

Phenomics of antimicrobial resistance in *Streptococcus uberis*

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Introduction

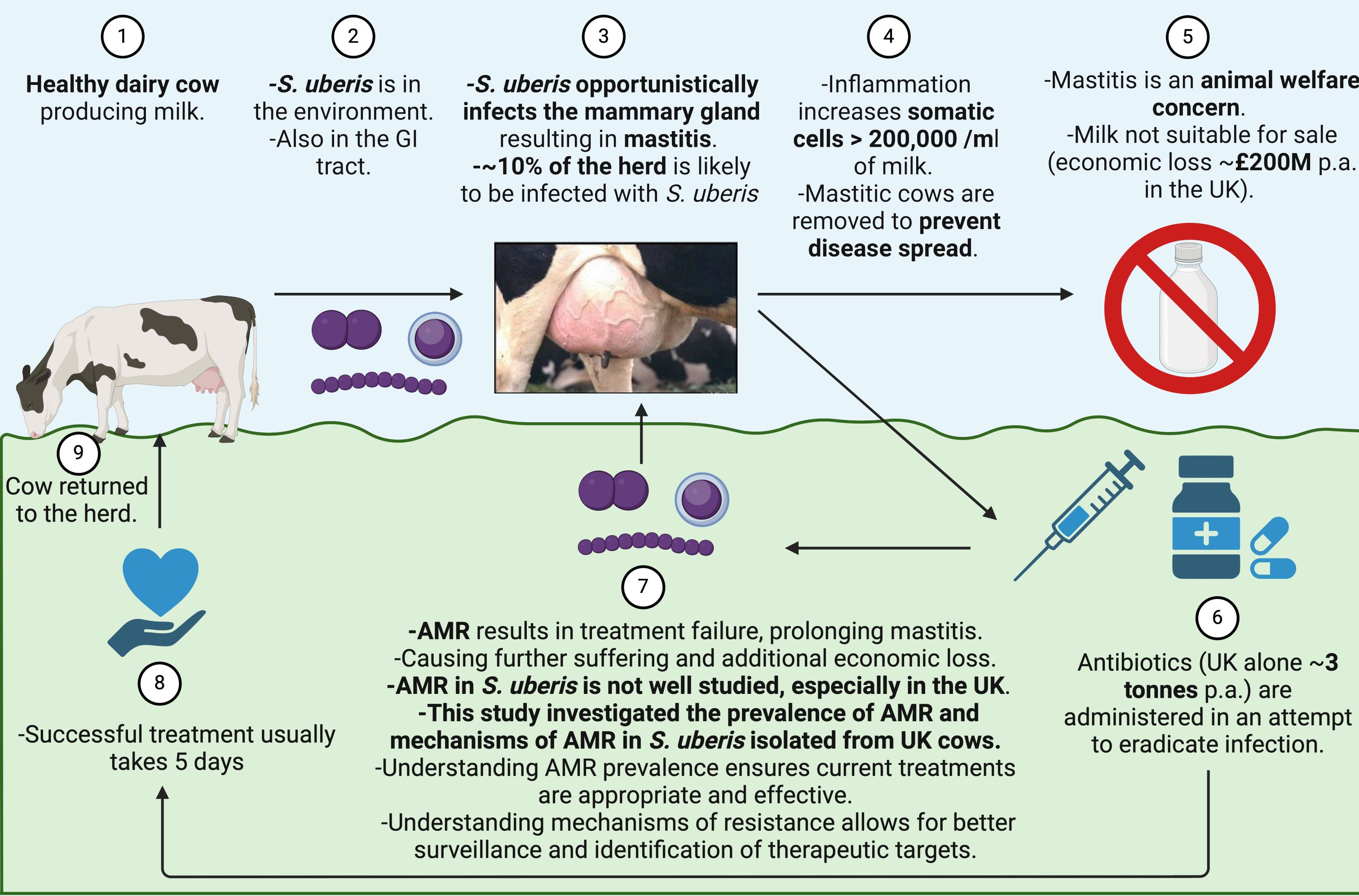


Figure 1. *S. uberis*, mastitis and the implications of antimicrobial resistance.

Methods

-1037 *S. uberis* whole genome sequenced isolates were used in this study¹.
-250 UK *S. uberis* isolates were phenotyped against 11 antibiotics (Table 1).
-A genome wide association study (GWAS) was run for erythromycin (Figure 2)².
-Prophage were identified in all 1037 *S. uberis* genomes^{3,4}.
-Prophage regions from each strain were used to create a phylogenetic tree via ViPTree⁵ (Figure 4). Coding regions were re-annotated through GHOSTX (Figure 3).

Results

Antibiotics	Concentrations of antibiotics in ug/ml										MIC 50%	MIC 90%
	0.125	0.25	0.5	1	2	4	8	16	32	64		
Penicillin	244	1	1	1	1	1	1				0.125	0.125
Ampicillin							250	0	0		4	4
Cefazolin						247	1	0	1	1	4	4
Cefoperazone				245	3	1	0	0	1	1	2	2
Cefquinome		249	0	0	0	0	1				1	1
Oxacillin		246	2	0	0	2					1	1
Pirlimycin		199	5	18	28						1	>4
Erythromycin	219	6	1	0	4	2	18				0.125	0.5
Marbofloxacin		19	108	106	16	1					1	1
					4/2	8/4	16/8	32/16				
Amoxicillin/Clavulanic acid						250	0	0	0		4/2	4/2
Kanamycin/Cephalixin					4/0.4	8/0.8	16/1.6	32/3.2				

Table 1. Minimum inhibition concentrations of 250 *S. uberis* isolates from the UK (1997-2022) against 11 different antibiotics.

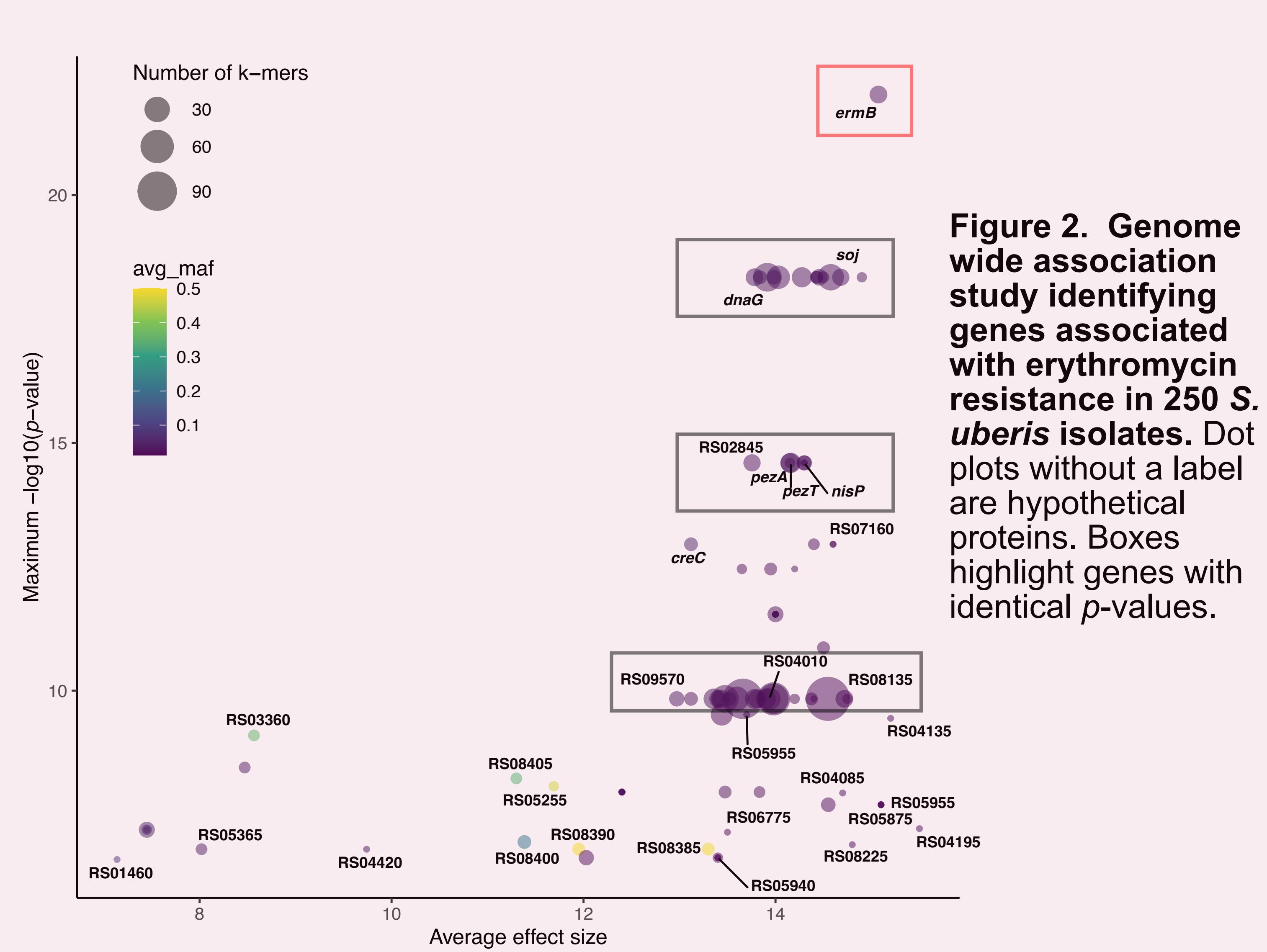


Figure 2. Genome wide association study identifying genes associated with erythromycin resistance in 250 *S. uberis* isolates. Dot plots without a label are hypothetical proteins. Boxes highlight genes with identical p-values.

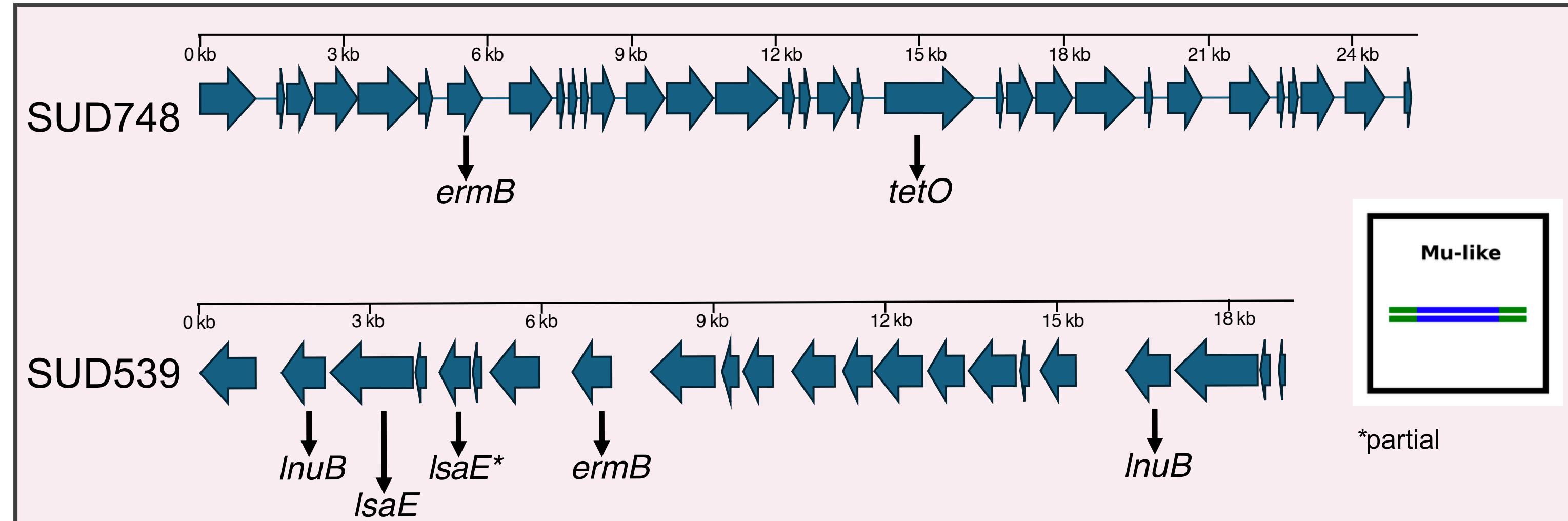


Figure 3. Prophage regions annotated through GHOSTX. Example isolates with prophage regions harbouring known resistance genes. All phage regions were mu-like.

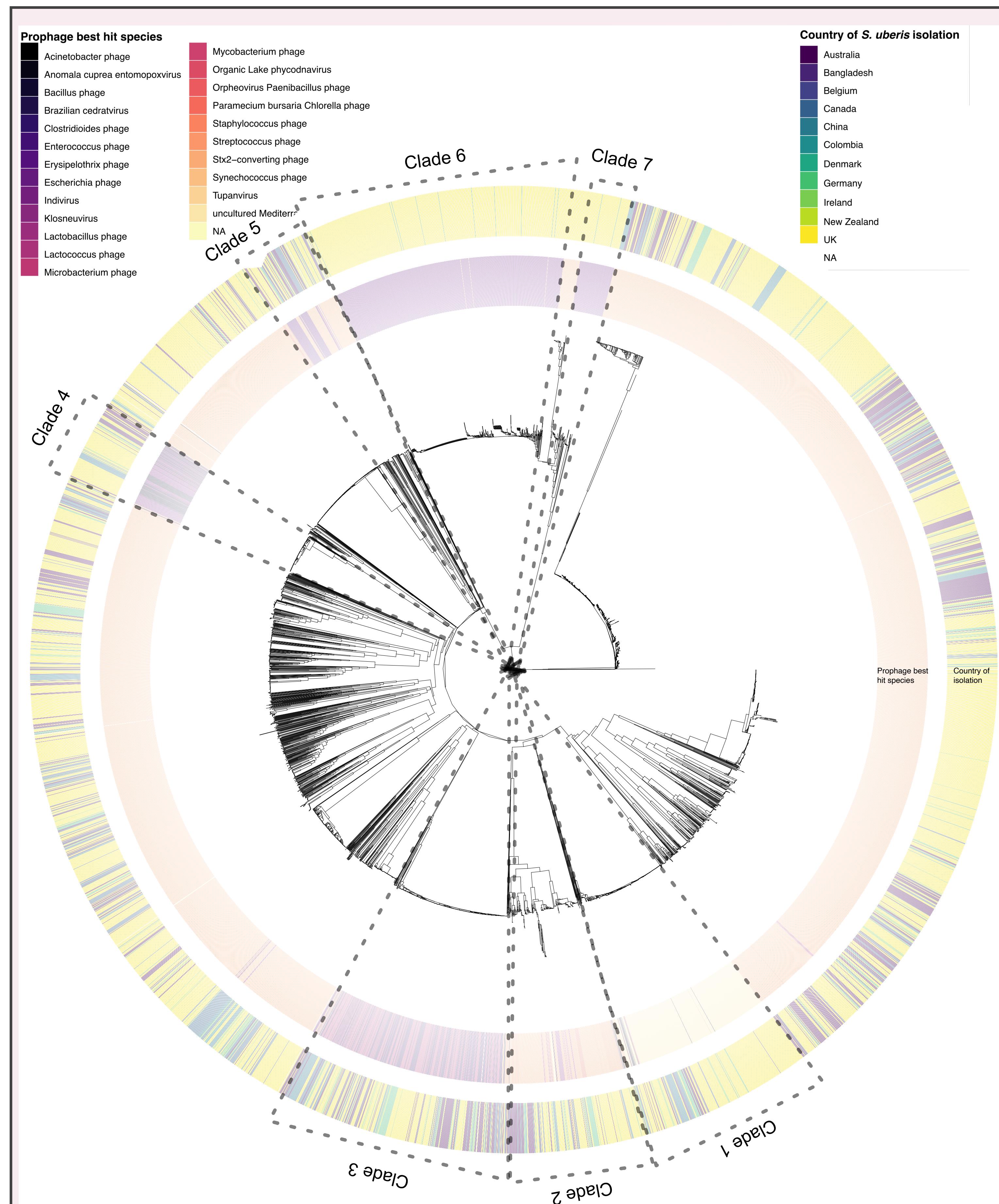


Figure 4. Phylogenetic tree and associated best hit species of all prophage regions. There were 5565 prophage regions in 1037 *S. uberis* genomes (median 5 prophage per isolate). Prophage were diverse. Clades 1-7 highlight regions not associated with known Streptococcal phage.

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Conclusion: Diverse prophage in *S. uberis* harbour known and putative AMR genes that likely confer resistance in these isolates