Assessing multidrug resistance patterns in bacteria isolated from canine urine samples submitted to the Veterinary Diagnostic Laboratory, University of Illinois

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INTRODUCTION

- The emergence of multidrug-resistant (MDR) bacteria in dogs is a threat to animal and public health[1,2].
- A common source of MDR bacteria (i.e., bacteria that are resistant to at least 3 antimicrobial classes[3]) is urinary infections.
- Providing local antibiogram information on urinary pathogens can help veterinarians with their UTI therapy choices and prevents the emergence of MDR bacteria.

References:
[1]Blondeau, et al. (2020). Persistent infection with *Staphylococcus pseudintermedius* in an adult oncology patient with transmission from a family dog. Journal of Chemotherapy, 32(3), 151-155.
[2]Leite-Martins, et al. (2015). Spread of multidrug-resistant *Escherichia coli* within domestic aggregates (humans, pets, and household environment). Journal of Veterinary Behavior, 10(6), 549-555.
[3]Magiorakos, et al. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clinical microbiology and infection, 18(3), 268-281.

OBJECTIVES

To evaluate multidrug resistance patterns of the most common bacteria isolated from canine urine samples submitted to the Veterinary Diagnostic Laboratory, University of Illinois.

METHODS

- A total of 2,583 de-identified isolates obtained from canine urine samples submitted to the Veterinary Diagnostic Laboratory, University of Illinois, between 2019 and 2020 were analyzed.

- Urine samples were cultured aerobically and MALDI-TOF MS was used to identify bacterial strains.

- Antimicrobial susceptibility of bacteria was assessed by using the broth microdilution method with Sensititre® COMPGP1F (24 antibiotics) and COMPGN1F (19 antibiotics) standard plates.

- Isolates were classified as resistant or susceptible based on their minimum inhibition concentrations (MIC) breakpoints obtained from the Vet01S Clinical Laboratory Standards Institute (CLSI) guidelines

- Statistical analysis including the descriptive and hierarchical clustering dendrograms (heatmaps) was done using the R software.

DATA MANAGEMENT
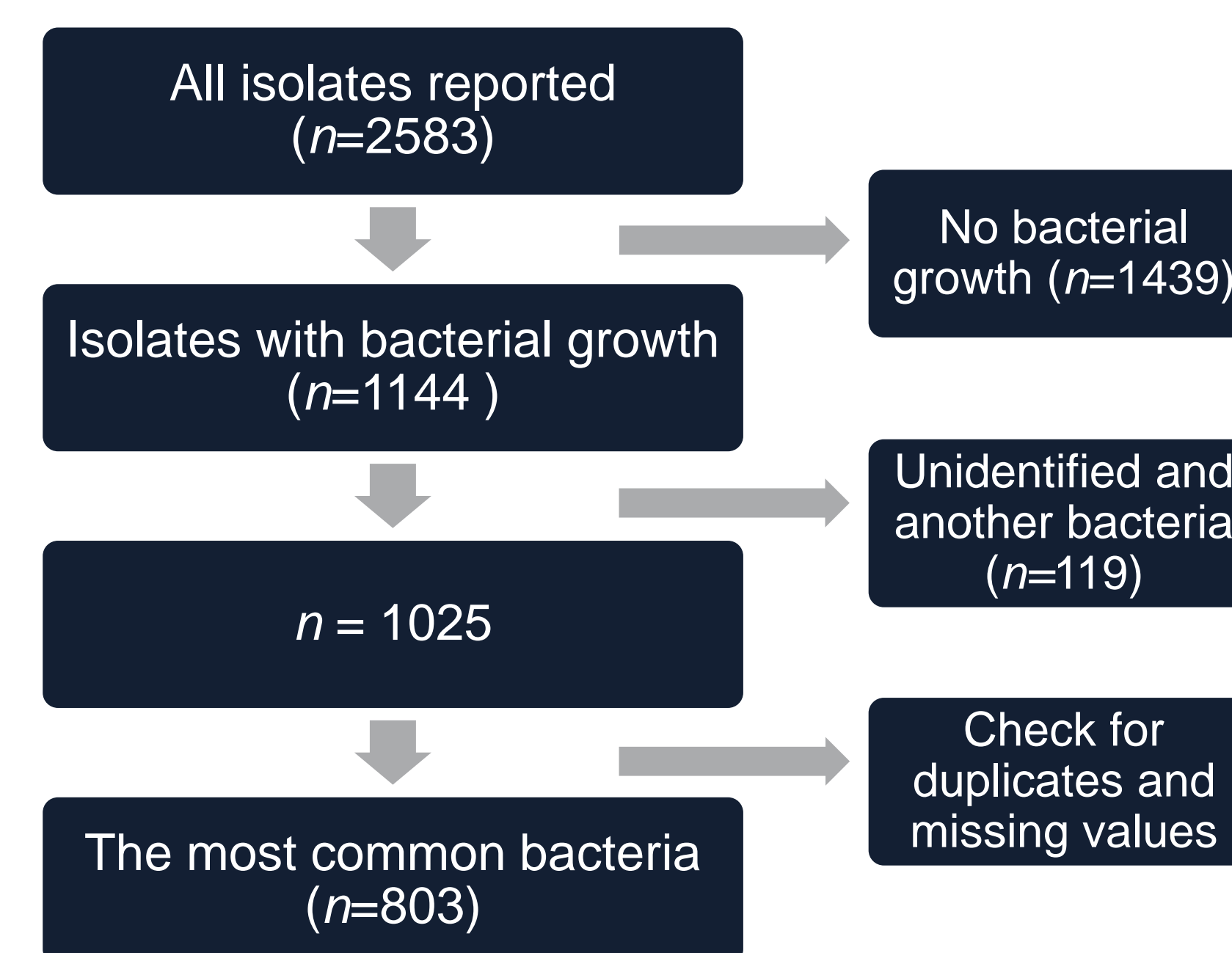
RESULTS

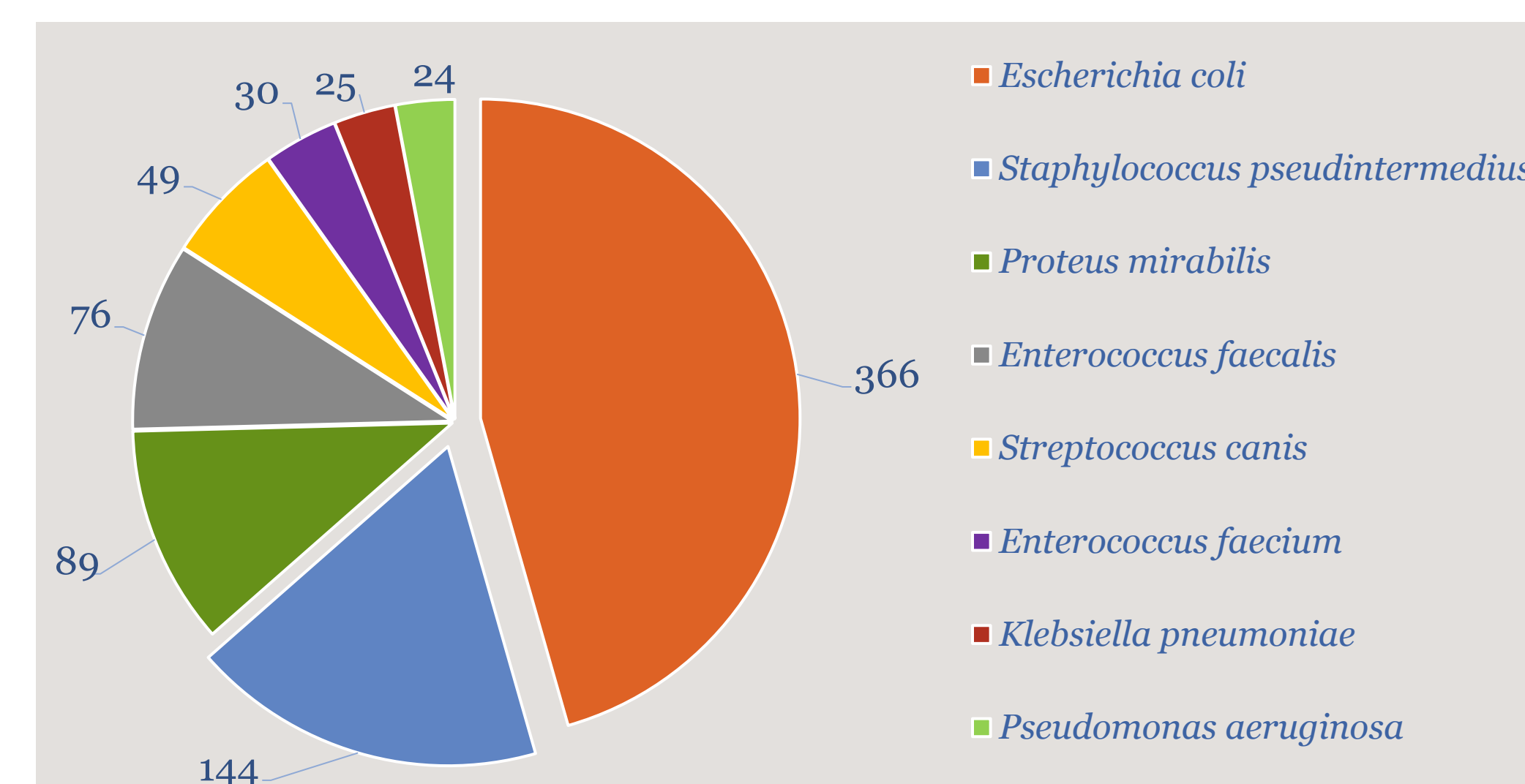- **Total bacterial isolates, Gram-positive (*n*= 299) and Gram-negative (*n*= 504).**

Fig.1. Positive culture results of urine samples (*n*=803)

- **The proportion of MDR bacterial isolates detected in canine urine samples***

Bacteria	Number of MDR (%, 95% CI**)
Staphylococcus pseudintermedius (N = 144)	16 (43.75, 35.51 – 52.26)
Streptococcus canis (N = 49)	5 (10.20, 3.40 – 22.23)
E. coli (N = 366)	85 (23.22, 18.99 – 27.89)
Proteus mirabilis (N = 89)	16 (17.98, 10.64 – 27.55)
Klebsiella pneumoniae (N = 25)	11 (44.00, 24.40 – 65.07)

* The MDR analysis for *Enterococcus faecalis, Enterococcus faecium*, and *Pseudomonas aeruginosa* isolates, were not included due to limited availability of MIC breakpoints. ** Confidence interval.
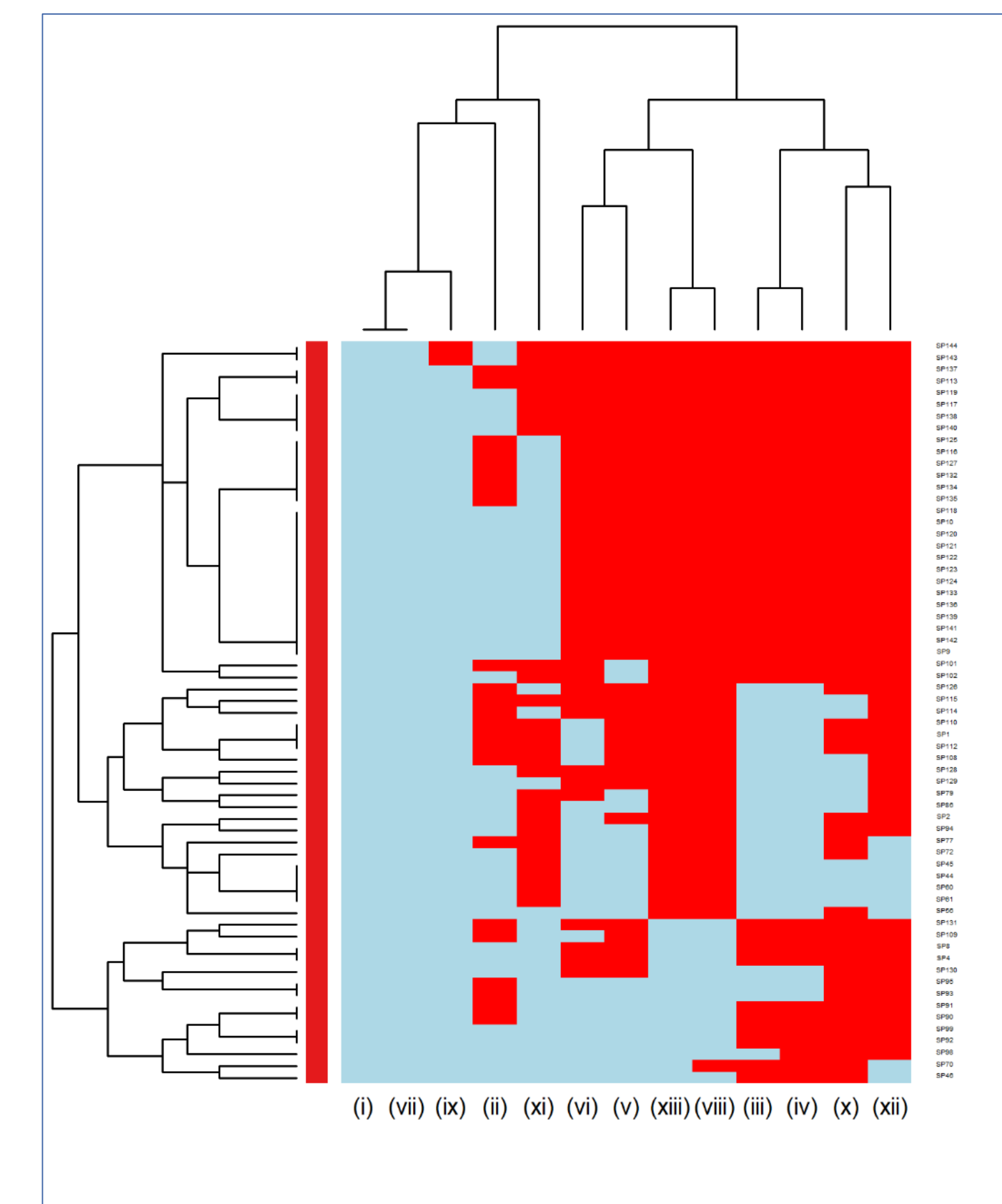
RESULTS

- **Multidrug resistance patterns**

Fig. 2. Heatmap of resistance to multiple antimicrobial classes in *S. pseudintermedius* isolates[a,b,c,d] | [a] (i) Ansamycins; (ii) Aminoglycosides/Aminocyclitols; (iii) β-Lactam Combination Agents; (iv) Cephalosporins; (v) Folate Pathway Antagonists; (vi) Fluoroquinolones; (vii) Glycopeptides; (viii) Lincosamides; (ix) Nitrofurans; (x) Penicillins; (xi) Phenicols; (xii) Tetracyclines; (xiii) Macrolides. [b] Heatmap generated by hierarchical clustering of the antimicrobial resistance determinants (columns) of bacterial isolates (rows). [c] Red color = resistant and light blue color = susceptible. [d] The isolates included in the heatmap were isolates that were resistance to at least 3 antimicrobial classes (Multidrug resistance).
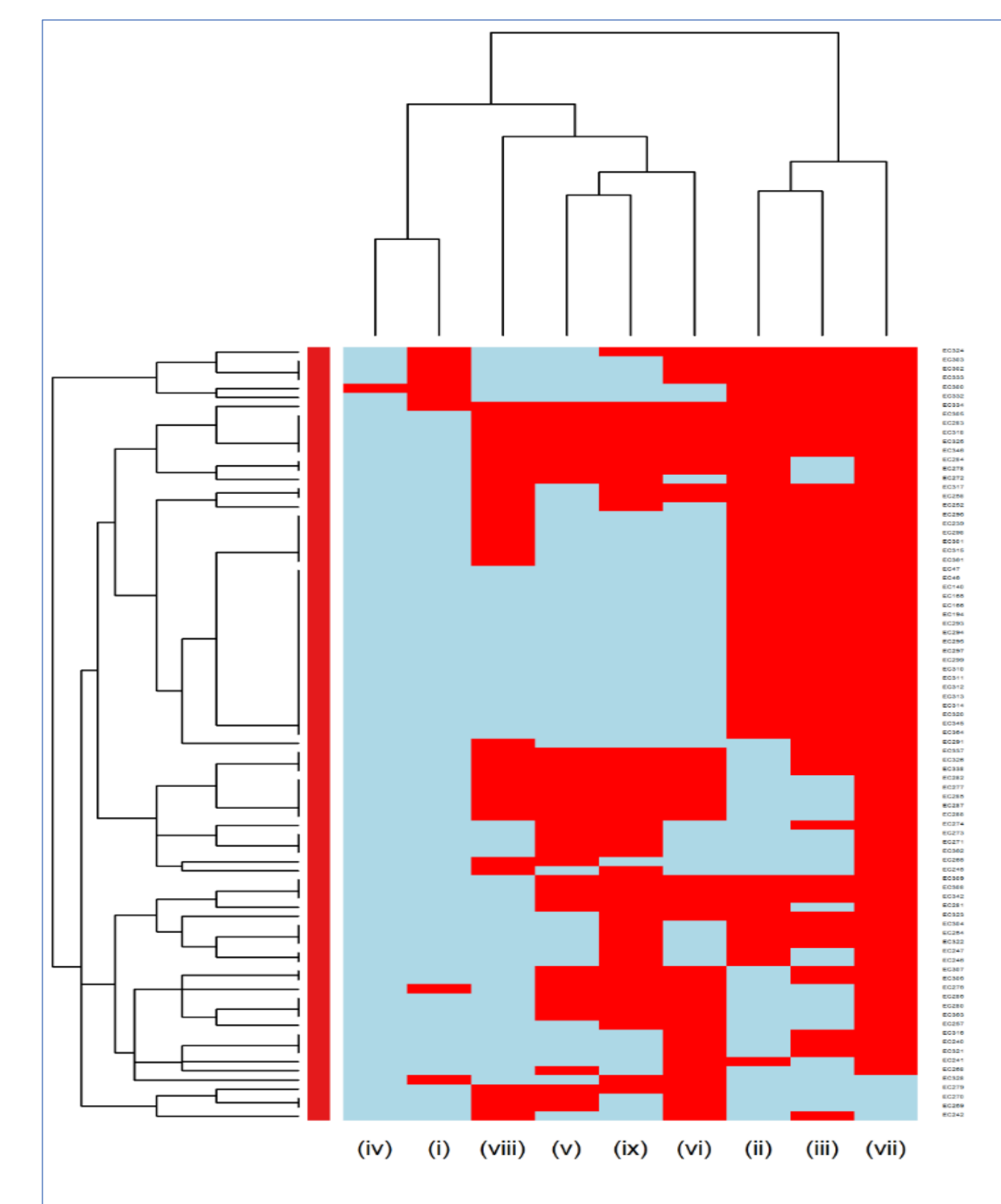

Fig. 3. Heatmap of resistance to multiple antimicrobial classes in *E. coli* isolates[a,b,c,d] | [a] (i) Aminoglycosides/Aminocyclitols; (ii) β-Lactam Combination Agents; (iii) Cephalosporins; (iv) Carbapenems; (v) Folate Pathway Antagonists; (vi) Fluoroquinolones; (vii) Penicillins; (viii) Phenicols; (ix) Tetracyclines. [b] Heatmap generated by hierarchical clustering of the antimicrobial resistance determinants (columns) of bacterial isolates (rows). [c] Red color = resistant and light blue color = susceptible. [d] The isolates included in the heatmap were isolates that were resistance to at least 3 antimicrobial classes (Multidrug resistance).

RESULTS

- **The most common resistance patterns**

Bacteria	Antimicrobial resistance patterns[a, b]	Number of antimicrobial classes in the pattern	n (%)
Staphylococcus pseudintermedius	PEN	1	15 (10.42)
	AUG2-AMP-FAZ-FOV-POD-CEP-CLI-DOX-ENRO-ERY-MAR-MIN-PEN-OXA-PRA-TET-SXT	8	10 (6.94)
	AUG2-AMP-FAZ-FOV-POD-CEP-CLI-DOX-ENRO-ERY-GEN-MAR-MIN-PEN-OXA-PRA-TET-SXT	9	7 (4.86)
	DOX-MIN-TET	1	7 (4.86)
	Susceptible	0	36 (25.00)
Escherichia coli	AMP	1	18 (4.92)
	CHL	1	16 (4.37)
	AUG2-AMP-FAZ-FOV-POD-TAZ-LEX	3	10 (2.73)
	DOX-TET	1	7 (1.91)
	AMP-CHL-DOX-ENRO-MAR-ORB-PRA-TET-SXT	5	5 (1.37)
	Susceptible	0	205 (56.01)

Amikacin (AMI), gentamicin (GEN), amoxicillin-clavulanic acid (AUG2), piperacillin-tazobactam (PT4), cefazolin (FAZ), cefovecin (FOV), cefpodoxime (POD), ceftazidime (TAZ), cephalexin (LEX), cephalothin (CEP), clindamycin (CLI), imipenem (IMI), trimethoprim-sulfamethoxazole (SXT), enrofloxacin (ENRO), marbofloxacin (MAR), orbifloxacin (ORB), pradofloxacin (PRA), ampicillin (AMP), penicillin (PEN), oxacillin (OXA), chloramphenicol (CHL), doxycycline (DOX), tetracycline (TET).

CONCLUSION

- The high prevalence of resistance to antimicrobials commonly used to treat UTI is concerning.

- Collecting urine samples for bacterial culture and susceptibility testing before initiating the UTI therapy is recommended to reduce the severity and length of infections, avoid treatment failures, and prevent the emergence of MDR bacteria.

- Considering the risk of zoonotic transmission of MDR bacteria, veterinarians should inform dog owners about this risk when treating UTI.

LIMITATIONS

- Recurrent UTI cases might be overrepresented as we evaluated urine samples from a veterinary referral laboratory.

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