RES-265

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Genomic Surveillance Uncovers High Diversity and Regional Resistance in *Streptococcus uberis* from Dairy Cows

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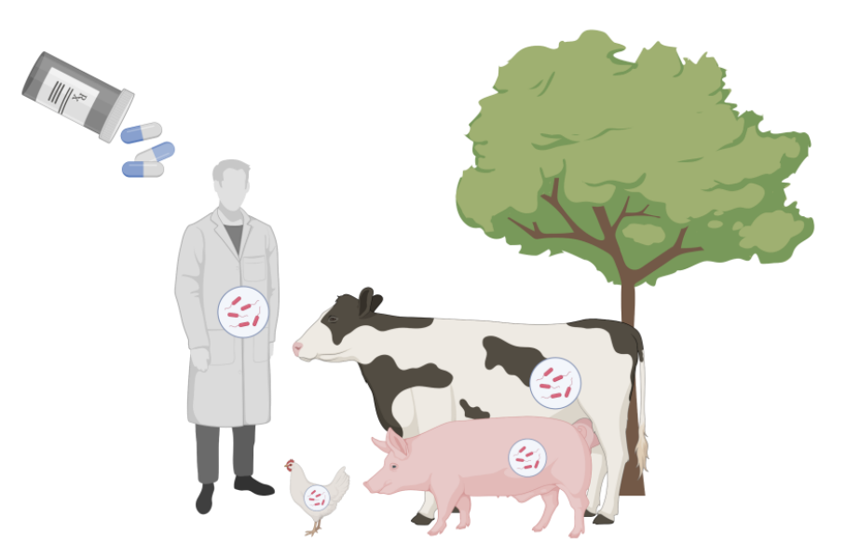
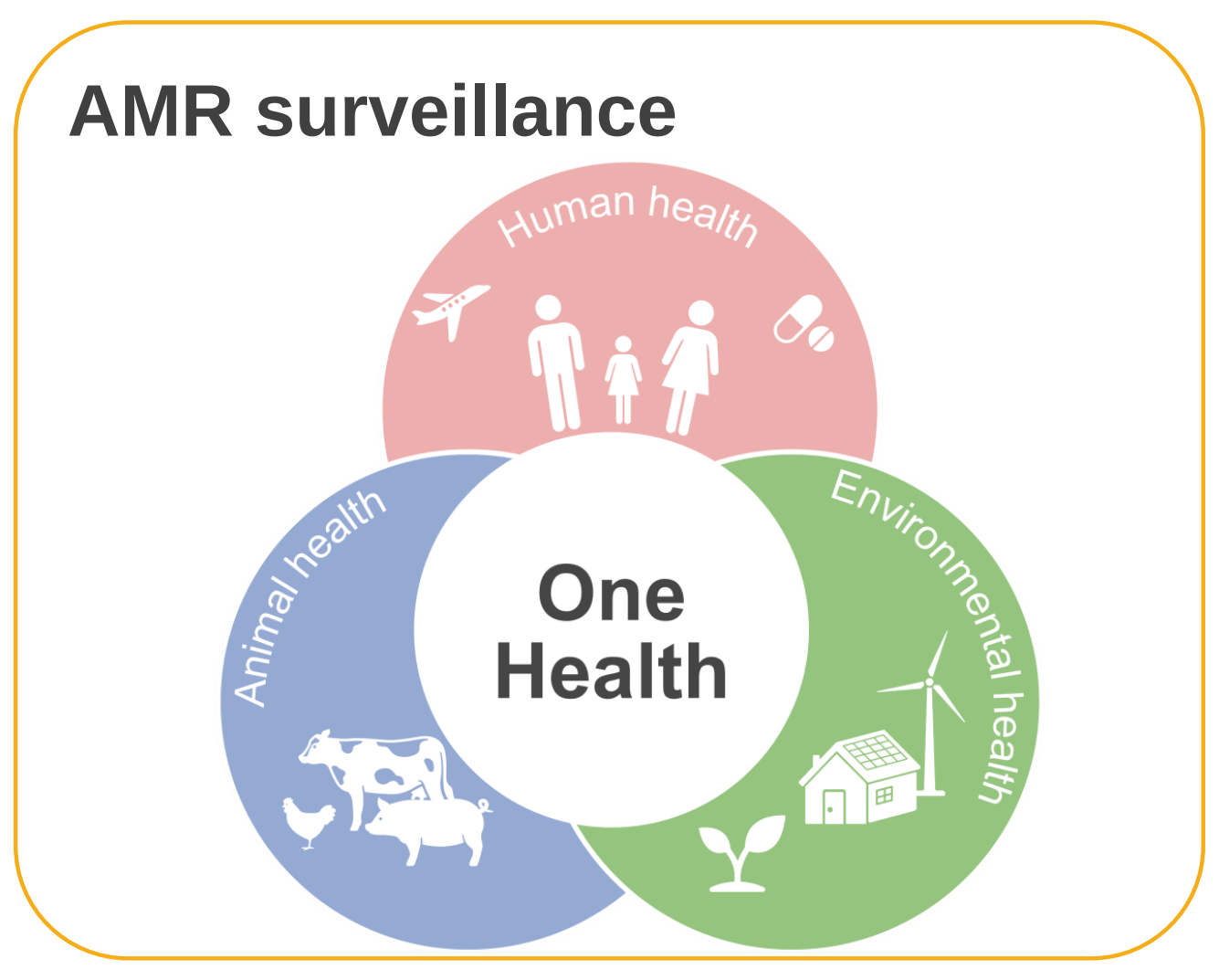
Introduction

Antimicrobial resistance (AMR) is a global health threat requiring coordinated One Health surveillance across human and veterinary medicine. *Streptococcus uberis*, a major cause of bovine mastitis, leads to economic losses in dairy production and is often treated with broad-spectrum antimicrobials critical to human medicine. Despite its importance, genomic data on *S. uberis* from East Asia, particularly Japan, are scarce. This study aimed to characterize the genomic and antimicrobial resistance features of Japanese *S. uberis* isolates in comparison with global strains.

AMR: A global health threat





AMR surveillance

Results

Antibiotic susceptibility tests of 37 strains in this study

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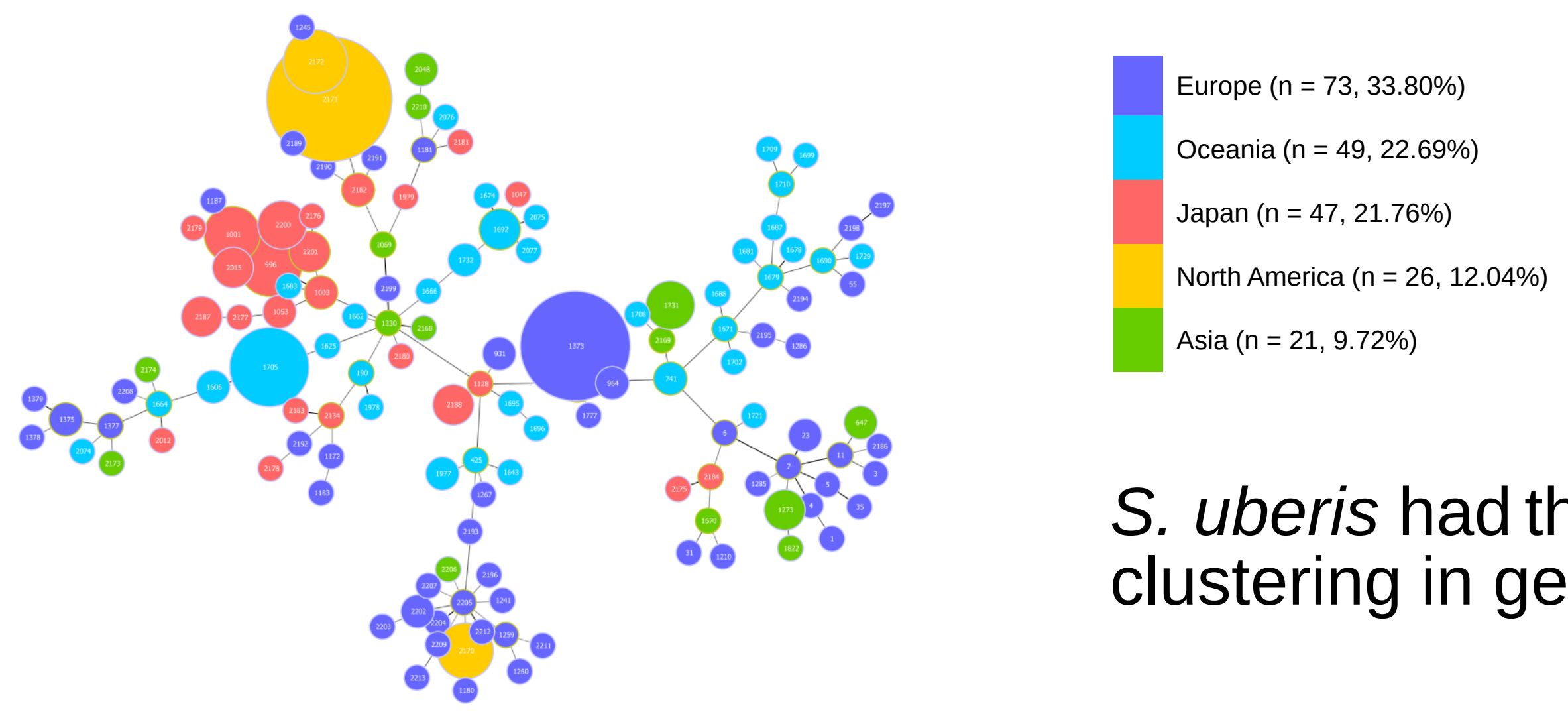
	MIC (µg/mL)													Resistance rate (%)
	≤0.31	0.63	0.125	0.25	0.5	1	2	4	8	16	32	64	>64	
Penicillin G	4	1	16	13	3									0
Ampicillin	5	1	17	12	2									0
Amoxicillin	4	1	4	23	5									0
Cefazolin			4		19	13	1							0
Cefoperazone				4		5	20	8						0
Cefquinome	5	2	19	10	1									0
Ceftiofur			5		2	13	12	5						0
Erythromycin	15	11			1								10	**27.03**
Lincomycin		1	17	1	1	3		2					12	**32.43**
Gentamicin							1	3	7	10	15	1		0
Oxytetracycline			4	17	3					2	9	2		**35.14**
Ciprofloxacin				1	29	7								0
Enrofloxacin				2	14	20	1							0
Sulfamethoxazole / Trimethoprim			8	22	6	1								0

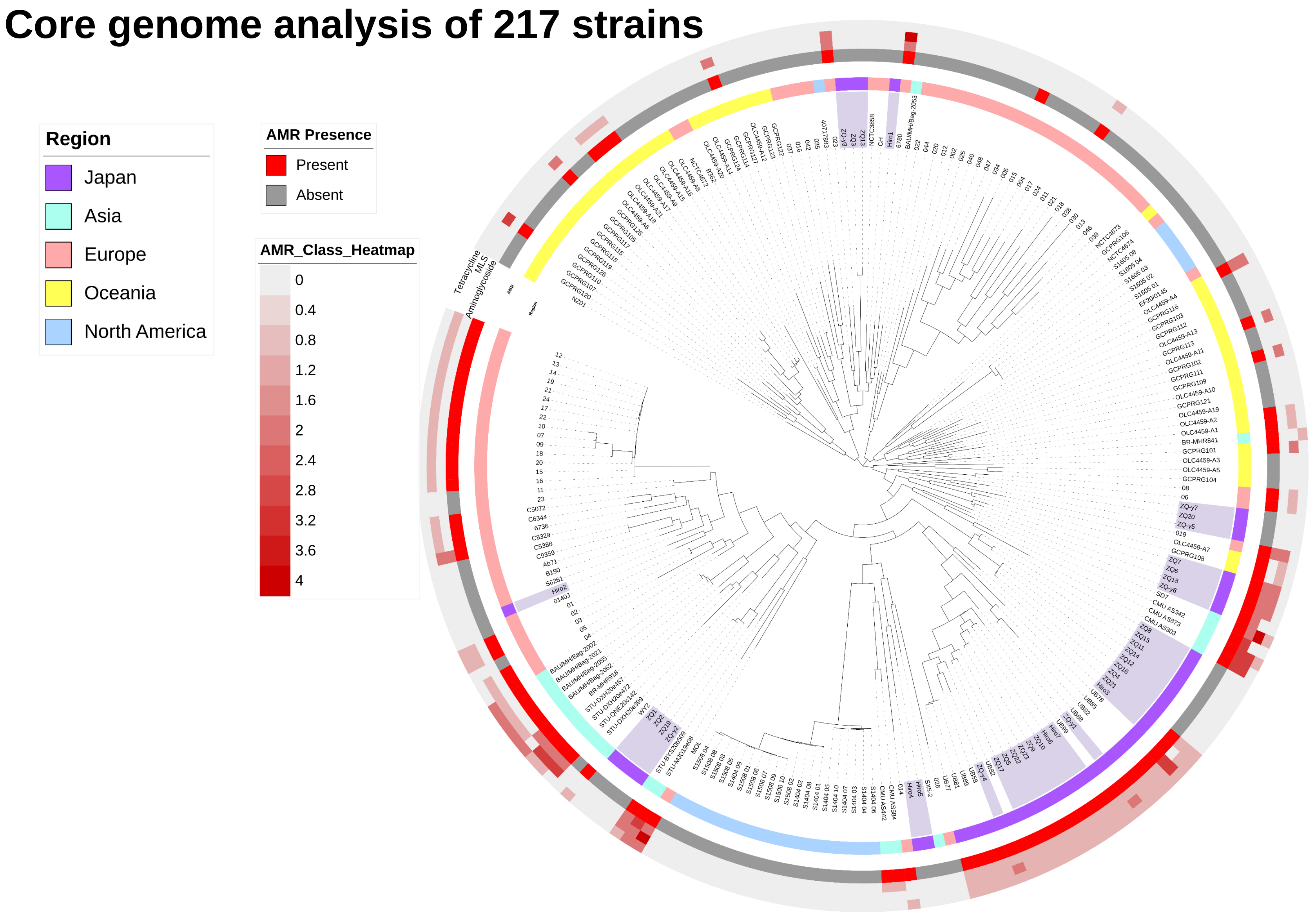
CLSI, VET01S, 7th ed., 2024., Zouharova et al., Antibiotics, 12(10), 1527, 2023., Monistero et al., Antibiotics, 10(6), 644, 2021.

MLST and regional patterns in *S. uberis*



S. uberis had the regional clustering in genomics.

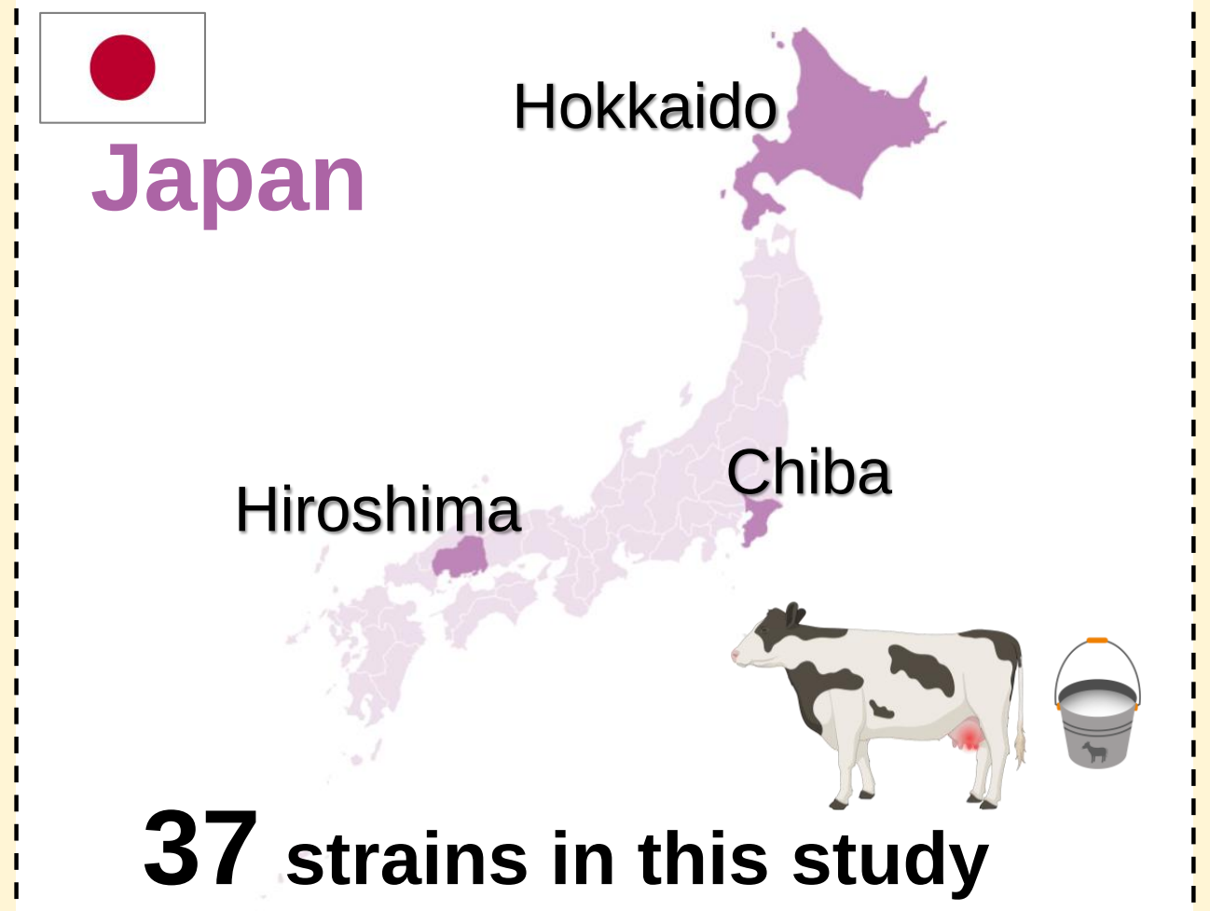
Core genome analysis of 217 strains



Japan had one major group with a high prevalence of AMR genes which are resistant to antibiotics, including aminoglycosides, tetracyclines, and macrolide-lincosamide-streptogramin (MLS).

Methods

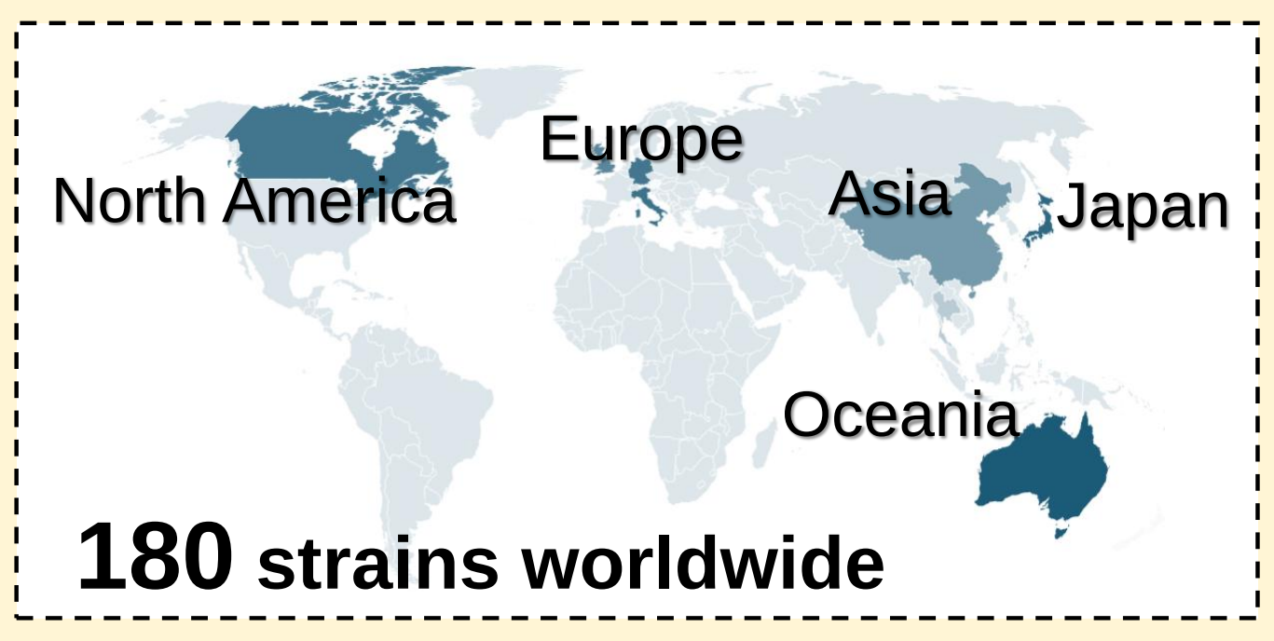
Collected milk from mastitis cow



37 strains in this study

+

Downloaded genome from GenBank database



180 strains worldwide

217 ***S. uberis* strains**

- Antibiotic susceptibility tests
- Whole genome sequencing

Genome analysis

- Core genomics
- Multilocus sequence typing (MLST)
- AMR genes analysis
- Virulence genes analysis

Conclusions

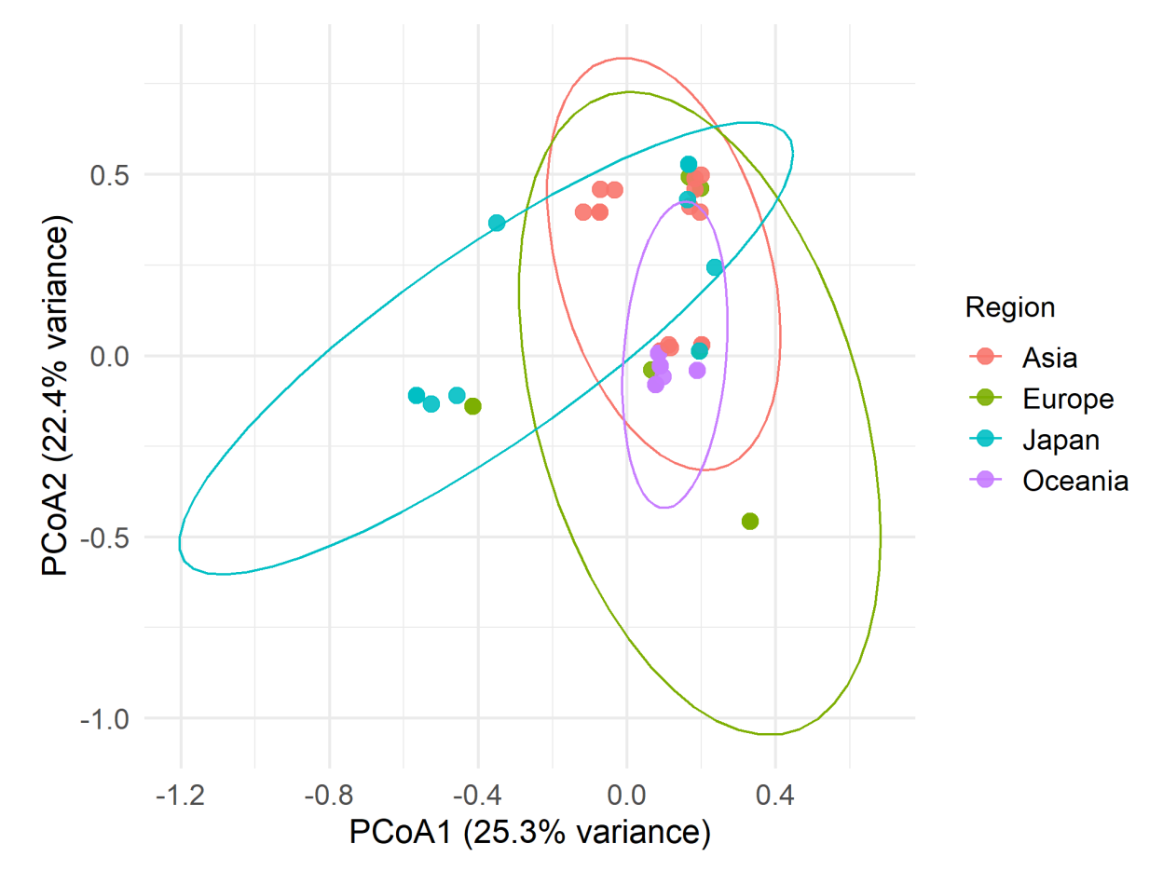
S. uberis isolates from Japan exhibit distinct AMR gene profiles compared to global strains. These findings highlight the need for region-specific genomic surveillance to guide targeted mastitis control and inform One Health strategies for AMR mitigation.

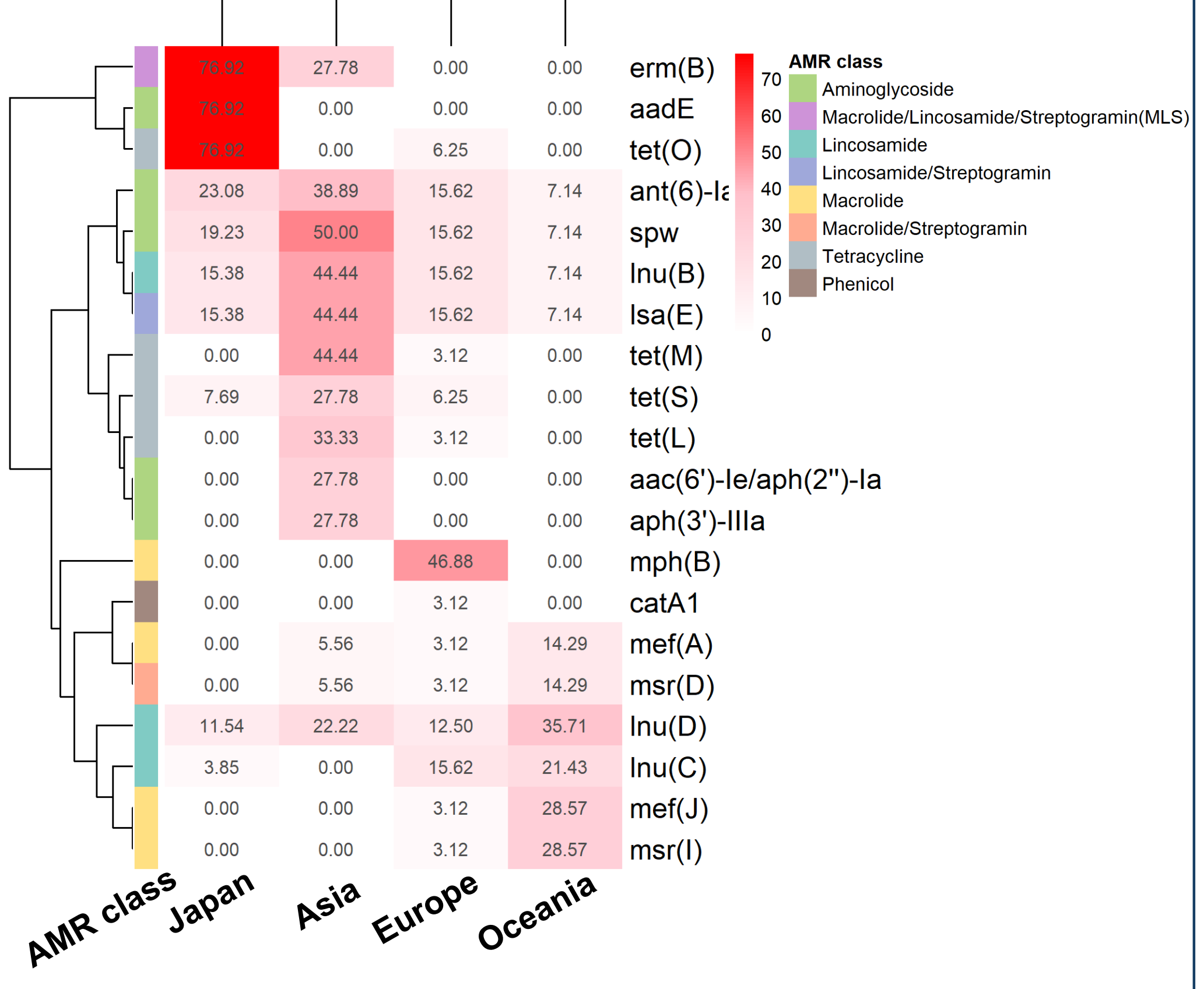
Results

Multivariate and differential abundance analyses across regions

AMR genes

Principal coordinate analysis (PCoA)

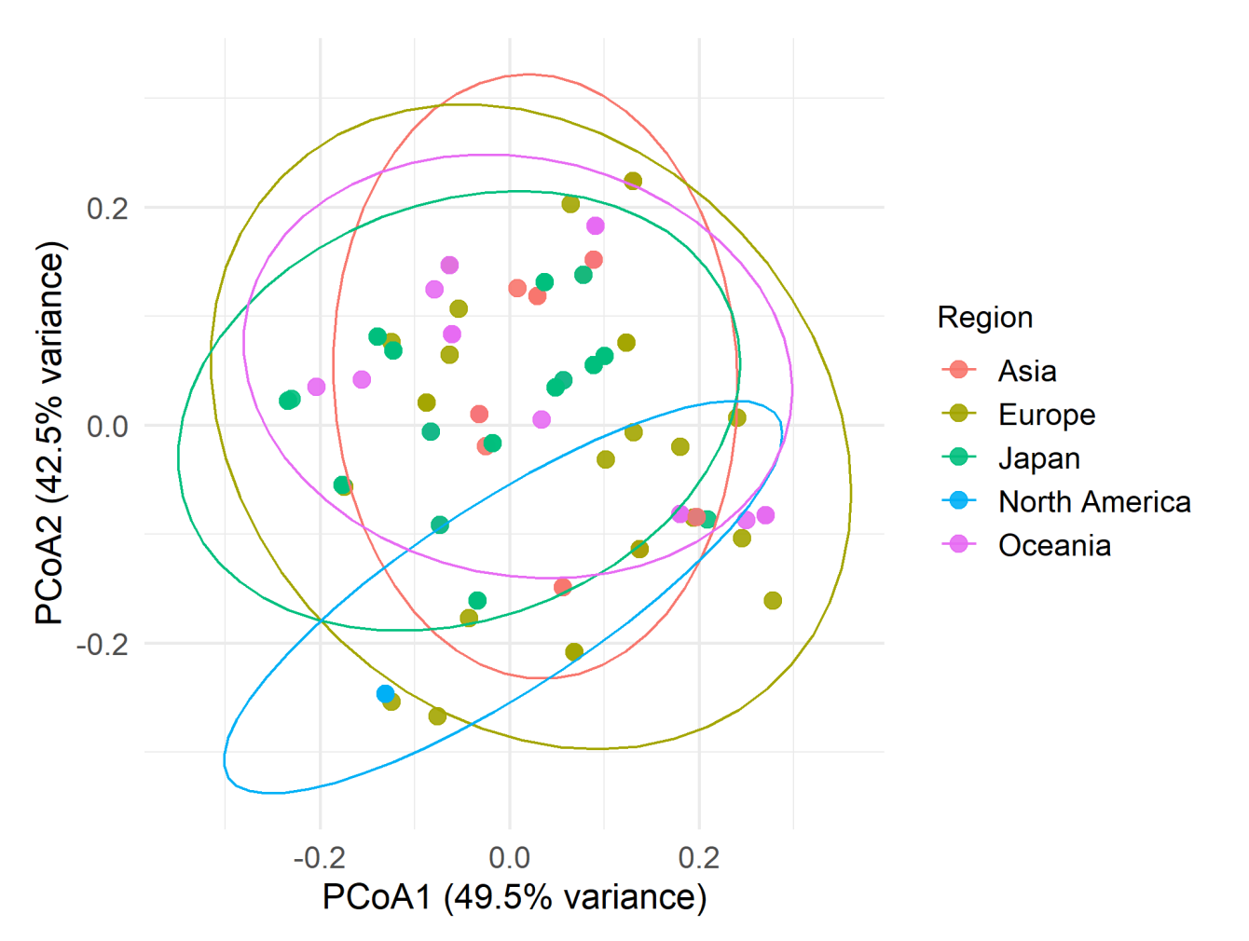


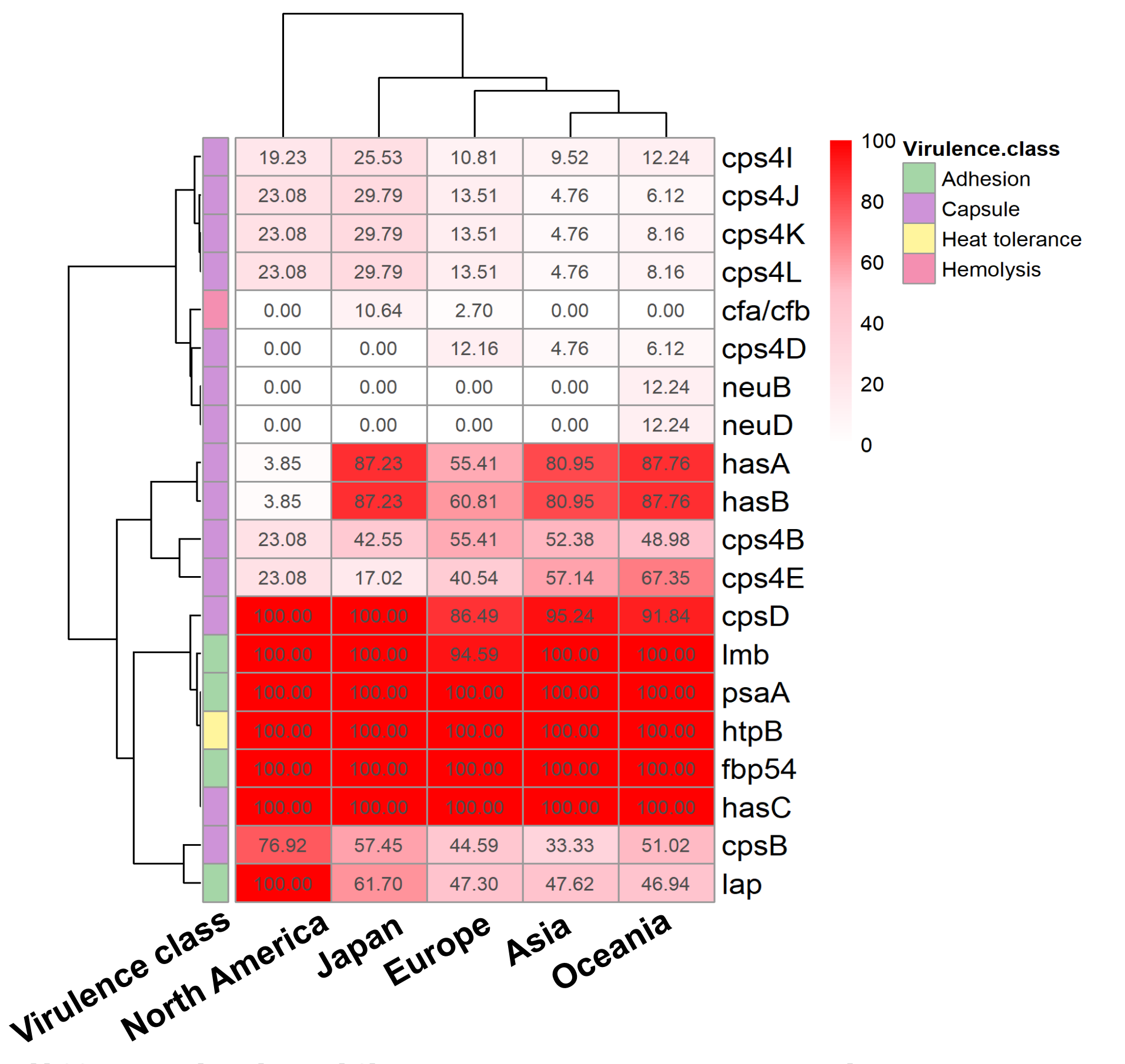


- The region significantly affects AMR gene profiles.
- Japan displayed a unique AMR gene profile, distinct from other regions [*erm(B), aadE,* and *tet(O)* genes]. This indicated potential regional-specific antimicrobial pressures or reservoirs of strains in Japan.

Virulence genes

Principal coordinate analysis (PCoA)





- The virulence gene profiles differed significantly among regions.
- Strains from Japan carried all core virulence genes but no region-specific markers.
- The *psaA, htpB, fbp54,* and *hasC* were consistently detected across all regions.