Article DOI: https://doi.org/10.3201/eid2908.221770

EID cannot ensure accessibility for Supplemental Materials supplied by authors. Readers who have difficulty accessing supplementary content should contact the authors for assistance.

Soft Tissue Infection of Immunocompetent Man with Cat-Derived *Globicatella* Species

Appendix

Appendix Table.	Biochemical	profiling a	and	antimicrobial	susceptibility
-----------------	-------------	-------------	-----	---------------	----------------

Test	Novel <i>Globicatella</i> isolate G1610988	Globicatella sanguinis Type strain*	Globicatella sulfidifaciens Type strain†
Component test of the API RAPID ID 32 STREP assay			
ADH	Negative	Negative	Negative
BGLU	Negative	Positive	Positive
BGAR	Positive	Positive	Positive
BGUR	Negative	Negative	Positive
AGAL	Negative	Negative	Positive
PAL	Negative	Negative	Negative
RIB	Negative	Negative	Negative
MAN	Negative	Positive	Negative
SOR	Negative	Negative	Negative
LAC	Negative	Negative	Positive
TRE	Negative	Positive	Positive
RAF	Negative	Positive	Positive
VP	Negative	Negative	Negative
APPA	Negative	Positive	Positive
BGAL	Negative	Positive	Positive
PYRA	Positive	Negative	Positive
BNAG	Negative	Negative	Negative
GTA	Negative	Negative	Negative
HIP	Negative	Positive	Positive
GLYG	Negative	Positive	Positive
PUL	Negative	Negative	Positive
MAL	Negative	Positive	Positive
MEL	Negative	Positive	Positive
MLZ	Negative	Negative	Negative
SAC	Negative	Positive	Positive
LARA	Negative	Negative	Negative
DARL	Negative	Negative	Negative
MBDG	Negative	Negative	Positive
TAG	Negative	Negative	Negative

Test	Novel <i>Globicatella</i> isolate G1610988			Globicatella sanguinis Type strain*	Globicatella sulfidifaciens Type strain†
BMAN	Negative		Negative	Negative	
CDEX		Negative		Negative	Negative
URE		Negative		Negative	Negative
Overall	Erysip	Good identification Erysipelothrix rhusiopathiae (98.7%)		Very good identification G. sanguinis (99.9%)	Very good identification G. sanguinis (99.7%)
Other tests	7-7		,	J (,	J. 1 (11)
Pyrrolidonyl aminopeptidase Leucine aminopeptidase Bile aesculin Initial MALDI-TOF MS	Negative *positive by API Negative Positive No reliable identification (score 1.31)		Positive Negative Positive N/A	Positive Negative Positive N/A	
Repeat MALDI-TOF MS		No reli̇̀able ider		G. sanguinis	G. sanguinis
(reference laboratory)		(score 1.4	,	(score 2.54)	(score 2.36)
Antibiotic susceptibility	MIC‡ (mg/L)	PK/PD non- species related breakpoint (mg/L)	Interpretation§		
Gentamicin	1	0.5	Do not use		
Ampicillin	≤0.016	2	Use with		
Cefotaxime	0.004	1	caution Use with caution		
Penicillin	≤0.016	0.25	Use with caution		
Teicoplanin	0.032	No breakpoint	-		
Vancomycin	0.25	No breakpoint	-		
Clindamycin	1	No breakpoint	-		
Erythromycin	0.032	No breakpoint	-		
Linezolid	1	2	Use with caution		
Ciprofloxacin	0.032	0.25	Use with caution		
Moxifloxacin	0.016	0.25	Use with caution		
Tetracycline	0.064	No breakpoint	-		
Chloramphenicol	2	No breakpoint	-		
Rifampin	0.004	No breakpoint	-		

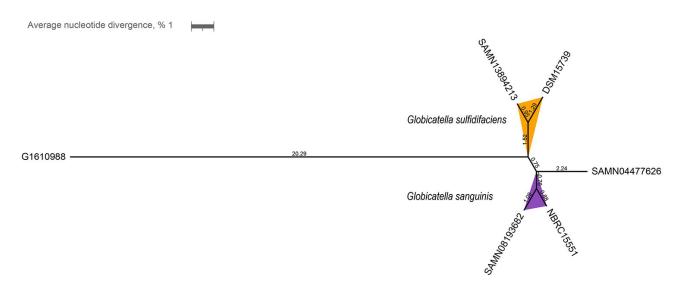
^{*}Globicatella sanguinis strain NCFB 2835 (American Type Culture Collection).

Reference

1. Letunic I, Bork P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. Nucleic Acids Res. 2021;49(W1):W293-6. PubMed https://doi.org/10.1093/nar/gkab301

[†] Globicatella sulfidifaciens strain LMG 18844 (Belgian Coordinated Collections of Microorganisms), also known as DSM 15739.

^{\$\}text{\$\text{MIC.}} \text{\$\text{SINC.}} \text{\$\text{SINC.}} \text{\$\text{PD non-species related breakpoint, as recommended by EUCAST.}



Appendix Figure. Average nucleotide divergence between isolate G1610988 and published *Globicatella* genomes. DSM15739 (NCBI Assembly accession: GCA_900167405.1) and NBRC15551 (GCA_001552295.1) are type strains of *G. sanguinis* and *G. sulfidifaciens*, respectively. Other published genomes: SAMN04477626 (GCA_001811625.1), SAMN08193682 (GCA_002847845.1), SAMN13894213 (GCA_012518335.1). Isolates of the same species are highlighted by colored shades. Numbers along branches are average percentage nucleotide divergencies of all orthologous regions shared between genomes. This figure was created by using iTOL (1).