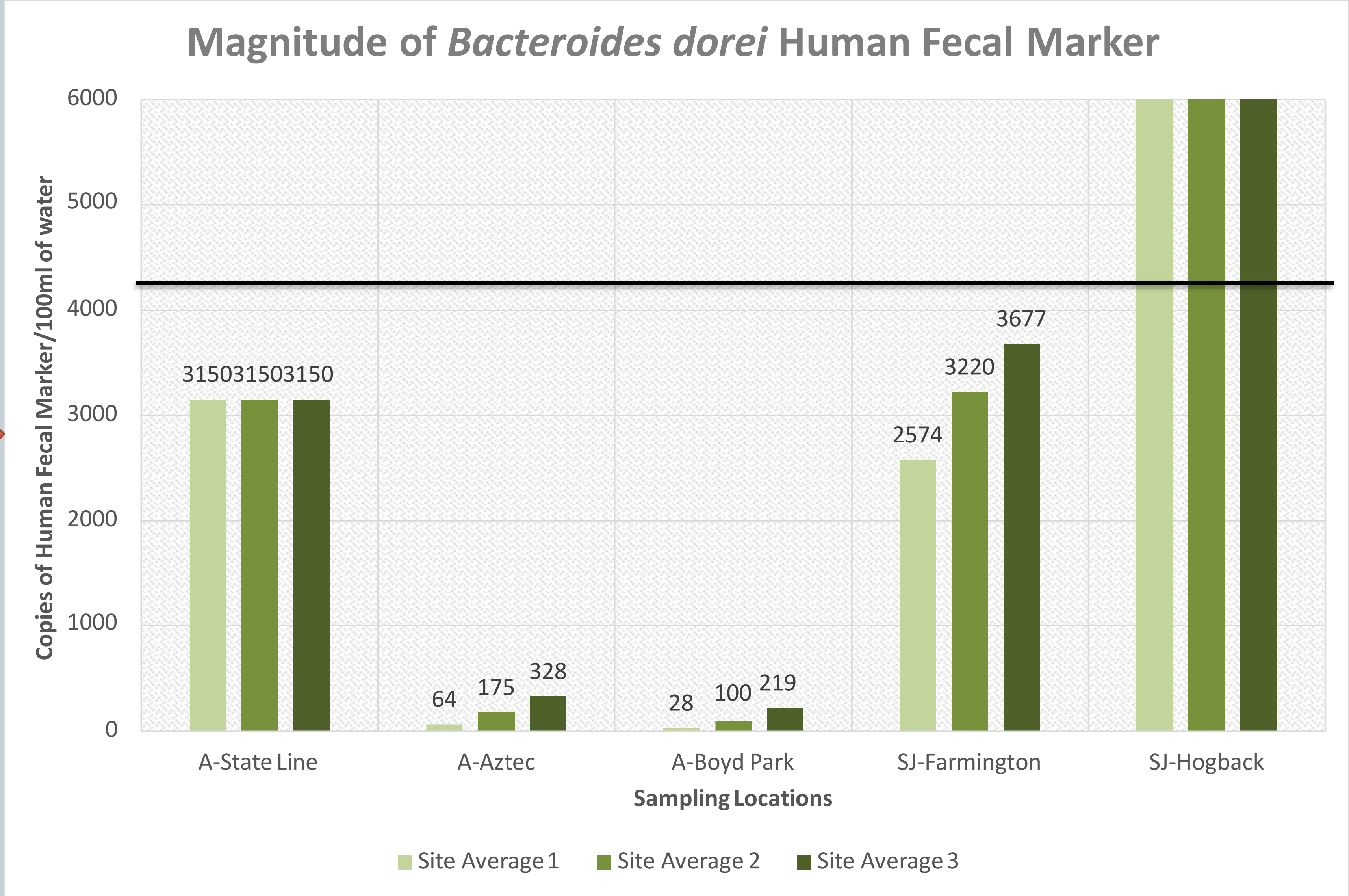
All sites showed a consistent presence of ruminant source bacteria



San Juan River at Hogback had significantly higher human bacteria than all other sites

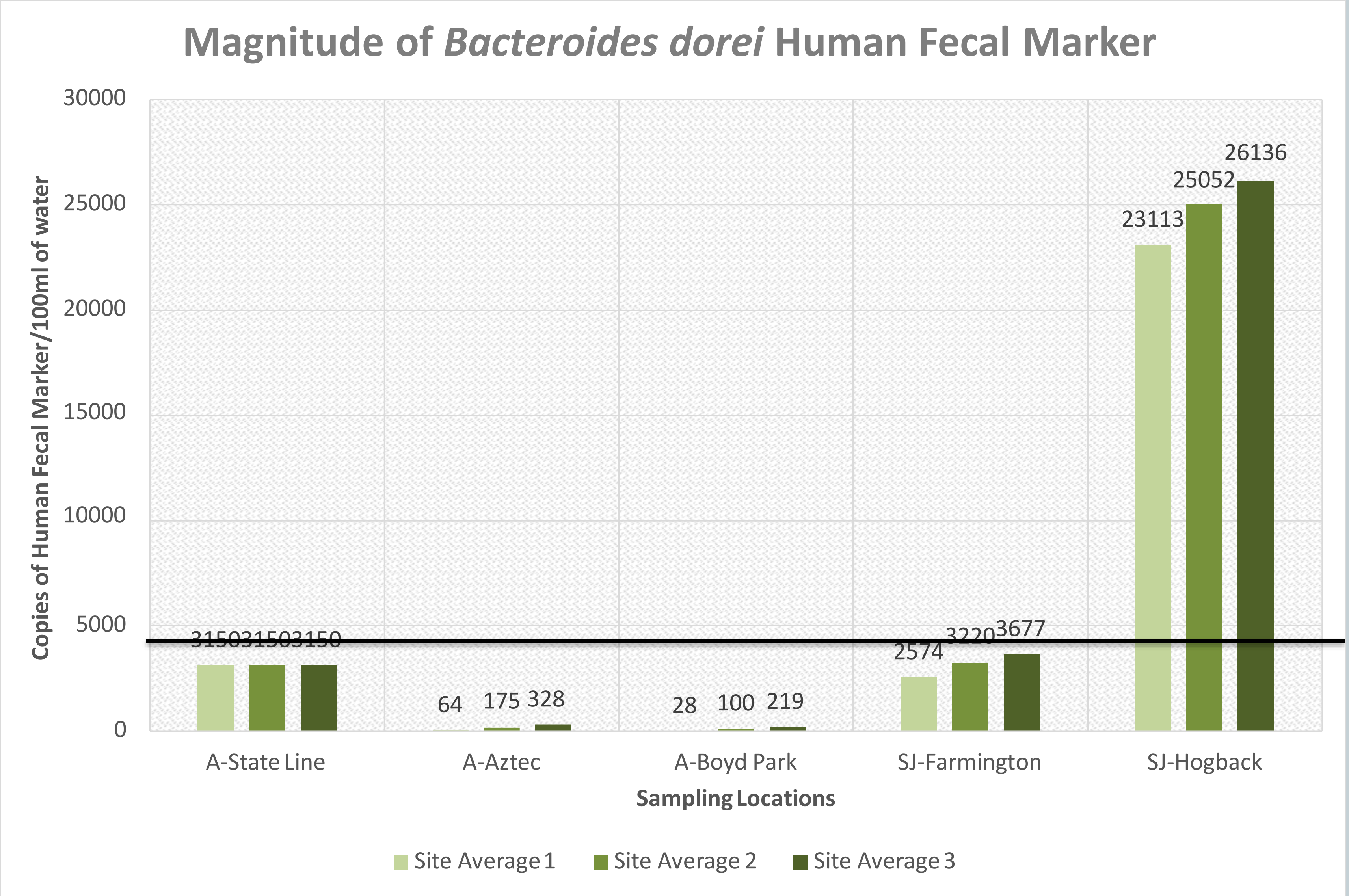
How Much Are Humans Contributing *Bacteroides dorei* to Our Rivers?

DATA GAP



4200 copies/100ml is a benchmark illness rate of 30 illnesses per 1000 swimmers

How Much Are Humans Contributing *Bacteroides dorei* to Our Rivers?



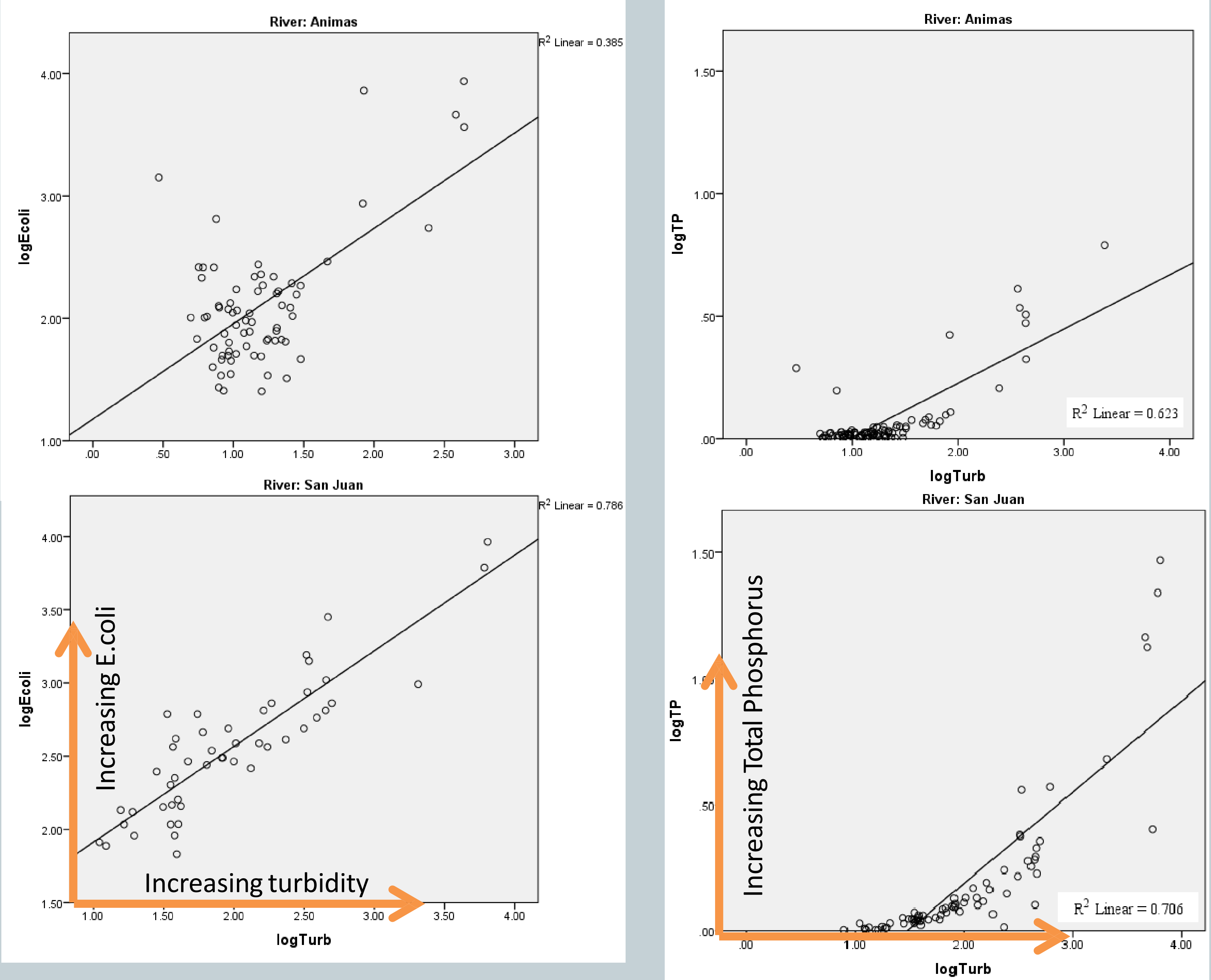
4200 copies/100ml is a benchmark illness rate of 30 illnesses per 1000 swimmers

How would specific bacteria sources travel to the river?

Biological Source	Source Activity Pathway to River:	Groundwater	Direct Discharge	Irrigation Return	Stormwater
Human	Faulty septic tanks	X			X
	Illegal septic (straight pipes, cess pits, etc.)	X	X	X	X
	Leaking sewer pipes	X	X		
	Illegal dumping – waste disposal companies		X		X
	Illegal dumping – recreational vehicles		X		X
	Wastewater treatment plants		X		
	Outdoor defecation				X
Ruminant – (includes cattle, deer, elk, sheep, goats)					
	Animals with direct access to river		X		X
	Grazing on irrigated fields			X	X
	Grazing in uplands and riparian areas				X
	Improper manure disposal		X		X

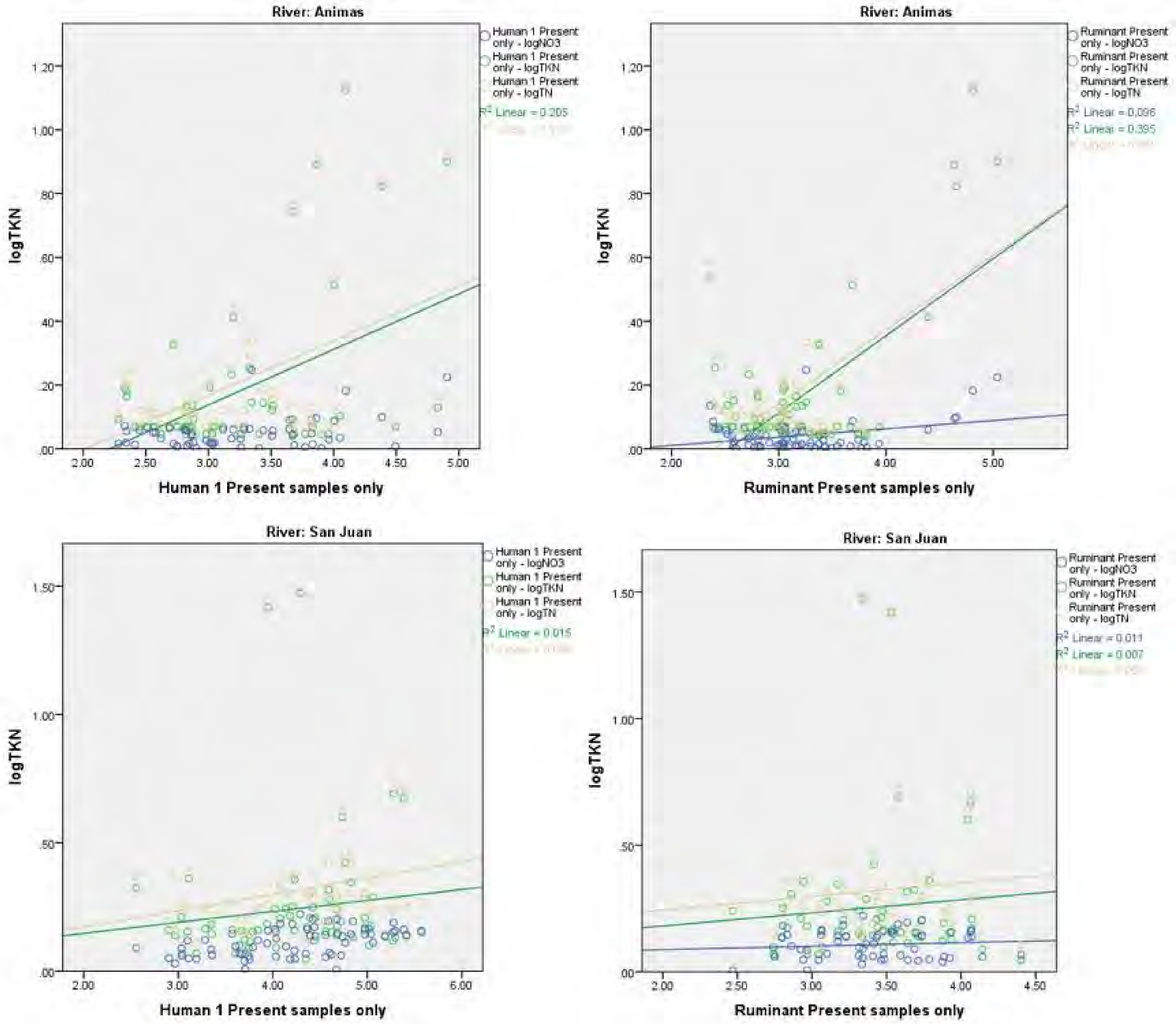
Can we relate trends in the data back to specific pathways and source activities?

Hypothesis	Expected trend in the data
Storm runoff is a primary pathway for bacteria to reach the rivers	-E.coli, TP, and TKN increase with turbidity -High E.coli, TP, and TKN at highest flows -High Human and/or Ruminant bacteria at highest flows


River: Animas
R^2 Linear = 0.385
logEcoli
4.00
3.00
2.00
1.00
.00
.50
1.00
1.50
2.00
2.50
3.00
River: Animas
logTP
1.50
1.00
.50
.00
R^2 Linear = 0.623
.00
1.00
2.00
3.00
4.00
logTurb
River: San Juan
R^2 Linear = 0.786
logEcoli
4.00
3.50
3.00
2.50
2.00
1.50
Increasing E.coli
Increasing turbidity
1.00
1.50
2.00
2.50
3.00
3.50
4.00
logTurb
River: San Juan
logTP
1.50
.50
.00
Increasing Total Phosphorus
R^2 Linear = 0.706
.00
1.00
2.00
3.00
4.00
logTurb

E.coli, Total Phosphorus, & Total Nitrogen all positively correlated with turbidity, but no clear trend with human and ruminant markers

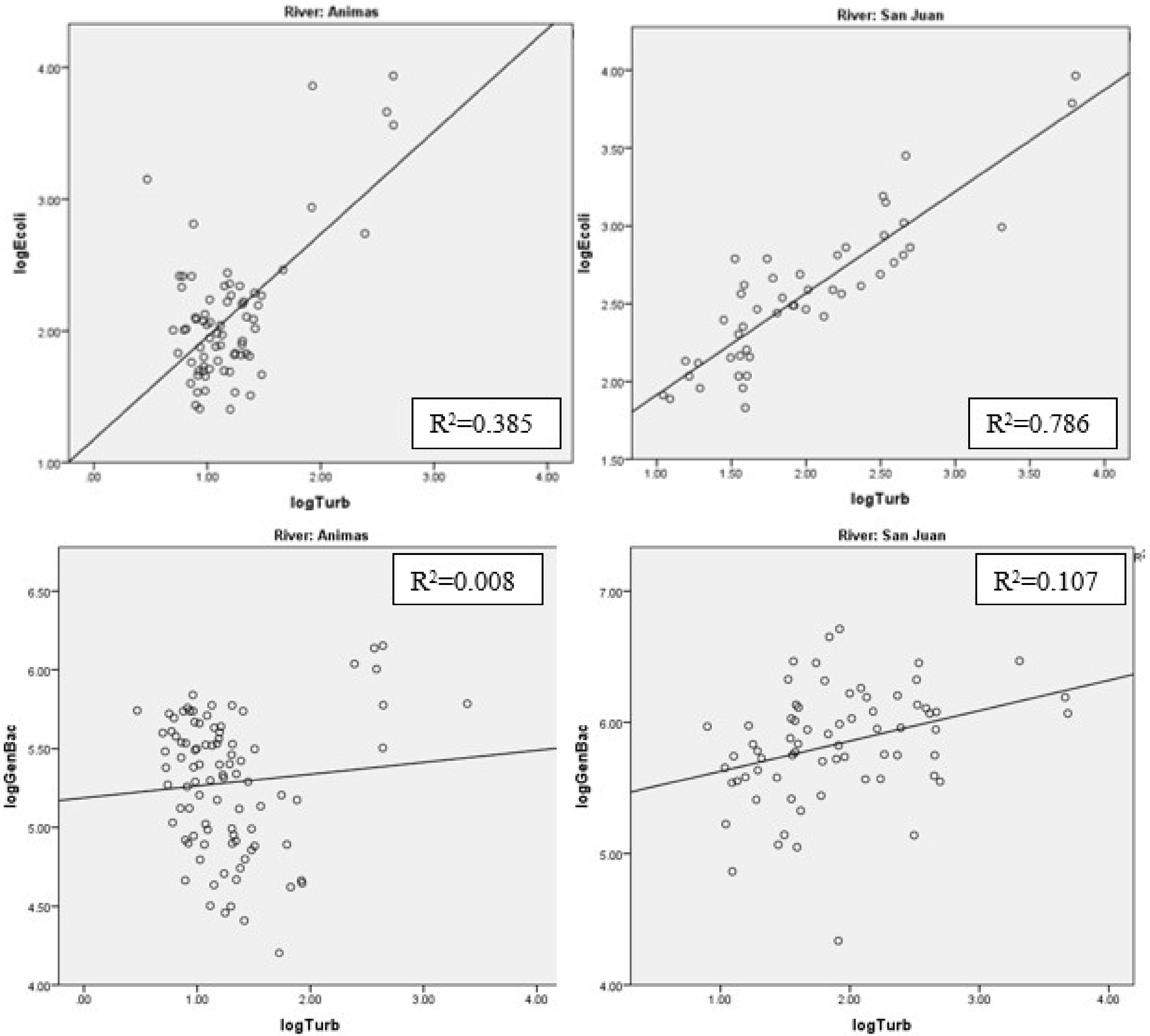
DATA GAP



Frequent presence of multiple bacteria sources clouds relationship to both stormwater and base flow – more analysis needed.

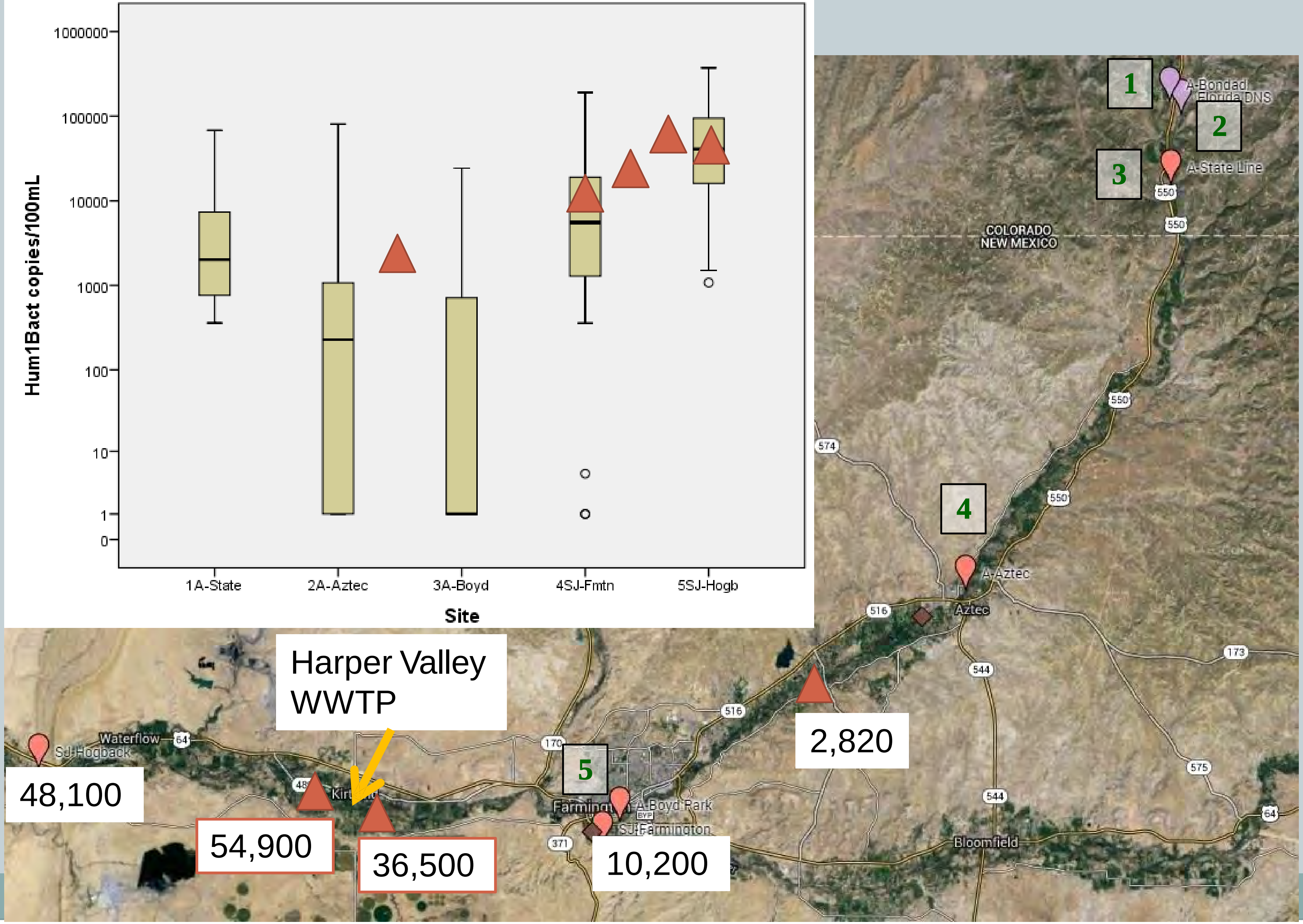
DATA GAP

- Connection between E.coli concentrations and Bacteroides
- Difference in assumptions re: human health risk based on E.coli vs. Bacteroides
- Patterns in Bacteroides concentration (general, human ruminant) as related to flow, turbidity, other parameters
- Relationship between E.coli and “new” USGS continuous turbidity measurement



Dec 2016 Targeted Sampling

Human1Bacteria Quantification Dec 2016



Conclusions and Opportunities for Future Research and Projects

Conclusions

- Bacteria pollution is reaching the Animas and San Juan Rivers via multiple sources (human, ruminant) and pathways (stormwater, direct, groundwater)
- **All available data point to the San Juan River between Farmington and Hogback having a more severe bacteria impairment than the Animas or reach of the San Juan upstream of Farmington**

Data Gaps and Suggestions for Future Work

- What is the extent of bacteria pollution downstream of Hogback? Are there hotspots of primary contact in this reach that should be priorities for future outreach and targeted sampling?

- What is the relationship between E.coli and Bacteroides concentrations?
  - At the NM- CO/SUIT boundary, what is contributing to significant concentrations of human bacteria but low concentrations of E.coli?
  - How much of human fecal signal could be coming from treated wastewater?
  - How long can dead anaerobic Bacteroides be detected in the environment (ie: detectable but now longer indicators of a human health risk)

- Is bacteria pollution upstream of Farmington improving, or just hard to capture in monthly baseflow sampling?