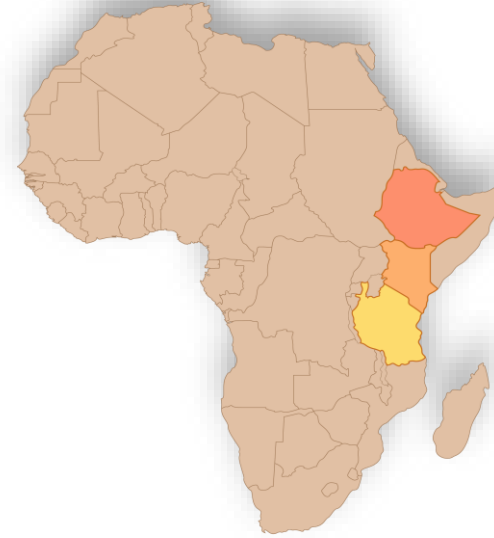




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## Molecular Epidemiology of Enteric infections in Eastern Africa

[Wondwossen A. Gebreyes]

Feed the Future Innovation Lab for Livestock Systems, University of Florida

Photo credits: Ohio State University



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## BILL & MELINDA GATES FOUNDATION AWARD

- **Equip project:** Strengthening smallholder livestock systems for the future

### Subprojects:

- **FEED:** Improving supply of quality feed for dairy cows in Ethiopia and small ruminants in Burkina Faso
- **CAGED:** *Campylobacter* genomics and environmental enteric dysfunction
- **Project duration:** 5 years (2017-2022)
- **Target countries:** Burkina Faso & Ethiopia





## RATIONALE

- Part of the Global One Health initiative (GOHi)
- Food- Water- and Vector-borne pathogens remain major concerns in the region
- Invasive and multi-drug resistant strains are major concerns
- The capacity/ skilled-manpower to address these issues is critically lacking
- Partnership with academic and research institutes:

Ethiopia- Addis Ababa Univ./ Gondar/ Haramaya (also EPHI/ NAHDIC)

Kenya- University of Nairobi and Kenya Medical Research Institute

Tanzania- Sokoine Univ.Agriculture (SUA)

Others- ILRI/ ICIPE

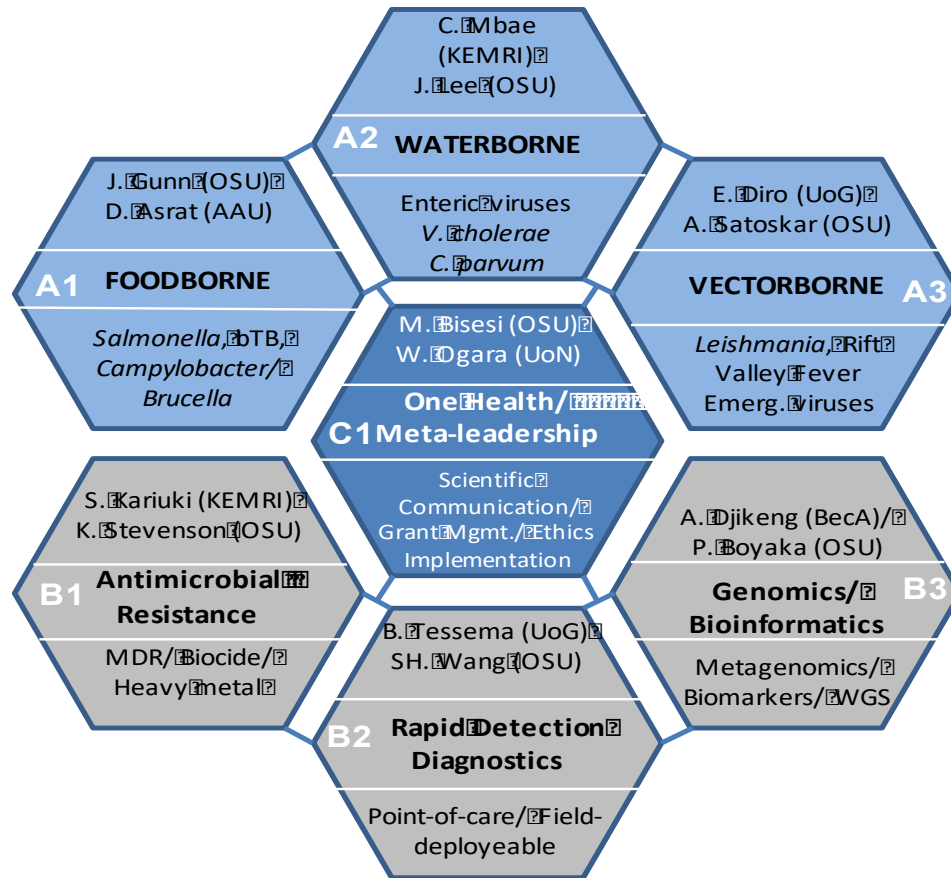




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## NIH-D43: MOLECULAR EPIDEMIOLOGY OF PATHOGENS- OHEART (2010-22)



Training grant- always looking for research project partners!!!



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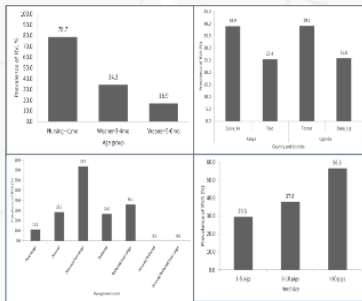
Figure 3. Priority topics and thematic area co-leaders.

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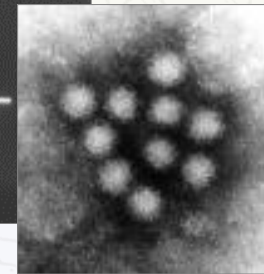
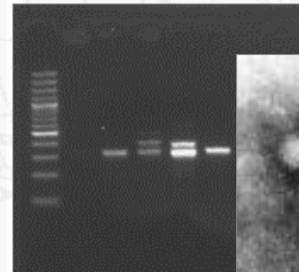


# Molec, epid, of Viruses and parasites

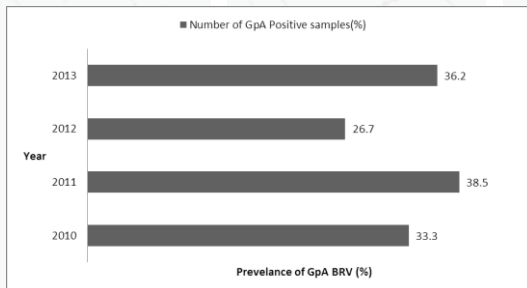
## Detection & genetic characterization of porcine rotaviruses in pigs in smallholder farms in East Africa (Joshua Amimo- Univ. Nairobi)



## Enteric caliciviruses in pigs and cattle (Zufan Sisay- AAU, Ethiopia)

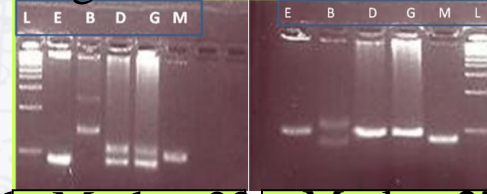


## Genotyping of Rotaviruses (Khadija Said, SUA, Tanzania)



## Clinical and Molecular Epidemiology of *Leishmania aethiopica* (Nigatu Wubie, AAU, Ethiopia)

Figure 1 a. Markers 1,4,6



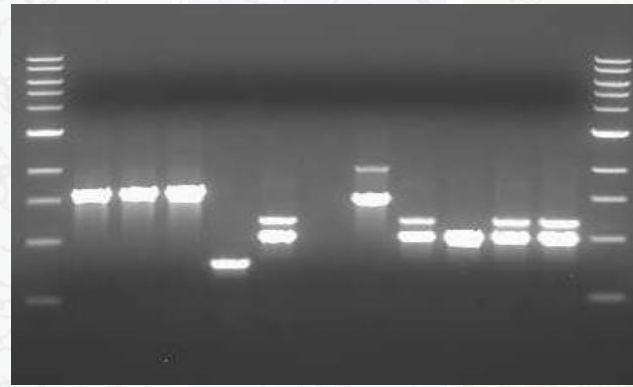
b. Marker 22 c. Marker 27





# Molecular Epid. of MDR *Salmonella* in Ethiopia

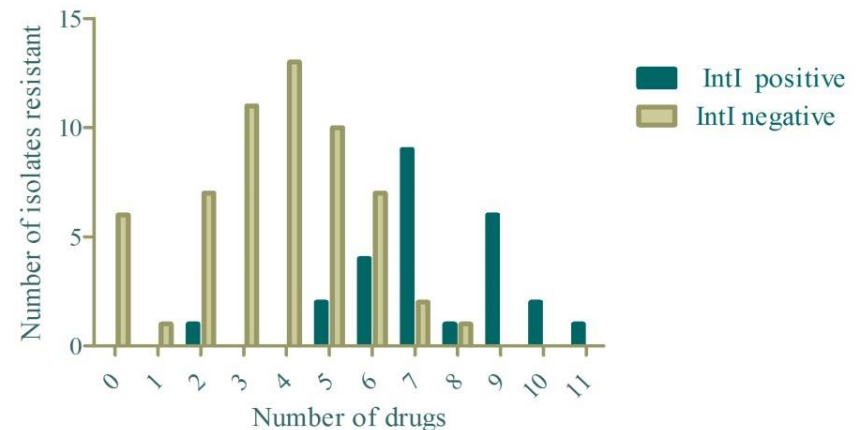
Drug	% resistant
Streptomycin	77
Tetracycline	65.5
Sulfisoxazole	52.9
Neomycin	41.38
Nalidixic acid	41.38
Cephalothin	33.3
Ampicillin	31
Nitrofurantoin	28.75
SXT	24.1
Amoxi+clavulonic acid	20.7
<b>Ciprofloxacin</b>	<b>14.9</b>
Gentamicin	14.94
Chloramphenicol	5.75



Class 1 Integrons



**T. Eguale**  
AAU, Ethiopia





RESEARCH

Open Access



## Genetic markers associated with resistance to beta-lactam and quinolone antimicrobials in non-typhoidal *Salmonella* isolates from humans and animals in central Ethiopia

Tadesse Egualé<sup>1\*</sup>, Josephine Birungi<sup>2</sup>, Daniel Asrat<sup>3</sup>, Moses N. Njahira<sup>4</sup>, Joyce Njuguna<sup>2</sup>, Wondwossen A. Gebreyes<sup>5</sup>, John S. Gunn<sup>6</sup>, Appolinaire Djikeng<sup>2</sup> and Ephrem Engidawork<sup>7</sup>

### Abstract

**Background:** Beta-lactam and quinolone antimicrobials are commonly used for treatment of infections caused by non-typhoidal *Salmonella* (NTS) and other pathogens. Resistance to these classes of antimicrobials has increased significantly in the recent years. However, little is known on the genetic basis of resistance to these drugs in *Salmonella* isolates from Ethiopia.

**Methods:** *Salmonella* isolates with reduced susceptibility to beta-lactams ( $n = 43$ ) were tested for genes encoding for beta-lactamase enzymes, and those resistant to quinolones ( $n = 29$ ) for mutations in the quinolone resistance determining region (QRDR) as well as plasmid mediated quinolone resistance (PMQR) genes using PCR and sequencing.

**Results:** Beta-lactamase genes (*bla*) were detected in 34 (79.1%) of the isolates. The dominant *bla* gene was *bla*TEM, recovered from 33 (76.7%) of the isolates, majority being TEM-1 (24, 72.7%) followed by TEM-57, (10, 30.3%). The *bla*OXA-10 and *bla*CTX-M-15 were detected only in a single *S. Concord* human isolate. Double substitutions in *gyrA* (Ser83-Phe + Asp87-Gly) as well as *parC* (Thr57-Ser + Ser80-Ile) subunits of the quinolone resistance determining

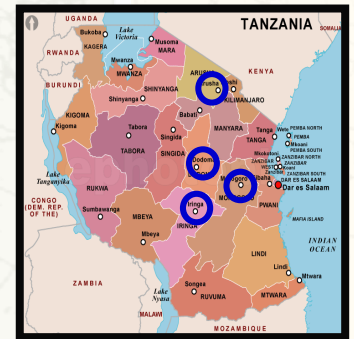
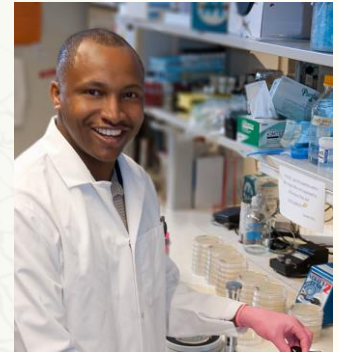


# Molecular Epidemiology of MDR *Salmonella*: Tanzania

GOAL: Understand epidemiology and transmission dynamics in pastoral and agro-pastoral zones; decipher the role of ecosystem such as heavy metal and association with MDR;

WGS- understand the various genetic components for HM tolerance, AMR and virulence in parallel

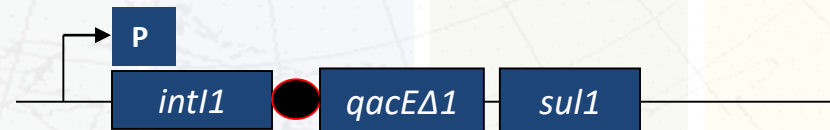
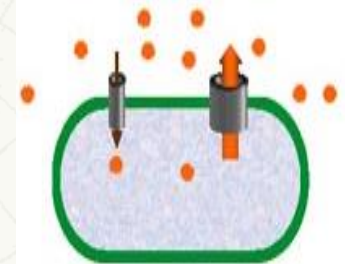
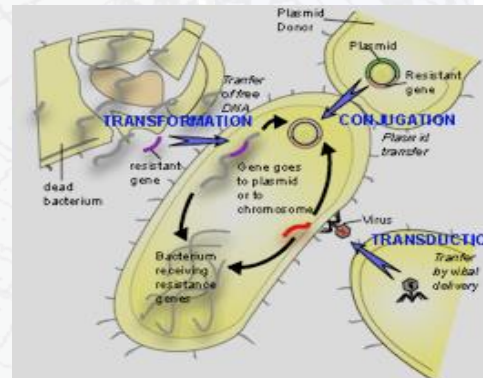
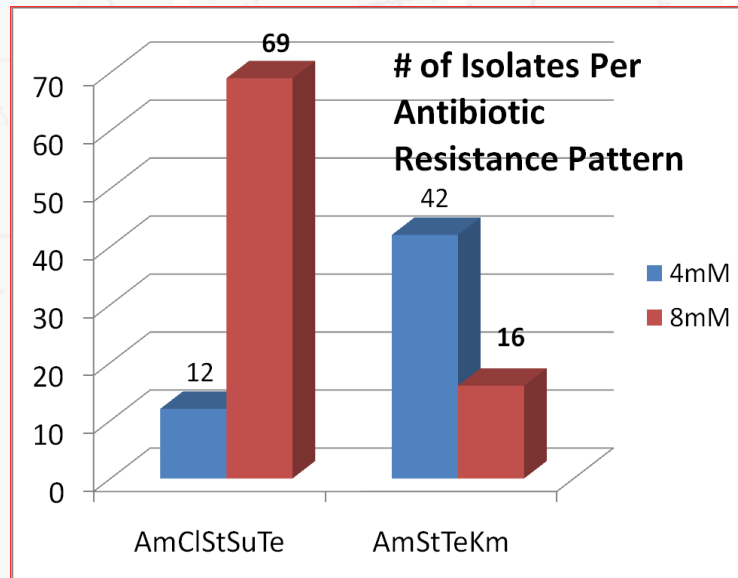
NIH Fogarty Int'l Center (D43)- (2011-22)/ GID Research Training capacity building; Co-funding- WHO-AGISAR/ USAID/ FDA-CFSAN/ PAHO/ etc- consider in Brazil





# Heavy metal micronutrients in swine feed and association with MDR *Salmonella*

Association determined between	OR	P-value
Zn tolerance, R-types and MDR (AmClStSuTe v. AmStTeKm)	14.66	<0.0001
Zn tolerance & czcD gene carriage (low v. high MIC)	5.92	<0.0001





## In-Feed Use of Heavy Metal Micronutrients in U.S. Swine Production Systems and Its Role in Persistence of Multidrug-Resistant *Salmonellae*

Julius J. Medardus,<sup>a,c,d</sup> Bayleyegn Z. Molla,<sup>a,d</sup> Matthew Nicol,<sup>a</sup> W. Morgan Morrow,<sup>b</sup> Paivi J. Rajala-Schultz,<sup>a</sup> Rudovick Kazwala,<sup>c,d</sup> Wondwossen A. Gebreyes<sup>a,d</sup>

Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio, USA<sup>a</sup>; Department of Animal Science, College of Agriculture and Life Sciences, North Carolina State University, Raleigh, North Carolina, USA<sup>b</sup>; Sokoine University of Agriculture, Faculty of Veterinary Medicine, Morogoro, Tanzania<sup>c</sup>; VPH-Biotech Global Consortium<sup>d</sup>†

The study aimed to characterize the role of heavy metal micronutrients in swine feed in emergence of heavy-metal-tolerant and multidrug-resistant *Salmonella* organisms. We conducted a longitudinal study in 36 swine barns over a 2-year period. The feed and fecal levels of  $\text{Cu}^{2+}$  and  $\text{Zn}^{2+}$  were measured. *Salmonella* was isolated at early and late finishing. MICs of copper sulfate and zinc chloride were measured using agar dilution. Antimicrobial susceptibility was tested using the Kirby-Bauer method, and 283 isolates were serotyped. We amplified *pcoA* and *czcD* genes that encode  $\text{Cu}^{2+}$  and  $\text{Zn}^{2+}$  tolerance, respectively. Of the 283 isolates, 113 (48%) showed  $\text{Cu}^{2+}$  tolerance at 24 mM and 164 (58%) showed  $\text{Zn}^{2+}$  tolerance at 8 mM. In multivariate analysis, serotype and source of isolates were significantly associated with  $\text{Cu}^{2+}$  tolerance ( $P < 0.001$ ). Fecal isolates were more likely to be  $\text{Cu}^{2+}$  tolerant than those of feed origin (odds ratio [OR], 27.0; 95% confidence interval [CI], 2.8 to 250;  $P = 0.0042$ ) or environ-

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## GENOMETRKR PARTNERSHIP

**Salmonella enterica**  
Accession: PRJNA275961 ID: 275961

**GenomeTrakr: OSU-ICOPHA project**  
Whole genome sequencing of cultured *Salmonella enterica* as part of the US Food and Drug Administration's WGS surveillance effort for the rapid detection of foodborne illness outbreaks.

**Related Resources:**  
International Congress on Pathogens at the Human-Animal Interface (ICOPHA)

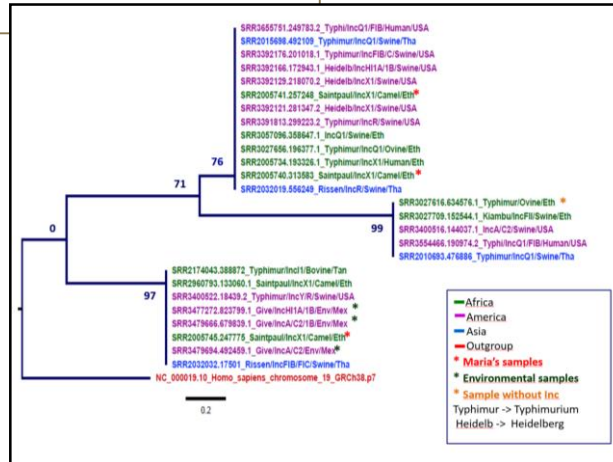
**Project Type:** Genome sequencing and assembly  
**Attributes:** Scope: Multisite; Material: Genome; Capture: Whole; Method type: Sequencing  
**Relevance:** Medical  
**Project Data:**

Resource Name	Number of Links
BioSample	924

**SRA Data Details**

Parameter	Value
Data volume, Gbases	4
Data volume, Mbytes	2749

**Lineage:** Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica* [Taxonomy ID: 28901]  
**Submission:** Registration date: 20-Feb-2015  
US Food and Drug Administration



### 1000+ MDR *Salmonella* WGS partnership

- Brazil (104)
- Ethiopia (401)
- Kenya (86)
- Mexico (63)
- Tanzania (64)
- Thailand (60)
- U.S. –OSU (247)



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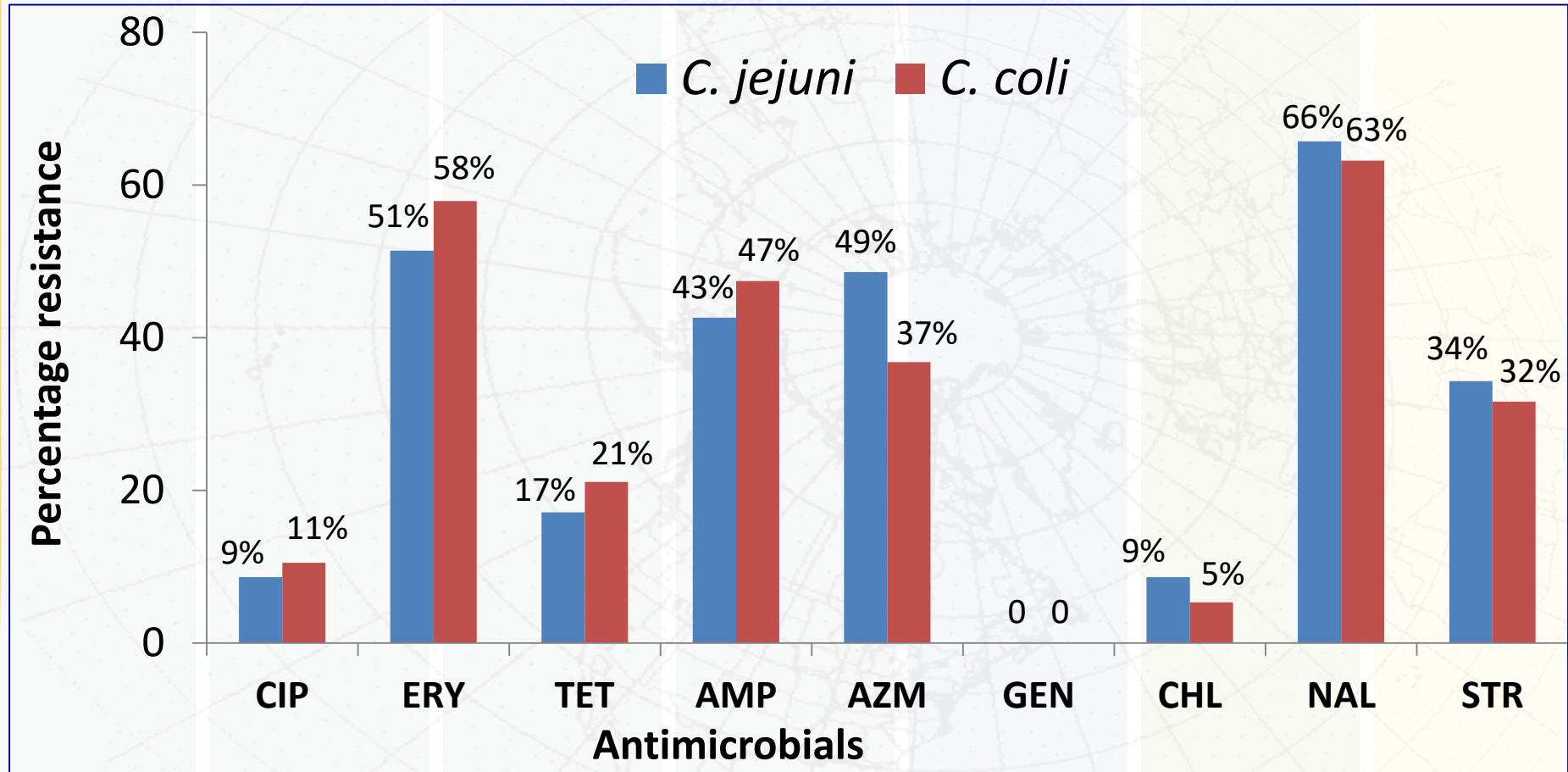
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# MOLEC. EPID OF CAMPYLOBACTER IN TANZANIA

Source	No. of Sample	Morphological Positive samples		No. (%) of PCR analyzed positive for:			
		No.	%	<i>C. jejuni</i>	<i>C. coli</i>	<i>C. jejuni</i> / <i>C. coli</i>	OTC*
Milk	284	38	13.4	21 (55.3)	12 (31.6)	0	5 (1.8)
Carcass swabs	253	24	9.5	15 (62.5)	7 (29.2)	1 (4.2)	1 (4.2)
<b>Total</b>	<b>537</b>	<b>62</b>	<b>11.6</b>	<b>36 (58.1)</b>	<b>19 (30.7)</b>	<b>1 (1.6)</b>	<b>6 (9.7)</b>

# ANTIMICROBIAL RESISTANCE

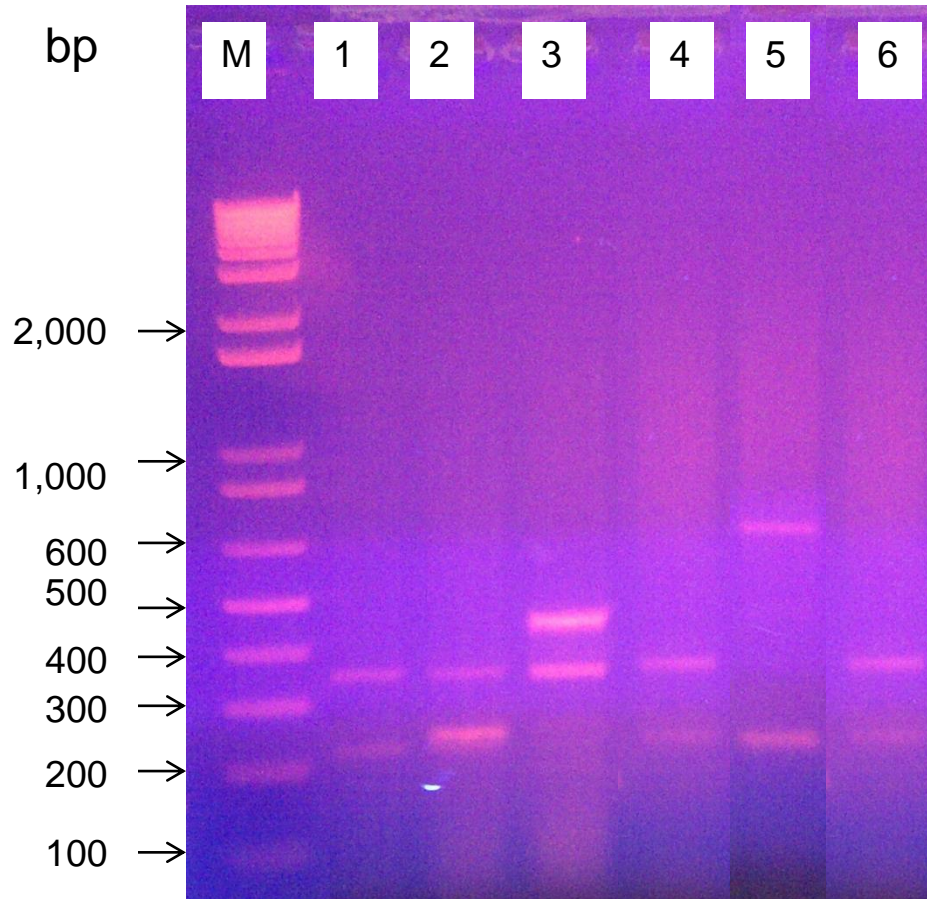






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Resistance genes detected	Sources of isolates	
	Milk [No. (%)]	Meat [No. (%)]
<i>tet (O)</i>	7 (21.2)	2 (9.5)
<i>aph -3-1</i>	-	1 (4.8)
<i>bla</i> <sub>OXA-61</sub>	3 (9.1)	3 (14.3)
<i>cmeB</i>	4 (12.1)	1 (4.8)
<i>cmeB / bla</i> <sub>OXA-61</sub>	2 (6.1)	5 (23.8)
<i>tet (O) / bla</i> <sub>OXA-61</sub>	1 (3)	1 (4.8)
<i>cmeB / tet (O)</i>	1 (3)	-
<i>tet(O)/cmeB / bla</i> <sub>OXA-61</sub>	1 (3)	1 (4.8)



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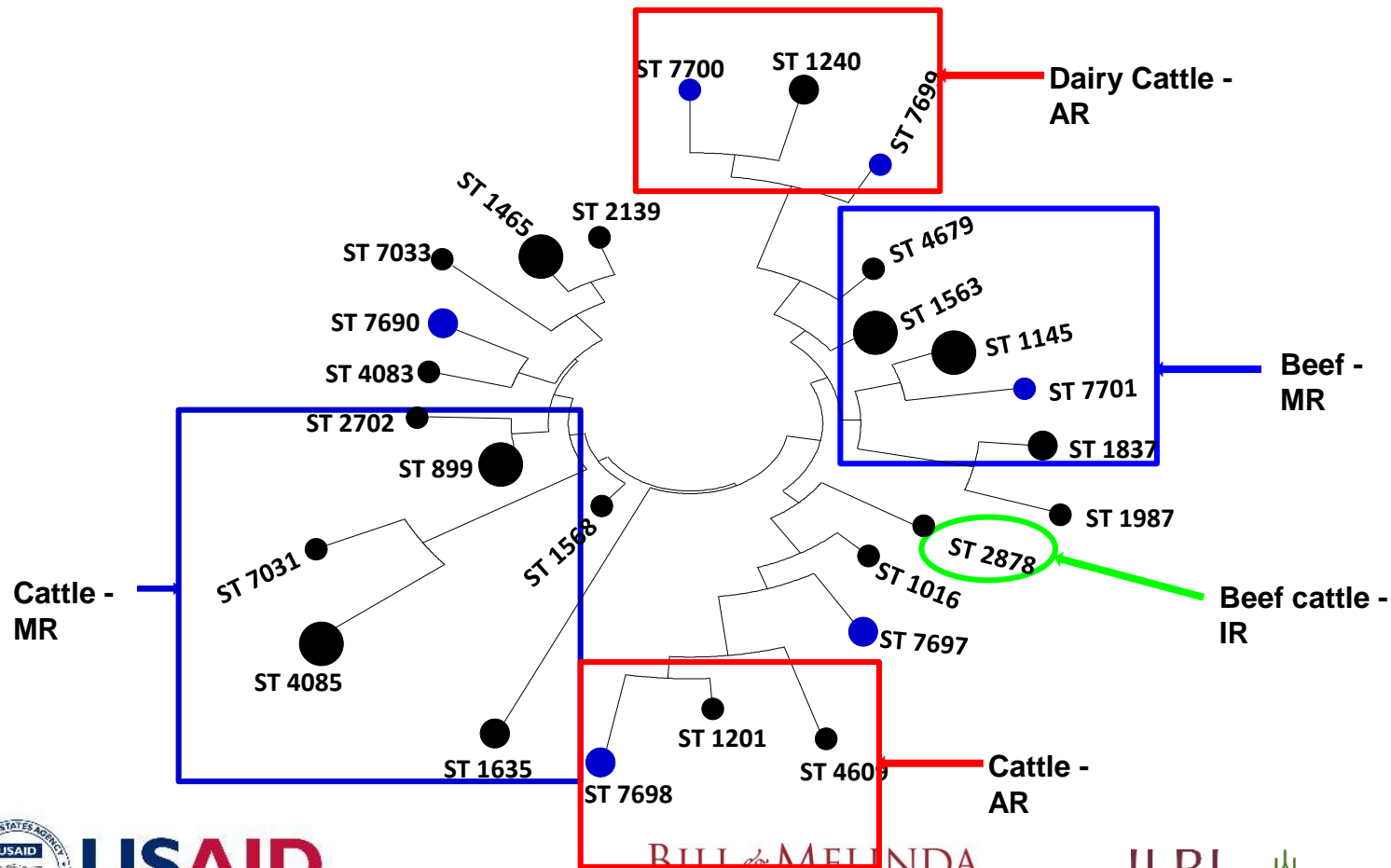
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## MULTI-LOCUS SEQUENCE TYPING (MLST)



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FOODBORNE PATHOGENS AND DISEASE  
Volume 11, Number 11, 2014  
© Mary Ann Liebert, Inc.  
DOI: 10.1089/fpd.2014.1794

## Phenotypic and Genotypic Diversity of Thermophilic *Campylobacter* spp. in Commercial Turkey Flocks: A Longitudinal Study

Isaac P. Kashoma,<sup>1-3</sup> Anand Kumar,<sup>1,2</sup> Yasser M. Sanad,<sup>1,2</sup> Wondwossen Gebreyes,<sup>2,4</sup>  
Rudovick R. Kazwala,<sup>3,4</sup> Rebecca Garabed,<sup>2</sup> and Gireesh Rajashekara<sup>1,2,4</sup>

MICROBIAL DRUG RESISTANCE  
Volume 22, Number 1, 2016  
© Mary Ann Liebert, Inc.  
DOI: 10.1089/mdr.2015.0079

## Prevalence and Antimicrobial Resistance of *Campylobacter* Isolated from Dressed Beef Carcasses and Raw Milk in Tanzania

Isaac P. Kashoma,<sup>1,2</sup> Issmat I. Kassem,<sup>3</sup> Julius John,<sup>1,2</sup> Beda M. Kessy,<sup>1</sup> Wondwossen Gebreyes,<sup>2,4</sup>  
Rudovick R. Kazwala,<sup>1,2</sup> and Gireesh Rajashekara<sup>1-3</sup>

frontiers  
in Microbiology

ORIGINAL RESEARCH  
published: 12 November 2015  
doi: 10.3389/fmicb.2015.01240



## Antimicrobial Resistance and Genotypic Diversity of *Campylobacter* Isolated from Pigs, Dairy, and Beef Cattle in Tanzania

Isaac P. Kashoma<sup>1,2,3</sup>, Issmat I. Kassem<sup>1</sup>, Anand Kumar<sup>1</sup>, Beda M. Kessy<sup>2</sup>,  
Wondwossen Gebreyes<sup>2,4</sup>, Rudovick R. Kazwala<sup>2,3</sup> and Gireesh Rajashekara<sup>1,2,4\*</sup>



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## OHIO STATE- GLOBAL ONE HEALTH



THE OHIO STATE UNIVERSITY

Global One Health initiative (GOHi)

**The global dynamics makes One Health a critical need.**

### **The Global Risk;**

- Water Crises;
- Failure of climate change adaptation;
- Global travel;
- Man-made environmental catastrophes;
- Biodiversity loss and ecosystem collapse;
- Large-scale migration...

**Consequences-** Much complex and wider in spectrum incl. cancer and other NCDs.



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Global One Health initiative (GOHi)

## Mission

*To expand capacity Globally (local, national, regional and international) for a One Health approach via education, training, implementation science and outreach to efficiently and effectively address diseases at the interface of humans, animals, plants and the environment.*

## Vision

*Capable institutional systems and professionals for a healthy and enduring community.*



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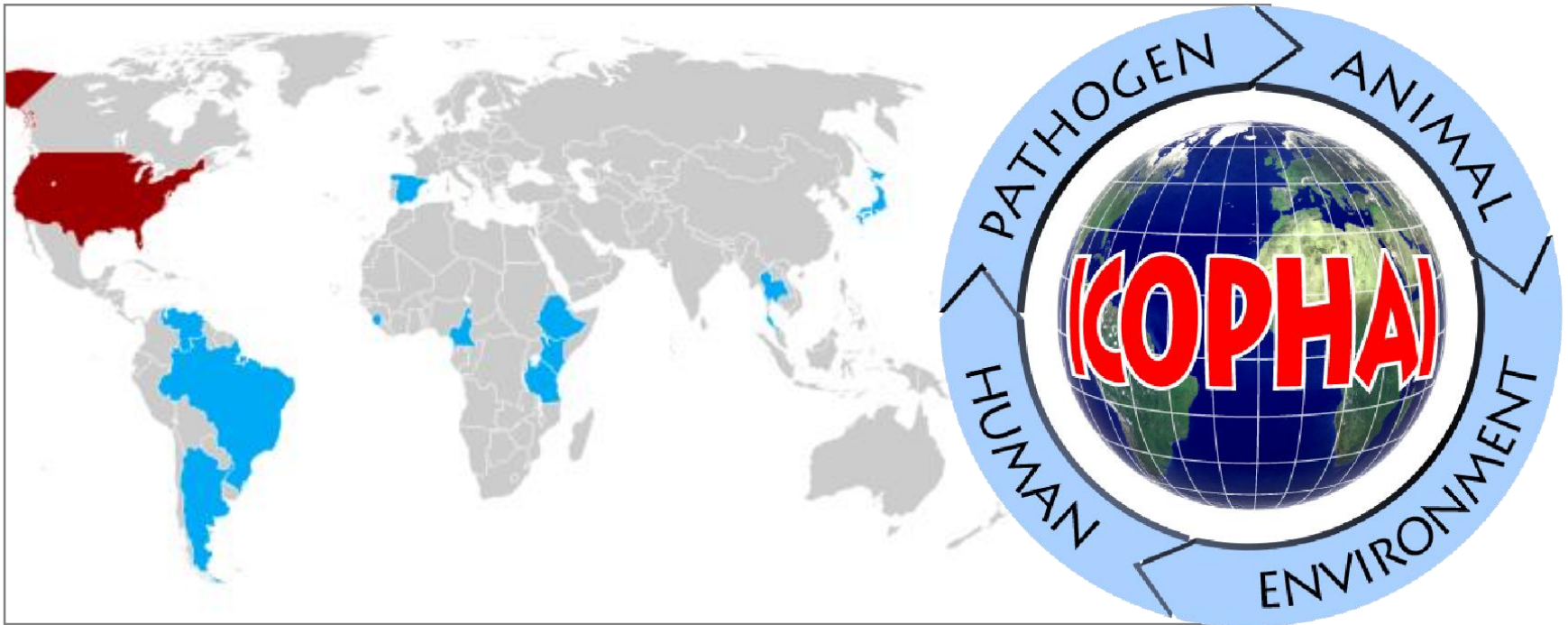
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## GLOBAL ONE HEALTH KNOWLEDGE-SHARING



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