Investigation of Antimicrobial Resistance in *Escherichia Coli* Isolated from Wild Animals Presented to a Regional Wildlife Health Centre in Sri Lanka

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Introduction

Resistance to antimicrobials is a worldwide problem in both human and veterinary medicine. Exposure to antimicrobials is commonly attributed to maintenance of resistance in bacterial populations and commensals like *Escherichia coli* (*E. coli*), can easily acquire and transfer resistance genes. Antimicrobial Resistance (AMR) bacteria are extremely important to human health, but the wild reservoirs of resistance determinants are poorly understood [1]. Wild animals provide a biological mechanism for the spread of antibiotic resistance genes [1]. Even though significant resistance cannot be expected in wild animals, confirmation is important. The present study was conducted to identify antimicrobial resistant profiles of *E. coli* isolated from faecal samples of wild birds, mammals and reptiles (n=54) over a 6 month period starting from December 2015.

Objective

To identify the level of antimicrobial resistance among faecal isolates of *E. coli* in wild animal species in the Eastern Wildlife Health Region (EHWHR) of Sri Lanka.

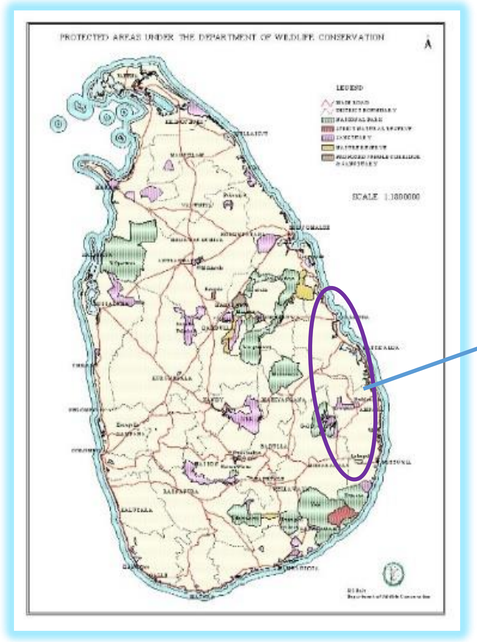

Figure 1: Map of Sri Lanka

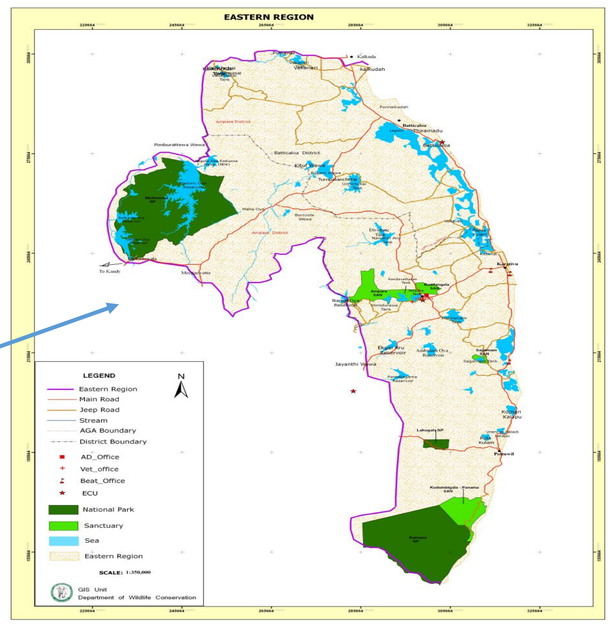

Figure 2: Map of Eastern Wildlife Health Region

Materials & Methods

- Wild animals brought to the EWHR (Fig. 2) for treatment and rehabilitation during the period December 2015 to May 2016 were subjected to the study.
- A single faecal sample (clinical rectal swab or swab from freshly voided faeces) was taken from each animal (N=54) before any treatment or feed was given.
- Isolation and identification of *E. coli* were done according to modified SLS 516: part 3: 1982 protocols.
- Identified isolates were subjected to disk diffusion assay with 12 antimicrobials according to CLSI (2013) guidelines.

Results & Discussion

- Of the 54 wild animal samples, 25 (46.3%) were from mammals, 26 (48.1%) were from birds and 3 (5.6%) were from reptiles. Out of these, 9 (36%) samples from wild mammals were positive for *E. coli* and 11 (42.3%) samples from wild birds were positive. No *E. coli* isolates were recovered from reptiles.

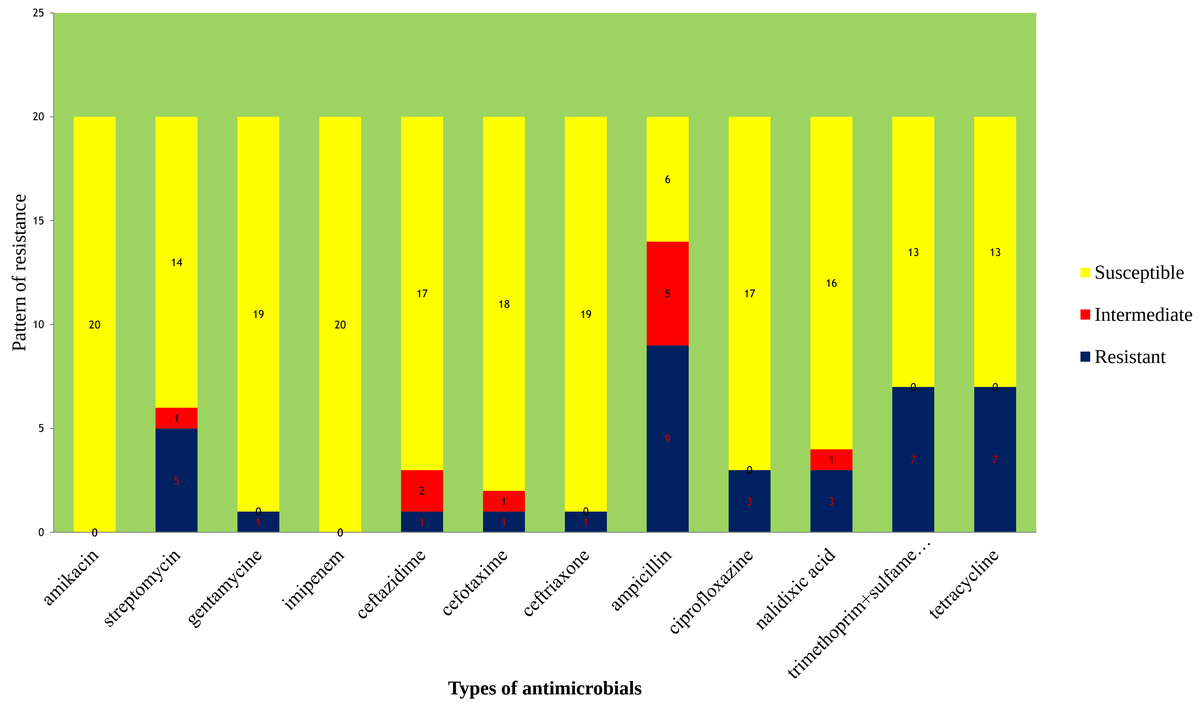

Figure 3: Numbers of *E. coli* isolates with their respective antimicrobial susceptibility levels

- Forty five percent (9/20) of *E. coli* isolates were resistant to ampicillin while 35% (7/20) were resistant to each of trimethoprim-sulfamethoxazole and tetracycline. The percentages of *E. coli* isolates that were resistant to streptomycin, ciprofloxacin and nalidixic acid were 25%, 15% and 15% respectively (Fig. 3).
- There are degrees to which wildlife are really wild, and there is good evidence that proximity to human populations, rather than direct antibiotic use on the land, is sufficient to substantially affect the gut flora of local wildlife [2]. In our study there were two *E. coli* isolates from wild animals which showed multi resistance (resistance to more than 6 antimicrobials). These species were Jungle Cat (*Felis chaus*, Fig. 4) and Jungle Fowl (*Gallus lafayetti*. Fig. 5), both of which are found close to human habitats and may be frequently feed on domestic animals and their wastes.

Figure 4: Jungle cat (*Felis chaus*)

Figure 5: Jungle fowl (*Gallus lafayettii*)

Conclusion and a further study

- Based on our data, although majority of the isolates were susceptible to tested antimicrobials, the resistant isolates indicate the possible environmental contamination with resistant genes.
- Further detailed study including wild animals representing all the local wild life health regions is warranted for proper understanding of the AMR levels of bacterial pathogens in wild animals in Sri Lanka.

References

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