

1 **Full Title:** Strain typing and characterization of virulence genes in clinical *Staphylococcus aureus*
2 isolates from Kenya.

3 Short title: *S.aureus* strain typing and virulence gene detection.

4 **Authors**

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14 **Abstract**

15 *Staphylococcus aureus* strain typing is an important surveillance tool as particular strains have
16 been associated with virulence and community and hospital acquired MRSA outbreaks globally.
17 This study sought to determine the circulating strain types of *S.aureus* in Kenya and establish
18 the virulence genes among the strains. Clinical *S.aureus* isolates from 3 hospitals in Kenya were
19 sequenced on the Illumina Miseq and genomes assembled and annotated on PATRIC. Results
20 demonstrated great diversity among the isolates with identification of 6 distinct CC
21 (8,22,15,80,121,152), 8 ST types (8, 15, 22,80,121,152,241, 1633) and 8 spa types (t005, t037, t064,
22 t084, t233, t2029, t272,t355). Novel STs (4705, 4707) and a novel spa type (t17826) were
23 identified. The most prominent clonal complex was CC 152 comprised of only MSSA. A majority
24 of MRSA isolates (3/4) typed to ST 241, CC8. One MRSA isolate typed to a novel ST 4705. All
25 isolates were screened for a panel of 56 known virulence genes (19 adhesins, 9 hemolysins, 5
26 immune evasion proteins, 6 exo-enzymes and 19 toxins). 9 toxin genes were detected among
27 the isolates with CC8 isolates having the highest numbers of toxin genes. An MSSA isolate (CC8)
28 from a severe burn infection had the highest number of toxin genes (5). All MRSA isolates (CC8)
29 had only 2 toxins, SEK and SEQ, whereas a majority of the MSSA isolates either had 0 or ≥ 2
30 toxins. SEK+SEQ and TSST-1+SEB+SEL toxin combinations were observed among patients
31 whose disease resulted in hospitalization, an indicator of severe infections. This study confirms
32 the highly heterogeneous *S.aureus* population in Kenya. MSSA appear to have the potential of
33 accumulating more toxin genes than MRSA. This co-occurrence of major toxin genes, some

34 associated with MRSA, highlights the potential risks of outbreaks of highly virulent MRSA
35 infections which would pose treatment challenges.

36 **Keywords:** MRSA, MSSA, Kenya, virulence, whole genome

37 **Introduction**

38 *Staphylococcus aureus* is one of the leading causes of nosocomial infections but in recent years
39 it has been increasingly associated with community acquired infections [1]. *S.aureus* causes a
40 wide spectrum of diseases including bacteremia, pneumonia, urinary tract, skin and soft tissue
41 infections (SSTI) [2,3]. Since the emergence of methicillin resistance (MRSA) in the 1940s
42 epidemics initiated by successful MRSA clones have been observed [4,5] . For instance, USA 300,
43 a highly virulent MRSA strain that emerged in the USA is currently associated with community
44 outbreaks globally [6]. E-MRSA 15 which emerged in the UK has been linked to various hospital
45 outbreaks [7]. Clonal success has been attributed to factors that enhance binding to host tissues
46 and to the acquisition of virulence genes. For example, USA 300 has acquired the arginine
47 catabolic mobile element, *sek* and *seq* virulence genes [8-10].

48 Strain typing is necessary for identification of emerging and outbreak associated strains. Multi
49 locus sequence typing (MLST) and typing of the staphylococcal protein A (*spa*) gene have been
50 widely used over the last 10 years to identify different strain types [11,12]. MLST examines
51 differences in 7 housekeeping genes, assigns allele numbers and sequence types (ST) from the
52 allelic profiles. These ST are then grouped into larger groups known as clonal complexes [13].
53 Spa typing is based on the number, sequence and type of repeats in the hypervariable region of

54 protein A. For MRSA, additional typing of the staphylococcal cassette chromosome (SSC mec)
55 which harbors the gene encoding methicillin resistance allows for additional discrimination
56 between MRSA strains. Staphylococcal cassettes differ in gene arrangement and at least 11
57 types have been reported [14-16].

58 The *S.aureus* genome bears a plethora of virulence determinants [17,18] some of which are
59 encoded in the core genome while others are borne on accessory genomes such as plasmids,
60 conjugative transposons, plasmids and cassettes [19]. Virulence factors are grouped according
61 to function into adhesins, immune evasion proteins, toxins and pore forming proteins. Cell wall
62 adhesins mediate binding to host tissues and biofilm formation e.g. clumping factor A and
63 polysaccharide intracellular adhesin. Pore forming proteins include leukocidins (LukE, LukD, and
64 PVL) and hemolysins (gamma, beta, alpha). *S.aureus* toxins have been associated with severe food
65 poisoning (SEB, SEA) exfoliative skin conditions (ETA, ETB) and systemic shock (TSST-1) [20-24].
66 The distribution of virulence genes has been shown to differ between strain types [25].

67 Previous Kenyan studies have largely focused on susceptibility profiles [26,27] of *S.aureus* and
68 strain typing with limited testing for virulence determinants which can influence infection
69 severity. Virulence genes reported in both *S.aureus* carriage and infection studies in Kenya
70 include Panton Valentine leukocidin (*PVL*), Toxic shock syndrome (TSST1), exfoliative toxin A and
71 enterotoxin A with a notably high prevalence of *PVL* reported [28,29]. These studies were limited
72 to 4 healthcare institutions in close geographic proximity therefore there is limited information
73 on the diversity and distribution of the *S.aureus* population across Kenya. This study sought to
74 fill this gap by typing isolates from a wider geographical area and identifying the relationships

75 between Kenyan strains and known global strains using phylogeny. In addition, isolates were
76 screened for a panel of known virulence genes and attempts made to correlate their presence
77 with disease severity. By broadening our understanding of the *S.aureus* population in Kenya, this
78 study provides baseline data for tracking emerging hypervirulent or outbreak associated strains
79 of *S.aureus*.

80 **Materials and methods**

81 **Ethics**

82 This study was approved by the Walter Reed Army Institute of Research (#2089) and Kenya
83 Medical Research Institute (#2767) IRBs.

84 **Bacterial isolates identification**

85 Clinical *S.aureus* isolates from patients enrolled in an ongoing surveillance study (WRAIR#2089,
86 KEMRI#2767) in public hospitals in three counties (Kisumu, Kericho and Nairobi) in Kenya were
87 analyzed for this study. *S.aureus* isolates were identified based on beta hemolysis on sheep
88 blood agar plates, gram positive, clustered cocci by gram stain, catalase and coagulase positive
89 phenotypes. Isolate identity was confirmed using the MALDI-TOF biotyper (Bruker Daltonics,
90 Millerica, MA, USA) and using the GP card on the Vitek 2 platform (bioMérieux, Hazelwood, MO,
91 USA). 19 isolates (4 MRSA, 15 MSSA) obtained between April 2015 and December 2015 were
92 studied. A majority of the *S.aureus* isolates were from skin and soft tissue infections (18/19).
93 84.2% were community acquired infections and 15.8% (3/19) were hospital acquired infections

94 as per the CDC classification (29). Outpatient infections were considered mild infections (10/19,
95 52.6%) whereas inpatient infections (9/19, 47.3%) were considered severe infections, Table 1.

97

98 **Table 1: Clinical characteristics of the Kenyan *S.aureus* isolates in this study**

ISOLATE #	INFECTION TYPE ^d	MRSA/MSSA ^b	CA/HA ^c	IP/OP ^a	SEVERITY
SAKEN01	UTI	MRSA	CA	OP	Mild
SAKEN05	SSTI	MRSA	HA	IP	Severe
SAKEN06	SSTI	MRSA	CA	IP	Severe
SAKEN13	SSTI	MSSA	CA	OP	Mild
SAKEN14	SSTI	MSSA	HA	IP	Severe
SAKEN15	SSTI	MSSA	HA	IP	Severe
SAKEN16	SSTI	MSSA	CA	OP	Mild
SAKEN17	SSTI	MSSA	CA	OP	Mild
SAKEN18	SSTI	MSSA	CA	IP	Severe
SAKEN19	SSTI	MSSA	CA	IP	Severe
SAKEN20	SSTI	MSSA	CA	IP	Severe
SAKEN21	SSTI	MRSA	CA	IP	Severe
SAKEN22	SSTI	MSSA	CA	OP	Mild
SAKEN23	SSTI	MSSA	CA	IP	Severe
SAKEN24	SSTI	MSSA	CA	OP	Mild
SAKEN25	SSTI	MSSA	CA	OP	Mild
SAKEN26	SSTI	MSSA	CA	IP	Severe
SAKEN27	SSTI	MSSA	CA	OP	Mild
SAKEN29	SSTI	MSSA	CA	OP	Mild

99 Table legend: ^aIP-Inpatient, OP-Outpatient. Inpatient infections are considered severe infections in this

100 study. ^bMethicillin Resistant *Staphylococcus aureus* (MRSA), Methicillin Susceptible *Staphylococcus aureus*.

101 ^cCA – Community acquired infection, HA - Hospital associated infection. ^dSSTI – Skin and soft tissue

102 infection, UTI – Urinary tract infection

103 **Isolate typing**

104 In-vitro spa typing was performed using conventional PCR [30] and Sanger sequencing. Contigs
105 were assembled on CLC bio Main-Workbench (CLC bio, Aarhus, Denmark) and spa types
106 analyzed using Ridom StaphType (Ridom GmbH, Münster, Germany). In-silico spa typing was
107 done by analyzing assembled genomes on the online analysis pipeline
108 <https://cge.cbs.dtu.dk/services/spatyper/>. Spa types obtained by both methods were compared.
109 Sequences of isolates with novel spa repeats were submitted to the Ridom Spa Server for
110 assignment of spa type.

111 MLST sequence type (ST) was determined in-vitro using published primers [11]. Gene sequences
112 for each of the 7 loci were queried against the *S.aureus* database, allele numbers obtained and
113 allelic profiles analyzed on <http://www.mlst.net/> [13] to assign ST. Isolates were grouped into
114 clonal complexes using the BURST clustering algorithm available on <http://eburst.mlst.net/>,
115 allowing a minimum of 6 identical loci for group definition. Sequences of novel ST were
116 submitted to <https://pubmlst.org/saureus/> for ST assignment.

117 **Staphylococcal cassette chromosome typing**

118 Staphylococcal cassette types for the MRSA isolates were determined using previously published
119 primers [14]. PCR products were visualized on agarose gels and SSC mec types determined
120 based on different amplicon size.

121 **Whole genome sequencing and sequence analysis**

122 Genomic DNA was extracted from freshly cultured *S.aureus* isolates using ZR Fungal/Bacterial
123 DNA MiniPrep Kit (Zymo research, California, United States). DNA concentrations were
124 determined using the Qubit (Thermo Fisher Scientific, Massachusetts, United States) and 1ng of
125 DNA used for library preparation with the Nextera XT kit (Illumina) as per manufacturer's
126 instructions to generate 300bp paired end libraries. Libraries were sequenced on an Illumina
127 MiSeq platform.

128 Raw reads were uploaded onto the Pathosystems Resource Integration Center (PATRIC 3.5)
129 <https://www.PATRICbrc.org/> [31]. Genome assembly was carried out on PATRIC using the
130 assembly pipeline 'miseq' as the assembly strategy which runs both Velvet [32] and SPAdes [33]
131 algorithms and uses ARAST, an in-house scoring script. Annotation was performed using the
132 RASTk pipeline [34] on PATRIC with 'Bacteria' as the domain and 'Staphylococcus aureus' as the
133 taxonomy ID. Genome assemblies were uploaded onto NCBI under BioProject ID PRJNA481322.
134 A summary of the genome characteristics can be found in Table 2.

135 **Bioinformatic analysis**

136 In-silico MLST was determined by analyzing the assembly files on both the PATRIC genome
137 characterization pipeline and on MLST 1.8 <https://cge.cbs.dtu.dk/services/MLST/> [35] at the
138 Centre for Genomic Epidemiology (CGE). Novel ST types were submitted to
139 <https://pubmlst.org/saureus/> for typing [36].

140 To establish the relationships between the isolates of this study, MLST sequences for the query
141 genomes were concatenated on FASconCAT [37] and maximum likelihood phylogeny inferred
142 using PhyML 3.1 [38] utilizing the TMP model with gamma variation.

143 To infer relationships between genomes of this study and known global strains, phylogenetic
144 analysis was performed on the 19 Kenyan *S.aureus* whole genomes and 26 global strains.
145 Reference strains were selected to include at least one whole genome for all the sequence types
146 identified and common global and regional strains. The reference strains used in the
147 phylogenetic analysis are under supplementary information appendix S1, Table 1. To generate a
148 whole genome sequence phylogeny on PATRIC, genome assemblies were analyzed on the
149 phylogenetic tree building service. The tree building service filtered genome protein files and
150 used BLAST to determine the best bi-directional hit, clustered protein files into homolog sets
151 and filtered out homolog sets representing <80% of the genomes and eventually protein sets
152 meeting the threshold were trimmed and aligned with MUSCLE [39]. Tree alignments were
153 concatenated and a main tree built using RAxML [40]. Progressive tree refinement was
154 employed for analysis of poorly refined sub – trees [31,41]. Phylogenetic trees generated from
155 both the MLST loci and WGS (Figure 1-2) were compared.

156 To investigate the presence of known virulence genes, whole genomes of Kenyan isolates were
157 screened for 56 virulence genes. Virulence genes were identified under the specialty genes on
158 PATRIC with 'Virulence' as the search term. Targeted virulence genes and pathogenicity islands
159 were identified across all isolates on PATRIC. To verify the virulence genes identified, contigs

160 were analyzed on VirulenceFinder 1.5 <https://cge.cbs.dtu.dk/services/VirulenceFinder/> [42]. The

161 virulence genes identified were then grouped according to function.

163 **Results and Discussion**

164 **Table 2: Genome characteristics of *S.aureus* isolates analyzed in this study**

ISOLATE ID	GC CONTENT	GENOME SIZE(MB)	CONTIGS	coding sequences	# of repeat regions	# of tRNA present	# of rRNA
SAKEN01	32.65	3	66	2918	125	57	7
SAKEN05	32.7	2.97	83	2864	156	60	9
SAKEN06	32.7	2.97	73	2868	151	58	9
SAKEN13	32.7	2.7	73	2613	90	60	2
SAKEN14	32.7	2.73	68	2595	85	56	9
SAKEN15	32.7	2.71	50	2568	79	56	8
SAKEN16	32.78	2.71	91	2564	86	61	13
SAKEN17	32.79	2.74	103	2641	91	59	8
SAKEN18	32.77	2.6	98	2555	80	54	6
SAKEN19	32.74	2.8	44	2700	115	59	10
SAKEN20	32.76	2.79	96	2703	102	58	6
SAKEN21	32.69	2.9	83	2896	116	55	8
SAKEN22	32.73	2.76	56	2654	94	58	8
SAKEN23	32.69	2.72	58	2575	84	58	9
SAKEN24	32.82	2.72	145	2622	110	55	6
SAKEN25	32.87	2.69	183	2604	73	51	7
SAKEN26	32.74	2.83	89	2784	133	58	8
SAKEN27	32.8	2.74	52	2592	83	59	8
SAKEN29	32.69	2.83	111	2749	132	57	8

165 **Spa typing**

166 Study isolates typed into 8 distinct spa types (t005, t037, t064, t084, t233, t2029, t272, t355). t355
167 was the dominant spa type (7/19; 36.8%). A single novel spa type, assigned t17826, was

168 reported. MRSA isolates typed to t007 (1) and t037 (3) while MSSA isolates showed great spa
169 diversity with t005, t17826, t272, t13194 being represented by singletons. Discrepancies
170 between in-vitro and in-silico spa typing were observed for SAKEN 01, (t007 vs t2029) and
171 SAKEN 13, (t084 vs t233) (Table 2).

172 **MLST typing**

173 Multi locus sequence typing results were consistent on both CGE and PATRIC analysis platforms.
174 There was great diversity among the isolates with the identification of 6 distinct CC
175 (8,22,15,80,121,152) and 8 ST types (8, 15, 22,80,121,152,241, 1633) (Table 3). 2 novel STs
176 assigned ST 4705 (CC 8, MRSA) and ST 4707 (CC 5, MSSA) by PubMLST [36] were reported. A
177 majority of the isolates belonged to CC 152 (7/19) and CC 8 (5/19). ST 152 was the most
178 dominant 6/19 (31%) with all isolates being MSSA geographically distributed across the 3
179 counties. 4 of the STs were represented by singletons.

180 All the MRSA in this study belonged to CC 8. A majority of MRSA (3/4) in this study typed to ST
181 241 and spa type t037. One isolate typed to the novel ST 4705 and spa type t007. This isolate
182 only differed from the other isolates in the acetyl coenzyme A acetyltransferase (*yqiI*) loci. In-
183 vitro SSC mec typing identified 2 SSC mec types with a majority of the MRSA typing to SSC mec
184 IVc (3/4). The remaining isolate with the novel ST 4705, typed to SSC mec II.

186

187 **Table 3: Table showing STs, CCs of Kenyan *S.aureus* isolates**

Isolate	Clonal complex	MLST type (ST)	SPA type (in-vitro)	SPA type (in- silico)	MRSA/MSSA	REGION ^a
SAKEN01	8	4705*	t007	t2029	MRSA	KDH
SAKEN05	8	241	t037	t037	MRSA	KDH
SAKEN06	8	241	t037	t037	MRSA	KDH
SAKEN21	8	241	t037	t037	MRSA	KDH
SAKEN19	8	8	t064	t064	MSSA	KDH
SAKEN26	8	8	t064	t064	MSSA	KDH
SAKEN16	152	152	t355	t355	MSSA	KCH
SAKEN18	152	152	t355	t355	MSSA	KCH
SAKEN20	152	152	t355	t355	MSSA	KDH
SAKEN14	152	152	t355	t355	MSSA	NRB
SAKEN22	152	152	t355	t355	MSSA	NRB
SAKEN23	152	152	t355	t355	MSSA	NRB
SAKEN15	152	1633	t355	t355	MSSA	NRB
SAKEN24	22	22	t005	t005	MSSA	KCH
SAKEN13	22	22	t084	t233	MSSA	NRB
SAKEN25	5	4707*	t17826*	unknown	MSSA	KDH
SAKEN17	15	15	t084	t084	MSSA	KCH
SAKEN27	80	80	t13194	t13194	MSSA	KCH
SAKEN29	121	121	t272	t272	MSSA	KDH

188 Table legend. * denotes novel ST and spa types reported by this study. ^a Three regions in Kenya where the

189 isolates were obtained from: KCH- Kericho, KDH – Kisumu County, NRB- Nairobi County

190 Each region showed a unique genetic fingerprint with CC 8 (ST 8 and ST 241) detected in Kisumu
191 County only while CC 152 showed a wide geographic distribution. Kericho County showed
192 greatest heterogeneity in CC/ST.

193 **Phylogenetic analysis**

194 Maximum likelihood phylogenies reconstructed on PATRIC and on PhyML gave similar tree
195 topologies with isolates clustering according to sequence types and/or clonal complexes Fig 1-2.

196

197 **Fig 1: Dendrogram of an MLST phylogeny of Kenyan *S.aureus* isolates.** Maximum likelihood was phylogeny
198 inferred using a custom model and 100 boot strap replicates. ST and CC associated with MRSA isolates of this study
199 are depicted in bold font.

200 The phylogenetic tree inferred using MLST depicted a multifurcating tree with distribution of
201 MRSA and MSSA isolates in distinct clusters. ST 121 was ancestral to ST 152 while ST 80 was
202 ancestral to ST 22. CC 8 cluster encompassed all MRSA isolates (ST 241, ST 4705) and ST 8
203 MSSA isolates. The MRSA clade (ST 241) and MSSA (ST 8) clade are sister groups sharing a
204 recent common ancestor. The MRSA isolate (SAKEN 01) which has a novel ST grouped within the
205 MRSA clade.

206

207 **Fig 2: Dendrogram showing whole genome phylogeny of Kenyan isolates** (SAKEN prefix and in blue)
208 relative to known global strains. MRSA isolates are depicted in green. Reference isolates are in black with
209 a country/regional prefix. Phylogeny inferred using maximum likelihood with progressive refinement on
210 PATRIC.

211 Whole genome phylogeny with global strains showed Kenyan ST 152 isolates clustered with the
212 asymptomatic Malian BB155 strain. MRSA in this study were closely related to TW20 strain 582
213 (ST 239) which is a successful HA MRSA lineage in the United Kingdom [7]. Kenyan ST8 MSSA
214 isolates grouped closely with the highly virulent Newman strain [43]. ST/CC 22 was represented
215 by 2 MSSA isolates which clustered with EMRSA-15 (MRSA-15), associated with widespread
216 outbreak of HA-MRSA in Europe [44]. It was also observed that Kenyan strains in this study were
217 closely related to MRSA and MSSA isolates from Tanzania and Sudan respectively. Tanzanian
218 MRSA isolates clustered with the Kenyan ST 8 MSSA isolates and Kenyan ST 15 MSSA.

219 **Virulence genes screen.**

220 The 19 *S.aureus* genomes were screened in-silico for a panel of 56 known virulence genes (19
221 adhesins, 9 hemolysins, 5 immune evasion proteins, 6 exo-enzymes and 19 toxins). Of the 19
222 adhesins investigated, 10 were identified in all the isolates (ClfA, ClfB, FnbA, EbpS, IcaA,
223 Eap/Map, SasA, SacC, SasF, and SasH) (S2 table). Since these adhesins are ubiquitously
224 expressed as they are essential for successful host invasion by facilitating binding to extra
225 cellular matrix proteins [45], they are not discussed further in this paper. Efb (Extracellular
226 Fibrinogen – binding protein) was detected in 84% of the isolates. 18/19 of the isolates bore ≥ 2
227 of the Ser-Asp rich fibrinogen binding proteins whereas collagen binding protein (cna) was
228 present in 63% of the isolates. It was observed that the presence of the adhesin genes was
229 loosely correlated with the clonal complex. For example, isolates lacking Efb (3) belonged to CC
230 152 while all CC 152 isolates lacked SdrC, SasG cell wall adhesion protein and CC8 isolates
231 lacked the SasK adhesion protein.

232 A majority of the hemolysins screened for (6/9) were identified in the isolates (gamma A, B, C,
233 delta, alpha hemolysin and PVL). 63% (12/19) of the isolates had ≥ 5 of the hemolysins screened
234 for with Leukocidin D and E being present in 94% and 89% of the isolates respectively.
235 Hemolysins damage the host cell plasma membrane which is a critical process during *S.aureus*
236 infection and disease progression [46]. Of note, all isolates typing to CC 152 lacked beta
237 hemolysin whereas the bi-component protein Panton Valentine leukocidin was detected in all
238 the Kenyan isolates.

239 Of the 19 toxins screened for 9 were detected; TSST-1, ETA/ETB, SEB, SEG, SEH, SEK, SEL, SEQ,
240 and SPEG. Toxins were found to be randomly distributed among the CCs. TSST-1 was detected
241 in 3/19 of the isolates obtained from various soft tissue infections (burns, abscesses and cuts).
242 All the isolates with TSST-1 were MSSA of which 2/3 were from hospitalized patients an indicator
243 of severe infection. Staphylococcal pathogenicity island 1 (SaP1) was detected in all isolates with
244 TSST-1 (S2 Table 1). SEB was present in 2/19 of the isolates obtained from hospitalized patients
245 presenting with a burn and an abscess. SEL, SEG enterotoxins and ETA/ETB exfoliative toxins
246 were each detected in 2/19 of the isolates. Isolates with ETA and ETB exfoliative toxins were
247 obtained from outpatient subjects with mild abscess and skin lesion infections. Staphylococcal
248 pathogenicity island 2 (SaPln2) was detected in isolates with one or both exfoliative toxins.

249 Some toxin combinations were observed to always co-occur: SEK+SEQ, SEB+SEL, TSST-1+SEG,
250 TSST-1+SEB+SEL, TSST-1+SEB+SEK+SEL. The SEK+SEQ combination was present in all the
251 MRSA isolates in this study a majority (3/4) of which were from hospitalized subjects. TSST-1
252 detected in this study was from both hospitalized (2) and outpatient (1) subjects. In the

253 hospitalized patients TSST-1 co-occurred with SEB and SEL while in an outpatient TSST-1 co-
254 occurred with SEG suggesting that TSST-1+SEB+SEL combination could cause severe infections.
255 Comparison of the number of toxin genes between MRSA and MSSA isolates revealed that all
256 Kenyan MRSA isolates only had 2 toxins whereas MSSA isolates had between 0-5 toxins. The
257 isolate with the highest number of toxins (5) was an MSSA isolate obtained from a hospitalized
258 burn patient. This MSSA isolate was in the same CC as the MRSA isolates suggesting the
259 potential risk of emergence of CC 8 strains that are both highly virulent and difficult to treat. A
260 majority (2/3) of the hospital acquired infections had no toxin genes detected in their genomes
261 with the remaining isolate having 2 toxin genes.

262 **Discussion**

263 This study typed *S.aureus* isolates from widespread geographical areas in Kenya and inferred
264 phylogenetic relationships between the isolates and known global and regional strains. To
265 understand the virulence potential of the Kenyan strains, virulence genes in the Kenyan strains
266 were identified and the presence of these genes investigated in relation to CC and clinical
267 presentation.

268 Strain typing revealed 8 STs and 8 spa types among the 19 Kenyan isolates confirming the great
269 heterogeneity previously described among *S.aureus* both regionally and globally [28,29,47-49].
270 The isolates grouped into 6 distinct clonal complexes with CC 152 being most dominant and
271 widely distributed across the three counties. CCs 8 and 22 known to harbor MRSA globally were

272 also reported. All MRSA isolates in this study typed to CC 8 while MSSA isolates showed
273 heterogeneous distribution across a number of CCs.

274 Globally, MRSA strains have been shown to belong to 3 major CC: CC 8, CC 5 and CC 22 [50].
275 For instance, EMRSA15/UK that is responsible for hospital acquired MRSA infections in the UK
276 types to CC 22. In this study CC 22 was comprised of only MSSA isolates whereas CC 8 was
277 composed of both MSSA and MRSA isolates. Previous Kenyan studies carried out in hospitals in
278 Nairobi [47] and Thika [28] identified CC 5 as the predominant circulating MRSA clone within
279 hospitals in Nairobi and its environs. MRSA isolates from hospitals in Nairobi were
280 predominantly ST 241, t037 while ST 239, t037 prevailed in the hospital in Thika. In this study, all
281 MRSA isolates typed to ST 241, t037; similar to that reported by Omuse et al [47] in 3 hospitals
282 in Nairobi. All MRSA isolates in this study (CC 8, ST 241 and novel ST 4705) were obtained from
283 Western Kenya which is situated 300km from Nairobi. This identification of ST 241 MRSA strains
284 in both Western Kenya and Nairobi suggests a widespread geographical distribution of this
285 MRSA strain in Kenya. Schaumburg et al [48] reported ST 241 MRSA clone to be widespread in
286 Africa though with varying SSCmec types; Senegal (SSCmec III), Tunisia (SSCmec III), Niger
287 (SSCmec III and V) Nigeria (SSCmec III and IV) and Algeria (SSCmec III) [51]. A majority of the
288 MRSA isolates of this study bore SSCmec IV similar to that reported in Nigeria.

289 Spa typing showed a greater discriminatory power than ST with multiple spa types belonging to
290 the same STs. Discrepancies between in-vitro and in-silico spa types (t007 vs t2029 and t084 vs
291 t2330) was due to shorter repeat sequences in-silico. The shorter repeats observed in silico can
292 be attributed to filtering out of low quality reads in the sequence analysis pipeline. Thus, we

293 recommend the use of conventional in-vitro spa typing as a surveillance tool more so in regions
294 with great *S.aureus* population diversity.

295 Inferred phylogeny of the Kenyan isolates showed distinctive clustering by CC. CC 8 cluster
296 composed of two clades ST 8 (MSSA) and ST 241 (MRSA) with the two clades sharing a recent
297 common ancestor. Studies have shown that MSSA isolates of CC 8 act as reservoirs for MRSA
298 pending acquisition of the staphylococcal cassette [52,53].

299 Relationships between isolates of this study and known global strains using whole genome
300 phylogeny revealed close clustering of MRSA strains in this study with the well-known TW20
301 strain 582, which is a successful HA MRSA clone which originated from London in the UK [7].
302 TW20 is a hospital associated outbreak MRSA strain known for its high transmissibility and
303 multi-drug resistant properties due to a plethora of resistance genes carried on mobile elements
304 [54]. TW20 and the MRSA strains in this study both type to CC 8. CC 8 MRSA strains have been
305 linked to community acquired infections and is the predominant MRSA strain in this study. This
306 clonal complex encompasses well known strains such as USA 300 which is a lineage linked to the
307 acquisition of SSCmec IV, PVL and SEQ and SEK genes [10,55]. EMRSA-15 strain belongs to the
308 same clade as Kenyan ST 22 MSSA isolates. EMRSA-15 is a well-known strain associated with the
309 widespread outbreak of HA-MRSA in Europe [44] and MSSA isolates typing to ST 22 have been
310 identified as the MSSA reservoir from which EMRSA-15 emerged [56]. ST 152, the dominant
311 Kenyan strain is related to both carriage strains in Mali [57] and pathogenic strains in Europe
312 [58-60].

313 Bacterial virulence factors are key for successful host colonization and infection. Adhesins
314 facilitate successful binding to the host extra cellular matrix promoting subsequent biofilm
315 formation. Worth noting is that ST 152 isolates in this study lacked some adhesins (SasG and
316 SdrC) and hemolysin (beta) genes. SasG surface protein mediates successful bacterial adhesion
317 to squamous epithelial cells of the nostrils and promotes biofilm formation. Expression of SasG
318 has been shown to mask the effect of adhesins binding to ligands such as fibrinogen and
319 fibronectin [61]. Both Malian BB155 and Kenyan ST 152 isolate genomes lack SasG which we
320 speculate could promote successful host colonization and provide a fitness advantage. All CC8
321 isolates lacked SasK cell wall adhesion, the significance of this putative adhesin is yet to be
322 determined [62]. Previous studies by McCarthy and Lindsay [25] noted similar observation of
323 variation in surface adhesions between clonal complexes and lineages.

324 PVL, a bi-component leukocidin causing destruction of leukocytes and tissue necrosis, was
325 widespread across all isolates in this study. PVL positive MRSA clones were identified in this
326 study and in other Kenyan and African studies [27,29,63,64]. A Nigerian study pointed out the
327 possibility of emergence of PVL positive MRSA clones as a result of the co-existence of MRSA
328 clones and PVL positive MSSA [65]. This study reports extensive (100%) PVL presence in Kenyan
329 MSSA and MRSA isolates supporting this hypothesis.

330 Staphylococcal toxin (SEB) is a super antigenic toxin associated with food poisoning, non-
331 menstrual toxic shock syndrome, dermatitis and asthma [20]. Kenyan isolates bearing SEB typed
332 to CC 8 and CC 152 consistent with previous observations where SEB was identified most often
333 in CC8 isolates in New York [66]. A Taiwanese study identified SEB to be the cause of

334 Staphylococcal scarlet fever [67]. In this study, SEB was detected in MSSA isolates obtained from
335 a burn and from an abscess. In both cases these were inpatients indicative of severe infections.

336 Toxic shock syndrome toxin (TSST-1) was initially reported as the cause of menstrual toxic shock
337 but over the years non-menstrual toxic shock syndrome has been reported [68-70]. TSST-1 is
338 encoded by *tstH* gene borne on the staphylococcal pathogenicity island 1 [71]. SaP1 was
339 identified in all the isolates positive for TSST-1. TSST-1 was observed to co-occur with up to 4
340 staphylococcal enterotoxins and most often with SEB and SEL. The presence of TSST-1 and SEB
341 toxins in isolates obtained from severe infections resulting in hospital admissions suggests the
342 severity of this toxin combination.

343 SEK and SEQ have been linked to a number of food poisoning cases [24,72] . Among the Kenyan
344 isolates these enterotoxins were associated with SSTIs. SEQ+SEK combination was consistently
345 observed in Kenyan MRSA isolates. SEQ and SEK toxin genes were reported to significantly co-
346 occur in Chinese MRSA isolates [73]. These toxins co-occur on genomic islands and have been
347 associated with the HA SSC *mec II* clone [21,66]. CC 8 isolates have been reported to
348 consistently bear SEQ, SEL and SEK toxin genes [19]. This pattern of distribution was observed
349 among isolates in this study.

350 Of the 4 MRSA isolates 3 were MRSA ST 241, *mec IVc* and the remaining isolate was the novel
351 MRSA ST 4705, *mec II*. Worth noting was the difference between the SSC *mec* cassettes present
352 in the isolates and that the MRSA ST 4705, *mec II* was the sole MRSA isolate associated with a
353 community acquired UTI infection.

354 It was also observed that a majority of MRSA isolates from this study were community acquired
355 and bore PVL, enterotoxin Q and K toxin genes. Studies by Voyich et al [74] have suggested the
356 highly virulent nature of community acquired MRSA in comparison to hospital acquired strains a
357 hypothesis that is not supported by this study which showed no differences in numbers and
358 types of virulence genes between the hospital acquired and the community acquired strains.

359 **Conclusion**

360 Despite the low number of isolates analyzed, this study provides a glimpse into the diversity and
361 distribution of Kenyan MSSA and MRSA isolates and their relatedness to global strains. The
362 study highlighted the potential impact of particular toxin combinations on clinical severity and
363 provided evidence that co-occurrence of methicillin resistance and virulence genes could
364 portend the emergence of highly virulent MRSA infections. There is demonstrated need for
365 continued trend monitoring through surveillance which will continue as part of this ongoing
366 surveillance program.

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377 **Author contributions**

378 Conceptualization: LM
379 Data Curation: LM, CK
380 Formal analysis: CK, JN, LM
381 Funding Acquisition: LM
382 Investigation: CK, JN, DM, VO, SW
383 Methodology: LM
384 Supervision: VO, LM, WS
385 Validation: LM, CK
386 Visualization: LM, CK
387 Writing- Original draft preparation: CK, LM
388 Writing- Review and Editing: JN, CK, VO, SW, DM, WS, LM

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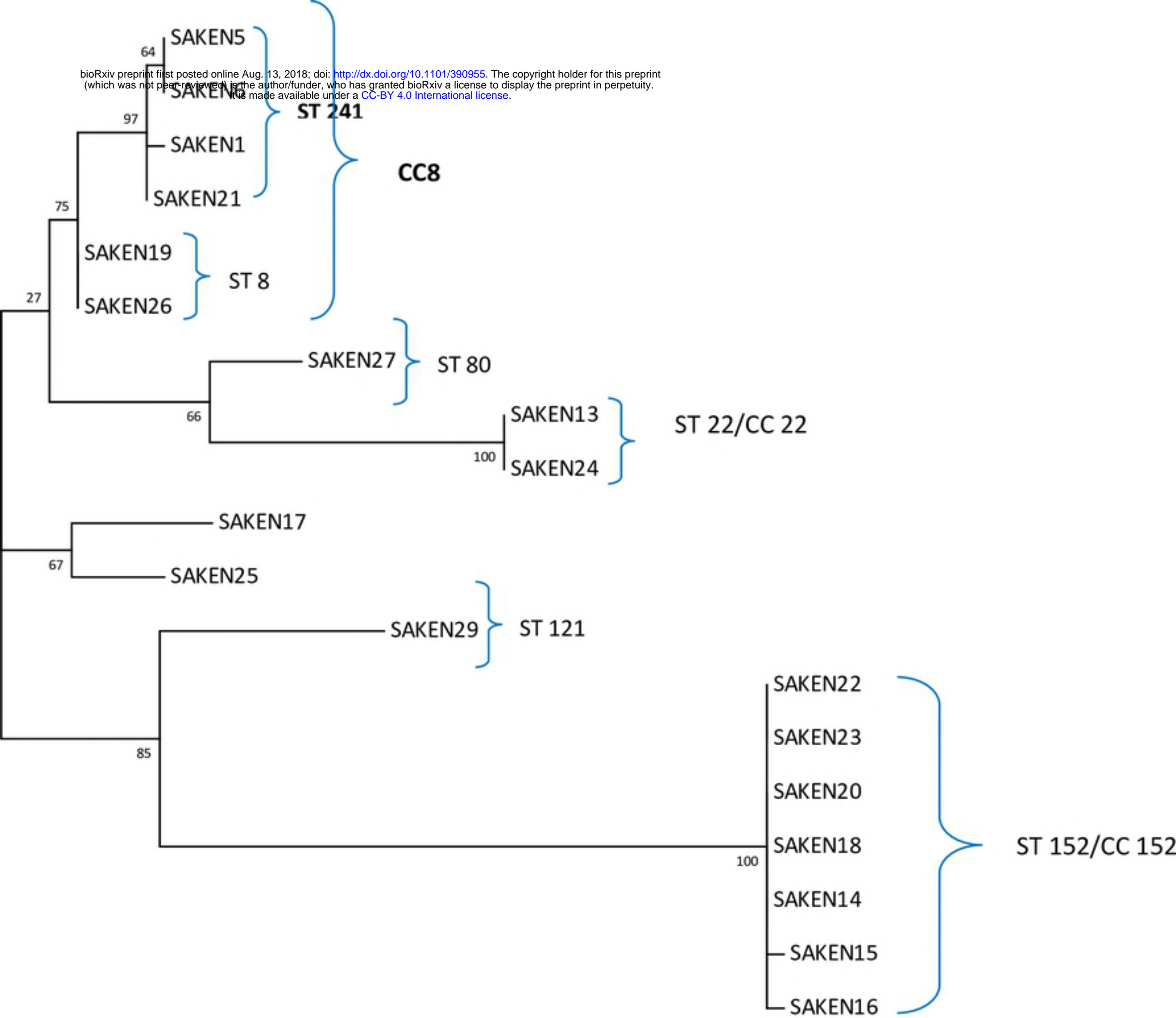
599 **SUPPLEMENTARY INFORMATION**

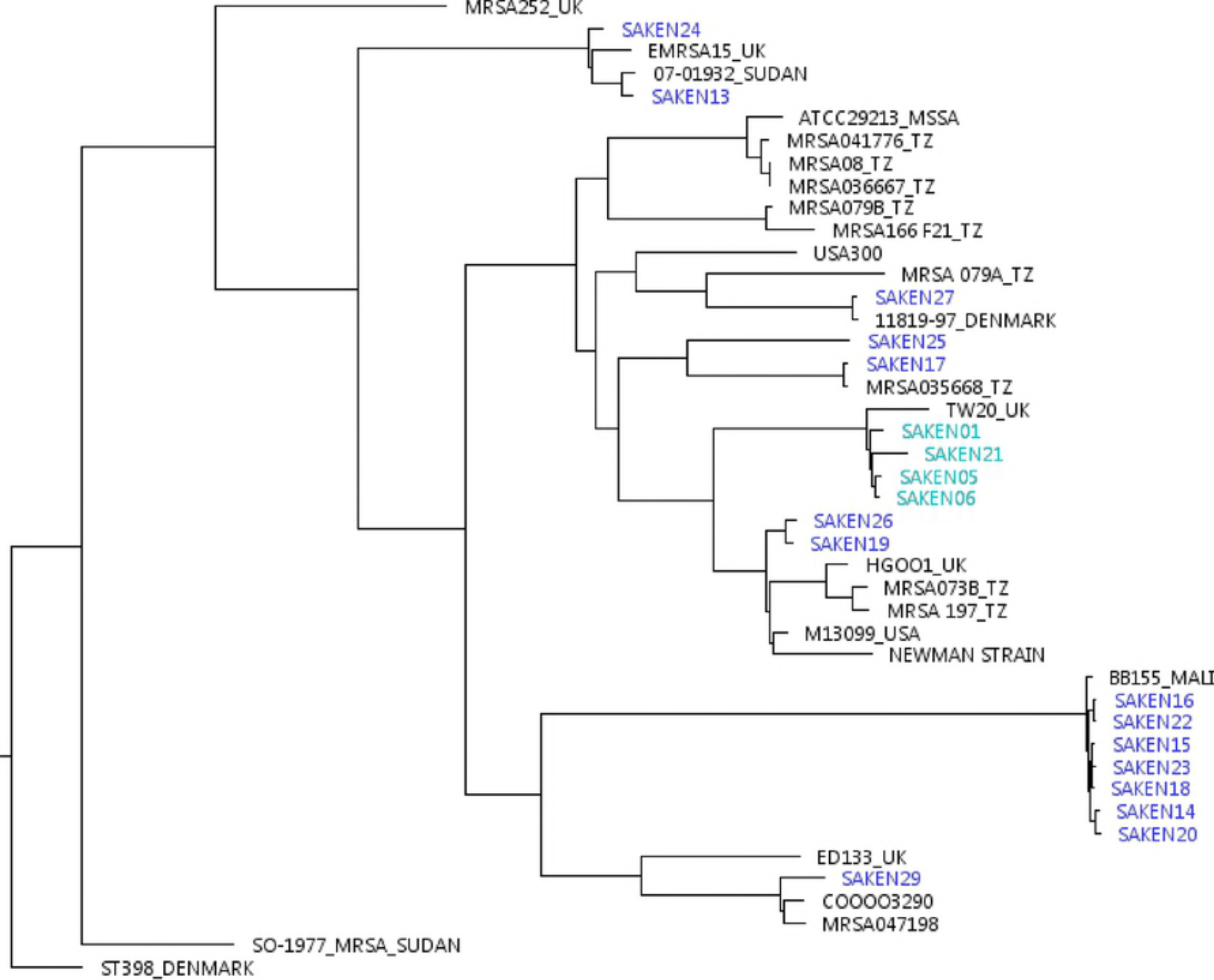
600 **S1 Table 1: List of reference genomes used in this study**

601 **S2 Table 2: Virulence gene profiles across *S. aureus* isolates**

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