

Prevalence of resistance and virulence genes among *S. aureus* isolated from ready-to-eat foods in Switzerland.

Group	Gene/Probe	Prevalence	
Markers	rnnD1 ( <i>S. aureus</i> )	99%	
	gapA	100%	
	katA	100%	
	coA	100%	
	nuc1	100%	
	spa	100%	
	sbi	100%	
	sarA	100%	
	saeS	100%	
	vraS	100%	
agr typing	agrI (total)	57%	
	agrB-I	56%	
	agrC-I	57%	
	agrD-I	57%	
	agrII (total)	22%	
	agrB-II	22%	
	agrC-II	22%	
	agrD-II	22%	
	agrIII (total)	21%	
	agrB-III	21%	
	agrC-III	21%	
	agrD-III	21%	
	agrIV (total)	0%	
	agrB-IV	2%	
agrC-IV	0%		
Resistance	blaZ	72%	
	blaI	75%	
	blaR	72%	
	erm(A)	1%	
	erm(B)	0%	
	erm(C)	1%	
	lnu(A)	0%	
	msr(A)	2%	
	mef(A)	0%	
	mph(C)	0%	
	vat(A)	0%	
	vat(B)	0%	
	vga(A)	0%	
	vga(A) (BM 3327)	0%	
	vgB(A)	0%	
	aacA-aphD	0%	
	aadD	3%	
	aphA3	0%	
	sat	0%	
	dfrS1	0%	
	far1	0%	
	Q6GD50	1%	
	mupA	0%	
	tet(K)	5%	
	tet(M)	1%	
	cat (total)	1%	
	cat (pC221)	1%	
	cat (pc223)	0%	
	cat (pMC524)	0%	
	cat (pSBK203R)	0%	
	cfr	0%	
	fexA	0%	
	fosB	64%	
	fosB (plasmid)	26%	
	qacA	0%	
	qacC (total)	1%	
	qacC (consensus)	1%	
	qacC (equine)	0%	
	qacC (SA5)	0%	
	qacC (Ssap)	0%	
	qacC (ST94)	0%	
	sdrM	94%	
	vanA	0%	
	vanB	1%	
	vanZ	0%	
	SCCmec typing	mecA	1%
		delta_mecR	1%
ugpQ		1%	
ccrA-1		1%	
ccrB-1		0%	
plsSCC (COL)		0%	
Q9XB68-dcs		1%	
ccrA-2		7%	
ccrB-2		7%	
kdpA-SCC		0%	
kdpB-SCC		0%	
kdpC-SCC		0%	
kdpD-SCC		0%	
kdpE-SCC		0%	
mecI		0%	
mecR		0%	
xyIR		0%	
ccrA-3		0%	
ccrB-3		0%	
merA		0%	
merB		0%	
ccrAA (MRSZAH47)_probe 1		0%	
ccrAA (MRSZAH47)_probe 2		1%	
ccrC (85-2082)	0%		
ccrA-4	0%		

	ccrB-4	0%
Toxic shock syndrome	tst1 (consensus)	18%
	tst1 ("human" allele)	17%
	tst1 ("bovine" allele, from RF122)	1%
Enterotoxins/ enterotoxin-like superantigens	sea	16%
	sea (320E)	0%
	sea (N315)	15%
	seb	4%
	sec	11%
	sed	7%
	see	1%
	seg	50%
	seh	4%
	sei	49%
	sej	7%
	sek	3%
	sel	11%
	selm	49%
	seln (consensus)	49%
	seln (other than RF122)	49%
	selo	50%
	egc enterotoxin gene cluster	52%
	seq	3%
	ser	7%
selu	49%	
ORF CM14_ probe1	5%	
ORF CM14_ probe2	5%	
Leukocidins/ hemolysins	lukF	98%
	lukS	78%
	lukS (ST22+ST45)	59%
	hlgA	100%
	lukF-PV	0%
	lukS-PV	0%
	lukF-PV (P83)	2%
	lukM	1%
	lukD	57%
	lukE	57%
	lukX	98%
	lukY	72%
	lukY (ST30+ST45)	28%
	hld	100%
	hl	100%
	hla	98%
	hlIII (consensus)	94%
	hlIII (other than RF122)	79%
	hIb_probe 1	76%
	hIb_probe 2	78%
hIb_probe 3	56%	
un-disrupted hIb	24%	
Exfoliative toxins	etA	1%
	etB	0%
	etD	2%
Capsule/ biofilm	cap1 (total)	0%
	capH1	0%
	capJ1	0%
	capK1	5%
	cap5 (total)	39%
	capH5	39%
	capJ5	39%
	capK5	42%
	cap8 (total)	61%
	capH8	61%
	capI8	61%
	capJ8	61%
	capK8	66%
	icaA	98%
	icaC	98%
	icaD	85%
bap	12%	
MSCRAMMs/ adhesion	bbp (total)	88%
	bbp (consensus)	80%
	bbp (COL+MW2)	28%
	bbp (MRSA252)	19%
	bbp (Mu50)	21%
	bbp (RF122)	2%
	bbp (ST45)	22%
	clfA (total)	100%
	clfA (consensus)	93%
	clfA (COL+RF122)	40%
	clfA (MRSA252)	32%
	clfA (Mu50+MW2)	78%
	clfB (total)	100%
	clfB (consensus)	88%
	clfB (COL+Mu50)	22%
	clfB (MW2)	26%
	clfB (RF122)	33%
	cna	48%
	ebh (consensus)	95%
	ebpS (total)	97%
	ebpS_probe 612	87%
	ebpS_probe 614	90%
	ebpS (01-1111)	19%
	ebpS (COL)	53%
	eno	94%
	fib	61%
	fib (MRSA252)	45%
	fnbA (total)	100%
fnbA (consensus)	89%	
fnbA (COL)	22%	

	fnbA (MRSA252)	28%
	fnbA (Mu50+MW2)	25%
	fnbA (RF122)	14%
	fnbB (total)	77%
	fnbB (COL)	14%
	fnbB (COL+Mu50+MW2)	45%
	fnbB (Mu50)	24%
	fnbB (MW2)	36%
	fnbB (ST15)	6%
	fnbB (ST45-2)	24%
	map (total)	93%
	map (COL)	41%
	map (MRSA252)	33%
	map (Mu50+MW2)	55%
	sasG (total)	43%
	sasG (COL+Mu50)	25%
	sasG (MW2)	25%
	sasG (other than MRSA252+RF122)	54%
	sdrC (total)	100%
	sdrC (consensus)	88%
	sdrC (B1)	14%
	sdrC (COL)	33%
	sdrC (Mu50)	28%
	sdrC (MW2+MRSA252+RF122)	20%
	sdrC (other than MRSA252+RF122)	67%
	sdrD (total)	88%
	sdrD (consensus)	80%
	sdrD (COL+MW2)	25%
	sdrD (Mu50)	28%
	sdrD (other)	37%
	vwb (total)	98%
	vwb (consensus)	81%
	vwb (COL+MW2)	17%
	vwb (MRSA252)	27%
	vwb (Mu50)	12%
	vwb (RF122)	14%
Others	sak	71%
	chp	55%
	scn	83%
	edinA	0%
	edinB	3%
	edinC	0%
	ACME cluster	0%
	arcA-SCC	0%
	arcB-SCC	0%
	arcC-SCC	0%
	arcD-SCC	13%
	aur (consensus)	88%
	aur (other than MRSA252)	60%
	aur (MRSA252)	39%
	splA	60%
	splB	59%
	splE	67%
	sspA	100%
	sspB	100%
	sspP (consensus)	100%
	sspP (other than ST93)	97%
	setC/setx	68%
	ssi01/set6_probe1_11	44%
	ssi01/set6_probe2_11	59%
	ssi01/set6_probe1_12	45%
	ssi01/set6_probe2_12	29%
	ssi01/set6_probe4_11	55%
	ssi01/set6_probeRF122	8%
	ssi01/set6 (COL)	14%
	ssi01/set6 (Mu50+N315)	15%
	ssi01/set6 (MW2+MSSA476)	12%
	ssi01/set6 (MRSA252)	25%
	ssi01/set6 (RF122)	0%
	ssi01/set6 (other alleles)	8%
	ssi02/set7	65%
	ssi02/set7 (MRSA252)	41%
	ssi03/set8_probe 1	62%
	ssi03/set8_probe 2	57%
	ssi03/set8 (MRSA252, SAR0424)	26%
	ssi04/set9	58%
	ssi04/set9 (MRSA252, SAR0425)	39%
	ssi05/set3_probe 1	55%
	ssi05/set3 (RF122, probe-611)	28%
	ssi05/set3_probe 2 (612)	51%
	ssi05/set3 (MRSA252)	35%
	ssi06/set21	36%
	ssi06 (NCTC8325+MW2)	42%
	ssi07/set1	63%
	ssi07/set1 (MRSA252)	33%
	ssi07/set1 (AF188836)	22%
	ssi08/set12_probe 1	55%
	ssi08/set12_probe 2	63%
	ssi09/set5_probe 1	68%
	ssi09/set5_probe 2	64%
	ssi09/set5 (MRSA252)	38%
	ssi10/set4	86%
	ssi10 (RF122)	12%
	ssi10/set4 (MRSA252)	55%
	ssi11/set2 (COL)	12%
	ssi11+set2(Mu50+N315)	9%
	ssi11+set2(MW2+MSSA476)	6%
	ssi11/set2 (MRSA252)	33%
	setB3	59%

setB3 (MRSA252)	34%
setB2	58%
setB2 (MRSA252)	32%
setB1	76%
isaB	66%
isaB (MRSA252)	92%
mprF (COL+MW2)	74%
mprF (Mu50+MRSA252)	73%
isdA (consensus)	92%
isdA (MRSA252)	47%
isdA (other than MRSA252 )	61%
lmrP (other than RF122)_probe1	94%
lmrP (other than RF122)_probe2	82%
lmrP (RF122)_probe1	8%
lmrP (RF122)_probe2	6%
hsdS1 (RF122)	5%
hsdS2 (Mu50+N315+COL+USA300+NCTC8325)	42%
hsdS2 (MW2+MSSA476)	86%
hsdS2 (RF122)	4%
hsdS2 (MRSA252)	28%
hsdS3 (all other than RF122+ MRSA252)	26%
hsdS3 (COL+USA300+NCTC8325+MW2+MSSA476+RF122)	14%
hsdS3 (Mu50+N315)	13%
hsdS3 (CC51+ MRSA252)	21%
hsdS3 (MRSA252)	25%
hsdSx (CC25)	59%
hsdSx (CC15)	13%
hsdSx (etd)	23%
Q2FXC0	25%
Q2YUB3	20%
Q7A4X2	57%
hysA1 (MRSA252)	36%
hysA1 (MRSA252+RF122) and/or hysA2 (consensus)	92%
hysA1 (MRSA252+RF122) and/or hysA2 (COL+USA300)	46%
hysA2 (all other than MRSA252)	35%
hysA2 (COL+USA300+NCTC8325)	51%
hysA2 (all other than COL+USA300+NCTC8325)_probe1	67%
hysA2 (MRSA252)	14%