



RESEARCH USING SAVSNET DATA

TEMPORAL, SPATIAL AND GENOMIC ANALYSES OF ENTEROBACTERIACEAE CLINICAL ANTIMICROBIAL RESISTANCE IN COMPANION ANIMALS REVEALS PHENOTYPES AND GENOTYPES OF ONE HEALTH CONCERN

Full paper published in the *Frontiers in Microbiology* available [here](#)

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ONE HEALTH

Antimicrobial resistance (AMR) is a globally important one health threat. The impact of resistant infections on companion animals, and the potential public health implications of such infections, has not been widely explored, largely due to an absence of structured population-level data.

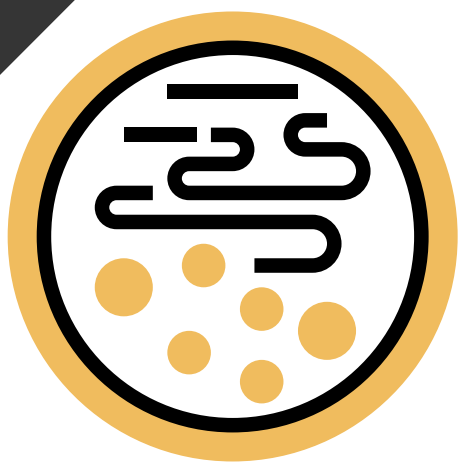
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AIM OF STUDY

We aimed to efficiently capture and repurpose antimicrobial susceptibility test (AST) results data from several veterinary diagnostic laboratories (VDLs) across the United Kingdom to facilitate national companion animal clinical AMR surveillance. We also sought to harness and genotypically characterize isolates of potential AMR importance from these laboratories.

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METHODS

We summarized AST results for 29,330 canine and 8,279 feline Enterobacteriaceae isolates originating from companion animal clinical practice, performed between April 2016 and July 2018 from four laboratories, with submissions from 2,237 UK veterinary practice sites.

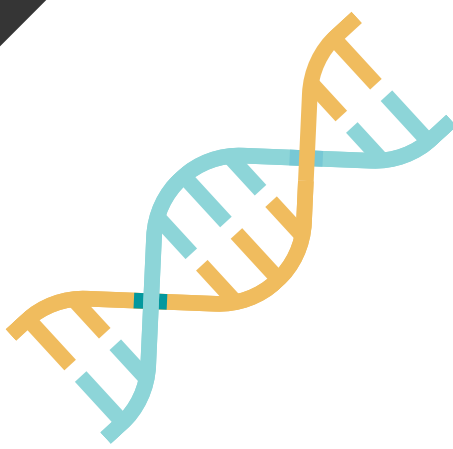
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E. COLI

E. coli was the most commonly isolated Enterobacteriaceae in dogs (69.4% of AST results, 95% confidence interval, CI, 68.7–70.0) and cats (90.5%, CI 89.8–91.3). Multi-drug resistance was reported in 14.1% (CI 13.5–14.8) of canine and 12.0% (CI 11.1–12.9) of feline *E. coli* isolates.

5



SEQUENCING

We selected 95 *E. coli* isolates for whole genome analyses, of which seven belonged to sequence type 131, also carrying the plasmid-associated extended spectrum β -lactamase gene *bla*CTX-M-15. The plasmid-mediated colistin gene *mcr-9* was also identified for the first time in companion animals.

6



RESISTANCE TRENDS

Linking clinical AMR data with genotypic characterization represents an efficient means of identifying important resistance trends in companion animals on a national scale.

Thank you to all veterinary practices and laboratories who contributed to this work.

“ Veterinary diagnostic laboratories routinely and voluntarily contributing data to projects like SAVSNET offers a unique opportunity to monitor clinical resistance trends in companion animals over unprecedented geographies and time. It is hoped these data will help remind practitioners of the importance of AMR in clinical practice, and of the need to regularly culture samples from animals who are suspected of suffering from a bacterial infection. Without samples from veterinary diagnostic laboratories the sequence data produced in this work would not have been possible. We are forever grateful. ”

Dr David Singleton

