

## Supplementary Materials: Detection of Methicillin-Resistant Staphylococci Isolated from Food Producing Animals: A Public Health Implication

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**Table S1.** Antimicrobial agents, disc content and zone diameter interpretative standards for *Staphylococcus* species.

Antibiotics Group	Antimicrobial Agent	Disc Content	Zone Diameter (mm)		
			Resistant	Intermediate	Sensitive
Penicillins	Methicillin	5 µg	≤9	10–13	≥14
	Cloxacillin	5 µg	≤10	11–12	≥13
	Penicillin	10 µg	≤28	-	≥29
	Amoxicillin	10 µg	≤19	-	≥20
Macrolides	Erythromycin	15 µg	≤13	14–22	≥23
Aminoglycosides	Gentamycin	10 µg	≤12	13–14	≥15
	Kanamycin	30 µg	≤13	14–17	≥18
Lincosamides	Clindamycin	2 µg	≤14	15–20	≥21
Phenicol	Chloramphenicol	30 µg	≤12	13–17	≥18
Folates	Trimethoprim-Sulfamethoxazole	1.25 µg	≤10	11–15	≥16
Glycopeptides	Vancomycin	30 µg	-	-	≥15

Source: CLSI [1].

Table S2. Staphylococci species isolated from nasal samples.

Isolates Code	Identification	Max Score	Total Score	Query Cover %	E-Value	Identity %	Accession
N001	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720173.1
N002	<i>Staphylococcus intermedius</i>	97.6	97.6	100%	1E – 17	100%	FN646071.1
N003	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KR709233.1
N004	<i>Staphylococcus intermedius</i>	97.6	97.6	100%	1E – 17	100%	FN646071.1
N005	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT719854.1
N006	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720164.1
N007	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720168.1
N008	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N009	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N010	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720171.1
N011	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	CP009046.1
N012	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720172.1
N013	<i>Staphylococcus intermedius</i>	97.6	97.6	100%	1E – 17	100%	FN646071.1
N014	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	CP009046.1
N015	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	CP009046.1
N016	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N017	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N018	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N019	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N020	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N021	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N022	<i>Staphylococcus aureus</i>	75.8	75.8	93%	4E – 11	96%	KR028437.1
N023	<i>Staphylococcus aureus</i>	75.8	75.8	93%	4E – 11	96%	KR028437.1
N024	<i>Staphylococcus aureus</i>	75.8	75.8	93%	4E – 11	96%	KR028437.1
N025	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N026	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	CP009046.1
N027	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N028	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N029	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1

Table S2. Cont.

Isolates Code	Identification	Max Score	Total Score	Query Cover %	E-Value	Identity %	Accession
N030	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720173.1
N031	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	EU659874.1
N032	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	EU659874.1
N033	<i>Staphylococcus aureus</i>	75.8	75.8	93%	4E – 11	96%	KR028437.1
N034	<i>Staphylococcus intermedius</i>	97.6	97.6	100%	1E – 17	100%	FN646071.1
N035	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1
N036	<i>Staphylococcus intermedius</i>	97.6	97.6	100%	1E – 17	100%	FN646071.1
N037	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1
N038	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N039	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1
N040	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1
N041	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N042	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N043	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1
N044	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577634.1
N045	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
N046	<i>Staphylococcus intermedius</i>	97.6	97.6	100%	1E – 17	100%	FN646071.1
N047	<i>Staphylococcus xylosus</i>	97.6	97.6	100%	1E – 17	100%	KT351728.1
N048	<i>Staphylococcus xylosus</i>	97.6	97.6	100%	1E – 17	100%	KT021502.1
N049	<i>Staphylococcus xylosus</i>	97.6	97.6	100%	1E – 17	100%	KR856344.1
N050	<i>Staphylococcus xylosus</i>	97.6	97.6	100%	1E – 17	100%	KP668813.1

Table S3. Staphylococci species isolated from raw milk samples.

Isolates Code	Identification	Max Score	Total Score	Query Cover %	E-Value	Identity %	Accession
M001	<i>Staphylococcus chromogenes</i>	93.7	93.7	95%	2E – 16	100%	KC481609.1
M002	<i>Staphylococcus chromogenes</i>	93.7	93.7	95%	2E – 16	100%	KC481609.1
M003	<i>Staphylococcus chromogenes</i>	97.6	97.6	100%	1E – 17	100%	EU622581.1
M004	<i>Staphylococcus chromogenes</i>	97.6	97.6	100%	1E – 17	100%	EU622581.1
M005	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577582.1
M006	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	HG813242.1
M007	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	HG813242.1
M008	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M010	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KT696497.1
M011	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M012	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M013	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M014	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M015	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KT696497.1
M016	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KT696497.1
M017	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KT696497.1
M018	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M019	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M020	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M021	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M022	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M023	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M024	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M025	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720164.1
M026	<i>Staphylococcus epidermidis</i>	89.7	89.7	100%	3E – 15	98%	FJ577582.1
M027	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720168.1
M028	<i>Staphylococcus chromogenes</i>	93.7	93.7	95%	2E – 16	100%	KC481609.1
M029	<i>Staphylococcus chromogenes</i>	93.7	93.7	95%	2E – 16	100%	KC481609.1
M030	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1

Table S3. Cont.

Isolates Code	Identification	Max Score	Total Score	Query Cover %	E-Value	Identity %	Accession
M031	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M032	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1
M033	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1
M034	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1
M035	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M036	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M037	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M038	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1
M039	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720173.1
M040	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720172.1
M041	<i>Staphylococcus chromogenes</i>	97.6	97.6	100%	1E – 17	100%	EU622581.1
M042	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M043	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M044	<i>Staphylococcus haemolyticus</i>	97.6	97.6	100%	1E – 17	100%	KP324951.1
M045	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1
M046	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M047	<i>Staphylococcus simulans</i>	93.7	93.7	100%	2E – 16	100%	FN646077.1
M048	<i>Staphylococcus chromogenes</i>	97.6	97.6	100%	1E – 17	100%	EU622581.1
M049	<i>Staphylococcus aureus</i>	97.6	97.6	100%	1E – 17	100%	FN646074.1
M050	<i>Staphylococcus saprophyticus</i>	97.6	97.6	100%	1E – 17	100%	KT720171.1

## References

1. *Performance Standards for Antimicrobial Susceptibility Testing; Sixteen International Supplements*; Clinical and Laboratory Standards Institute: Wayne, PA, USA, 2006; p. 118-123.



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