

## Understanding the Diversity of Antimicrobial Resistance among Wild Animals, Livestock and Associated Environment in a Rural Ecosystem in Sri Lanka

**Authors :** B. M. Y. I. Basnayake, G. G. T. Nisansala, P. I. J. B. Wijewickrama, U. S. Weerathunga, K. W. M. Y. D. Gunasekara, N. K. Jayasekera, A. W. Kalupahana, R. S. Kalupahana, A. Silva- Fletcher, K. S. A. Kottawatta

**Abstract :** Antimicrobial resistance (AMR) has attracted significant attention worldwide as an emerging threat to public health. Understanding the role of livestock and wildlife with the shared environment in the maintenance and transmission of AMR is of utmost importance due to its interactions with humans for combating the issue in one health approach. This study aims to investigate the extent of AMR distribution among wild animals, livestock, and environment cohabiting in a rural ecosystem in Sri Lanka: Hambegamuwa. One square km area at Hambegamuwa was mapped using GPS as the sampling area. The study was conducted for a period of five months from November 2020. Voided fecal samples were collected from 130 wild animals, 123 livestock: buffalo, cattle, chicken, and turkey, with 36 soil and 30 water samples associated with livestock and wildlife. From the samples, *Escherichia coli* (*E. coli*) was isolated, and their AMR profiles were investigated for 12 antimicrobials using the disk diffusion method following the CLSI standard. Seventy percent (91/130) of wild animals, 93% (115/123) of livestock, 89% (32/36) of soil, and 63% (19/30) of water samples were positive for *E. coli*. Maximum of two *E. coli* from each sample to a total of 467 were tested for the sensitivity of which 157, 208, 62, and 40 were from wild animals, livestock, soil, and water, respectively. The highest resistance in *E. coli* from livestock (13.9%) and wild animals (13.3%) was for ampicillin, followed by streptomycin. Apart from that, *E. coli* from livestock and wild animals revealed resistance mainly against tetracycline, cefotaxime, trimethoprim/ sulfamethoxazole, and nalidixic acid at levels less than 10%. Ten cefotaxime resistant *E. coli* were reported from wild animals, including four elephants, two land monitors, a pigeon, a spotted dove, and a monkey which was a significant finding. *E. coli* from soil samples reflected resistance primarily against ampicillin, streptomycin, and tetracycline at levels less than in livestock/wildlife. Two water samples had cefotaxime resistant *E. coli* as the only resistant isolates out of 30 water samples tested. Of the total *E. coli* isolates, 6.4% (30/467) was multi-drug resistant (MDR) which included 18, 9, and 3 isolates from livestock, wild animals, and soil, respectively. Among 18 livestock MDRs, the highest (13/ 18) was from poultry. Nine wild animal MDRs were from spotted dove, pigeon, land monitor, and elephant. Based on CLSI standard criteria, 60 *E. coli* isolates, of which 40, 16, and 4 from livestock, wild animal, and environment, respectively, were screened for Extended Spectrum  $\beta$ -Lactamase (ESBL) producers. Despite being a rural ecosystem, AMR and MDR are prevalent even at low levels. *E. coli* from livestock, wild animals, and the environment reflected a similar spectrum of AMR where ampicillin, streptomycin, tetracycline, and cefotaxime being the predominant antimicrobials of resistance. Wild animals may have acquired AMR via direct contact with livestock or via the environment, as antimicrobials are rarely used in wild animals. A source attribution study including the effects of the natural environment to study AMR can be proposed as this less contaminated rural ecosystem alarms the presence of AMR.

**Keywords :** AMR, *Escherichia coli*, livestock, wildlife

**Conference Title :** ICOH 2022 : International Conference on One Health

**Conference Location :** London, United Kingdom

**Conference Dates :** May 26-27, 2022