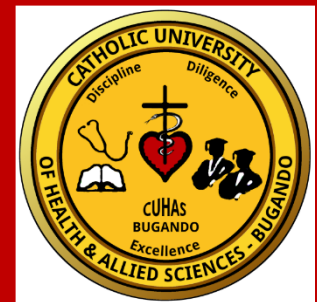




## **SOUTHERN AFRICAN CENTRE FOR INFECTIOUS DISEASE SURVEILLANCE**

# **The SACIDS One Health Approach to Genomics Driven Surveillance for Antimicrobial Resistance - a potential collaboration with EAIDSNet**

Stephen E. Mshana, MD, M.Med, PhD



# Background

- Burden of multidrug resistant bacteria across the globe is worrisome due to cost, complications and deaths.
- In Tanzania, infections like UTI which account for up to 39% of infections in children are no longer treatable.

## PRESS RELEASE: High-Level Meeting on Antimicrobial Resistance

21 September 2016 in Media, PGA Press Releases



OPGA/WHO/FAO/OIE Joint News Release



## HIGH-LEVEL MEETING ON ANTIMICROBIAL RESISTANCE



21 SEPTEMBER 2016, UN HEADQUARTERS, NEW YORK

## WHO PRIORITY PATHOGENS LIST FOR R&D OF NEW ANTIBIOTICS

### Priority 1: CRITICAL<sup>#</sup>

*Acinetobacter baumannii*, carbapenem-resistant

*Pseudomonas aeruginosa*, carbapenem-resistant

*Enterobacteriaceae*\*, carbapenem-resistant, 3<sup>rd</sup> generation  
cephalosporin-resistant

## Cont....

- In developing countries, limited information exists on circulating genotypes in humans, animals and environment
- WGS is a potential tool to delineate transmission potential
- SACIDS has been conducting studies to assess the circulating ESBL genotypes in humans, animals and environment in the North Western, Tanzania

# Methods

- A total of 600 humans, 984 animals, 70 environment samples were investigated
  - 300 neonates with clinical sepsis
- 100 ESBL producing Bacteria: *Escherichia coli* (55) and *Klebsiella pneumoniae* (53) underwent WGS
  - 36 PCR and sequencing typing
- Sequence analysis (Center for genomic epidemiology database software)

# RESULTS

## ESBL-PE in humans in the community

Mshana et al. *BMC Infectious Diseases* (2016) 16:187  
DOI 10.1186/s12879-016-1527-x

BMC Infectious Diseases

### RESEARCH ARTICLE

### Open Access



## Predictors of *bla*<sub>CTX-M-15</sub> in varieties of *Escherichia coli* genotypes from humans in community settings in Mwanza, Tanzania

Stephen E. Mshana<sup>1\*</sup>, Linda Falgenhauer<sup>2,3</sup>, Mariam M. Mirambo<sup>1</sup>, Martha F. Mushi<sup>1</sup>, Nyambura Moremi<sup>1</sup>, Rachel Julius<sup>1</sup>, Jeremiah Seni<sup>1</sup>, Can Imirzalioglu<sup>2,3</sup>, Mecky Matee<sup>4</sup> and Trinad Chakraborty<sup>2,3</sup>

- 334 humans, 55 (16.5 %) carried ESBL-PE
- The *bla*<sub>CTX-M-15</sub> allele was detected 37/42 (88.1%)
- The *bla*<sub>CTX-M-15</sub> was located in multiple IncY and IncF plasmids
- Eight Sequence types were obtained, ST 131, ST 38, ST 617

# Cont.....

PLoS One. 2017 Sep 12;12(9):e0184592. doi: 10.1371/journal.pone.0184592. eCollection 2017.

## **Faecal carriage of CTX-M extended-spectrum beta-lactamase-producing Enterobacteriaceae among street children dwelling in Mwanza city, Tanzania.**

Moremi N<sup>1,2</sup>, Claus H<sup>2</sup>, Vogel U<sup>2</sup>, Mshana SE<sup>1</sup>.

- Intestinal carriage of EPE was found in 34 (31.8%)
  - *bla*CTX-M-15 was detected in 75% (27/36) of ESBL isolates
- Sequence types (STs) 131, 10, 448 and 617 were the most prevalent in *E. coli*

# ESBL-PE in animals

- We detected 130 (21.7%) animals carrying ESBL-producing bacteria
- All isolates harbored the *bla*CTX-M-15 allele and resistance genes (strA , strB, aac(6')-Ib-cr, and qnrS1)
- Fourteen different sequence types were detected of which ST617 (7/25), ST131(6/25), ST2852(6/25), ST 38

## Multiple ESBL-Producing *Escherichia coli* Sequence Types Carrying Quinolone and Aminoglycoside Resistance Genes Circulating in Companion and Domestic Farm Animals in Mwanza, Tanzania, Harbor Commonly Occurring Plasmids

OPEN ACCESS

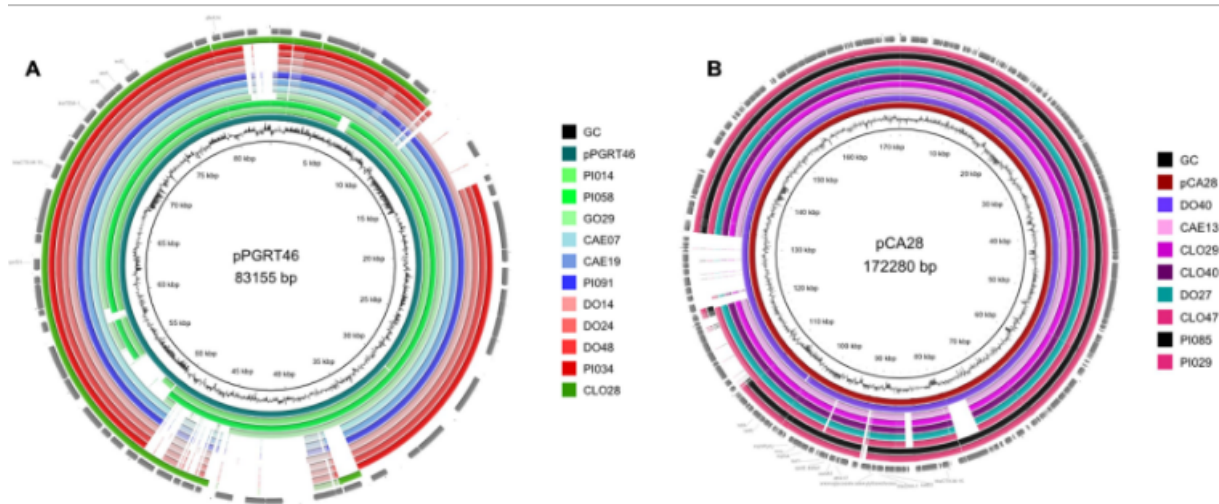
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# Plasmid analysis



pPGRT46 detected in Nigeria and pCA28, previously detected in isolates from the US.

**A novel plasmid carrying blaCTX-M-15 identified in commensal *Escherichia coli* from healthy pregnant women in Ibadan, Nigeria.**

Fortini D<sup>1</sup>, Fashae K<sup>2</sup>, Villa L<sup>1</sup>, Feudi C<sup>1</sup>, García-Fernández A<sup>1</sup>, Carattoli A<sup>3</sup>.

Antimicrob Agents Chemother. 2015;59(6):3002-7. doi: 10.1128/AAC.04772-14. Epub 2015 Mar 9.

**Complete nucleotide sequences of bla(CTX-M)-harboring IncF plasmids from community-associated *Escherichia coli* strains in the United States.**

Li JJ<sup>1</sup>, Spychala CN<sup>2</sup>, Hu F<sup>3</sup>, Sheng JF<sup>4</sup>, Doi Y<sup>5</sup>.



# ESBL-PE in environment and Fish

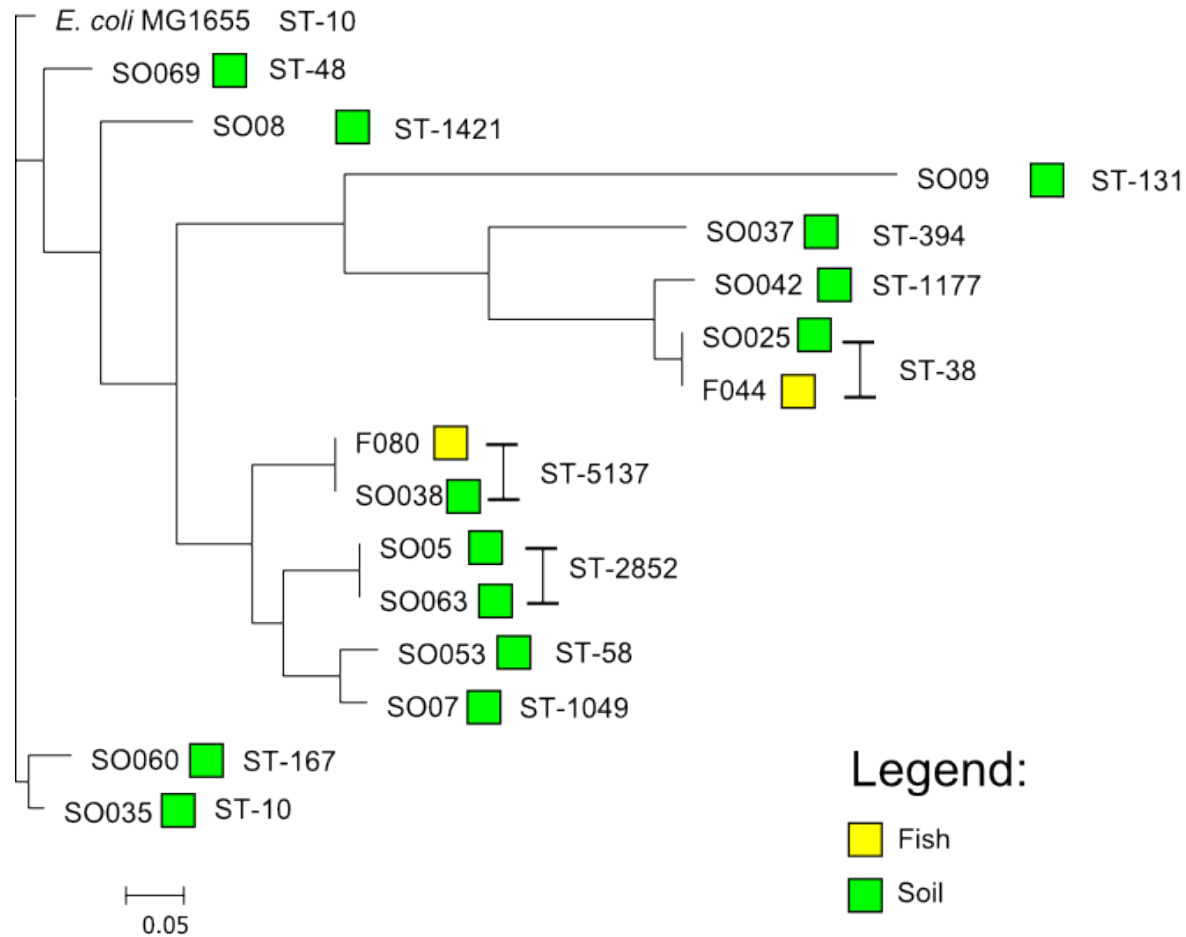


## Predominance of CTX-M-15 among ESBL Producers from Environment and Fish Gut from the Shores of Lake Victoria in Mwanza, Tanzania

Nyambura Moremi<sup>1</sup>, Elizabeth V. Manda<sup>1</sup>, Linda Falgenhauer<sup>2,3</sup>, Hiren Ghosh<sup>2,3</sup>, Can Imirzaloglu<sup>2,3</sup>, Mecky Matee<sup>4</sup>, Trinad Chakraborty<sup>2,3</sup> and Stephen E. Mshana<sup>1\*</sup>

- 26/196(13.3%) fish contained ESBL-PE
- 39/73(53.4%) environmental samples ESBL-PE
- IncY plasmids carrying *bla*CTX-M-15, qnrS1, strA and strB were detected in five environmental *E. coli* isolates and in one *E. coli* isolate from fish.

# Phylogenetic tree of Fish and environmental *E. coli*-PE



# Neonatal sepsis




- The high prevalence of *bla*<sub>CTX-M-15</sub> observed among ESBL producing *K. pneumoniae*
- Clones such as ST14 and ST45.
- Presence of *Acinetobacter baumannii* carrying blaNDM-1 colonizing a neonates
- ST-45 common both in blood and in colonization
- Change in epidemiology in 2010 predominant ST was ST-14 in 2016 ST-45

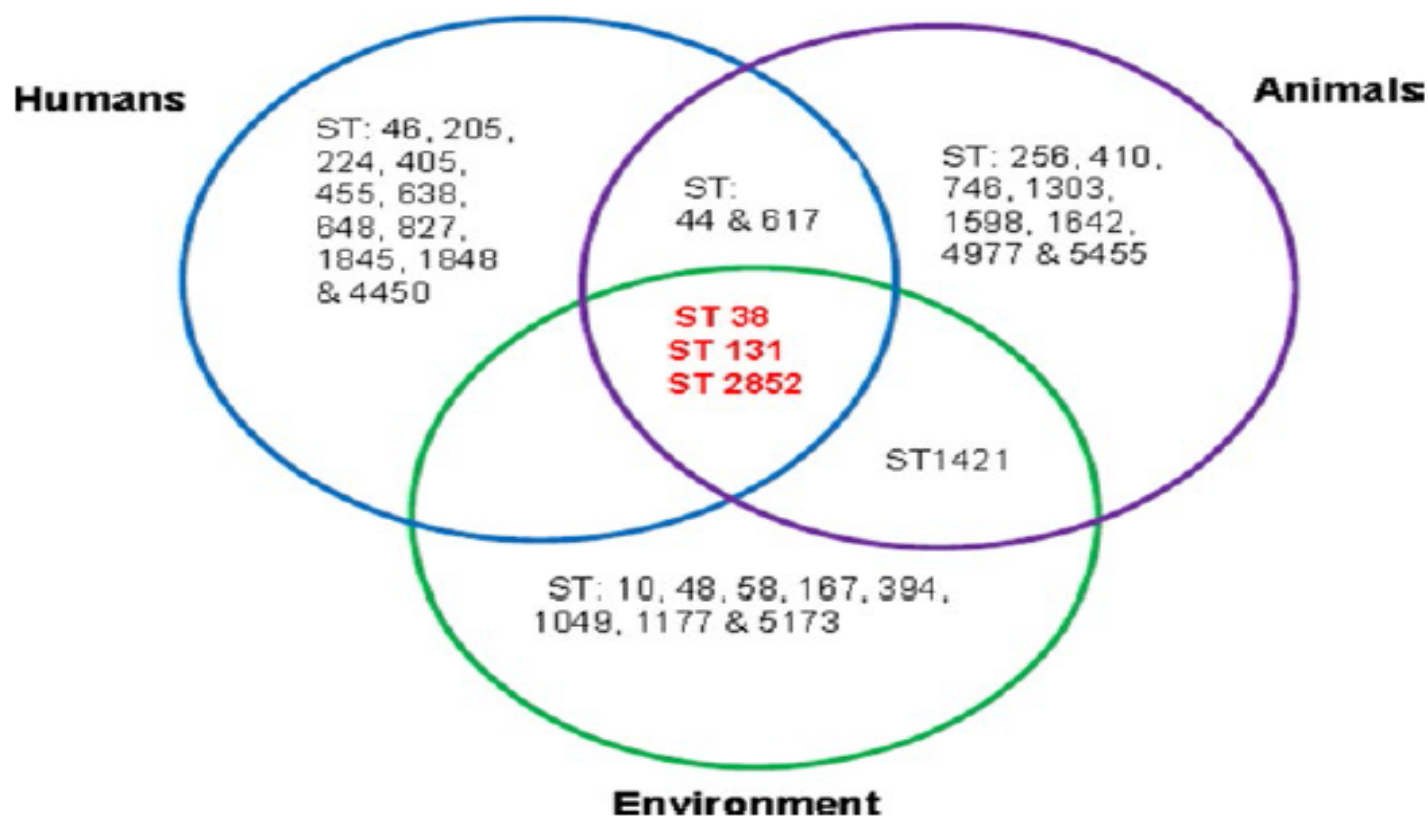
[BMC Infect Dis. 2013 Oct 7;13:466. doi: 10.1186/1471-2334-13-466.](#)

**Predominance of *Klebsiella pneumoniae* ST14 carrying CTX-M-15 causing neonatal sepsis in Tanzania.**

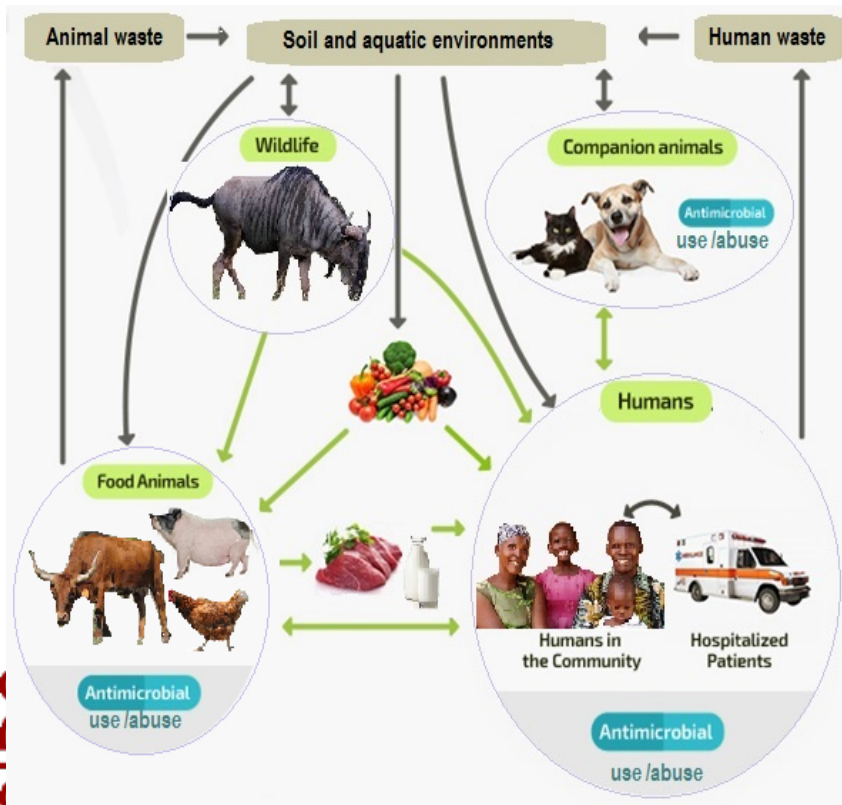
[Mshana SE<sup>1</sup>](#), [Hain T](#), [Domann E](#), [Lyamuya EF](#), [Chakraborty T](#), [Imirzalioglu C](#).

# Preliminary insights into the occurrence of similar clones of extended-spectrum beta-lactamase-producing bacteria in humans, animals and the environment in Tanzania: A systematic review and meta-analysis between 2005 and 2016

J. Seni<sup>1,2</sup>  | N. Moremi<sup>1</sup> | M. Matee<sup>3</sup> | F. van der Meer<sup>4</sup> |  
R. DeVinney<sup>2</sup> | S. E. Mshana<sup>1</sup> | J. D. D Pitout<sup>2</sup>



# SACIDS advocates a 2-Level One Health approach to Anti-microbial resistance surveillance



- **Level 1: phenotypic** screening/surveys by national public health and veterinary laboratories
- **Level 2: genomic** surveillance by SACIDS-ACE partnership and/or other specialised laboratories, to include resistome flows across human-animal-environment compartments

# Conclusion

- There is a pan-species distribution of ESBL-producing *E. coli* clonal groups in farming communities
- Persistence of *bla*CTX-M-15 in the Mwanza city is complex,
  - involves both clonal spread of resistant strains and dissemination by commonly occurring IncY plasmids
- Genomic surveillance of resistance pathogens is cost-effective approach to track AMR strains
- A One Health study of the flow of antimicrobial resistomes in different ecosystems will lead to:
  - Understanding of the antimicrobial resistance complexity,
  - rational selection/definition of cost-effective interventions and policy.

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