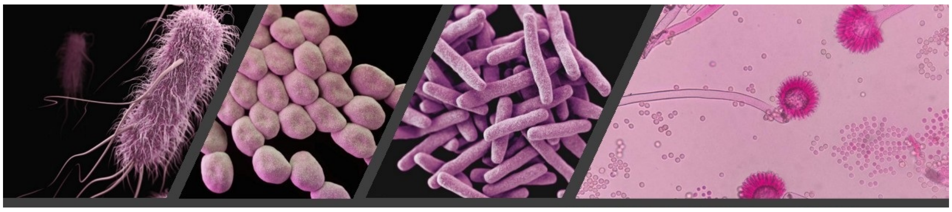

Abstract ID : **130**

The burden and drivers of antimicrobial resistance in commensal E.coli from shelter dogs in North Macedonia

Content

Dog shelters, with their dynamic populations from varied backgrounds, serve as critical environments for antimicrobial resistance (AMR). This study aimed to determine the prevalence of AMR in commensal E. coli in shelter dogs in North Macedonia and pinpoint contributing factors within shelter management.

A total of 112 E. coli isolates were recovered from 119 fecal samples across six shelters. Antimicrobial susceptibility profiles were established via broth microdilution and resistance genes were identified by PCR. Shelter practices were assessed through a questionnaire.

High resistance rates were observed for sulfamethoxazole (68.8%) and ampicillin (52.7%). Multidrug resistance (MDR) was detected in 50% of isolates. Notably, 15.1% of isolates were confirmed as ESBL producers, carrying the blaCTX-M and blaTEM genes. The plasmid-mediated AmpC gene blaCMY-2 was detected in 14.3% of all isolates, indicating potential for horizontal gene transfer. A strong statistical association was found between intensive antimicrobial use (AMU) and ESBL prevalence. All ESBL-producing isolates came from shelters with high AMU. Longer shelter stays also correlated significantly with increased AMR.

Shelter dogs in North Macedonia are reservoirs of MDR and ESBL-producing E. coli. The study highlights that specific shelter practices, especially intensive AMU, are critical drivers of AMR. These findings underscore the urgent need for antimicrobial stewardship programs in shelters.

Keywords

multidrug resistance, antimicrobial use, ESBL, canine

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