

Bacterial Source Tracking (BST) on Tributaries of Trinity and Galveston Bays

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What is Bacterial Source Tracking (BST)?

- Used to determine the sources of fecal contamination
- Based on uniqueness of bacteria from individual sources
- A variety of different methods are used
- Often works best as part of a “toolbox approach”



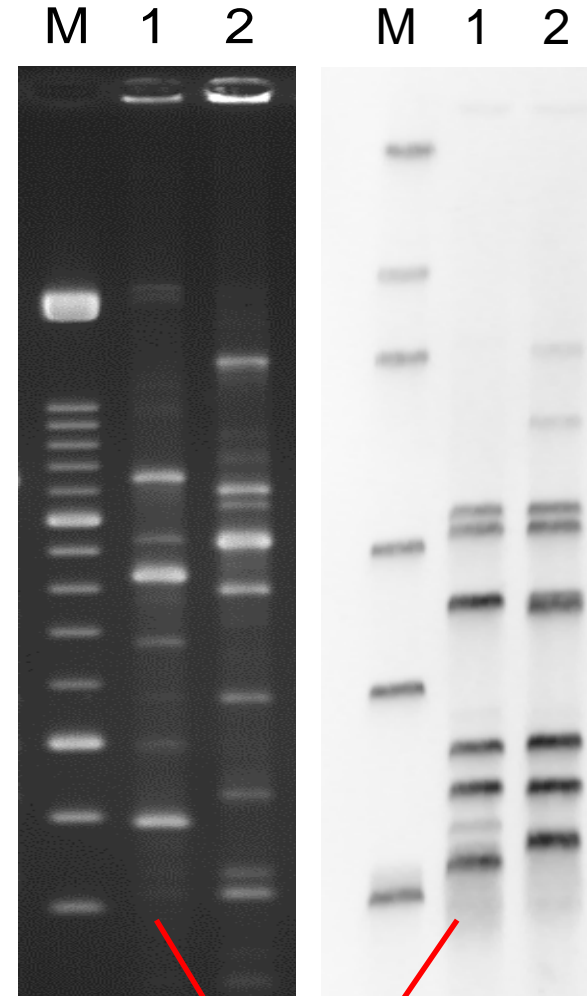
Library-Dependent BST Methods

Methods:

- DNA fingerprinting
 - Enterobacterial repetitive intergenic consensus sequence-polymerase chain reaction (ERIC-PCR)
 - RiboPrinting[®] (RP)

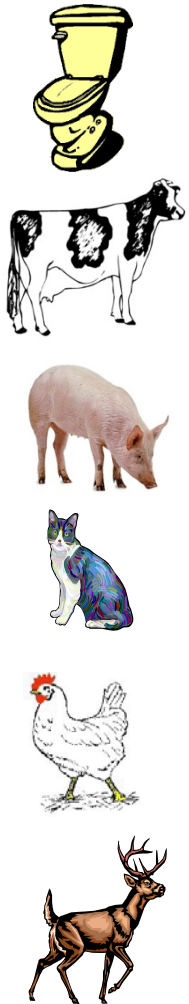
Advantages/Disadvantages:

- More discriminating
- Allows ranking of sources
- Detects wider range of sources
- More expensive

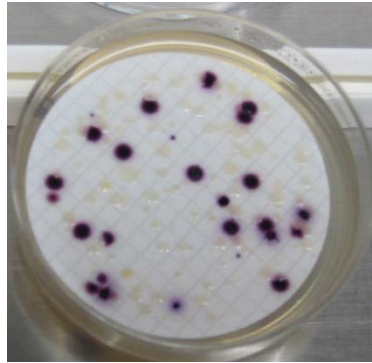


Development of Texas *E. coli* BST Library

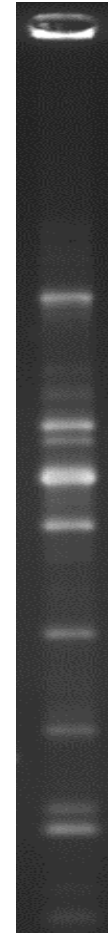
Sources



Isolate
→
E. coli



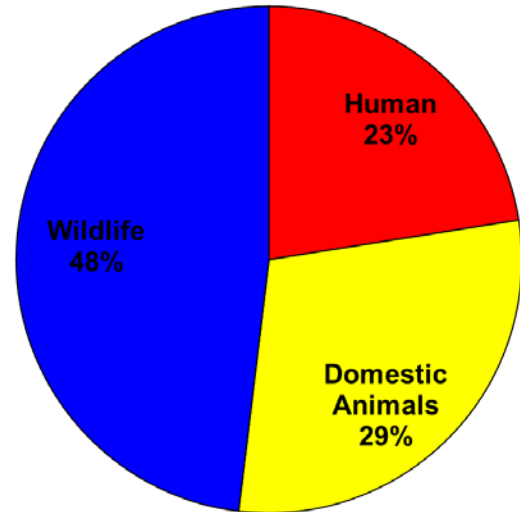
DNA
→
Fingerprint



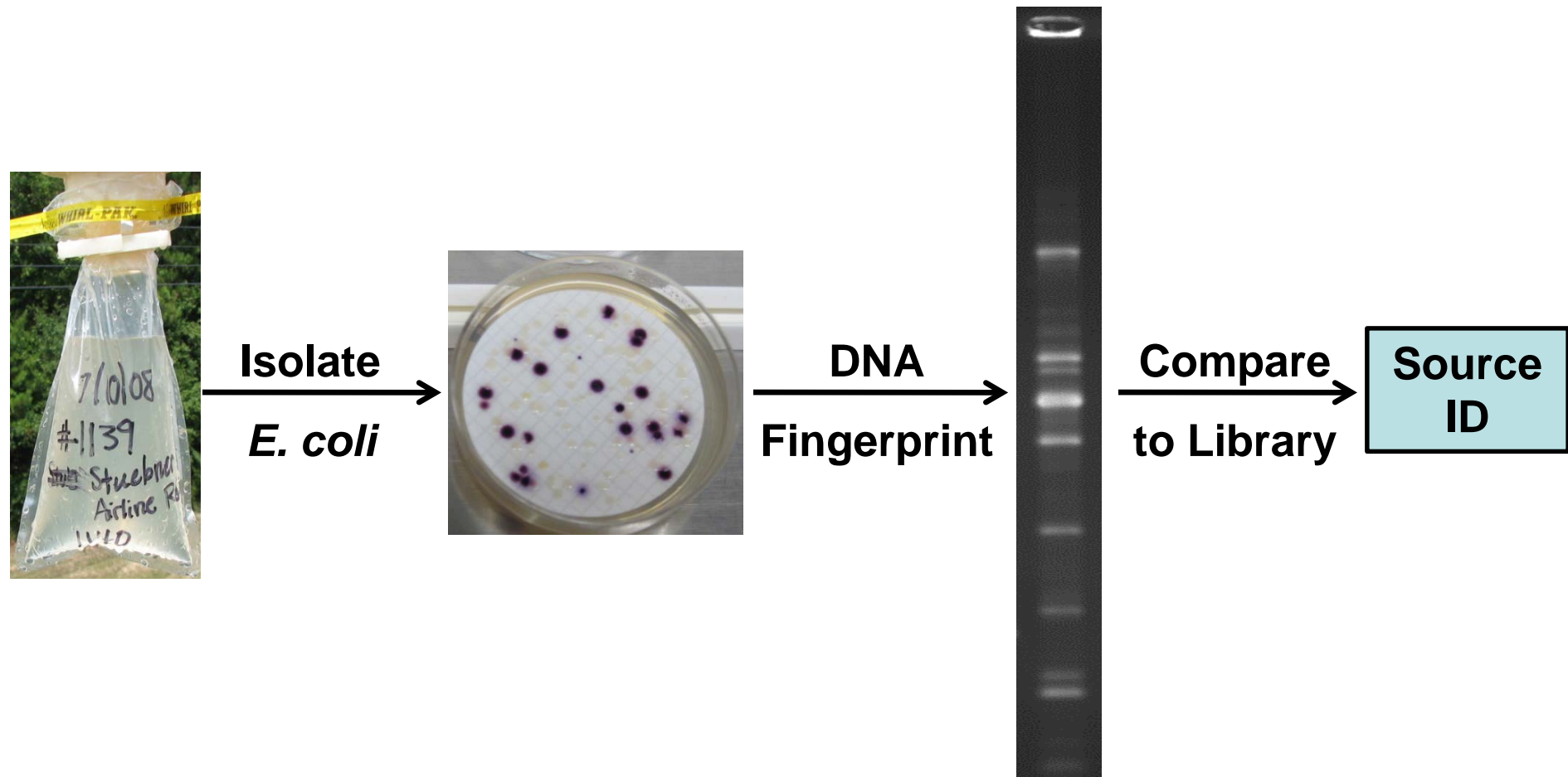
→
Add to
Library

Texas *E. coli* BST Library (v. 1-20)

- Contains 1,886 *E. coli* isolates from 1,645 different human and animal samples
- Developed by collecting over 4,000 domestic sewage, wildlife, livestock, and pet fecal samples and screening over 7,000 isolates for clones and host specificity
- Samples from over 20 watersheds across Texas for BST including:
 - Plum Creek
 - San Antonio
 - Lake Granbury
 - Oyster Creek / Trinity River
 - Waco / Belton Lake
 - Little Brazos River Tributaries
 - Attoyac Bayou
- Additional isolates being added from ongoing and future BST projects in other areas of Texas



Use of Texas *E. coli* BST Library for Identifying Water Isolates

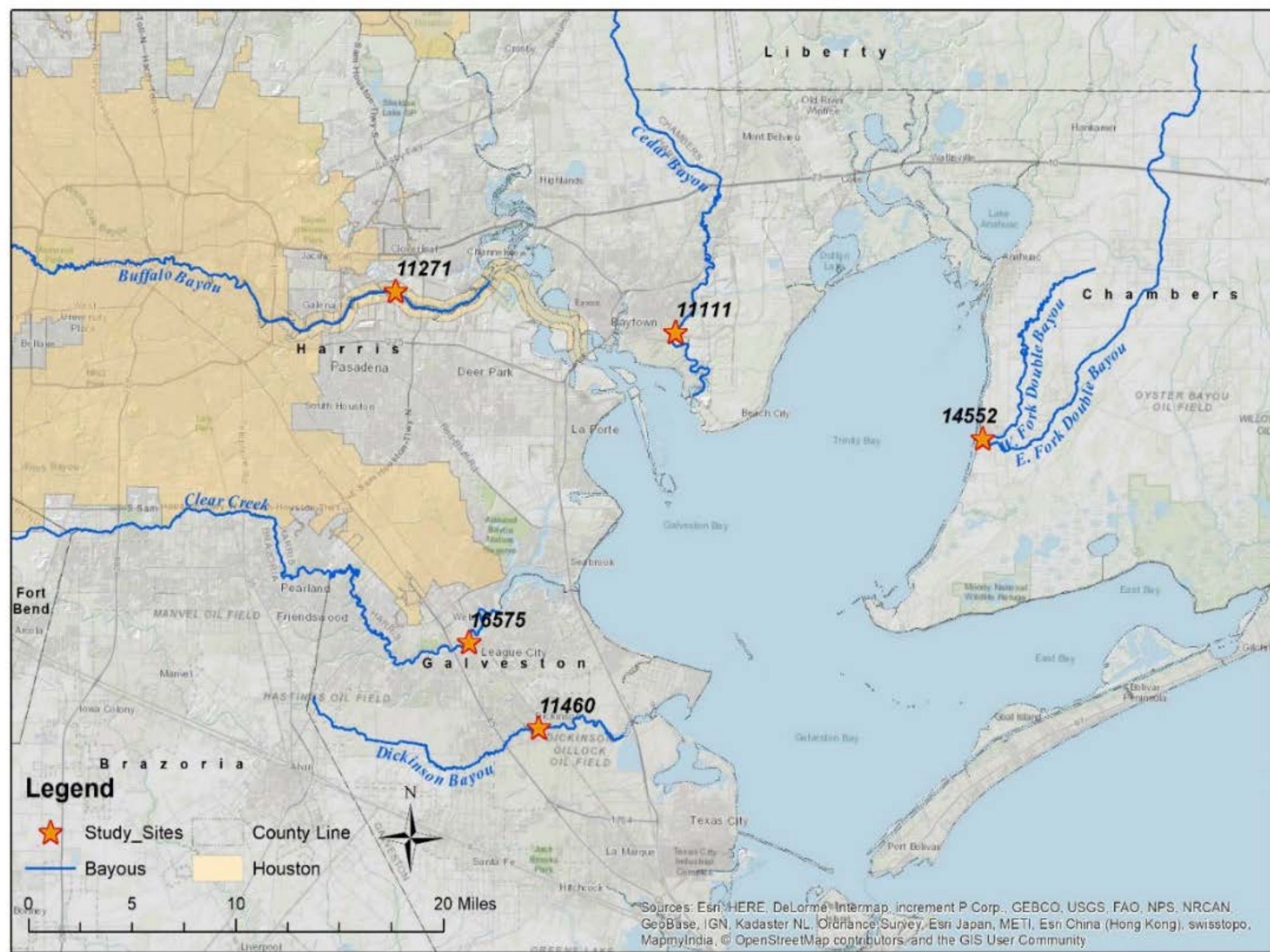


Texas *E. coli* BST Library Composition & Rates of Correct Classification (RCC)

Source Class	Number of Isolates	Number of Samples	Library Composition and Expected Random Rate of Correct Classification	Calculated Rate of Correct Classification (RCC)	RCC to Random Ratio***	Left Unidentified (unique patterns)
HUMAN	426	361	23%	100	4.3	22%
DOMESTIC ANIMALS	548	503	29%	100	3.4	20%
Pets	84	75	4%	84	21.0	42%
Cattle	245	226	13%	93	7.2	11%
Avian Livestock	96	84	5%	89	17.8	27%
Other Non-Avian Livestock	123	118	7%	90	12.9	15%
WILDLIFE	912	781	48%	100	2.1	16%
Avian Wildlife	273	251	14%	79	5.6	19%
Non-Avian Wildlife	639	530	34%	91	2.7	15%
Overall	1886	1645		ARCC** = 100% (3-way) 91% (7-way)		19%

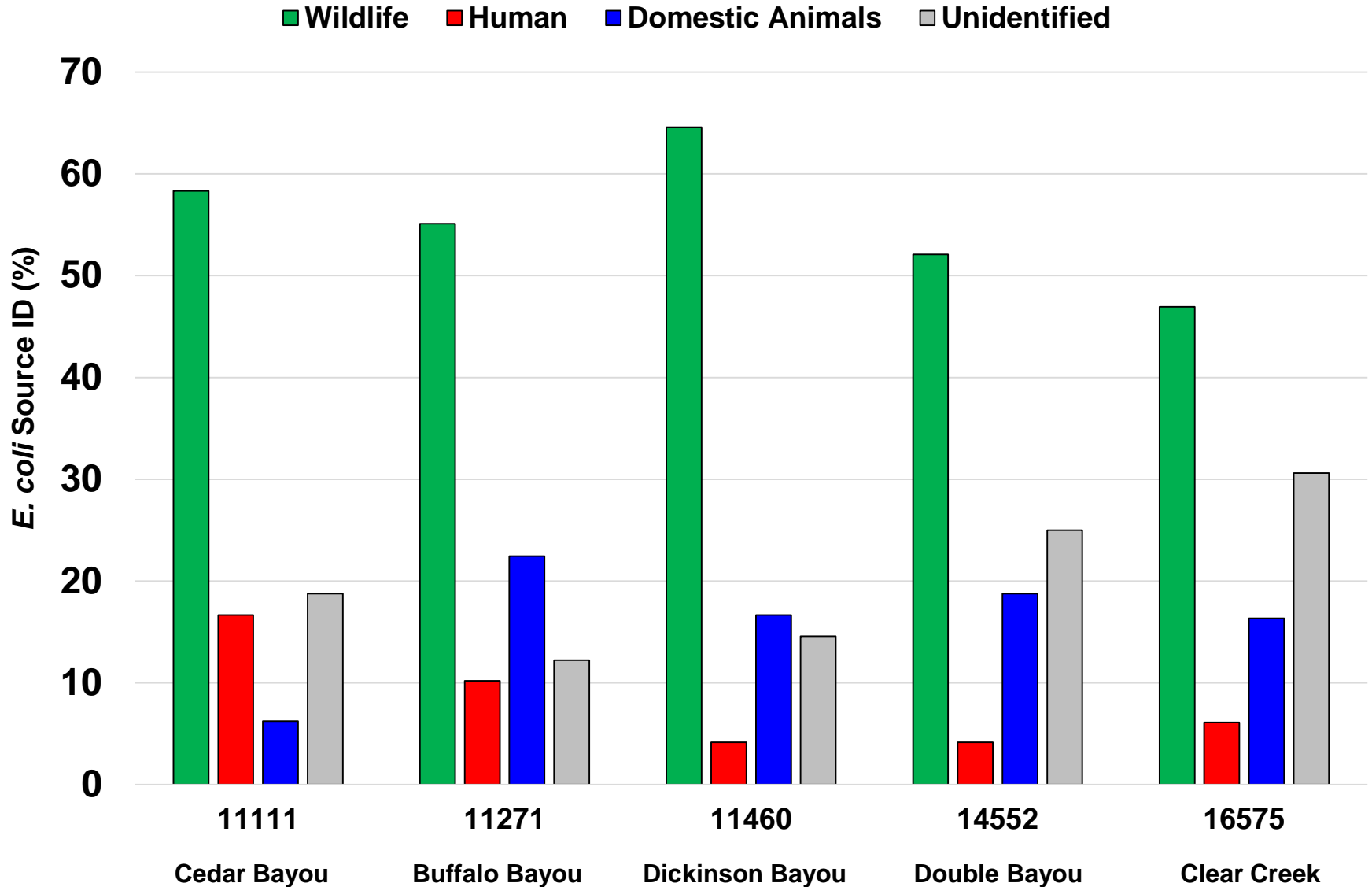
BST for Tributaries of Trinity and Galveston Bays

- **Addition of Known-Source *E. coli* Isolates**
 - **Isolated and DNA fingerprinted 77 *E. coli* for addition to the Texas *E. coli* BST Library**
 - **Non-avian wildlife (feral hogs, deer, opossums, etc.), sewage/septic, avian wildlife, pets, livestock, etc.**
- **Characterization of Water *E. coli* Isolates**
 - **Isolated *E. coli* from water samples collected monthly at five sites over one year (April 2018-2019; 60 samples)**
 - **DNA fingerprinted 241 *E. coli* isolates (4 per sample) and compared to Texas *E. coli* BST Library for source identification**



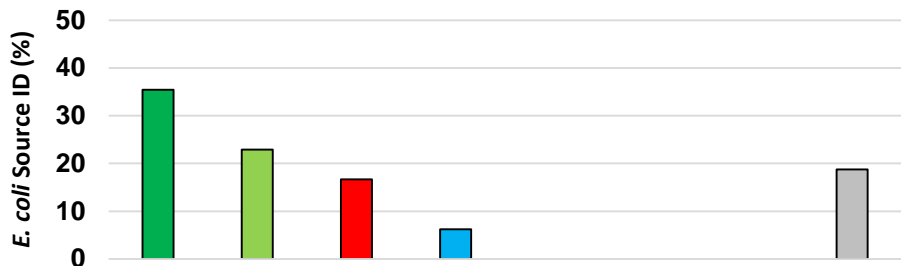
E. coli BST Results

5 Sampling Sites (3-Way Split)

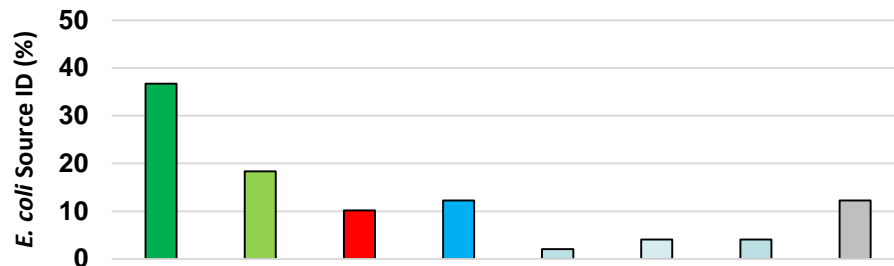


E. coli BST Results (7-Way Split)

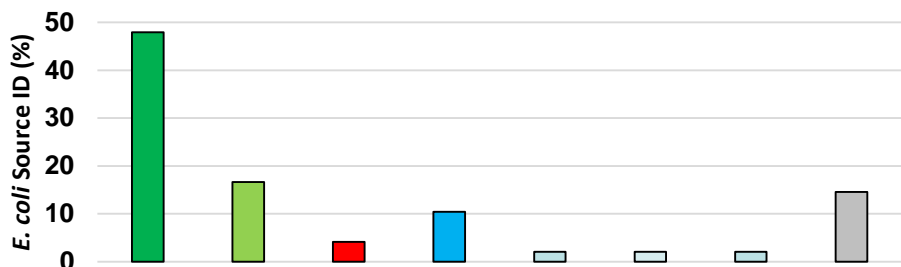
11111 (Cedar Bayou)



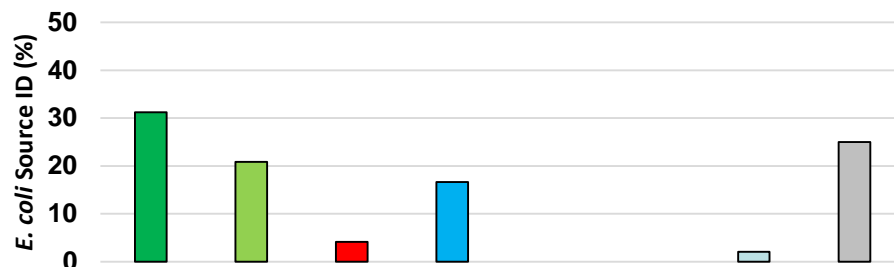
11271 (Buffalo Bayou)



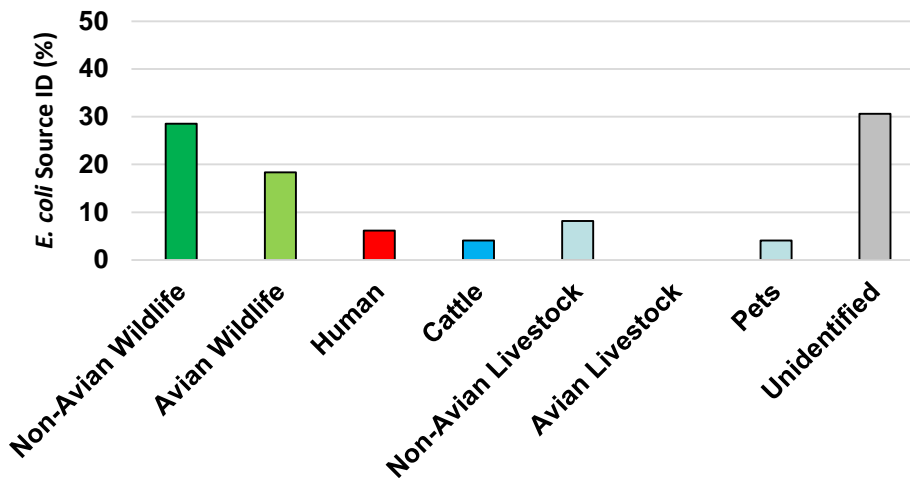
11460 (Dickinson Bayou)



14552 (Double Bayou)



16575 (Clear Creek)



BST Summary

- Major *E. coli* sources in tested samples appear to be non-avian wildlife (feral hogs, raccoons, opossums, mice, deer, etc.) and avian wildlife
- Some contributions from domesticated animals
- Human source contributions detected at all sites with variable levels across sites
- Relatively high proportion of unidentified isolates at some sites indicating 'unique' organisms not represented in library

Questions?

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