Fecal Bacteria Source Tracking and Loading Analysis of the Green River

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Problem and Study Goals

- Problem: Fecal coliform bacteria concentrations exceed state criteria for public health protection, requiring Total Maximum Daily Load (TMDL)
- Study 1: Evaluate spatial, hydrologic, and temporal variation of concentrations and loadings for development of the watershed model and TMDL
- Study 2: Evaluate the human and animal sources of bacteria for effective implementation of the TMDL

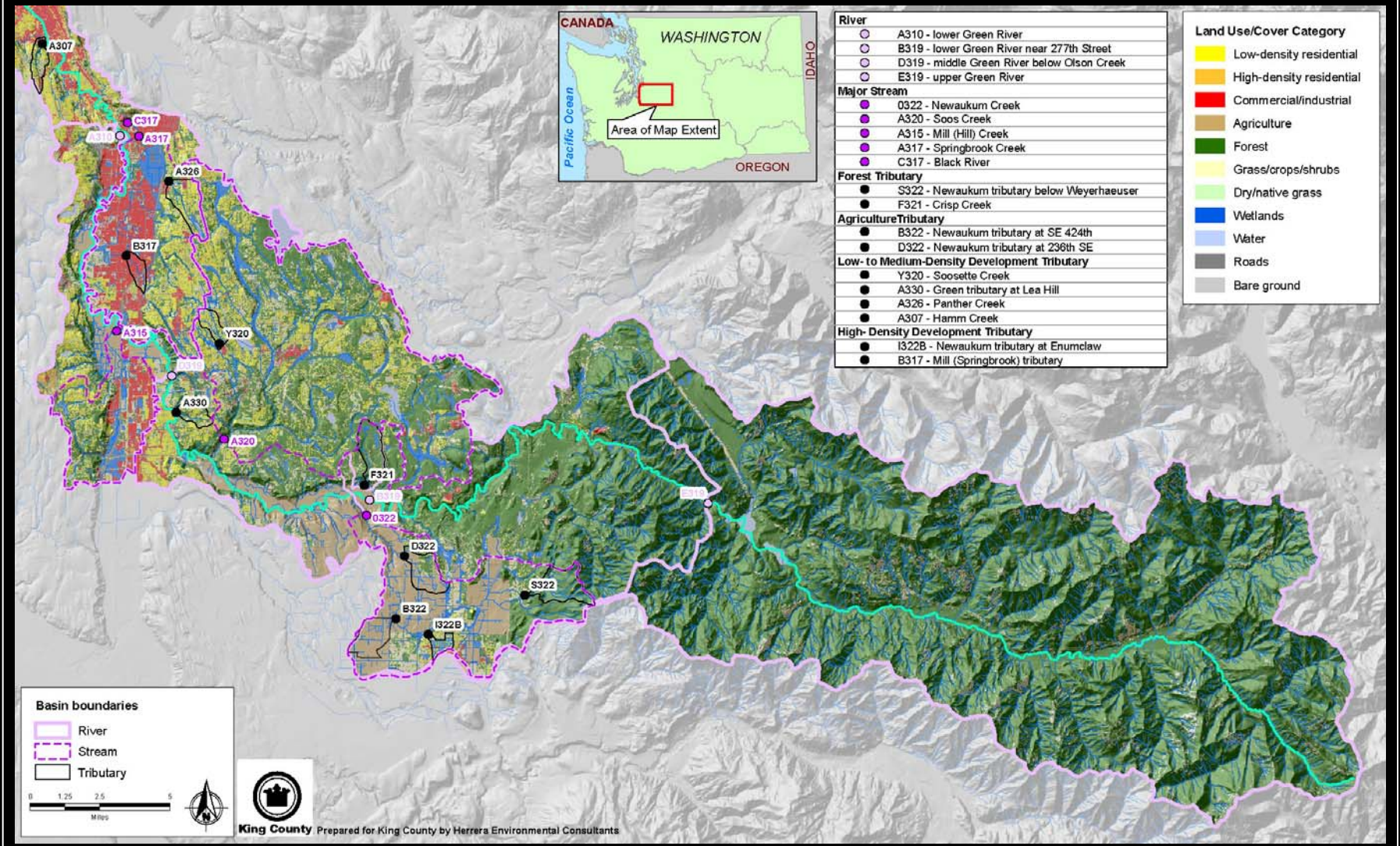
Bacteria Concentration and Loading Analysis Study Objectives

- Measure fecal coliform bacteria concentrations in storm flow and base flow at river, major stream, and tributaries representing specific land use types
- Correlate bacteria concentrations to water quality and hydrologic parameters
- Evaluate bacteria concentrations and annual areal bacteria loading rates in relation to hydrology and land use
- Data not for developing the bacteria TMDL or assessing public health risk

Microbial Source Tracking Study Objectives

- Identify sources of *E. coli* bacteria using the molecular ribotyping (genetic fingerprinting) technique at river and major stream sites
- Evaluate how human and animal sources of *E. coli* bacteria vary with hydrologic condition, season, and land use

Green-Duwamish Watershed



Study Design

	Concentration and Loading	Microbial Source Tracking
Stations		
River	2 (1 Flow)	4
Stream	5 (4 Flow)	4
Tributary	11 (8 Flow)	1
Sampling Events		
Base Flow	11 (2 years)	14 (3 years)
Storm Flow	13 (2 years)	15 (3 years)
Grab Samples		
Base Flow	332	284 (770 isolates)
Storm Flow	551	280 (733 isolates)

Monitoring Site Schematic Diagram

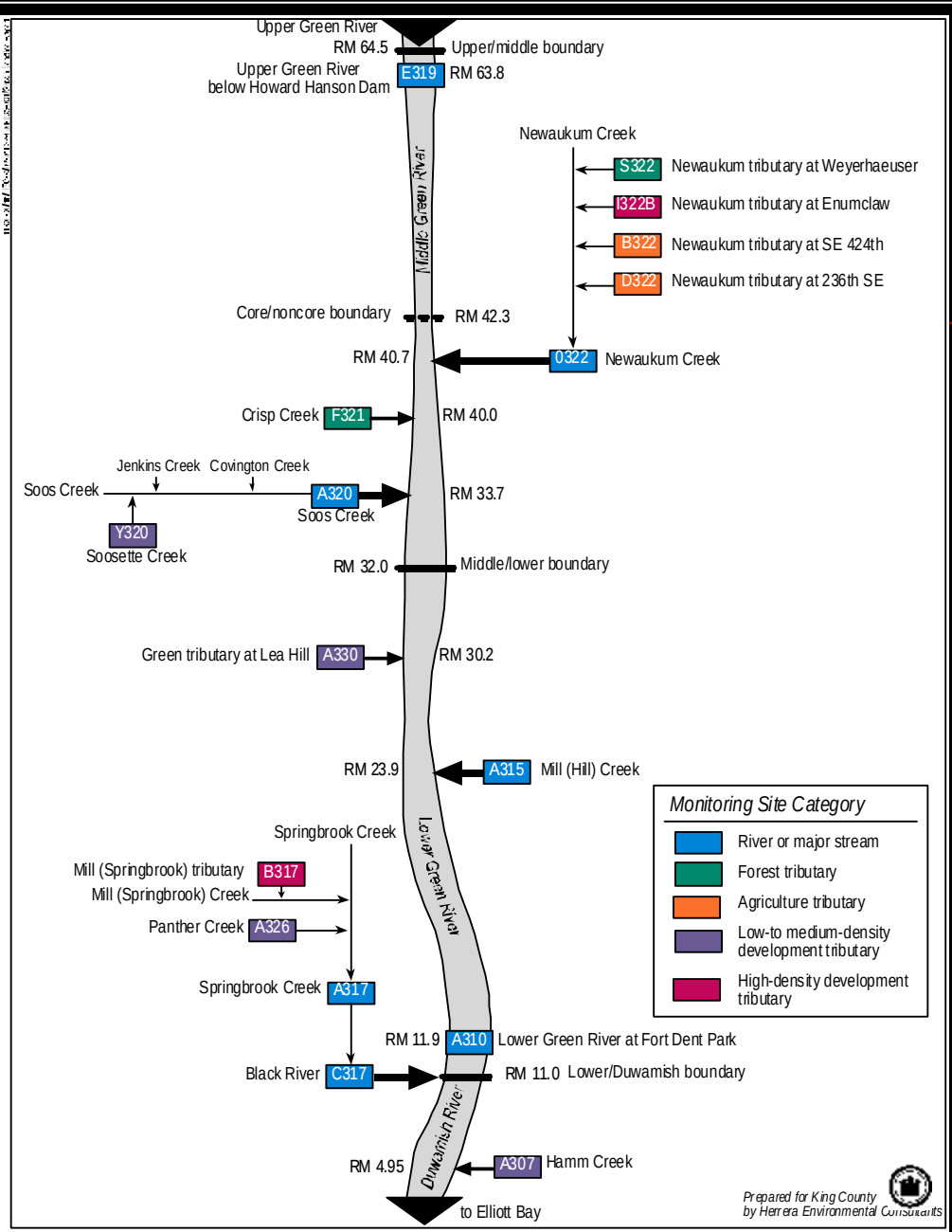
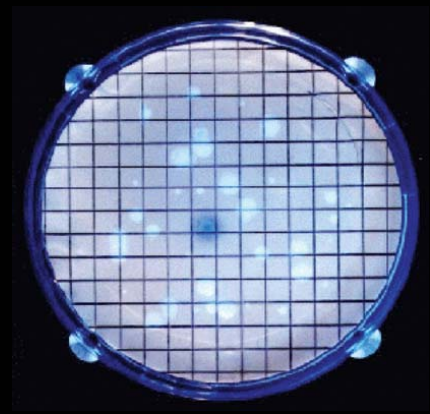
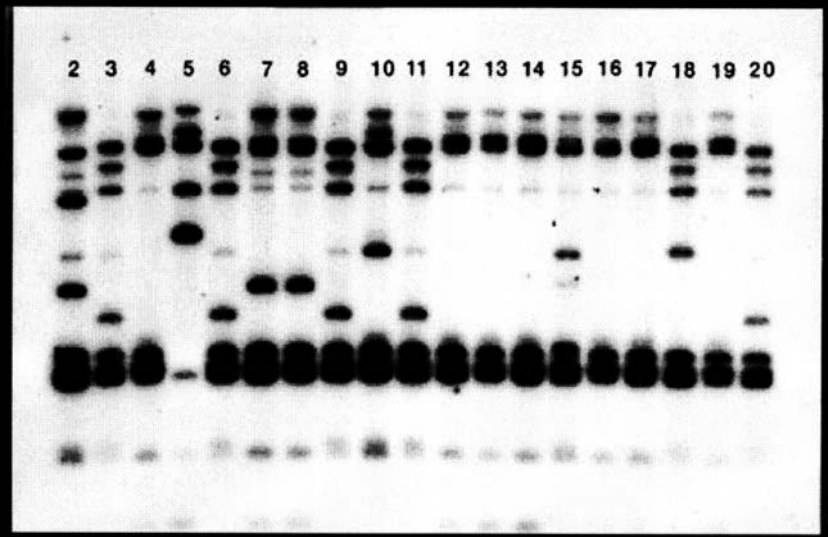


Figure 2-2. Schematic diagram of monitoring sites for the Green-Duwamish watershed water quality assessment.

Laboratory Methods

- Bacteria Concentration
  - Membrane filter by Standard Methods
- Ribotyping
  - Pure *E. coli* cultures isolated from culture plates
  - DNA is extracted, radio-labeled, and compared to genotype library containing over 50,000 known animal and human sources





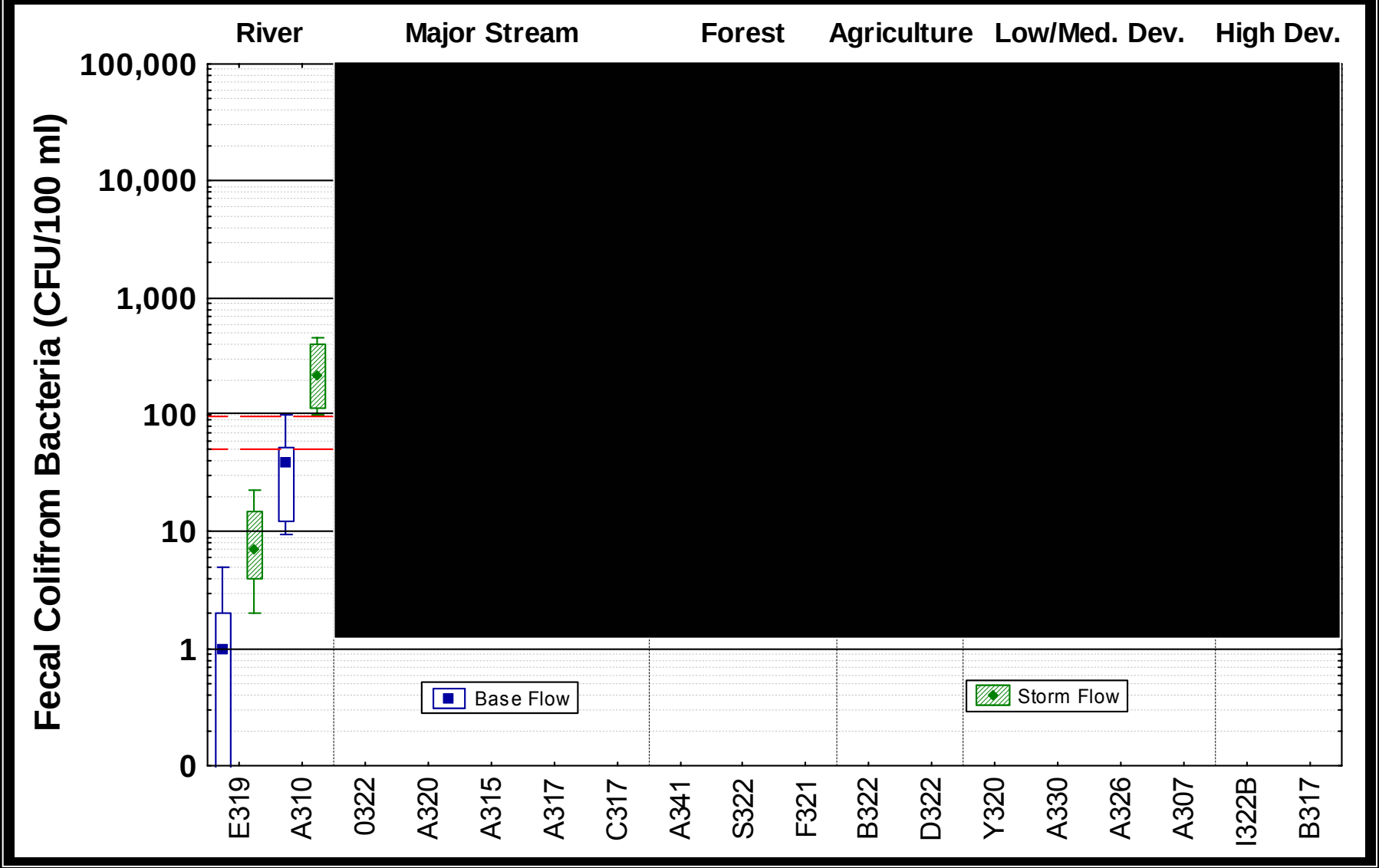
Data Analysis Methods

- Statistical difference using nonparametric Mann-Whitney U test at $\alpha = 0.05$
- Correlation analysis using Kendall's Tau at $\alpha = 0.05$
- Areal loading rates using:
  - Hydrograph separation and storm event delineation
  - Flow-weighted mean base flow concentration
  - Flow-weighted mean runoff concentration (storm – base)
- Bacteria source percentages by major source groups

Fecal Coliform Bacteria Concentration and Loading Results

- Box and whisker plots of concentrations at each site for base and storm flow
- Ratios of storm/base flow concentrations and runoff/base flow loading rates for each site
- Comparison of average loading rates to watershed model and literature values

Fecal Coliform Bacteria Concentrations by Site and Event Type



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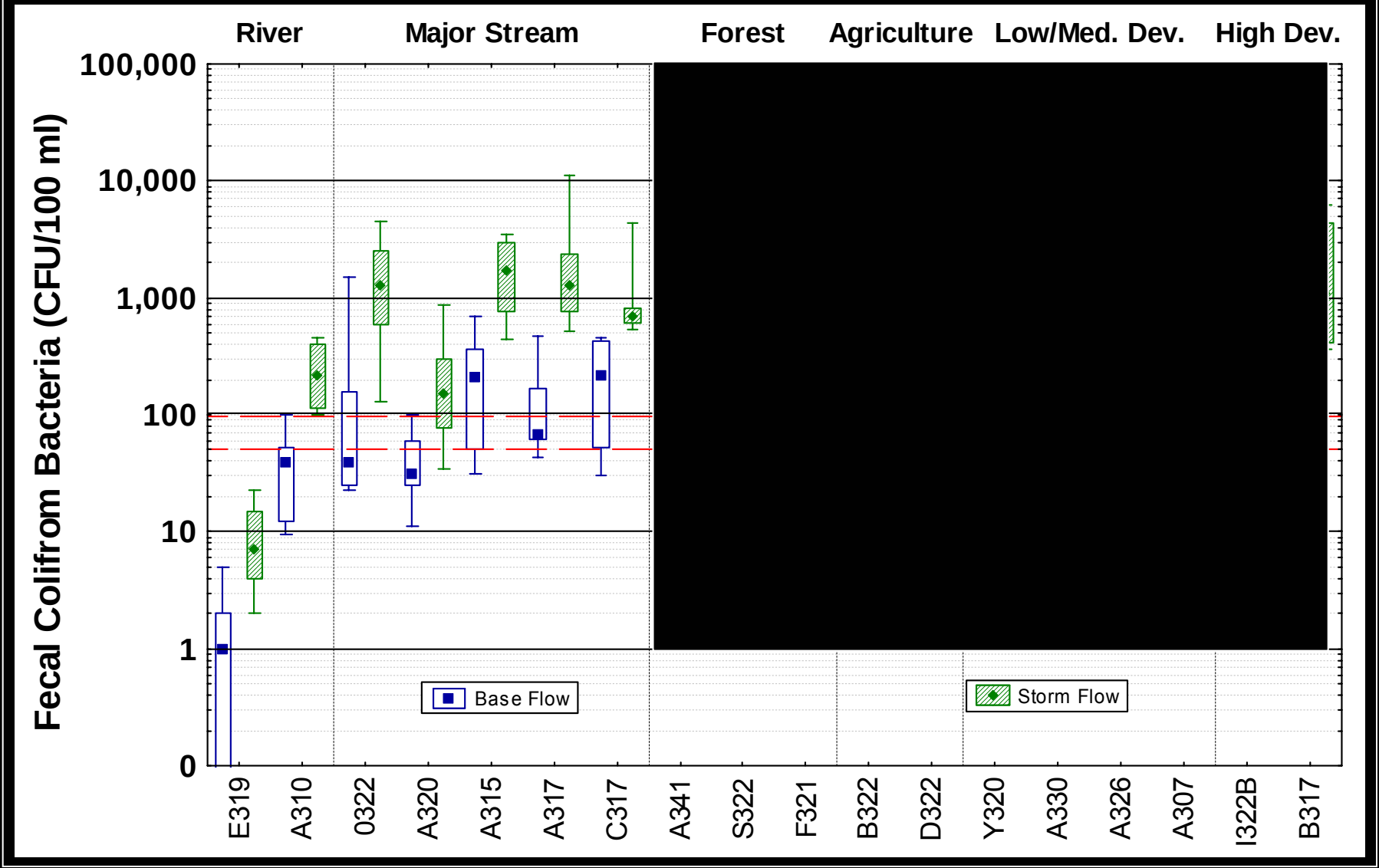

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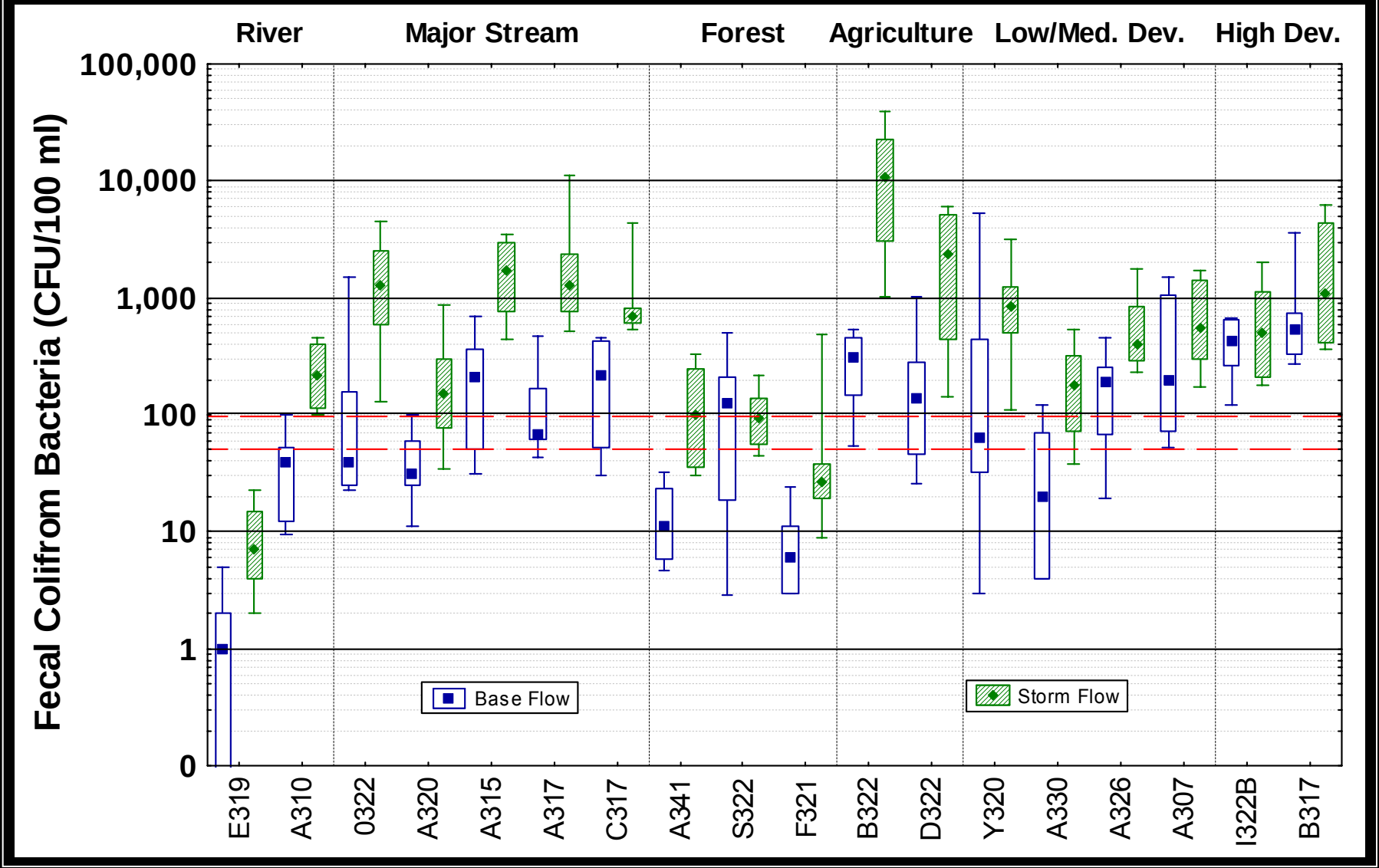

Significant Positive Correlation with Fecal Coliform Bacteria Concentration

	% of Sites
E. Coli	94
Copper, Total	83
Total Phosphorus	72
Total Suspended Solids	67
Mercury, Total	56
Zinc, Total	56
Turbidity	50
Copper, Dissolved	50

Significant Correlation with Fecal Coliform Bacteria Concentration

	Percent of All Sites Positive	Forest	Agriculture	Low/Med Development	High Development
E. Coli	94	+	+	+	+
Orthophosphate	39		+		
Total Phosphorus	72		+		+
Copper, Dissolved	50				
Copper, Total	83			+	
Mercury, Total	56				
Zinc, Total	56				
Suspended Solids	67				
Turbidity	50				
Dissolved Oxygen	36	−	−		
Total Storm Flow	NA	−			
Storm Flow Deviation	NA	−			

Bacteria Concentrations and Loads by Site and Event Type

	Median Concentration (CFU/100 mL)			Areal Loading (billion CFU/ha/yr)		
	Base	Storm	Storm/Base	Base	Runoff	Total
River						
E319 – Upper Green	1	8	8			
A310 – Lower Green	39	220	6	0.2	0.6	0.8
Major Stream						
0322 - Newaukum Creek	39	1,600	41	5.0	55	60
A320 - Soos Creek	31	150	5	1.7	6.2	7.8
A315 - Mill Creek	210	1,700	8	9.6	61	71
A317 - Springbrook Creek	68	1,306	19	3.8	146	150
C317 - Black River	220	690	3			
Forest						
A341 - TPU Diversion	11	101	9			
S322 - Weyerhaeuser	126	97	1	1.8	2.6	4.4
F321 - Crisp Creek	6	27	5	1.0	6.7	7.7
Agriculture						
B322 - SE 424th	310	10,636	34			
D322 - 236th SE	94	2429	26	1.2	47	48
Low/Med Development						
Y320 - Soosette Creek	56	900	16	5.0	133	138
A330 - Lea Hill	20	180	9			
A326 - Panther Creek	190	395	2	5.7	19	25
A307 - Hamm Creek	125	1,057	8	9.2	35	44
High Development						
I322B - Enumclaw	260	495	2	1.4	93	94
B317 - Mill (Springbrook)	540	800	2	54	131	185

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Bacteria Areal Loading Rates (billions/hectare-year)

Land Use/Cover	Green Study	King County	Literature[a]
Forest	6	8	4
Agriculture	48	215	16
Low/Med Development	69	82	9
High Development	140	159	21

[a] Horner et al. 1994

- Similar to watershed model values except for lower agriculture loading rates (one site)
- Higher than literature values

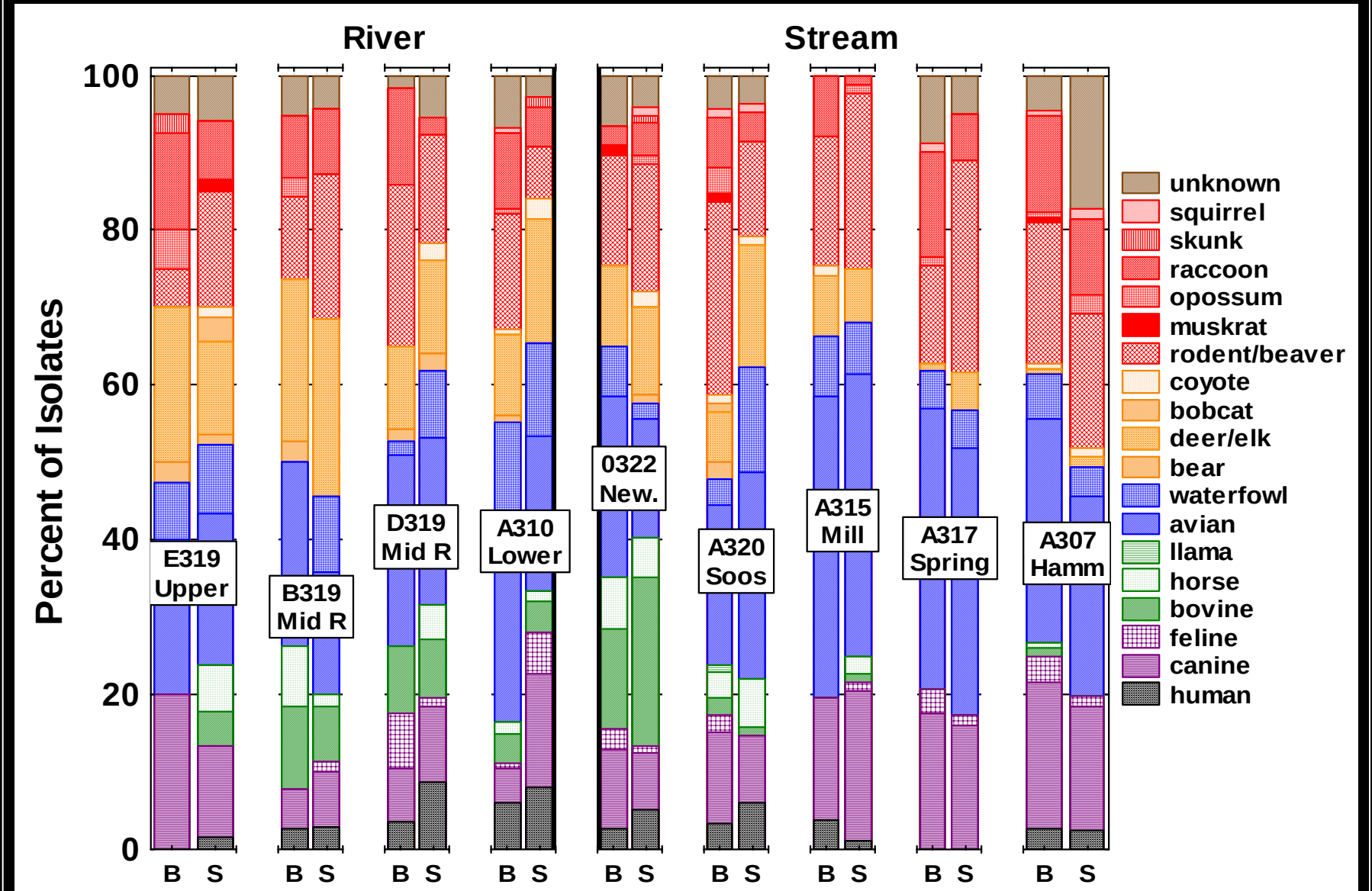
Bacteria Concentration and Loading Analysis Conclusions

- Bacteria concentrations increase from base to storm flow:
  - ~ 2X in high density development tribs (high base flow conc.)
  - ~ 6X in lower river and forest tributaries
  - ~ 10X in low/med density development tributaries
  - ~ 30X in agricultural tributaries
- Bacteria loading rates are:
  - ~ 10 to 100X higher in the major streams than the lower river
  - ~ 10 to 20X higher in the agriculture and development tributaries than the forest tributaries
- Stormwater runoff contributes ~75 percent of the bacteria load in the river and its tributaries

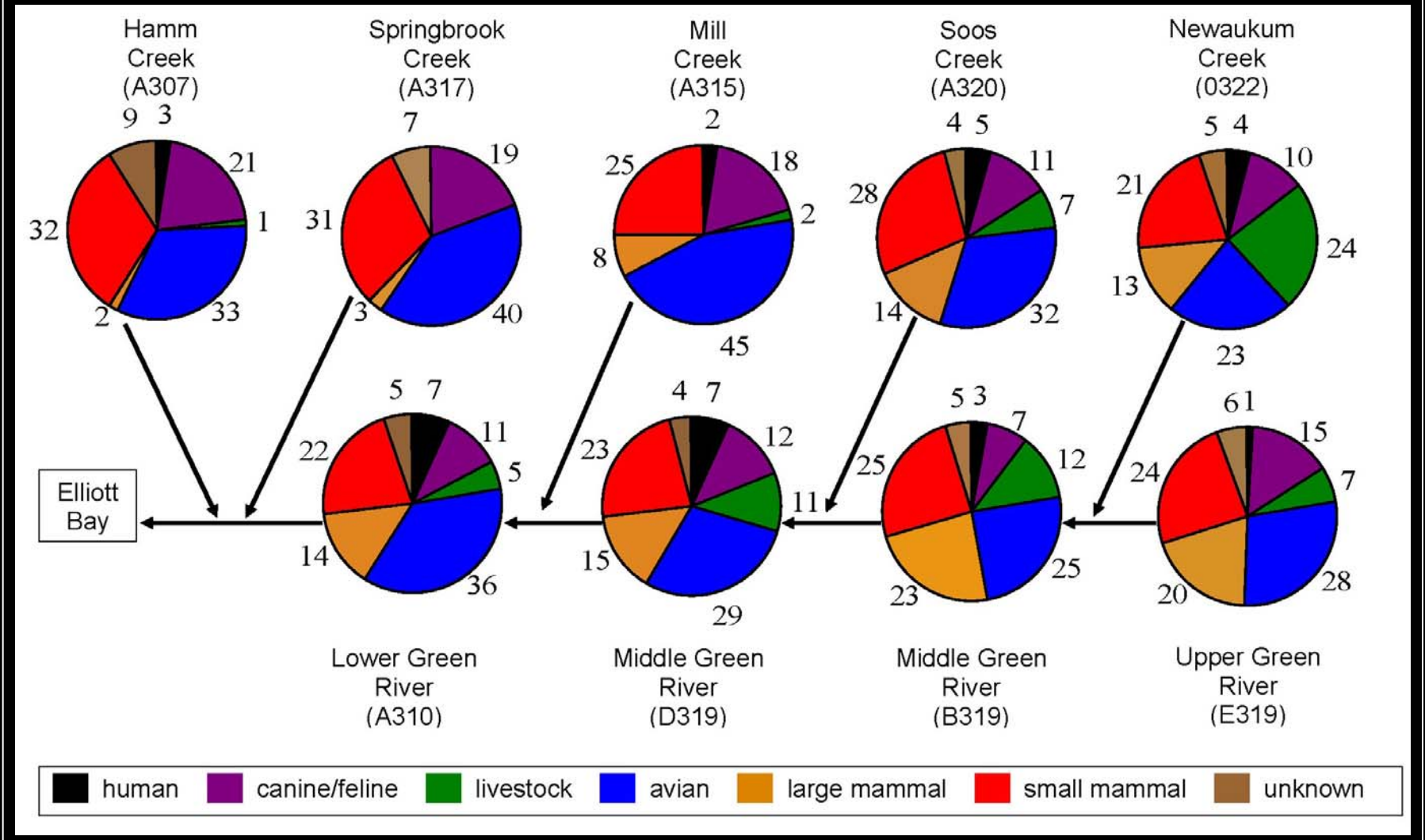
MST Analysis Results

- Stacked bar chart of *E. coli* sources at each site for base and storm flow
- Flow diagram of source groups in pie charts
- Correlation matrix of source percentages versus land use percentages

Bacteria Sources by Hydrologic Condition



Bacteria Source Flow Diagram



Correlation of Bacteria Sources with Land Use/Cover

	Forest	Agriculture	Low/Med Density Development	High Density Development	Effective Impervious Area
River and Stream Sites					
Human					
Canine/feline	–		+		+
Livestock	+		–	–	–
Avian					
Large Mammal	+		–	–	–
Small Mammal					
Rodent	–		+	+	+
Stream Sites Only					
Human	+			–	–
Canine/feline					
Livestock	+			–	–
Avian					
Large Mammal			–		
Small Mammal					
Rodent	–			+	+

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Stream Sites Only					
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Canine/feline					
Livestock	+			–	–
Avian					
Large Mammal			–		
Small Mammal					
Rodent	–			+	+

MST Analysis Conclusions

- Human = 4 %; none in Springbrook (100 % sewered); increased downstream
- Livestock = 7 %; highest in Newaukum (24 %) with most agriculture (45 %); decreased downstream in river
- Birds/Waterfowl = 26 %; most abundant at 8 of 9 sites
- Rodent/Beaver = 17 %; second most abundant source
- Canine = 12 %; more in streams than in river
- Deer/elk = 9 %, Raccoon = 8 %, other Wildlife < 2 %; Wildlife decreased downstream
- No consistent hydrologic or seasonal trends in sources
- Sources generally varied by land use as expected, but mixed land uses and inconsistent relationships limit predictability.

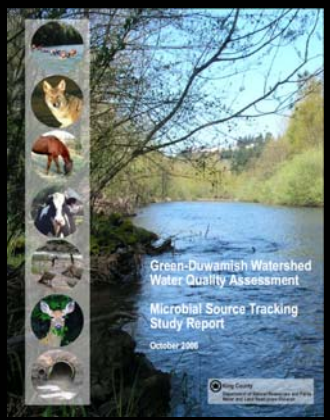
Emerging Issues and an Approach to Microbial Contamination

- Issues:
  - How to meet 90 % TMDL reduction if wildlife account for 75 % of sources (→implement costly water treatment)
  - Swimming beach closures are based on yesterday's bacteria test results (→revise closure or test procedures)
  - Bacteria concentrations generally do not correlate to the frequency of gastrointestinal illness and human health risk at swimming beaches (→develop new test procedures)
- Approach:
  - Use Pathogen Profiling with bacteria enumeration and source tracking data to assess human health risks from contact with waters containing varied bacteria populations originating from different human and animal sources.

More Information

- Water Quality Statistical and Pollutant Loadings Report:

http://dnr.metrokc.gov/wlr/waterres/streamsdata/reports/green-duwamish-loading-report.htm



- Microbial Source Tracking Report:

http://dnr.metrokc.gov/wlr/waterres/streamsdata/reports/Green-Duwamish-MST.htm

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