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rRNA Operon Copy Number Can Explain the Distinct Epidemiology of Hospital-Associated Methicillin-Resistant Staphylococcus aureus

Fluit, A.C.; Jansen, M.D.; Bosch, T.; Jansen, W.T.M.; Schouls, L.; Jonker, M.J.; Boel, C.H.E.

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Supplementary table 1. The annotation of the regions encoding the rRNA operons for strain COL.

locus	begin	end	gene	encodes
SACOL0521	527,373	527,690	-	conserved hypothetical protein
SACOL0522	527,697	528,293	*recR*	recombination protein RecR
SACOL_Sa16SA	529,146	530,700	*rrsA*	16S ribosomal RNA
SACOL_Sa23SA	531,065	533,987	*rrlA*	23S ribosomal RNA
SACOL_Sa5SA	534,060	534,174	*rrfA*	5S ribosomal RNA
SACOL0523	535,057	536,394	-	Orn/Lys/Arg decarboxylase
SACOL0524	536,396	537,013	*tmk*	thymidylate kinase
\\				
SACOL_Sa5SG	572,452	572,566	*rrfG*	5S ribosomal RNA
SACOL_tRNA-Ala-1	572,579	572,654	-	tRNA-Ala
SACOL_Sa16SB	572,776	574,330	*rrsB*	16S ribosomal RNA
SACOL_tRNA-Ile-1	574,423	574,499	-	tRNA-Ile
SACOL_Sa23SB	574,667	577,589	*rrlB*	23S ribosomal RNA
SACOL_Sa5SB	577,662	577,776	*rrfB*	5S ribosomal RNA
SACOL_Sa16SC	577,988	579,542	*rrsC*	16S ribosomal RNA
SACOL_Sa23SC	579,845	582,767	*rrlC*	23S ribosomal RNA
SACOL_Sa5SC	582,840	582,954	*rrfC*	5S ribosomal RNA
SACOL0563	583,479	584,861	-	transcriptional regulator, GntR family
SACOL0564	584,965	585,852	-	pyridoxine biosynthesis protein
\\				
SACOL_tRNA-Thr-2	1,976,762	1,976,837	-	tRNA-Thr
SACOL_tRNA-Val-1	1,976,854	1,976,929	-	tRNA-Val
SACOL_Sa5SD	1,976,941	1.977.055	*rrfD*	5S ribosomal RNA
SACOL_Sa23SD	1,977,128	1980,050	*rrlD*	23S ribosomal RNA
SACOL_tRNA-Ala-3	1,980,264	1,980,339	-	tRNA-Ala
SACOL_tRNA-Ile-2	1,980,358	1,980,434	-	tRNA-Ile
SACOL_Sa16SD	1,980,524	1,982,078	*rrsD*	16S ribosomal RNA
SACOL1919	1,982,818	1,983,264	-	transcriptional regulator, Fur family
SACOL1920	1,983,361	1,984,311	-	D-isomer specific 2-hydroxyacid dehydrogenase family protein
\\				
SACOL2050	2,110,529	2,111,797	*ilvA2*	threonine dehydratase
SACOL2051	2,111,846	2,112,001	-	hypothetical protein
SACOL_Sa5SE	2,112,007	2,112,121	*rrfE*	5S ribosomal RNA
SACOL_Sa23SE	2,112,194	2,115,116	*rrlE*	23S ribosomal RNA
SACOL_Sa16SE	2,115,663	2,117,217	*rrsE*	16S ribosomal RNA
SACOL_tRNA-Gly-4	2,117,335	2,117,408	-	tRNA-Gly
SACOL_tRNA-Leu-4	2,117,428	2,117,513	-	tRNA-Leu
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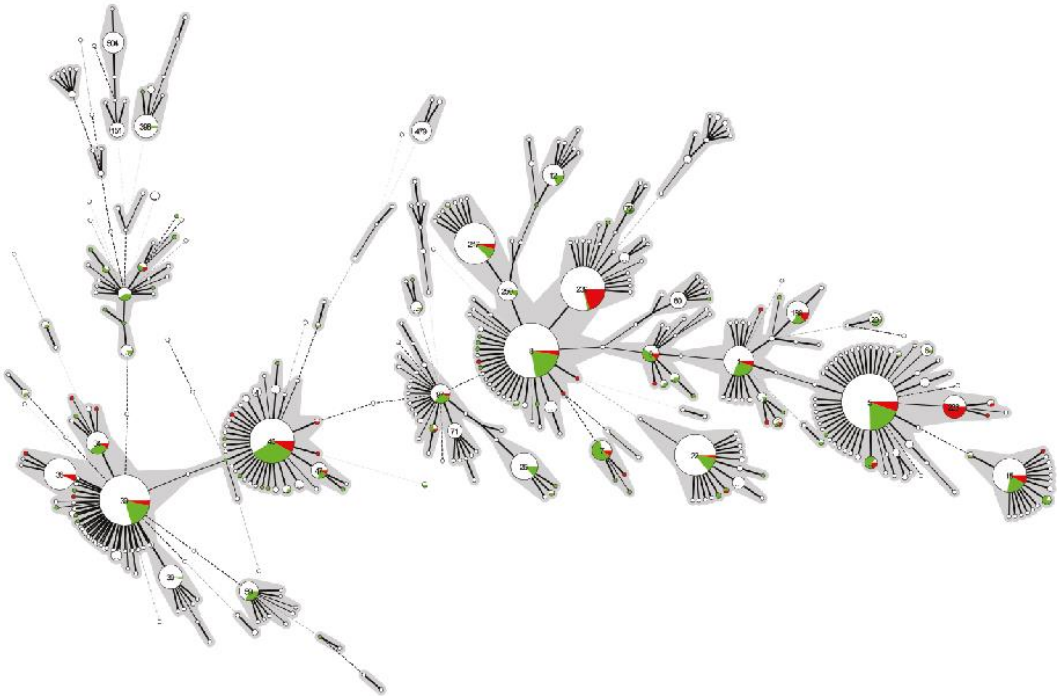
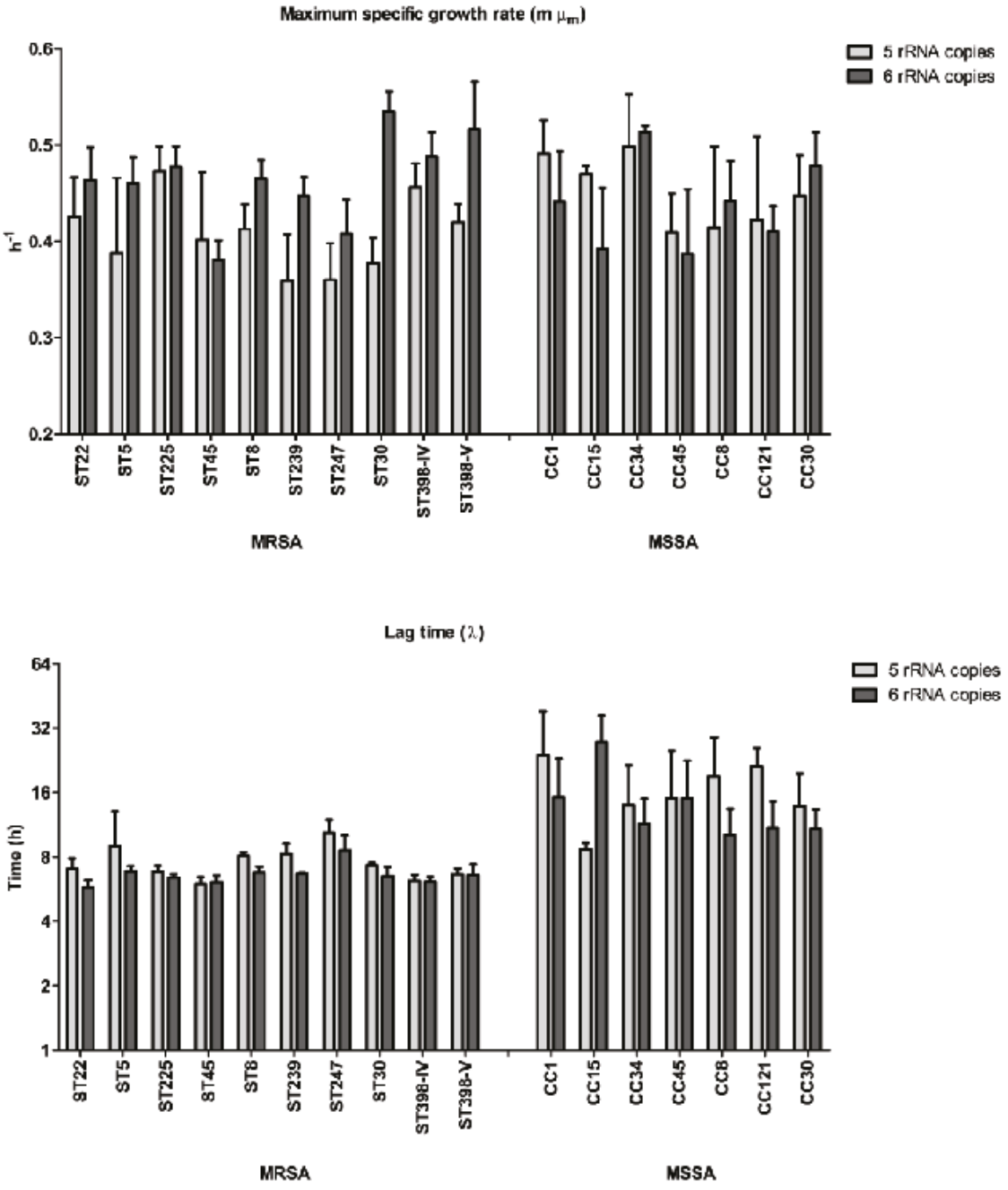
SACOL_tRNA-Asn-3	2,228,412	2,228,486	-	tRNA-Asn
SACOL_tRNA-Glu-3	2,228,339	2,228,410	-	tRNA-Glu
SACOL_Sa5SF	2,228,497	2,228,611	*rrfF*	5S ribosomal RNA
SACOL_Sa23SF	2,228,684	2,231,606	*rrlF*	23S ribosomal RNA
SACOL_Sa16SF	2,232,153	2,233,707	*rrsF*	16S ribosomal RNA
SACOL2156	2,234,163	2,235,227	-	ATP-binding protein, Mrp/Nbp35 family
SACOL2157	2,235,375	2,236,817	-	drug resistance transporter, EmrB/QacA subfamily



Supplementary figure 1. MLST-based Minimal Spanning Tree of *S. aureus*
A minimal spanning tree was constructed of 1350 strains from http://saureus.mlst.net/ supplemented with 146 MRSA, 195 MSSA and 105 CF isolates from our collection. The pie chart indicates the distribution of isolates used in this study within the total *S. aureus* population. The colors of the pie indicate the number of rRNA operons, red corresponds with 5 rRNA operons and green with 6 rRNA operons. Each sequence type (ST) is represented by a circle in which the circle size corresponds to the number of isolates. Heavy lines between two STs denote a difference in a single locus, thin lines denote double-locus variants, and dotted lines connect STs differing in more than 2 loci.



Supplementary figure 2. ***In vitro*** **growth analysis for individual STs/CCs**
The growth parameters for each ST (MRSA) or CC (MSSA) are shown, maximum specific growth rate (upper panel) and lag time (lower panel).