

Table S1. Sequences of the primers used for genotyping MRSA strains.

Gen	Primers (5' – 3')	Amplicon (pb)	Control strain	Reference
<i>mecA</i>	P4: TCCAGATTACAACCTTCACCAGG P7: CCACTTCATATCTTGTAAACG	162	ATCC 40142	[17]
Scmec typing Boye et al [17]				
β $\alpha 3$	ATTGCCTTGATAATAGCCYTCT TAAAGGCATCAATGCACAAACACT	937 (II and IV)	I: BAA 44 II: BAA 41 III: BAA 39 IV: NRS 643 V: NRS 745	[18]
<i>ccrCF</i> <i>ccrCR</i>	CGTCTATTACAAGATGTTAAGGATAAT CCTTTATAGACTGGATTATTCAAAATAT	518 (III and V)		
1271F1 1272R1	GCCACTCATAACATATGGAA CATCCGAGTGAAACCCAAA	415 (I and IV)		
5R <i>mecA</i> 5R431	TATACCAAACCCGACAACACTAC CGGCTACAGTGATAACATCC	359 (V)		
Scmec typing Oliveira et al [16]				
CIF2 F2 CIF2 R2	TTCGAGTTGCTGATGAAGAAGG ATTTACCACAAGGACTACCAGC	495 (I)	I: BAA 44 II: BAA 41 III: BAA 39 IV: NRS 643 V: NRS 745	[17]
KDP F1 KDPR1	AATCATCTGCCATTGGTGATGC CGAATGAAGTGAAAGAAAGTGG	284 (II)		
MECI P2 MECI P3	ATCAAGACTTGCATTACAGGC GCGGTTTCAATTCACTTGTC	209 (II and III)		
DSC F2 DSC R1	CATCCTATGATAGCTTGGTC CTAAATCATAGCCATGACCG	342 (I, II and IV)		
RIF4 F3 RIF4 R9	GTGATTGTTGAGATATGTGG CGCTTTATCTGTATCTATCGC	243 (III)		
Virulence factors				
<i>arcA</i>	F: CACGTAACCTTGCTAGAACGAG R: GAGCCAGAAGTACGCGAG	724	NRS 643	[22]
<i>lukFS-PV</i>	F: GCATCAASTGTATTGGATAGCAAAAGC R: ATCATTAGGTAAAATGTCTGGACATGATCCA	433	BAA 1556	[31]
<i>lukED-PV</i>	F: TGTATTGATAGCAAAAGCAGTGCA R: TGAAAAAGGTTCAAAGTTGATACGAG	269	NRS 111	[31]
<i>luk-M</i>	F: GAAGATATTGGCGACGATGCAGAAGT R: GTATTTTGGTCTTTTGATGTAAGACC	253	ATCC 31890	[32]
<i>psm</i>	F: TCCTTCCTTTTCGATGTCGTT R: CCATCTTTTACGATGGTGGTTT	221	NRS 101	[30]
<i>nucA</i>	F: GATGGTGATACGGTT R: AGCCAAGCCTTGACGAACTAAAGC	270	ATCC 43300	[23]
<i>gyrA</i>	F: AGTACATCGTCGTATACTATATGG R: ATCACGTAACAGTTCAAGTGTG	283	ATCC 12600	[24]
<i>coa</i>	F: CACGGATACCTGTACCAGCA R: ACCACAAGGTAAGTGAATCAACG	170	ATCC 43300	[25]
<i>fnbA</i>	F: CTGTGTGGTAATCAATGTC R: CACAACCAGCAAATATAG	1369	ATCC 29213	[26]
<i>fnbB</i>	F: GCCGTCGCCTTGAGCGT R: GGAGAAGGAATTAAGGCG	813	ATCC 29213	[27]
<i>cna</i>	F: CAGGATAGATTGGTTTA R: AGTGGTTACTAATACT	560, or 1120, or 1739	NRS 123	[26]
<i>clfA</i>	F: CTCATCAGGTTGTTTCAGG R: GTAGGTACGTTAATCGGTT	1584	BAA 1556	[26]
<i>clfB</i>	F: TCGGTCTGTAATAAAGGTA R: TGCAAGATCAAACCTGTTCCCT	596	BAA 1556	[26]
<i>icaA</i>	F: ACTACTGCTGCGTTAATAAT R: GATTATGTAATGTGCTTGGA	770	BAA 1556	[26]
<i>icaD</i>	F: GGCAATATGATCAAGATAC R: AAACGTAAGAGAGGTGG	381	BAA 1556	[28]
<i>srdC</i>	F: CTGGACGGAAATATTGACCA R: CGCATGGCAGTGAATACTGTTGCAGC	238	BAA 1556	[29]
<i>sea</i>	F: GAAAAAAGTCTGAATTGCAGGGAACA R: CAAATAATCGTAATTAACCGAAGGTTT	561	NRS 111	[31]
<i>seb</i>	F: ATTCTATTAAGGACACTAAGTTAGGGA R: ATCCCGTTTCATAAGGCGAGT	405	NRS 266	[31]
<i>sec</i>	F: GTAAAGTTACAGGTGGCAAACTTG R: CATATCATACCAAAAAGTATTGCCGT	296	NRS 111	[31]
<i>sed</i>	F: GAATTAAGTAGTACCGCGCTAAATAATAG R: GCTGTATTTTTTCTCCGAGAGT	493	NRS 110	[31]

<i>see</i>	F: CAAAGAAATGCTTTAAGCAATCTTAGGC R: CACCTTACCGCCAAAGCTG	483	NRS 111	[31]
<i>eta</i>	F: ACTGTAGGAGCTAGTGCATTGT R: TGGATACTTTTGTCTATCTTTTTCATCAAC	189	NRS 266	[31]
<i>etb</i>	F: CAGATAAAGAGCTTTATACACACATTAC R: AGTGAACCTATCTTTCTATTGAAAAACACTC	610	NRS 266	[31]
<i>hla</i>	F: CTGATTACTATCCAAGAAATTCGATTG R: CTTTCCAGCCTACTTTTTTATCAGT	210	NRS 111	[31]
<i>hlb</i>	F: GTGCACCTACTGACAATAGTGC R: GTTGATGAGTAGCTACCTTCAGT	310	NCTC 7428	[31]
<i>hld</i>	F: TTAGTGAATTTGTCACTGTGTGCGA R: AAGAATTTTATCTTAATTAAGGAAGGAGTG	111	NCTC 9393	[31]
<i>hlg</i>	F: GTCAYAGAGTCCATAATGCATTTAA R: CACCAAATGTATAGCCTAAAGTG	533	NRS 266	[31]
<i>tst</i>	F: TACTAATGAATTTTTTATCGTAAGCCCTT R: TTCACTATTTGTAAGAGTGTGACACCCACT	180	NRS 111	[31]
<i>spa</i>	F: TAAAGACGATCCTTCGGTGAGC R: CAGCAGTAGTGCCGTTTGCTT	300 to 600	ATCC 43300	[33]

Table S2. Presence of virulence factor genes in MRSA strains isolated from the pharynx and nose

Gene	Nose strains (n= 68)	Pharynx strains (n= 67)	Total (N= 135)
Resistance			
<i>mecA</i>	68 (100%)	67 (100%)	135 (100%)
Enzymes			
<i>arcA</i>	15 (22.05%)	15 (22.38%)	30 (22.22%)
<i>nucA</i>	68 (100%)	67 (100%)	135 (100%)
<i>gyrA</i>	61 (89.70%)	63 (94.02%)	124 (91.85%)
Adhesines			
<i>fnbA</i>	42 (61.76%)	37 (55.22%)	79 (58.51%)
<i>fnbB</i>	43 (63.23%)	41 (61.19%)	84 (62.22%)
<i>cna</i>	47 (69.11%)	49 (73.13%)	96 (71.11%)
<i>clfA</i>	45 (66.17%)	42 (62.68%)	87 (64.44%)
<i>clfB</i>	41 (60.29%)	37 (55.22%)	78 (57.77%)
<i>coa</i>	60 (88.23%)	62 (92.53%)	122 (90.37%)
Biofilms			
<i>psm</i>	10 (14.70%)	9 (13.43%)	19 (14.07%)
<i>icaA</i>	65 (95.58%)	61 (91.04%)	126 (93.33%)
<i>icaD</i>	51 (75%)	46 (68.65%)	97 (71.85%)
<i>sdrC</i>	63 (92.64%)	58 (86.56%)	121 (89.62%)
Toxins			
<i>sea</i>	15 (22.05%)	15 (22.38%)	30 (22.22%)
<i>seb</i>	6 (8.82%)	7 (10.44%)	13 (9.62%)
<i>sec</i>	7	11	18

	(10.29%)	(16.41%)	(13.33%)
<i>sed</i>	11 (16.17%)	8 (11.94%)	19 (14.07%)
<i>see</i>	1 (1.47%)	0	1 (0.74%)
<i>eta</i>	4 (5.88%)	3 (4.47%)	7 (5.18%)
<i>etb</i>	1 (1.47%)	1 (1.49%)	2 (1.48%)
<i>hla</i>	35 (51.47%)	35 (52.23%)	70 (51.85%)
<i>hlb</i>	18 (26.47%)	19 (28.35%)	37 (27.40%)
<i>hld</i>	49 (72.05%)	50 (74.62%)	99 (73.33%)
<i>hlg</i>	40 (58.82%)	36 (53.73%)	76 (56.29%)
<i>tst</i>	31 (45.58%)*	17 (25.37%)	48 (35.55%)
<i>lukS-PV/lukF-PV</i>	18 (26.47%)	15 (22.38%)	33 (24.44%)
<i>lukE-D</i>	65 (95.58%)	63 (94.02%)	128 (94.81%)
<i>luk-M</i>	0	0	0

* $p < 0.05$

Table S3. *spa*-typing of isolated MRSA strains.

<i>spa</i> -Type	Nose strains (n= 68)	Pharynx strains (n= 67)	Total (n= 135)
t-002	0	5	5
t-008	3	3	6
t-010	1	1	2
t-012	6	3	9
t-018	1	1	2
t-021	3	3	6
t-024	2	0	2
t-034	0	1	1
t-056	0	1	1
t-078	0	1	1
t-084	0	2	2
t-136	1	1	2
t-148	0	1	1
t-159	0	2	2
t-164	1	1	2
t-189	6	11	17
t-190	1	0	1

t-209	1	0	1
t-213	0	2	2
t-214	1	0	1
t-233	1	0	1
t-253	1	1	2
t-304	1	0	1
t-346	2	6	8
t-416	1	0	1
t-426	1	0	1
t-527	1	1	2
t-586	1	0	1
t-587	1	0	1
t-645	1	1	2
t-688	1	0	1
t-701	3	2	5
t-706	0	1	1
t-723	3	0	3
t-810	0	1	1
t-816	1	0	1
t-878	0	1	1
t-895	1	0	1
t-909	1	1	2
t-922	4	2	6
t-1406	2	2	4
t-1710	1	1	2
t-1885	1	0	1
t-2651	1	0	1
t-3380	1	0	1
t-3955	0	1	1
t-4318	1	0	1
t-4395	0	1	1
t-4468	1	1	2
t-4656	0	1	1
t-4976	2	0	2
t-5410	1	0	1
t-5747	0	1	1

t-6367	1	0	1
t-8163	1	0	1
t-11978	1	0	1
t-14362	0	1	1
t-16143	0	1	1
t-16164	0	1	1
t-16665	1	0	1
t-18475	1	0	1