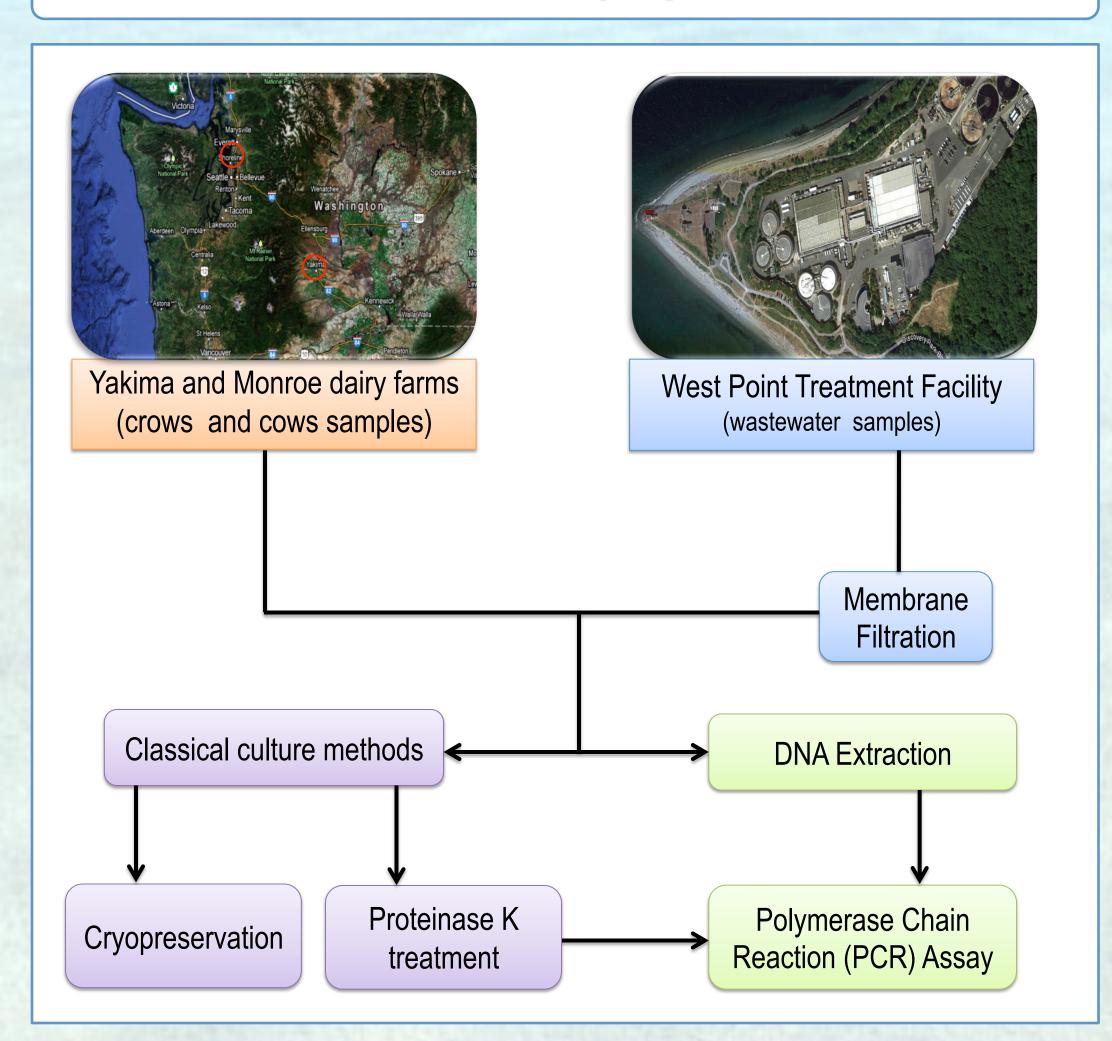


# Isolation of pathogens and drugs resistant genes from crows and their environment

#### INTRODUCTION

The objective of this study was to determine if we could isolate pathogens and detect antibiotic resistant bacteria and genes in crow feces and their environments (urban wastewater and agricultural cow feces). Crows were captured at wastewater and agricultural locations, and feces were obtained under UW IACUC approval. Primary and secondary wastewater samples were collected, and cow feces obtained from agricultural lands. Twenty-six samples were processed (crows n=20 [14 urban; 6 agricultural], dairy barns n=2 and wastewater n=4) using classical culture methods for Campylobacter spp., E. coli O157:H7, Salmonella spp., Staphylococcus aureus and methicillin resistant Staphylococcus aureus [MRSA] and vancomycin-resistant Enterococcus (VRE) and drug resistant bacteria. By culturing, in the urban setting *Campylobacter* spp. was identified in 21% crows vs. 25% wastewater while at agricultural sites 33% crows vs. 50% cows; Salmonella spp. in 14% vs. 75%; S. aureus urban 7% vs. 0% and agricultural 50% vs. 50%; and VRE in urban 14% vs. 100% and agricultural 33% vs. 0%. Culture of antibiotic resistant Gram-negative bacteria ranged from 29-57% in the urban crows and 50-100% in wastewater and 17-100% in agricultural crows and 50-100% of cows. Percentage of PCR positive samples for antibiotic resistant genes in urban crows vs. wastewater were identical for macrolide resistant genes *mef*(A) and *erm*(B) [33%], and tetracycline resistant genes *tet*(B) [67%], and *tet*(Q) [33%] while in agricultural areas macrolide resistant genes between crows at 17% and 50%-100% in cows and tetracycline resistant genes *tet*(B) 50% vs. 100%, and *tet*(Q) 0% vs. 100%. The pilot study identified four pathogens and a variety of drug resistant genes in both crow populations. There seems to be differences in what the crows carried in their feces depending on where they lived (urban vs. agricultural) but the total number of samples are too low to determine if this is a real trend.

#### METHODS



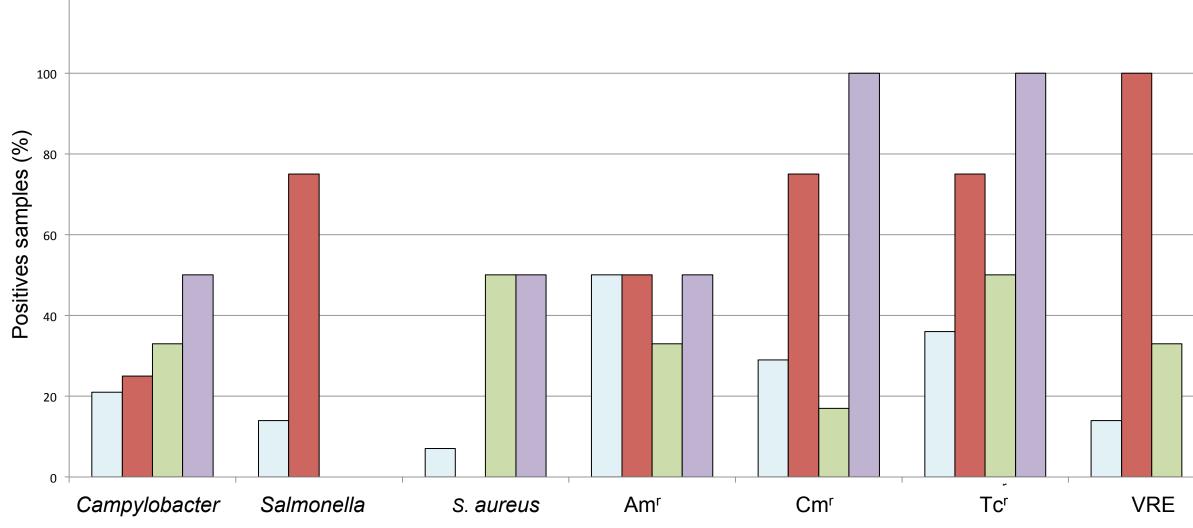
Sheila F. Cubero-Rodríguez<sup>1</sup>, David No<sup>2</sup>, Karen Michael<sup>2,</sup> Jack DeLap<sup>3</sup>, John M. Marzluff<sup>3</sup> & Marilyn C. Roberts<sup>2</sup> <sup>1</sup>URGREAT-MBRS-RISE, School of Sciences and Technology, Universidad del Este, Carolina, PR <sup>2</sup>Deparment of Environmental & Occupational Health Sciences, University of Washington, Seattle, USA <sup>3</sup>School of Environmental and Forest Sciences, University of Washington, Seattle, USA

#### RESULTS

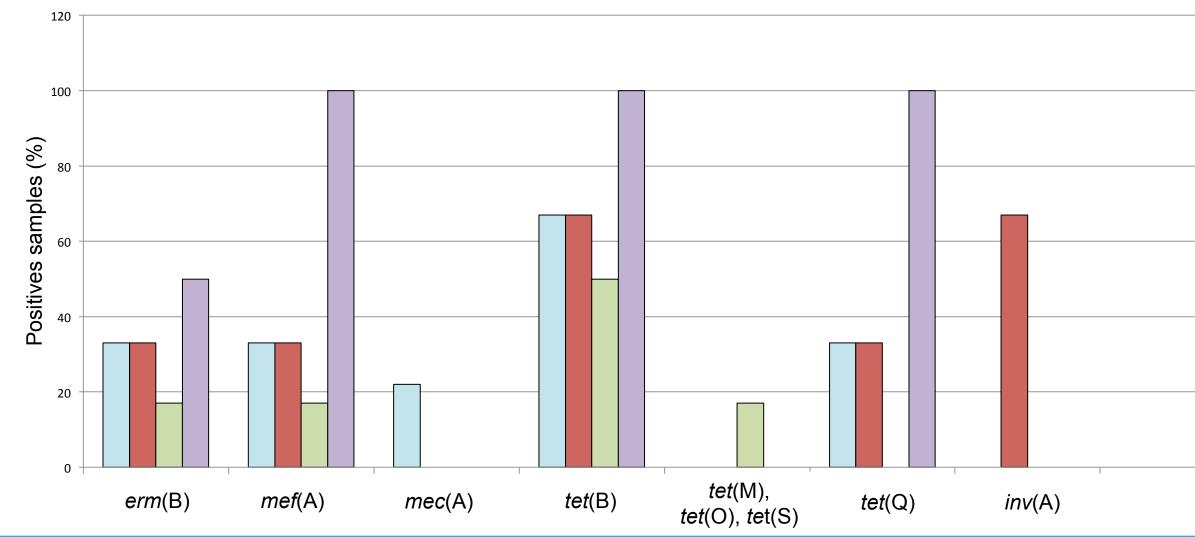
#### Table 1. Positives urban and agricultural samples in selective media and antibiotic resistant genes present by PCR

resistant genes present by rork					
	Urban EnvironmentalAgricultural EnvironSewage Treatment SamplesMonroe and Yakima Dair				
Isolated Bacteria	Crows n=14	Wastewater n=4	Crows n=6	Dairy Manure Pile n=2	
Campylobacter spp.	3	1	2	1	
Salmonella spp.	2	3	0	0	
Staphylococcus aureus	1	0	3	1	
Ampicillin-resistant <i>E. coli</i> (Am <sup>r</sup> )	7	2	2	1	
Chloramphenicol-resistant <i>E. coli</i> (Cm <sup>r</sup> )	4	3	1	2	
Tetracycline-resistant <i>E. coli</i> (Tc <sup>r</sup> )	5	3	3	2	
Vancomycin-resistant <i>Enterococcus</i>	2	4	2	0	
Gene	Crows n=9	Wastewater n=3	Crows n=6	Dairy Manure Pile n=2	
<i>erm</i> (B)	3	1	1	1	
mef(A)	3	1	1	2	
mec(A)	2	0	0	0	
tet(B)	6	2	3	2	
tet(M),tet(O), tet(S)	0	0	1	0	
tet(Q)	3	1	0 (n=5)	2	
<i>inv</i> (A) (for identification of <i>Salmonella</i> )	0	2	0	0	

### Fig 1. Percent of pathogens and antibiotic resistant bacteria from urban and agricultural environmental samples



#### Fig 2. Percent of antibiotic resistant genes present by PCR in urban and agricultural environmental samples





## CONCLUSION

urban crows	

- ■urban wastewater
- agricultural crows
- □ agricultural cows

- urban crows
- urban wastewater
- agricultural crows
- □ agricultural cows

- Pathogens (*Campylobacter* spp., *Salmonella* spp., Staphylococcus aureus, Vancomycin-resistant *Enterococcus*) were found in crow samples in urban and agricultural setting, which is the first time in crows.
- In both crows population (urban and agricultural) were identified antibiotic resistant bacteria and genes.
- All the samples in both environments presented the following drugs resistant genes: macrolide *mef*(A), *erm*(B) and tetracycline *tet*(B).
- The crow and wastewater samples from urban environmental, show a percentage similarity in *mef*(A), erm(B), tet(Q) and tet(B).
- There seems to be differences in what the crows carried in their feces depending on where they lived (urban vs. agricultural) but the total number of samples are too low to determine if this is a real trend.

### **FUTURE WORK**

- Collect more samples to determine if difference is real between urban and agricultural settings.
- Are pathogens found in crows genetically related to those isolated from their environment?

### ACKNOWLEDGMENTS

• This poster was supported in part by Award Number R25ES16150 from the National Institute of Environmental Health Sciences and a grant from DEOHS to Dr. Roberts. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

