



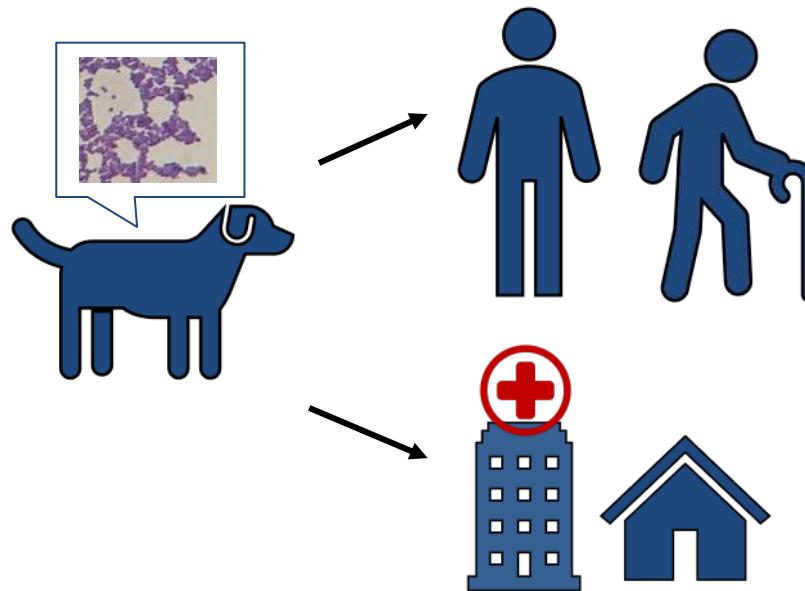
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with the 3rd International Conference of Advanced Veterinary Science and
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Antimicrobial resistance and genomic analysis of bacterial zoonosis in animals, One-health approach

Asst. Prof. Dr. Nathita Phumthanakorn, DVM, PhD
Department of Pre-clinic and Applied Animal Science,
Faculty of Veterinary Science, Mahidol University

Staphylococcus pseudintermedius

- Coagulase-positive staphylococci (CoPS)
- Commonly found in companion dogs
- Can cause opportunistic infections
- Methicillin-resistance *S. pseudintermedius* (MRSP)
- Zoonotic pathogen
- Contaminates the environment around dog areas



Staphylococcus pseudintermedius

- The **surface proteins** involved in host binding and colonization
- Developing rapid multiplex PCR tools for detecting surface proteins (**sps**) genes that responsible for colonization and infection in different hosts
- **spsP** and **spsQ** found more frequently in canine clinical isolates than in human or environmental isolates
 - May play a role in pathogenicity

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Development of a set of multiplex PCRs for detection of genes encoding cell wall-associated proteins in *Staphylococcus pseudintermedius* isolates from dogs, humans and the environment



Nathita Phumthanakorn^a, Pattrarat Chanchaitong^{a,b}, Nuvee Papasarakul^{a,b,*}

^a Department of Microbiology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok 10330, Thailand

^b STAR Diagnosis and Monitoring of Animal Pathogens, Faculty of Veterinary Science, Chulalongkorn University, Bangkok 10330, Thailand

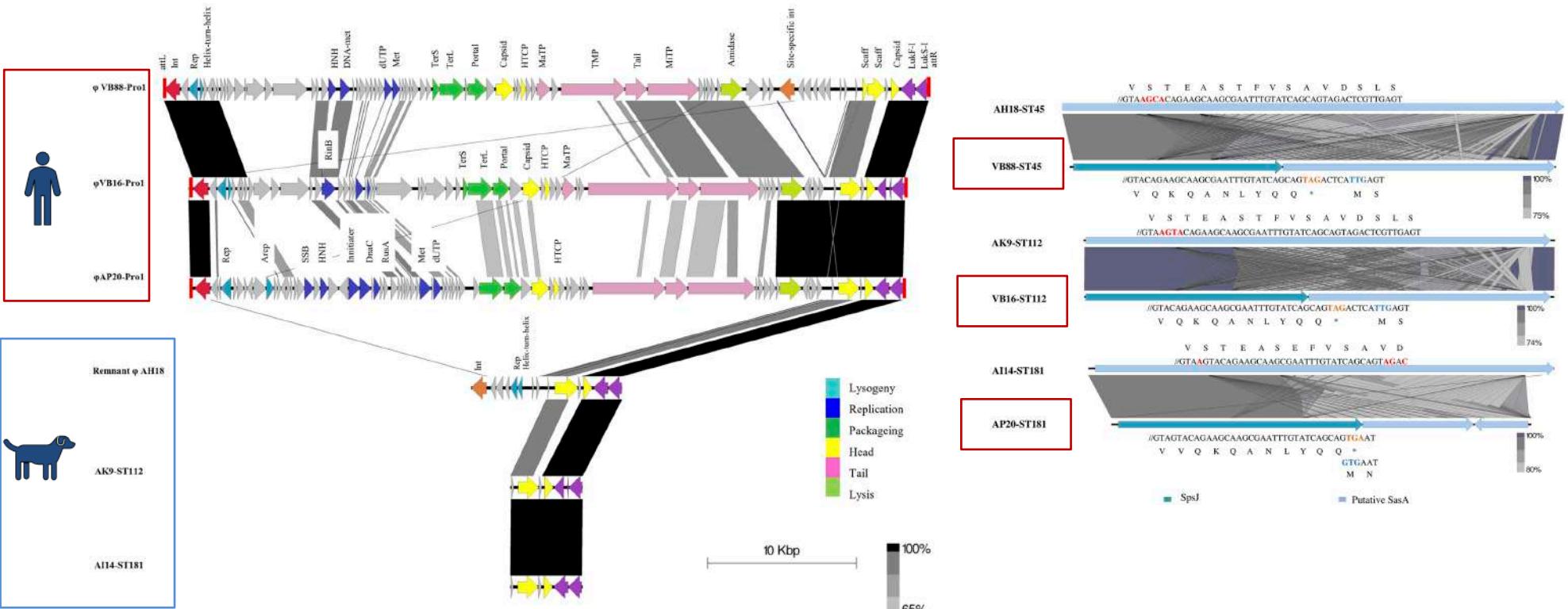
Percentage and numbers in parentheses of variable genes detected among *S. pseudintermedius* isolated from dogs, humans and the environment.

Genes	Dogs			Humans (n = 25)	Environment (n = 40)
	Carriage (n = 35)	Clinical (n = 35)	Total (n = 70)		
<i>spsD</i>	28.6 (10)	17.1 (6)	24.3 (16)	20.0 (5)	25.0 (10)
<i>spsF</i>	14.3 (5)	14.3 (5)	14.3 (10)	12.0 (3)	27.5 (11)
<i>spsI</i>	80.0 (28)	80.0 (28)	80.0 (56)	76.0 (19)	87.5 (35)
<i>spsO</i>	42.9 (15)	34.3 (12)	38.6 (27)	24.0 (6)	52.5 (21)
<i>spsP</i>	25.7 (9)	48.6 (17)*	37.1 (26)	48.0 (12)	40.0 (16)
<i>spsQ</i>	25.7 (9)	48.6 (17)*	37.1 (26)	48.0 (12)	40.0 (16)

* Statistically significant by χ^2 -test ($p < 0.05$) between carriage and clinical group of isolates.

Staphylococcus pseudintermedius

- Genomic comparative analyses of MRSP isolates from dogs and humans



The differences were mainly associated with the presence of two additional **prophages** as well as truncation of some of the **CWA protein genes** in the human ST45 isolate.

Coagulase-negative staphylococci (CoNS)

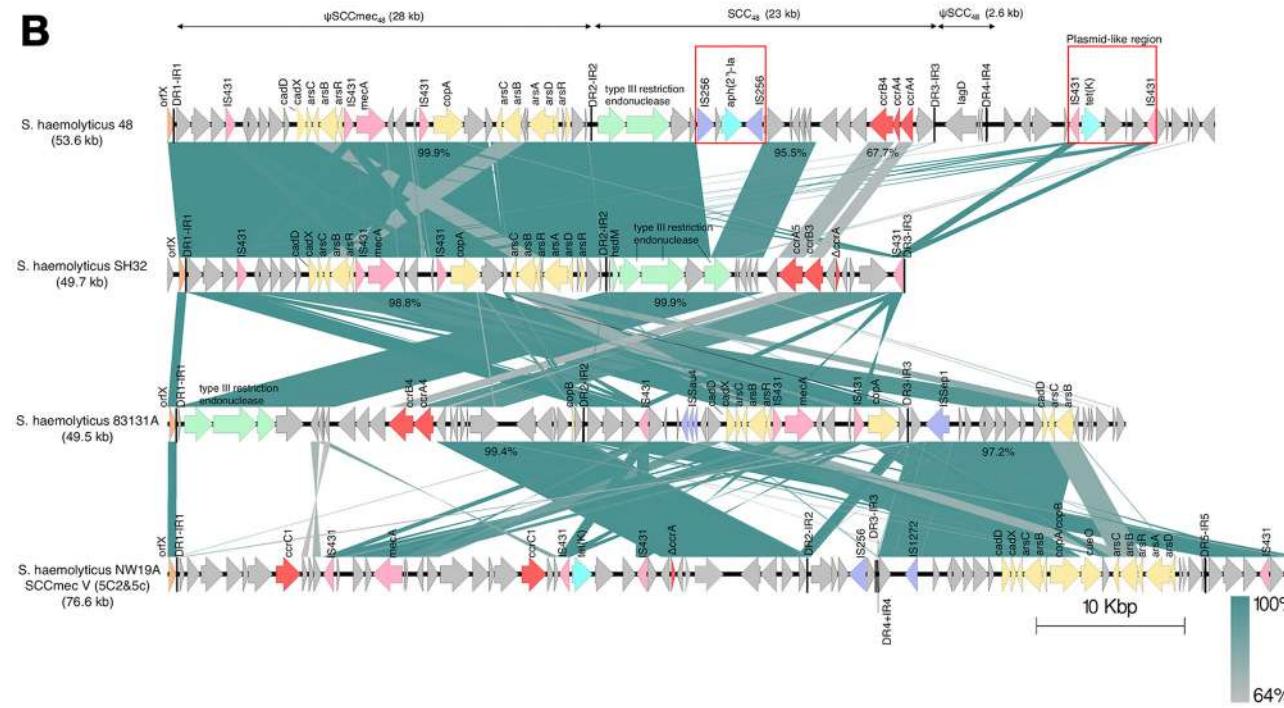
- There are fewer studies on CoNS compared with CoPS in pets.
- Zoonotic transmission of CoNS has been observed in pet owners.
- 185 CoNS (17.5%) were obtained and included 18 species from dogs (n = 116) and 14 species from cats (n = 69).

TABLE 1. *SCCmec* TYPES AND ANTIMICROBIAL RESISTANCE OF METHICILLIN-RESISTANT COAGULASE-NEGATIVE STAPHYLOCOCCI FOUND IN THIS STUDY

<i>CoNS</i> spp.	Strain	Animal	Sample	<i>SCCmec</i> type (<i>ccr</i> and <i>mec</i> complex)	Phenotypic resistance profiles ^a	Genotypic resistance profiles
<i>Staphylococcus haemolyticus</i> (n=8)	195	Dog	Skin (wound)	V (<i>ccrC</i> , C)	β-lactams, ERY, CLI, TET, FUS, SMX-TMP	<i>blaZ</i> , <i>erm</i> (C), <i>tet</i> (L), <i>fusB</i> , <i>dfrG</i>
	625	Cat	Skin (wound)	V (<i>ccrC</i> , C)	β-lactams, TET	<i>blaZ</i> , <i>tet</i> (K)
	1283	Dog	Skin (wound)	V (<i>ccrC</i> , C)	β-lactams, ENR, MAR, CLI, TET	<i>blaZ</i> , <i>gyrA</i> (S84L) ^b , <i>erm</i> (C), <i>tet</i> (K)
	521	Dog	Urine	V (<i>ccrC</i> , C)	β-lactams, ERY, CLI, CHL	<i>blaZ</i> , <i>erm</i> (C), <i>cat</i> _p C221
	50	Dog	Skin (crust)	V (<i>ccrC</i> and <i>ccrAB</i> , C)	β-lactams, ERY, CLI, CHL	<i>blaZ</i> , <i>mph</i> (C), <i>cat</i> _p C221
	48	Dog	Skin (wound)	NT (-/-)	β-lactams, GEN, ENR, MAR, ERY, CLI, TET, MUP, SMX-TMP	<i>blaZ</i> , <i>aph</i> (3')-IIIa, <i>gyrA</i> (S84L) ^b , <i>erm</i> (C), <i>tet</i> (K), <i>mupA</i> , <i>dfrG</i>
	289	Dog	Skin (wound)	NT (-/-)	β-lactams, ENR, MAR, CLI, TET, MUP, RIF	<i>blaZ</i> , <i>gyrA</i> (S84L) ^b , <i>erm</i> (C), <i>mph</i> (C), <i>msr</i> (A), <i>tet</i> (K), <i>mupA</i>
	1864	Dog	Urine	NT (-/-)	β-lactams, ENR, MAR, ERY, CLI, TET, MUP, SMX-TMP, RIF	<i>blaZ</i> , <i>gyrA</i> (S84L) ^b , <i>erm</i> (C), <i>mph</i> (C), <i>msr</i> (A), <i>tet</i> (K), <i>mupA</i> , <i>dfrG</i>
<i>Staphylococcus epidermidis</i> (n=6)	187	Dog	Pleural effusion	IV (<i>ccrAB2</i> , B)	β-lactams, ERY, CLI	<i>blaZ</i> , <i>msr</i> (A), <i>inu</i> (A)
	236	Dog	Skin (wound)	IV (<i>ccrAB2</i> , B)	β-lactams, GEN, TET, SMX-TMP,	<i>blaZ</i> , <i>aacA</i> - <i>aphD</i> , <i>tet</i> (K), <i>dfrG</i>
	459	Dog	Lung biopsy	IV (<i>ccrAB2</i> , B)	β-lactams, ERY, TET, FUS	<i>blaZ</i> , <i>msr</i> (A), <i>tet</i> (K), <i>fusB</i>
	1536	Cat	Nasal discharge	IV (<i>ccrAB2</i> , B)	β-lactams, ENR, MAR, TET	<i>blaZ</i> , <i>gyrA</i> (S84Y) ^b , <i>glrA</i> (S80Y), <i>tet</i> (K)
	1574	Dog	Pleural effusion	IV (<i>ccrAB2</i> , B)	β-lactams, ERY, CLI, TET, FUS, MUP	<i>blaZ</i> , <i>msr</i> (A), <i>tet</i> (K), <i>fusB</i> , <i>mupA</i>
<i>Staphylococcus hominis</i> spp. <i>hominis</i> (n=5)	1076	Dog	Urine	NT (<i>ccrAB2</i> /-)	β-lactams, MAR, CLI, TET,	<i>blaZ</i> , <i>gyrA</i> (S84F) ^b , <i>glrA</i> (S80F), <i>erm</i> (C), <i>tet</i> (K)
	1231	Dog	Cerebrospinal fluid	III (<i>ccrAB3</i> , A)	β-lactams, ERY, CLI, TET	<i>blaZ</i> , <i>erm</i> (C), <i>msr</i> (A)
	385	Cat	Skin (pustules)	V (<i>ccrC</i> , C)	β-lactams, GEN, ENR, MAR, ERY, CLI, TET, MUP, SMX-TMP	<i>blaZ</i> , <i>aacA</i> - <i>aphD</i> , <i>aph</i> (3')-IIIa, <i>gyrA</i> (S84L) ^b , <i>erm</i> (B), <i>tet</i> (M), <i>mupA</i> , <i>dfrG</i>
	371	Dog	Peritoneal effusion	NT (-/A)	β-lactams, CLI, SMX-TMP	<i>blaZ</i> , <i>dfrG</i>
	384	Dog	Skin (wound)	NT (-/A)	β-lactams, ERY, CLI	<i>blaZ</i> , <i>mph</i> (C), <i>msr</i> (A), <i>inu</i> (A)
	464	Dog	Skin	NT (-/-)	β-lactams, GEN, ENR, MAR, ERY, CLI, TET, CHL, SMX-TMP	<i>blaZ</i> , <i>aacA</i> - <i>aphD</i> , <i>aph</i> (3')-IIIa, <i>erm</i> (B), <i>tet</i> (M), <i>dfrG</i>

Coagulase-negative staphylococci (CoNS)

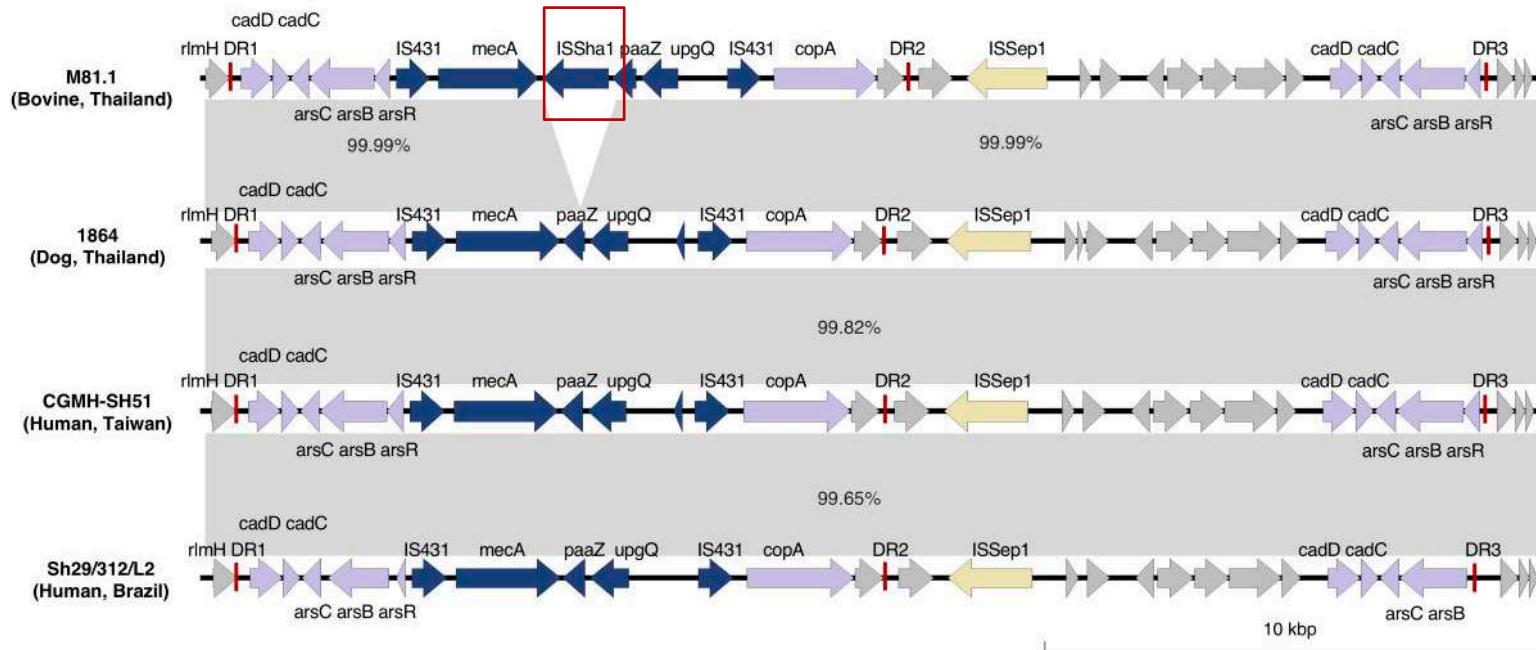
- Short- and long-read nucleotide sequencing was used to characterize nontypeable (NT)-SCCmec elements in *S. haemolyticus* and *S. hominis*.
- Several **antimicrobial resistance** and **heavy metal resistance genes** were identified on the SCCmec element.



Coagulase-negative staphylococci (CoNS)

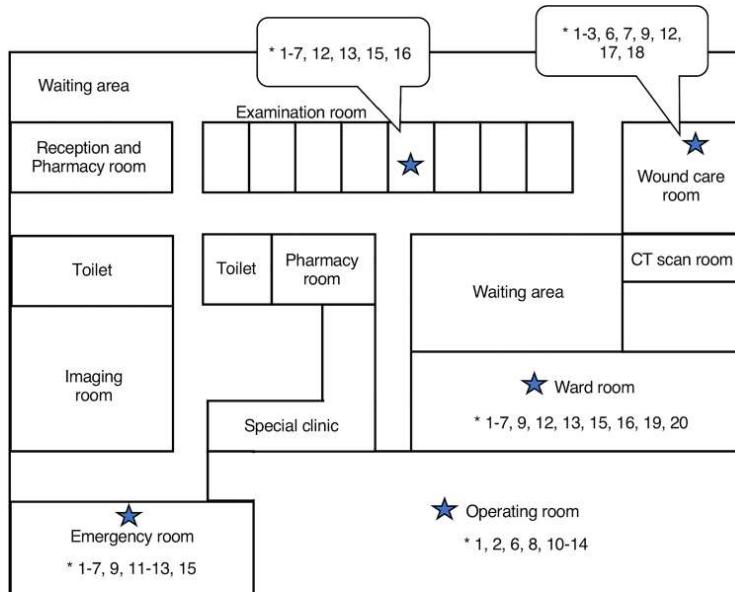
- *S. haemolyticus* from bovine mastitis milk
- MRSH-ST42 strain M81.1 contained a **novel variant of C1 mec complex**
- Distinct evolution of the MRSH lineage through *ISSha1* insertion, highlighting its role in SCCmec diversification

(b)



Pseudomonas aeruginosa

- Major nosocomial pathogen causing healthcare-associated infections
- Moist and water-rich hospital environments as key sources of infection
- Molecular epidemiology of *P. aeruginosa* from a **veterinary teaching hospital environment**



Collected 3 times every 2 months

* Sample collection sites

1. Sink
2. Faucet
3. Examination table
4. Equipment holder
5. Work bench
6. Liquid hand soap dispenser
7. Normal saline for irrigation
8. Povidone iodine solution
9. Rubber tube
10. Anesthesia-breathing circuit
11. Endotracheal tube
12. Tap water
13. Thermometer jar
14. Chlorhexidine solution
15. Keyboard
16. Detergent solution
17. Nebulizer machine
18. Water for nebulizer machine
19. Dog cage floor
20. Cat cage floor

Pseudomonas aeruginosa

- **Sinks** in exam and ward rooms consistently tested positive over 5 months
- Two **carbapenem-resistant** strains carried ***bla*_{VEB-1}**
- Low-**SNP**, same-**ST** strains in different rooms indicate transmission link to the **ward room**
- Findings support improved management of *P. aeruginosa* in veterinary hospitals

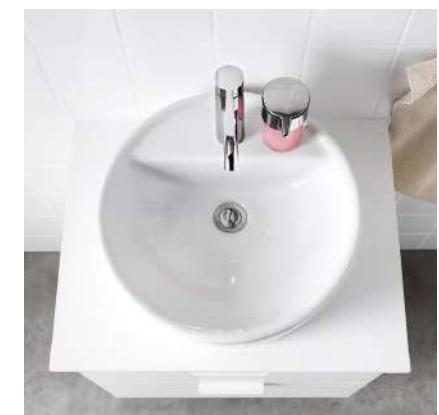
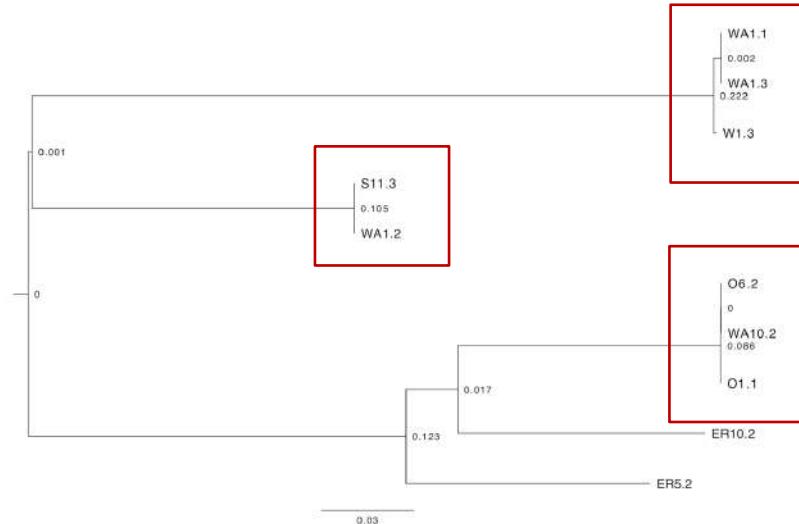


Table 1 Positive sampling sites of *P. aeruginosa* (n=19) found in this study^a

Sampling sites ^b	Examination room (n=5)			Wound care room (n=4)			Ward room (n=4)			Emergency room (n=4)			Operating room (n=2)		
	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
Sink (n=8)	+(O1.1)	+(O1.2)	+(O1.3)	-	-	-	+(W1.3)	+(WA1.1)	+(WA1.2)	+(WA1.3)	-	-	-	-	+(S1.3)
Rubber tube (n=4)	-	-	-	-	+(W10.1)	-	-	-	+(WA 10.2)	-	+(ER10.1)	+(ER10.2)	-	-	-
Liquid hand soap dispensers (n=3)	-	+(O6.2)	+(O6.3)	-	+(W6.2)	-	-	-	-	-	-	-	-	-	-
Normal saline for irrigate (n=1)	-	-	-	+(W7.1)	-	-	-	-	-	-	-	-	-	-	-
Work bench (n=1)	-	-	-	-	-	-	-	-	-	-	+(ER5.2)	-	-	-	-
Equipment holder (n=1)	-	-	-	-	-	-	-	-	-	-	-	+(ER4.3)	-	-	-
Anesthesia- breathing circuit (n=1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+(S11.3)

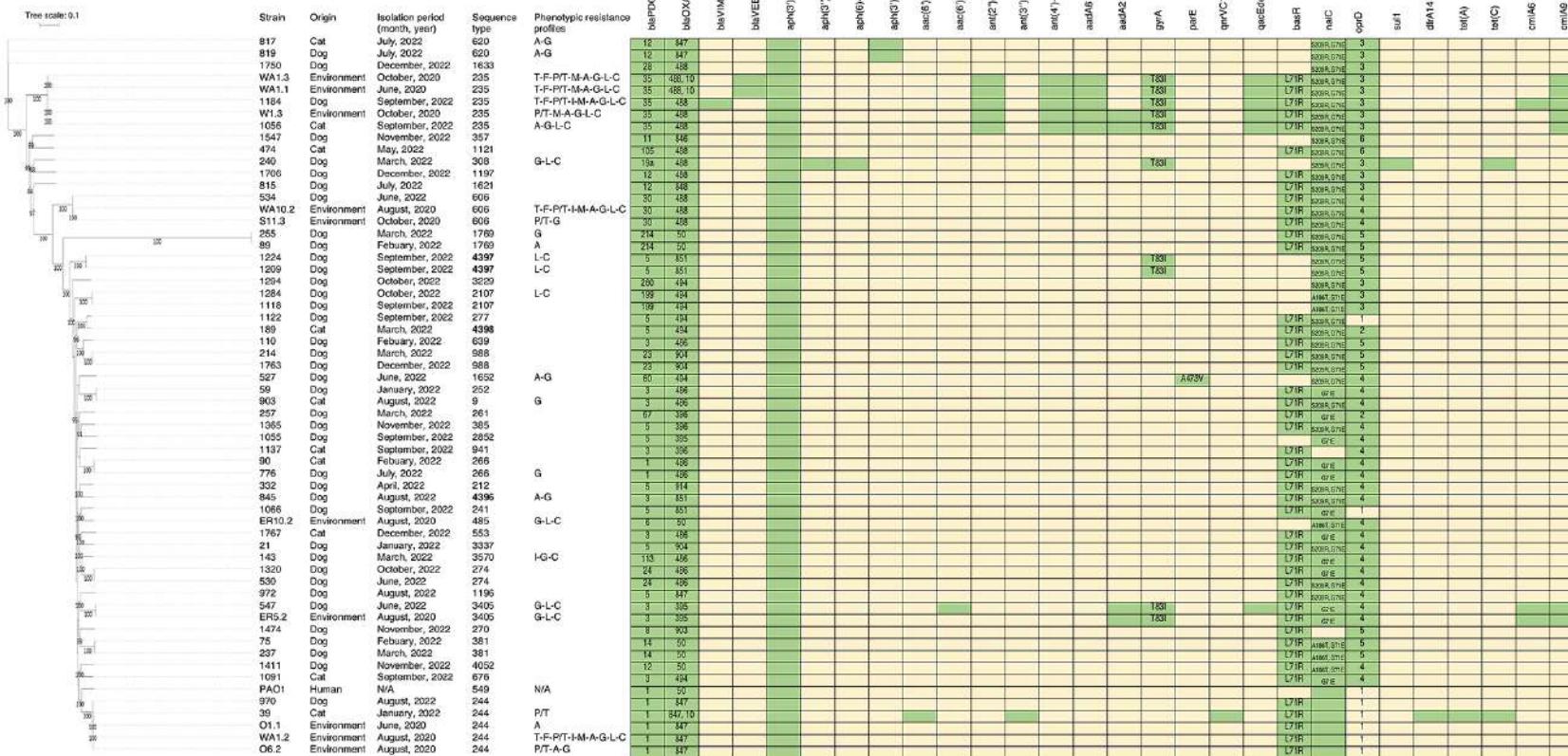
^a + and - represent positive and negative sampling sites, respectively

^b The number of positive *P. aeruginosa* is presented in parenthesis

Pseudomonas aeruginosa

Investigate the sequence typing and clones, and antimicrobial resistance of clinical *P. aeruginosa* isolates from the dogs and cats visiting a veterinary teaching hospital in Thailand within a 1-year period (2022).

High-risk clones



Current research

AMR and genomic analysis

- Genomic characterization of AMR in clinical bacterial isolates from ornamental fish over a 10-year period
- Investigation of antimicrobial resistance profiles of *Enterococcus* species isolated from dogs and cats

Metagenomics

- Application of metagenomic approaches to explore microbial communities and resistance gene diversity in animal hosts



Acknowledgement



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Thank you for your attention