Characterization of pathogens in non-human fecal matter

Session 2: What do we know about the pathogenicity of non-human source microbes?

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State-of-the-Science: Fecal Source Identification and Associated Risk Assessment Tools
SCCWRP, 3535 Harbor Blvd. Costa Mesa, CA Nov 28th, 2012

Key Points

- Zoonotic pathogens, by definition are infectious in humans
  - Issues for rec water: prevalence & survival
  - Common problem: resolution from non-pathogens
  - Gastrointestinal & other illness (sequelae)
- Fecal but also environmental pathogens
  - *Vibrio* spp. & *Ps. aeruginosa* via wound infections
    Mycobacterium avium (increased virulence via animals)

Zoonotic pathogens

Zoonosis – pathogen from animal-to-human

- A few are viral (e.g. HEV pigs, H5N1 birds, hantavirus), range of pathogenic bacterial & parasitic protozoa

Which animal groups of concern in rec water?

- **Water birds** (e.g. [H1N1], *Campylobacter jejuni, Cryptosporidium meleagridis, Salmonella enterica* [*Giardia lamblia*], microsporidia)
- **Mammals: cats & sea otters** (*Toxoplasma gondii*), **rodents** (*Leptospira* &* hantavirus), **dogs** (*Toxocara & Trichuris* spp.), **rabbits** (*Cryptosporidium cuniculus*)

* 35 cases/y in Hawaii, Katz *et al.* 2011 EID 17:221-6

Non-GI illness endpoints

- Prime interest is gastrointestinal (GI) disease
  - But other endpoints / sequelae possible, e.g.
- *E. coli* O157:H7 GI, but may also cause HUS (hemolytic uremic syndrome)
- *Campylobacter jejuni* causes reactive arthritis & Guillain Barré syndrome
- *Leptospira* spp. freshwater leptospirosis

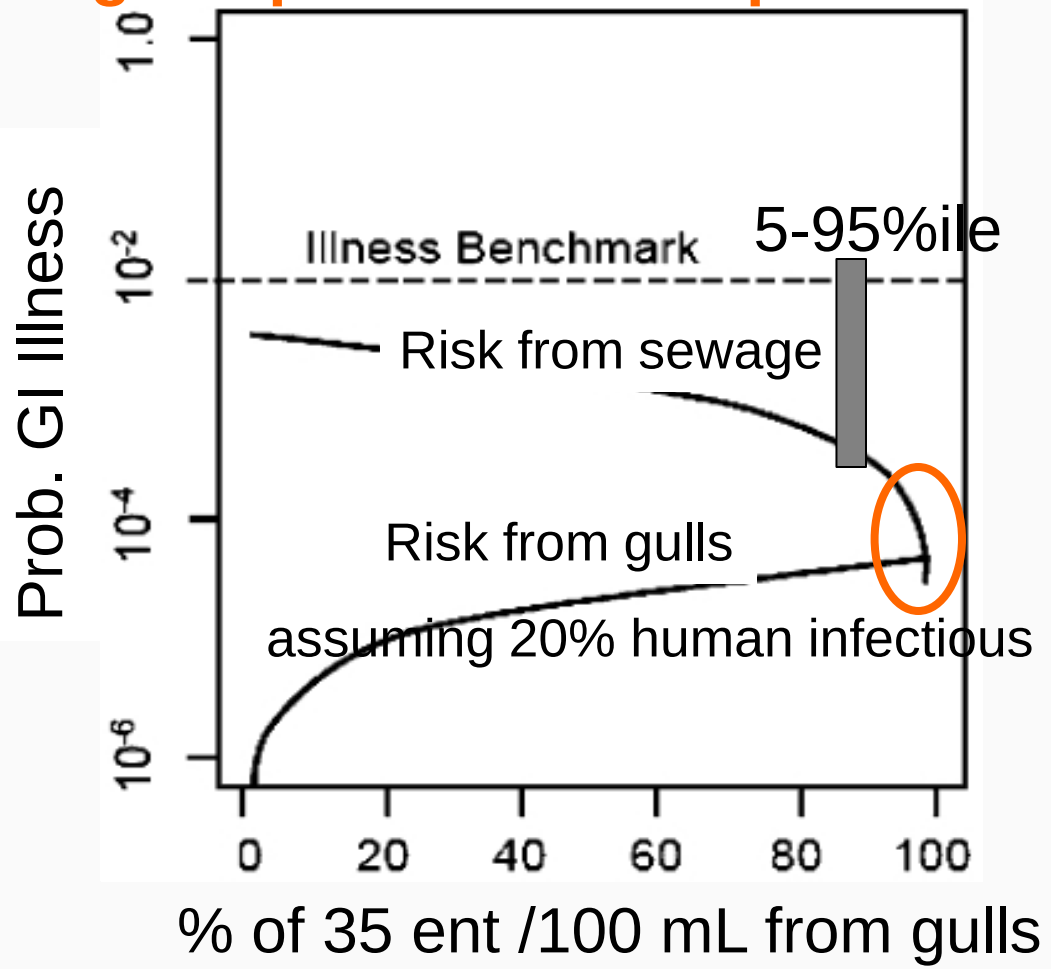
Understanding (fecal) sources

- Animal surveys / by season / risk periods
- qPCR for various pathogens / indicators
- Microbial Source Tracking (MST)
  - *Bacteroidales* targets, yet poorly developed for non-ruminants & birds (*Catellicoccus* ?)
  - Emerging use whole genome sequencing
- Chemical biomarkers to ID sources
  - Fecal sterols & other biomarkers are aids

Californian seagull risk?

- Most epidemiology studies to date have lacked statistical power, nor were they designed to specifically investigate health relationships to fecal indicators as well as other fecal source mixes

<20% human enterococci maybe sig: is qPCR MST that precise?

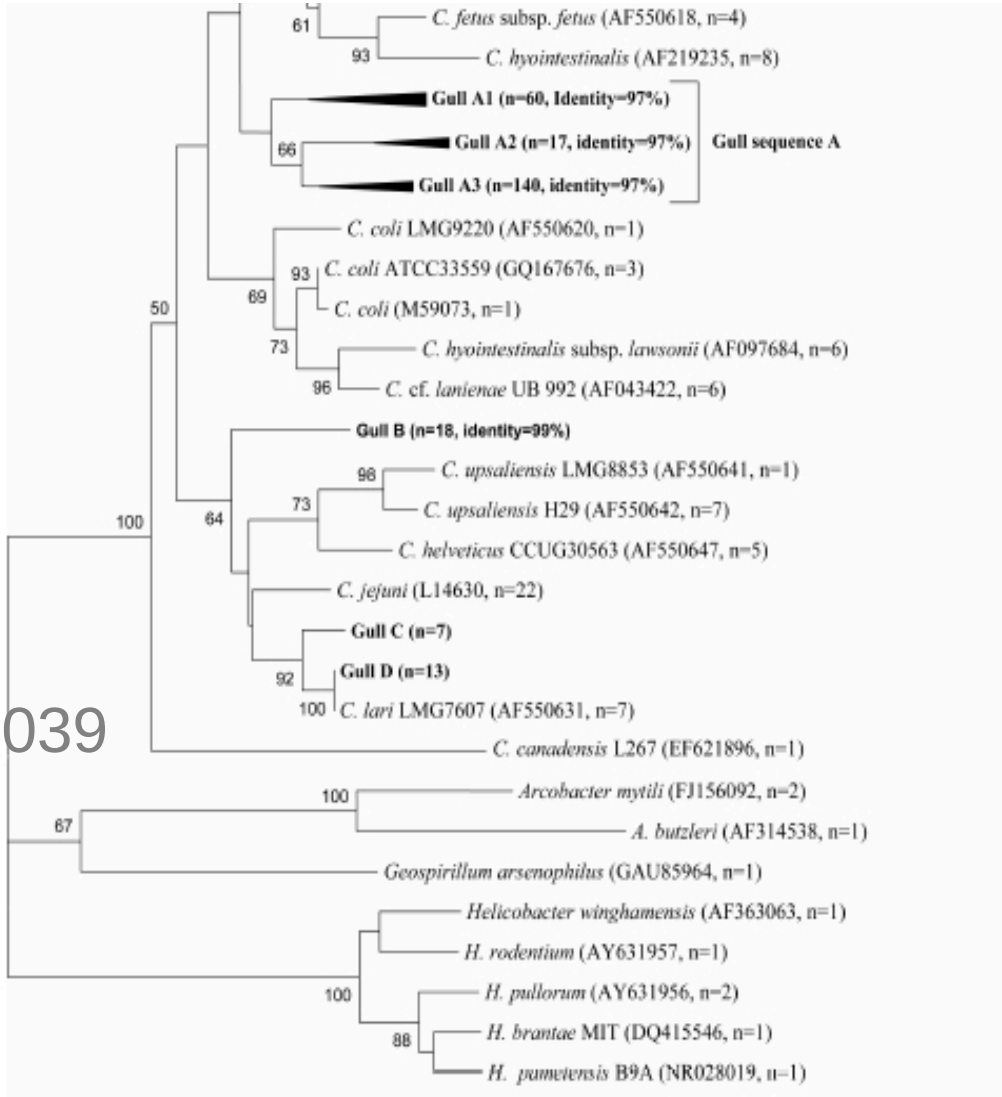


Schoen & Ashbolt (2010) Environ. Sci. Tech. 44:2286-91

A small portion (8%) of the fecal sequences were associated to *C. lari* or *C. jejuni* (clades C-D), while 85% constituted a distinct clade (A) away from *C. coli*, suggesting a novel species

Californian seagull *Campylobacter* 16S rRNA gene sequence (n=255) similarities (97-99%)

Lu *et al*. (2011) AEM 77:5034-5039



Sandhill crane (*Grus canadensis*) campylobacters

- *Campylobacter* spp. were detected in 39%, 25%, and 11% of DNA extracts of the Sandhill crane excreta, water, and sediments, respectively
- Most identified as *C. jejuni* by PCR

Lu *et al.* (2011) *ASM2011*, May 21-24 New Orleans, Louisiana

Further research gaps
Zoonotic pathogens & indicators ?

- Known pathogens (Sal, Campy, Ec O157 etc.):
  - Risk attributions? (human~cattle>pig/poultry)
- Emerging pathogens & what indicators?
  - HEV, *T. gondii*, *P. aeruginosa,* from pigs, cats, dogs, sea otters …
- Antibiotic-resistant bacteria/genes from animal feeding operations & environmental amplification

Conclusions: what next

- Probably need multiple qPCR targets to ID a source/mix with high sensitivity & specificity
- Then correlate to actual fecal (& environmental) pathogens for Fate &Transport modeling
  - Linking pathogen densities/behavior with surrogates
    - Noting differential die-off (of CFU) of FIB by fecal source!
  - Emerging roles for omics-ID/chemical markers
  - Emergence of ARG and antibiotic-resistant pathogens
- Dose-response models for various sequelae other than GI illness

Acknowledgements

Mary Schoen, Jeff Soller, Jingrang Lu,
Ian Struewing, Helen Buse, Jorge Santo Domingo, Randy Revetta