

**Prevalence and genomic structure of bacteriophage *phi3* in human derived livestock-associated MRSA from 2000 to 2015**

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Table S1: Oligonucleotide primers used for PCR amplification

Oligonucleotide	Sequence (5'-3')	Reference
<i>hlb-1-for</i>	CGGCGTAGCGATTGTAAG	This study
<i>hlb-2-rev</i>	GGGAACGCATATACATCCC	This study
<i>hlb-3-for</i>	GCTGCAACACTTGCATTAGC	This study
<i>hlb-4-rev</i>	GGATACAAAACGGTCGATAACA	This study
<i>chp-for</i>	TTTACTTTTGAACCGTTTCCTAC	This study
<i>chp-rev</i>	TATTCATTAGTTTTTCCAGGACCATT	This study
<i>sak-for</i>	AAGGCGATGACGCGAGTTAT	This study
<i>sak-rev</i>	GCGCTTGGATCTAATTCAAC	This study
<i>scn-for.2</i>	CTAGATAAAAATGAGGCACAAG	This study
<i>scn-rev.2</i>	CTTTTTAGTGCTTCGTCAATTTC	This study
<i>sea-for</i>	AGATCATTCGTGGTATAACG	This study
<i>sea-rev</i>	TTAACCGAAGGTTCTGTAGA	This study
<i>sep-for</i>	AATCATAACCAACCGAATCA	This study
<i>sep-rev</i>	TCATAATGGAAGTGCTATAA	This study

Table S2: Accession numbers of the *phi3*-positive isolates

Isolate	Isolation year	Accession number
1_1439	2006	LT992456; LT992457
2_LA_86	2008	LT992463
3_LA_115	2008	LT992464
4_LA_208	2010	LT992466
5_3949	2010	LT992462
6_LA_232	2010	LT992465
7_4623	2010	LT992458
8_LA_272	2011	LT992461
9_LA_281	2011	LT992460
10_5235	2011	LT992472
11_LA_290	2011	OVTT01000001; OVTT01000002; OVTT01000003
12_LA_293	2011	LT992468
13_LA_301	2011	LT992470
14_5418	2011	LT992473
15_LA_305	2012	LT992469
16_LA_309	2012	LT992467
17_LA_343	2012	LT992471
19_LA_388	2013	LT992474
20_LA_415	2013	LZ992475
21_LA_436	2014	LT992476
22_LA_562	2015	LT992477

Table S3: Resistance profile of *phi3*-positive MRSA *spa*-CC011

Gene	Description <sup>a</sup>	14 39	LA 86	LA 115	LA 208	39 49	LA 232	46 23	LA 272	LA 281	52 35	LA 290	LA 293	LA 301	54 18	LA 305	LA 309	LA 343	LA 388	LA 415	LA 436	LA 562
<i>mecA</i>	Alternate penicillin binding protein 2, defining MRSA	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>blaZ</i>	Beta-lactamase gene	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+
<i>blaI</i>	Beta lactamase repressor (inhibitor)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+
<i>blaR</i>	Beta-lactamase regulatory protein	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+
<i>tet(K)</i>	Tetracycline efflux protein	-	a	a	-	+	-	+	+	+	+	+	-	a	+	+	a	-	+	+	+	-
<i>tet(M)</i>	Ribosomal protection protein associated with tetracycline resistance	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

<sup>a</sup> Description as provided by the manufacturer (*S. aureus* Genotyping Kit 2.0 manual, Alere Technologies GmbH, Jena, Germany)

<sup>b</sup> a, ambiguous; +, positive; -, negative

Table S4: Presence of MGE-encoded genes associates with livestock or human origin in *phi3*-positive isolates<sup>a</sup>

Gene <sup>b</sup>	Description	143 9	LA 86	LA 115	LA 208	394 9	LA 232	462 3	LA 272	LA 281	523 5	LA 290	LA 293	LA 301	54 18	LA 305	LA 309	LA 343	LA 388	LA 415	LA 436	LA 562
<i>int phi2</i>	integrase gene of bacteriophage 2	+	-	-	-	+	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-
<i>int phi6</i>	integrase gene of bacteriophage 6	-	+	+	-	+	+	-	-	-	+	+	-	+	+	-	-	+	+	+	+	+
<i>int phi7</i>	integrase gene of bacteriophage 7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>cadDX</i>	operon of gene <i>cadX</i>	+	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>rep27</i>	replication protein 27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>rep7</i>	replication protein 7	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+

<sup>a</sup> MGE-located genes associated with C398 isolates of animal origin are highlighted in grey (1); MGE, mobile genetic element;

<sup>b</sup> Detection of genes by *in silico* PCR using oligonucleotides for *int phi2* (2) and *int phi6*, *int phi7*, *cadDX*, *rep27*, *rep7* (3).

## References

1. McCarthy AJ, van Wamel W, Vandendriessche S, Larsen J, Denis O, Garcia-Graells C, Uhlemann AC, Lowy FD, Skov R, Lindsay JA. 2012. *Staphylococcus aureus* CC398 clade associated with human-to-human transmission. *Appl Environ Microbiol* 78: 8845-8848. <https://doi.org/10.1128/AEM.02398-12>
2. Schijffelen MJ, Boel CHE, van Strijp JAG, Fluit AC. 2010. Whole genome analysis of a livestock-associated methicillin-resistant *Staphylococcus aureus* ST398 isolate from a case of human endocarditis. *BMC Genomics* 11:376. <https://doi.org/10.1186/1471-2164-11-376>
3. Lekkerkerk WSN, van Wamel WJB, Snijders S V, Willems RJ, van Duijkeren E, Broens EM, Wagenaar JA, Lindsay JA, Vos MC. 2015. What is the origin of livestock-associated Methicillin-resistant *Staphylococcus aureus* Clonal Complex 398 isolates from humans without livestock contact? An epidemiological and genetic analysis. *J Clin Microbiol* 53:1836–1841. <https://doi.org/10.1128/JCM.02702-14>