Transmission of antimicrobial resistance between dogs and humans

Luca Guardabassi[1]

[1] University of Copenhagen, Denmark, lg@sund.ku.dk

Keywords: antimicrobial resistance, companion animals, uropathogenic *Escherichia coli* (UPEC), One Health

1. Introduction

The pet population is increasing significantly in both size and diversity, reflecting a broader societal transformation in the human-animal bond. Companion animals, particularly dogs and cats, are now regarded as integral members of the family, sharing close physical contact and living environments with their human owners. Advances in veterinary medicine, alongside rising expectations for high standards of care, have led to increased antimicrobial use in companion animals, sometimes involving drugs that are critically important to human medicine, such as fluoroquinolones and extended-spectrum cephalosporins. This trend has raised concerns about pets acting as reservoirs and potential transmitters of antimicrobial resistance (AMR) to humans. As pets may serve as both sources and recipients of resistant bacteria, this phenomenon has important consequences for both human and animal health.

This lecture provides a comprehensive overview of the role of dogs in the transmission of AMR to humans. It focuses particularly on the shared intestinal microbiota, specifically *Escherichia coli*, and its implications for urinary tract infections (UTIs). *E. coli*, especially uropathogenic strains (UPEC), is the primary cause of UTIs in both dogs and humans. Up to 50% of women and approximately 15% of dogs experience a UTI at least once in their lifetime, with similar risk factors, recurrence rates, and potential for complications such as pyelonephritis. The significant overlap in clinical presentation and microbial aetiology makes UTIs an important One Health model for studying bacterial transmission and AMR exchange between dogs and their owners, with implications for both human and veterinary medicine.

2. Household studies on *E. coli* transmission between dogs and humans

Household-based investigations have provided compelling evidence that pets and humans can share *E. coli* strains, including multidrug-resistant variants. A large-scale study involving 85 households in Portugal and the UK examined ESBL-producing *E. coli* and identified shared CTX-M-15-producing strains in three households, including globally relevant lineages such as ST93 and ST457, both linked to pandemic dissemination in human populations [1]. In a subsequent study conducted during episodes of active infection in pets, 56% of animals and 36% of human household members were positive for ESBL-producing *Enterobacterales*. Transmission of ESBL-producing *E. coli* and *K. pneumoniae* to cohabitant humans was observed in three households, with repeated isolation of the index strains on faecal samples from the animals and their cohabiting humans. [2]. Earlier evidence from New Zealand corroborates these findings, as both pets and their owners were found to shed genetically indistinguishable resistant *E. coli* strains in in seven out of 27 households [3]. Although a longitudinal study from Switzerland did not detect concurrent carriage of the same multidrug-resistant organism in owner-pet pairs, several pets carried the same strain for

over four months following hospitalization [4]. This long-term colonization points to indirect routes of transmission, potentially via environmental contamination, that pose a continued risk to human household members.

To explore the frequency of *E. coli*-mediated UTI transmission from pets to humans, we recently performed a longitudinal study to assess transfer of UTI-causing strains by screening faecal samples from pets and their owners [5]. In two households, *E. coli* strains isolated from dogs were genetically indistinguishable (≤7 SNPs) from those causing UTI in the owner, with canine strains persisting months after the initial human infection episode. These findings indicate long-term carriage and underscore the potential of dogs to act as reservoirs for UTI-associated *E. coli*. Taken together, these studies demonstrate that the household environment facilitates the bidirectional exchange of *E. coli* strains and AMR. Companion animals, particularly dogs, can serve as both sources and recipients of resistant bacteria, with implications for recurrent infection, treatment outcomes, and broader One Health concerns.

3. Genomic Studies Comparing UPEC Isolated from Canine and Human UTIs

A growing body of genomic research has focused on evaluating the genetic relatedness between UPEC strains isolated from humans and dogs to assess potential cross-species transmission. A large-scale comparative study conducted in Australia analysed 5,471 E. coli genomes collected from a range of hosts and environmental sources, including both humans and companion animals [6]. Several common sequence types (STs) were found in both human and canine isolates, including pandemic lineages such as ST131. Complementary to this, a previous Australian study sequencing 377 canine UPEC isolates identified STs such as ST73, ST127, ST131, and ST58 among dogs, strongly overlapping with common human UTI lineages [7]. This supports the hypothesis that at least a subset of UPEC clones are generalist pathogens, capable of infecting both humans and dogs. Interestingly, ST372 emerged as a lineage predominantly found in dogs but only rarely in human datasets, indicating potential host adaptation and a possibly reduced zoonotic risk associated with this ST. A similar finding has been reported in a French study, where dog-associated ST372 (21%) and ST73 (20%), previously considered human-associated, were the most frequent lineages among canine clinical isolates [8]. ESBL-mediated resistance to extended-spectrum cephalosporins was found in only 5% of isolates. The B2 phylogroup was overrepresented (80%) and strongly associated with multiple virulence factors, including UPEC-specific genes (*cnf1*, *hlyD*).

Unpublished data from the U.S. indicate that human UTIs are more likely caused by ST131 and ST95, whereas ST372. ST73, ST38, and ST12 are equally represented among human and canine isolates, suggesting potential for cross species transfer. Despite some host-specific trends, plasmid replicon types and UPEC-associated virulence factors are often conserved across host species, indicating likely horizontal gene transfer and cross-host adaptability. Our ongoing comparative genomic analysis indicates that ST12 and ST131 are primarily found in human infections in Denmark, whereas ST73 and ST372 are more frequent in canine infections. However, the pandemic lineage ST131 occurs in both canine and human isolates, often carrying identical CTX-M-type ESBLs and shared virulence profiles. Notably, certain virulence genes, such as *iutA*, *fyuA*, and *papGII*, are more prevalent in canine isolates, suggesting subtle host-specific adaptations (unpublished data). Taken together, these findings demonstrate that a proportion of UPEC strains in dogs and humans share genetic background, resistance determinants, and virulence attributes.

4. Conclusion

Evidence increasingly supports the role of dogs as both reservoirs and vectors of antimicrobial-resistant *E. coli* within households. Genetically identical or closely related strains have been found in dogs and their human cohabitants, including during UTI in the human or dog patients. Genomic data confirm overlap in sequence types, resistance genes, and virulence factors between canine and human UPEC isolates. While some clones, like ST372, appear dog-adapted, the presence of generalist lineages shared across hosts suggests ongoing bidirectional transmission and cross-species adaptation.

5. References

1. Menezes J et al. Transmission dynamics of ESBL/AmpC and carbapenemase-producing Enterobacterales between companion animals and humans. *Front Microbiol.* 2024 Sep 3;15:1432240. doi: 10.3389/fmicb.2024.1432240.
2. Menezes J et al. Longitudinal study of ESBL/AmpC-producing Enterobacterales strains sharing between cohabiting healthy companion animals and humans in Portugal and in the United Kingdom. *Eur J Clin Microbiol Infect Dis.* 2023 Aug;42(8):1011-1024. doi: 10.1007/s10096-023-04629-2.
3. Toombs-Ruane LJ et al. Carriage of Extended-Spectrum-Beta-Lactamase- and AmpC Beta-Lactamase-Producing *Escherichia coli* Strains from Humans and Pets in the Same Households. *Appl Environ Microbiol* . 2020, 86:e01613-20. doi.org/10.1128/AEM.01613-20
4. Dazio V et al. Duration of carriage of multidrug-resistant bacteria in dogs and cats in veterinary care and co-carriage with their owners. One Health. 2021 Aug 31;13:100322. doi: 10.1016/j.onehlt.2021.100322.
5. Damborg P et al. Dogs can be reservoirs of *Escherichia coli* strains causing urinary tract infection in human household contacts. *Antibiotics*. 2023 Aug 1;12(8):1269. doi: 10.3390/antibiotics12081269.
6. Watt AE et al. Parameters for one health genomic surveillance of *Escherichia coli* from Australia. *Nat Commun.* 2025 Jan 2;16(1):17. doi: 10.1038/s41467-024-55103-
7. Elankumaran P et al. Genomic and temporal trends in canine ExPEC reflect those of human ExPEC. *Microbiol Spectr.* 2022 Jun 29;10(3):e0129122. doi: 10.1128/spectrum.01291-22.
8. Valat C et al. Pathogenic *Escherichia coli* in dogs reveals the predominance of ST372 and the human-associated ST73 extra-intestinal lineages. *Front Microbiol.* 2020 Apr 21;11:580. doi: 10.3389/fmicb.2020.00580.