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Oral Session 4: Antimicrobial ResistanceDate: Saturday, Nov 19, 2022 Time: 10:30-12:00Venue: Meeting Rooms 304 & 305

EXTENT OF ANTIMICROBIAL RESISTANCE (AMR) IN AN ECOSYSTEM WITH ORGANIZED LIVESTOCK FARMING IN SRI LANKA.

B.M.Y.I. Basnayake [1], G.G.T. Nisansala [1 2], P.I.J.B. Wijewickrama [1], U.S. Weerathunga [1], K.W.M.Y.D. Gunasekara [1], D.B.N. Pushpakumara [3], N.K. Jayasekera [4], A.W. Kalupahana [5], R.S. Kalupahana [1], A. Silva-Fletcher [6], K.S.A. Kottawatta [1]

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Intro

Combating AMR is a major challenge in current era. This study aims to investigate the distribution of AMR and the Extended Spectrum Beta Lactamase (ESBL) among livestock, wild animals and environment in an ecosystem with a high density of

organized livestock farms in Sri Lanka.

Methods

One square km area at Kosgama was mapped using GPS as the study area. In total 222 samples: feces from livestock and wild animals, soil and water from environment, were collected and *Escherichia coli* (*E. coli*) were isolated. Maximum of two *E. coli* per sample were tested to profile AMR for 12 antimicrobials. Among the *E. coli,* ESBL producers were screened and ESBL expressions were phenotypically detected using cefpodoxime combination disk kit. Prevalence of common ESBL genes: *bla*CTX-M, *bla*TEM, *bla*SHV was detected by PCR.

Findings

Seventy seven percent (61/79) of livestock, 62% (42/68) of wild animals, 79% (35/44) of soil and 68% (21/31) of water samples were positive for *E. coli*. Of the *E. coli* tested for AMR in livestock, the highest resistance (51.7%) was detected against tetracycline followed by ampicillin (39.4%) and nalidixic acid (37.7%). *E. coli* from wildlife (45%) and soil/ water (46.5%) reflected the highest resistance against streptomycin. Of the *E. coli* isolates, 31.5% (36/114) of livestock, 7.3% (6/82) of wildlife, 12.1% (8/66) of soil and 31.4% (11/35) of water were Multi Drug Resistant (MDR). Among 37 *E. coli* screened as ESBL, two from a mongoose (*Herpestes edwardsii*) were phenotypically positive for ESBL. Prevalence of ESBL genes were ~49% (18/37) of which 17 carried *blaTEM* gene and one that expressed ESBL phenotypically contained *bla*CTX-M gene. Gene *bla* SHV was not detected.

Conclusion

Unexpected presence of AMR, MDR and ESBL *E. coli* particularly in wild animals and environment throw light on necessity of prudent use of antimicrobials.

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Intro: Combating AMR is a major challenge in current era. This study aims to investigate the distribution of AMR and the Extended Spectrum Beta Lactamase (ESBL) among livestock, wild animals and environment in an ecosystem with a high density of organized livestock farms in Sri Lanka.

Methods: One square km area at Kosgama was mapped using GPS as the study area. In total 222 samples: feces from livestock and wild animals, soil and water from environment, were collected and *Escherichia coli* (*E. coli*) were isolated. Maximum of two *E. coli* per sample were tested to profile AMR for 12 antimicrobials. Among the *E. coli*, ESBL producers were screened and ESBL expressions were phenotypically detected using cefpodoxime combination disk kit. Prevalence of common ESBL genes: *bla*CTX-M, *bla*TEM, *bla*SHV was detected by PCR.

Findings: Seventy seven percent (61/79) of livestock, 62% (42/68) of wild animals, 79% (35/44) of soil and 68% (21/31) of water samples were positive for *E. coli*. Of the *E. coli* tested for AMR in livestock, the highest resistance (51.7%) was detected against tetracycline followed by ampicillin (39.4%) and nalidixic acid (37.7%). *E. coli* from wildlife (45%) and soil/ water (46.5%) reflected the highest resistance against streptomycin. Of the *E. coli* isolates, 31.5% (36/114) of livestock, 7.3% (6/82) of wildlife, 12.1% (8/66) of soil and 31.4% (11/35) of water were Multi Drug Resistant (MDR). Among 37 *E. coli* screened as ESBL, two from a mongoose (*Herpestes edwardsii*) were phenotypically positive for ESBL. Prevalence of ESBL genes were ~49% (18/37) of which 17 carried *blaTEM* gene and one that expressed ESBL phenotypically contained *bla*CTX-M gene. Gene *bla* SHV was not detected.

Conclusion: Unexpected presence of AMR, MDR and ESBL *E. coli* particularly in wild animals and environment throw light on necessity of prudent use of antimicrobials.

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Oral Session 4: Antimicrobial Resistance

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LARGE RETROSPECTIVE WGS STUDY DESCRI GENOMIC EPIDEMIOLOGY OF S. AUREUS IN AND REVEALS TWO NOVEL MULTI-DRUG RESISTANT SUB-LINEAGES OF S. AUREUS CL COMPLEX 22

V. Shamanna [1,2], M. Abrudan [3], G. Nagaraj [2], S. Gregorio [4], A. Underwood [3], S. Argimón [3], V. Govindan [2], S. Dharmavaram [2], D. Aanensen, K.L. Ravikumar [2]

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Intro: S. aureus is a major pathogen in In mial infections, but little is known about its ology and mechanisms of resistance in hospi use WGS to characterize 508 S. aureus clini across India and analyze them in a global co

Methods: Whole-genome sequencing wa clinical isolates of S. aureus collected from 17 India between 2014 and 2019 with the Illu genotypes were predicted using Staphopia. Is SCCmec cassettes were further characterized quencing. A temporal analysis of clonal compl lates from 14 different studies was performed

Findings: Sequencing results confirmed 4 reus. ST22, ST772 & ST239 were the major clo depth analysis of the 175 CC22 Indian isolate ST22 MRSA clones, PVL+ and one harboring poral analysis showed that these two ST22 cl mon ancestor in the 1980s and they became year 2000 in India. Analyzing these in a glob evidence of transmission of the two Indian cl the world.

Discussion: Temporal analysis shows tha originated around 2010 in India and we four mission of the two Indian clones in other pa novel SCCmec types identified in our study ar long reads to understand their genetic structu

Conclusion: Our study describes a large re sampled from India. By comparing the Indian show the evidence of the international transm isolates. Even though the two of the major do and ST239) using WGS have been reported, that describes the third dominant clone (ST22

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