

Table S2. Cellular fatty acid compositions (%) of strains Mo2-6^T, S9, KG4-3^T, and 50Mo3-2 and their closely related *Staphylococcus* type strains

Taxa: 1, strain Mo2-6^T; 2, strain S9; 3, strain KG4-3^T; 4, strain 50Mo3-2; 5, *S. equorum* subsp. *equorum* KACC 13255^T; 6, *S. pseudoxylosum* DSM 107950^T; 7, *S. xylosum* KACC 13239^T. All data were obtained from this study. Data are expressed as percentages of the total fatty acids, and fatty acids constituting less than 1.0% in all strains are not shown. Major components (> 10.0%) are highlighted in bold; symbols: tr, trace amount (< 1.0%); –, not detected

Fatty acid	1	2	3	4	5	6	7
Saturated:							
C _{14:0}	1.1	1.2	2.6	1.2	1.9	2.4	tr
C _{16:0}	3.4	3.6	9.9	2.1	15.0	9.2	1.8
C _{18:0}	2.0	2.5	7.3	2.6	12.5	7.2	2.2
C _{20:0}	tr	tr	tr	2.1	tr	tr	1.4
Unsaturated:							
iso-C _{17:1} ω10c	1.4	tr	–	tr	–	–	–
C _{18:1} ω9c	tr	tr	tr	tr	1.2	tr	tr
Branched:							
iso-C _{13:0}	2.1	1.0	9.9	6.7	1.7	6.9	tr
iso-C _{14:0}	1.0	tr	1.2	1.2	tr	tr	1.0
iso-C _{15:0}	23.6	19.2	13.8	18.9	11.5	10.7	15.4
iso-C _{16:0}	tr	tr	1.6	1.7	tr	1.4	1.4
iso-C _{17:0}	1.1	1.1	4.1	6.5	2.0	6.2	5.2
iso-C _{19:0}	tr	tr	1.1	1.8	tr	1.1	1.5
anteiso-C _{11:0}	1.6	–	tr	tr	–	tr	–
anteiso-C _{13:0}	2.1	tr	10.8	7.1	tr	8.9	tr
anteiso-C _{15:0}	53.6	61.6	25.2	35.9	41.9	27.7	56.5
anteiso-C _{17:0}	1.1	1.5	4.7	6.8	3.1	9.3	9.0
Summed feature*:							
8 (C _{18:1} ω6c and/or C _{18:1} ω7c)	tr	tr	tr	tr	1.8	1.9	–

*Summed feature is a group of typically two or three fatty acids that cannot be reliably separated from one another using the selected chromatographic conditions. The MIDI system combines these fatty acids into a single feature and assigns a single percentage of the total.