Table S1. All investigated resistance- and virulence genes in the 34 S. haemolyticus *isolates. P-values calculated with Fisher's exact test, comparing the outbreak clone to the non-outbreak isolates. Virulence genes previously associated with clinical* S. haemolyticus *isolates (1).*

Gene	Function/resistance	Outbreak clone n (%)	Non-outbreak isolates n (%)	p-value
Resistance genes				
aac(6')-aph(2'')	aminoglycoside	20 (100)	10 (71)	0.022
aadD	aminoglycoside	0	1 (7)	0.412
ant(9)-Ia	aminoglycoside	0	1 (7)	0.412
aph(3')-III	aminoglycoside	0	0	1
str	aminoglycoside	0	0	1
qacB	antiseptic	0	0	1
blaZ	β-lactam	20 (100)	14 (100)	1
cat (pC221)	chloramphenicol	0	4 (29)	0.022
qacA	disinfectant	17 (85)	12 (86)	1
fusB	fusidic acid	0	4 (29)	0.022
fusC	fusidic acid	0	1 (7)	0.412

lnuA	lincosamide	0	2 (14)	0.162
lsaA	lincosamides and streptogramin a	0	0	1
ermA	macrolide	0	1 (7)	0.412
ermC	macrolide	0	1 (7)	0.412
mphC	macrolide	18 (90)	7 (50)	0.017
vga(A)LC	macrolide	0	2 (14)	0,162
msrA	macrolide	18 (90)	7 (50)	0.017
mecA	methicillin	20 (100)	11 (79)	0.061
***tet*(K)**	tetracycline	0	4 (29)	0.022
***tet*(M)**	tetracycline	0	1 (7)	0.412
dfrG	trimethoprim	0	3 (21)	0.061
MDR		20 (100)	13 (93)	0.412

Virulence genes

ugpQ	Glycerophosphoryl diester phosphodiesterase	20 (100)	11 (79)	0.061
paaZ	Domain protein	20 (100)	11 (79)	0.061

mecA	Methicillin resistance	20 (100)	11 (79)	0.061
SH0155_NA	MFS transporter	20 (100)	14 (100)	1
nikA	Nickel-binding periplasmic protein	20 (100)	14 (100)	1
secA2	Protein translocase subunit seca2	20 (100)	13 (93)	0.412
fabG	Fabg	20 (100)	13 (93)	0.412
yjjG	Pyrimidine 5’-nucleotidase yjjg	20 (100)	14 (100)	1
ansA	Putative L-asparaginase	20 (100)	14 (100)	1
aacA-aphD	Bifunctional AAC/APH	20 (100)	10 (71)	0.022
SH1612_NA	Acetyltransferase GNAT	20 (100)	10 (71)	0.022
blaI	Penicillinase repressor	20 (100)	13 (93)	0.412
blaR1	Regulatory protein blar1	20 (100)	12 (86)	0.162
blaZ	B-lactamase	20 (100)	14 (100)	1
SH2156_NA	Ferrichrome ABC transporter truncated	20 (100)	13 (93)	0.412
tagE	Truncated glycosyltransferase	20 (100)	13 (93)	0.412

folB	Dihydroneopterin aldolase	20 (100)	8 (57)	0.002
folP	Dihydropteroate synthase	20 (100)	9 (64)	0.007
SH2607_NA	ATP-binding protein (plasmid)	20 (100)	4 (29)	<0.001
sraP	Serine-rich adhesin for platelets	20 (100)	13 (93)	0.412

Table S2. Frequency of combinations of antibiotic resistance phenotype, genotype and virulence seen in the 34 S. haemolyticus *isolates.*

Combination	**Antibiotic resistance phenotype**	**Outbreak clone n (%)**	**Non-outbreak isolates n (%)**
1	Aminoglycoside, Methicillin, β-lactam, Macrolide	16 (80)	5 (36)
2	Aminoglycoside, Methicillin, β-lactam	2 (10)	0 (0)
3	Aminoglycoside, Methicillin, β-lactam, Macrolide, Trimethoprim-sulfamethoxazole	2 (10)	0 (0)
4	Fusidic acid, β-lactam	0 (0)	1 (7)
5	Aminoglycoside, Methicillin, β-lactam, Fluoroquinolone	0	1 (7)
6	Aminoglycoside, Methicillin, β-lactam, Fusidic acid	0	1 (7)
7	Aminoglycoside, Methicillin, β-lactam, Fluoroquinolone, Fusidic acid, Lincosamide, Macrolide, Trimethoprim-sulfamethoxazole	0	2 (14)
8	Macrolide, β-lactam	0	1 (7)
9	Methicillin, β-lactam	0	1 (7)
10	Aminoglycoside, Methicillin, β-lactam, Fluoroquinolone, Lincosamide, Macrolide, Trimethoprim-sulfamethoxazole	0	1 (7)
11	β-lactam	0	1 (7)

Combination	**Antibiotic resistance genotype**	**Outbreak clone n (%)**	**Non-outbreak isolates n (%)**
1	*aac(6')-aph(2"), blaZ, qacA, mphC, msrA, mecA*	15 (75)	4 (29)
2	*aac(6')-aph(2"), blaZ, mphC, msrA, mecA*	3 (15)	0
3	*aac(6')-aph(2"), blaZ, qacA, mecA*	2 (10)	0
4	*blaZ, qacA*	0 (0)	1 (7)
5	*aadD, blaZ, cat (pC221), qacA, fusB*	0	1 (7)
6	*aac(6')-aph(2"), blaZ, mecA, tet*(M)	0	1 (7)
7	*aac(6')-aph(2"), blaZ, cat (pC221). qacA, fusB, lsaA, mphC, vga(A)LC, msrA, mecA, tet*(K), *dfrG*	0	2 (14)
8	*aac(6')-aph(2"), blaZ, cat (pC221), qacA, mecA, tet*(K)	0	1 (7)
9	*aph(3')-III*	0	1 (7)
10	*blaZ, qacA, mecA, tet*(K)	0	1 (7)
11	*aac(6')-aph(2"), blaZ, qacA, fusB, fusc, mecA*	0	1 (7)
12	*aac(6')-aph(2"), blaZ, qacA, ermC, mphC, msrA, mecA, dfrG*	0	1 (7)

Combination	**Virulence**	**Outbreak clone n (%)**	**Non-outbreak isolates n (%)**
1	All 20 virulence genes (Table S1)	20 (100)	2 (14)
2	All virulence genes except *SH2607_NA* (Table S1)	0	5 (36)
3	All virulence genes except *folB* (Table S1)	0	1 (7)
4	*SH0155_NA, nikA, yjjG, ansA, blaZ, SH2156_NA*	0	1 (7)
5	*SH0155_NA, nikA, secA2, fabG, yjjG, ansA, blaI, blaR1, blaZ, SH2156_NA, tagE, sraP*	0	2 (14)
6	*ugpQ, paaZ, mecA, SH0155_NA, nikA, secA2, fabG, yjjG, ansA, aacA-aphD, SH1612_NA, blaI, blaR1, blaZ, SH2156_NA, tagE, sraP*	0	1 (7)
7	*ugpQ, paaZ, mecA, SH0155_NA, nikA, secA2, fabG, yjjG, ansA, aacA-aphD, SH1612_NA, blaI, blaZ, tagE, folB, folP, SH2607_NA, sraP*	0	1 (7)
8	*ugpQ, paaZ, mecA, SH0155_NA, nikA, secA2, fabG, yjjG, ansA, blaI, blaR1, blaZ, SH2156_NA, tagE, sraP*	0	1 (7)

Supplementary reference

1. Pain M, Hjerde E, Klingenberg C, Cavanagh JP. 2019. Comparative Genomic Analysis of Staphylococcus haemolyticus Reveals Key to Hospital Adaptation and Pathogenicity. Front Microbiol 10:2096.