Estimating *Salmonella* and *Campylobacter* Cell Density in Animal Feces and Their Potential to Lead to Significant Contamination Events

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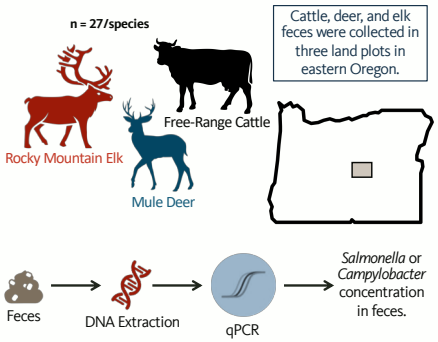
INTRO:

Significant foodborne outbreaks have been linked to the presence of wildlife and/or domesticated species in and around agricultural environments. Despite these linkages, there is little information about the likelihood of pathogens to be associated with certain species nor about the load that may be present in feces.

PURPOSE:

To estimate the quantity of *Salmonella* and/or *Campylobacter* in animal feces to identify species and/or individual animals that could contribute to the contamination of agricultural products.

METHODS:



RESULTS:

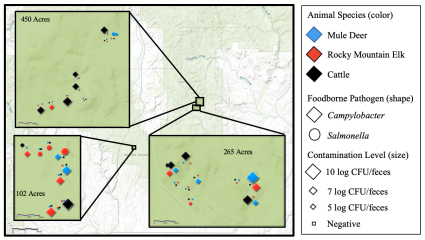


Figure 1. Distribution and concentration of *Campylobacter* and *Salmonella* in Mule Deer, Rocky Mountain Elk, and Free-Range Cattle in Eastern Oregon.

An individual **deer or elk** can shed

>1.3 MILLION

Salmonella or *Campylobacter* cells

per poop.

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Prevalence & Concentration Data:

Salmonella:
Mule Deer: 1/27; 6.4 log CFU/poop
Rocky Mt. Elk: 3/27; 6.1-7.7 log CFU/poop
Cattle: 1/27; 5.9 log CFU/poop

Campylobacter:
Mule Deer: 7/27; 6.2-10.3 log CFU/poop
Rocky Mt. Elk: 7/27; 5.6-8.0 log CFU/poop
Cattle: 10/27; 5.6-9.9 log CFU/poop

Other Wildlife Tested:

Salmonella:
Bobcat: 1/30; 5.1 log CFU/poop
Coyote: 0/30
Skunk: 0/5

Campylobacter:
Bobcat: 11/30; 4.5-8.9 log CFU/poop Coyote 6/30; 5.3-9.4 log CFU/poop
Skunk: 1/5; 4.7 log CFU/poop

Additional Method Details:

Fecal mass for calculations:
Deer: 27 g (dry weight);
Elk and Cattle: 58 g (dw)
Bobcat and Coyote: 17 g (dw)
Skunk: 10 g (dw)

DNA extraction: bead vortex and Qiagen DNeasy Blood and Tissue kit.

qPCR assays: SYBR Green

Salmonella invA primers:
invA_176F: CAACGTTTCCTGCGGTACTGT
invA_291R: CCCGAACGTGGCGATAATT

Campylobacter 16S primers:
R-camp-F2 CACGTGCTACAATGGCATAT
R-camp-RS GGCTTCATGCTCTGCAGTT

qPCR detection limit: 3.7 log CFU/g