Correction

Correction: Characterization of *Staphylococcus aureus* from Distinct Geographic Locations in China: An Increasing Prevalence of *spa*-t030 and SCCmec Type III

The PLOS ONE Staff

In Table 5, there are multiple errors in the “SCCmec type (no. of isolates)” column. Please see the corrected Table 5 here.

Table 5. The distribution of MLST types, SCCmec types and virulence genes in different MRSA clones according to *spa* clone complex.

<i>spa</i> -CC ^a	<i>spa</i> type	No. (%) of isolates	MLST (no. of isolates tested)	MLST allele profile ^b	SCCmec type (no. of isolates)	Carriage of virulence genes (no. of isolates)
CC030	t030	121(80.1)	ST239(12)	2-3-1-1-4-4-3	III (111), IV(1), V(3), NT (6)	<i>sea</i> (109), <i>seb</i> (1), <i>sec</i> (2), <i>sed</i> (1), <i>seg</i> (8), <i>seh</i> (2), <i>sei</i> (2), <i>sej</i> (5), <i>tst</i> (1), <i>sasX</i> (2)
	t037	6(4.0)	ST239(4)	2-3-1-1-4-4-3	III (6)	<i>sea</i> (6), <i>sasX</i> (3)
	t233	1(0.7)	ST239(1)	2-3-1-1-4-4-3	III (1)	<i>sea</i> (1), <i>sec</i> (1)
	t459	1(0.7)	ST239(1)	2-3-1-1-4-4-3	III (1)	<i>sea</i> (1)
	t748	1(0.7)	ST239(1)	2-3-1-1-4-4-3	IV(1)	<i>sea</i> (1)
CC437	t437	7(4.6)	ST59(6)	19-23-15-2-19-20-15	IV(6), V(1)	<i>pvl</i> (4), <i>sea</i> (1), <i>seb</i> (4), <i>sec</i> (1), <i>sed</i> (1), <i>sej</i> (1)
	t441	1(0.7)	ST59(1)	19-23-15-2-19-20-15	IV(1)	None
CC002	t002	3(2.0)	ST764(2)	1-136-1-4-12-1-10	II (3)	<i>sea</i> (1), <i>seb</i> (3), <i>sec</i> (3), <i>seg</i> (3), <i>sei</i> (3), <i>tst</i> (3)
Singleton	t4549	2(1.3)	ST630(2)	12-3-1-1-4-4-3	V(2)	<i>sea</i> (1)
CC127	t127	1(0.7)	ST1(1)	1-1-1-1-1-1-1	IV(1)	<i>sea</i> (1), <i>seh</i> (1)
CC227	t287	1(0.7)	ST25(1)	4-1-4-1-5-5-4	V(1)	<i>pvl</i> (1), <i>seb</i> (1), <i>seg</i> (1), <i>sei</i> (1)
CC701	t701	1(0.7)	ST6(1)	12-4-1-4-12-1-3	NT (1)	None
CC1376	t1376	1(0.7)	ST1298(1)	22-1-14-109-12-4-31	NT (1)	<i>sea</i> (1)
	t3622	1(0.7)	ST88(1)	22-1-14-23-12-4-31	IV(1)	<i>sea</i> (1)
Singleton	t078	1(0.7)	NT(1)	1-1-4-1-new-new-1	III (1)	<i>seg</i> (1)
Unkown	t5554	1(0.7)	ST630 SLV	12-334-1-1-4-4-3	V(1)	None
	NT	1(0.7)	NT(1)	1-4-new-169-new-57-11	NT (1)	None

^aCC: clone complex.

^bAllelic profile in order of *arcC-aroE-glpF-gmk-pta-tpi-yqiL*.

SLV: single locus variant.

NT: not typeable, the reasons for the nontypeable of some isolates were mainly due to that a low quality of sequence chromatogram was present for *spa* typing, or at least one new allele was identified in the seven housekeeping genes for MLST typing, or no corresponding band was found in the multiplex PCR for SCCmec typing. The typing experiments were repeated at least twice for the nontypeable isolates.

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Reference

- Chen Y, Liu Z, Duo L, Xiong J, Gong Y, et al. (2014) Characterization of *Staphylococcus aureus* from Distinct Geographic Locations in China: An Increasing Prevalence of *spa*-t030 and SCCmec Type III. PLoS ONE 9(4): e96255. doi:10.1371/journal.pone.0096255

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