

Supplementary materials for the article:

Huang F. et al. Comparative Genomic Analysis and Phenotypic Characterization of  
Bronchoscope-Associated *Klebsiella aerogenes*  
Pol J Microbiol. 2021, Vol. 70, No 3, 409–412.

Table SI  
Genome collection used in this study.

Sample	Accession	Host	Country	Source
NJBB01	SAMN07249743	environmental	USA	soil
QKNB01	SAMN09104666	<i>Homo sapiens</i>	Spain	urine
PKQD01	SAMN08239887	<i>Homo sapiens</i>	China	blood
VLPF01	SAMN12330825	<i>Homo sapiens</i>	China	urine
CP041925	SAMN12330869	<i>Homo sapiens</i>	China	sputum
VLOZ01	SAMN12330831	<i>Homo sapiens</i>	China	sputum
VLOY01	SAMN12330832	<i>Homo sapiens</i>	China	sputum
VLPB01	SAMN12330829	<i>Homo sapiens</i>	China	urine
VLPE01	SAMN12330826	<i>Homo sapiens</i>	China	urine
VLOW01	SAMN12330834	<i>Homo sapiens</i>	China	sputum
VLOO01	SAMN12330842	<i>Homo sapiens</i>	China	urine
VLOS01	SAMN12330838	<i>Homo sapiens</i>	China	urine
CP035466	SAMN10788268	cow	Poland	rumen content
CP042530	SAMN12289361	<i>Homo sapiens</i>	Australia	clinical sample
LPQB01	SAMN04252907	<i>Homo sapiens</i>	Tunisia	-
CP044214	SAMN12807522	<i>Homo sapiens</i>	United Kingdom	rectal swab
CABMNC01	SAMEA5852002	<i>Homo sapiens</i>	USA	human gut
CP011574	SAMN03733745	<i>Homo sapiens</i>	USA	perirectal
JSWV01	SAMN03145041	food	Malaysia	bitter gourd
WMHU01	SAMN12061310	<i>Homo sapiens</i>	South Korea	-
BGNU01	SAMD00126349	<i>Homo sapiens</i>	Singapore	-
BGNV01	SAMD00126350	<i>Homo sapiens</i>	Singapore	-
JUHZ01	SAMN03012837	<i>Homo sapiens</i>	USA	excreted bodily substance
NWEB01	SAMN07609119	<i>Homo sapiens</i>	China	-
CABGSS01	SAMEA104567694	<i>Homo sapiens</i>	United Kingdom	stool
PYHJ01	SAMN08743208	<i>Homo sapiens</i>	Lebanon	-
PXKM01	SAMN08623813	<i>Homo sapiens</i>	USA	bloodstream
PIBQ01	SAMN08095962	<i>Homo sapiens</i>	United Kingdom	blood
CP033817	SAMN10163207	<i>Homo sapiens</i>	USA	endotracheal aspirate
QYNY01	SAMN09981294	<i>Homo sapiens</i>	USA	stool

Sample	Accession	Host	Country	Source
JMUO01	SAMN02581251	<i>Homo sapiens</i>	USA	urine
JMUN01	SAMN02581250	<i>Homo sapiens</i>	USA	wound
FO203355	SAMEA3138432	<i>Homo sapiens</i>	France	-
CP014029	SAMN03996296	<i>Homo sapiens</i>	USA	urine
LSOH01	SAMN04496843	<i>Homo sapiens</i>	Brazil	catheter
CP024885	SAMN04014850	-	-	-
CP011539	SAMN03448049	<i>Homo sapiens</i>	France	-
CP031756	SAMN06173340	<i>Homo sapiens</i>	USA	skin swab
POVY01	SAMN04875568	<i>Homo sapiens</i>	USA	urine clean catch
LR607333	SAMEA104567454	<i>Homo sapiens</i>	United Kingdom	stool
RPDR01	SAMN10405433	<i>Homo sapiens</i>	USA	urine
MTLB01	SAMN06234924	environmental	Argentina	soil
VTUM01	SAMN12560212	plant	Germany	chives
NPJV01	SAMN07425777	<i>Homo sapiens</i>	China	ascites
CP044083	SAMN11056356	<i>Homo sapiens</i>	USA	-
CP002824	SAMN02603581	-	-	-
QVMZ01	SAMN09843510	<i>Homo sapiens</i>	USA	sputum
CP045870	SAMN12877717	<i>Homo sapiens</i>	South Korea	blood
RPEK01	SAMN10405414	<i>Homo sapiens</i>	USA	blood
LYDO01	SAMN05068064	<i>Homo sapiens</i>	Brazil	stool
MOAA01	SAMN05935553	<i>Homo sapiens</i>	China	-
04251141Q-3	SAMN14970464	environmental	China	surface
04250663Q-1	SAMN14970463	environmental	China	surface
04292179Q-1	SAMN14970465	environmental	China	surface
04160493Q-2	SAMN14970461	environmental	China	surface
04161141Q-1	SAMN14970462	environmental	China	surface
04304169Q-2	SAMN14970466	environmental	China	surface
05021124Q-3	SAMN14970467	environmental	China	surface

Table SII

The species, number and proportion of bacteria isolated in the sample before usual decontamination procedures.

Species	Number	Proportion (%)	ESBL-producers
<i>Staphylococcus epidermidis</i>	69	18.9	0
<i>Streptococcus salivarius</i>	42	11.5	0
<i>Klebsiella pneumoniae</i>	26	7.1	2
<i>Streptococcus oralis</i>	23	6.3	0
<i>Neisseria flavescens</i>	22	6	0
<i>Streptococcus mitis</i>	21	5.7	0
<i>Corynebacterium</i>	19	5.2	0
<i>Neisseria macaque</i>	19	5.2	0
<i>Streptococcus parahaemophilus</i>	13	3.5	0
<i>Streptococcus pneumoniae</i>	11	3	0
<i>Pseudomonas aeruginosa</i>	9	2.4	2
<i>Streptococcus pneumoniae</i>	9	2.4	0
<i>Staphylococcus haemolyticus</i>	7	1.9	0
<i>Klebsiella aerogenes</i>	6	1.6	0
<i>Escherichia coli</i>	6	1.6	0
<i>Acinetobacter baumannii</i>	5	1.3	2
<i>Corynebacterium pseudodiphtheriae</i>	3	0.8	0
<i>Citrobacter koseri</i>	3	0.8	0
<i>Proteus mirabilis</i>	3	0.8	0
<i>Neisseria perflava</i>	3	0.8	0
<i>Klebsiella oxytoca</i>	2	0.5	0
<i>Staphylococcus saprophyticus</i>	2	0.5	0
<i>Neisseria clavus</i>	2	0.5	0
<i>Moraxella catarrhalis</i>	2	0.5	0
<i>Citrobacter coase</i>	2	0.5	0
<i>Streptococcus cristae</i>	2	0.5	0
<i>Streptococcus sanguis</i>	2	0.5	0
<i>Actinobacillus ureae</i>	2	0.5	0
<i>Neisseria lactamica</i>	2	0.5	0
<i>Rothia mucilagenosus</i>	2	0.5	0
<i>Streptococcus australis</i>	2	0.5	0
<i>Streptococcus pandoralis</i>	1	0.2	0
<i>Streptococcus pneumoniae</i>	1	0.2	0
<i>Streptococcus gordonii</i>	1	0.2	0
<i>Bacillus circulans</i>	1	0.2	0
<i>Corynebacterium durum</i>	1	0.2	0
<i>Actinomycetes</i>	1	0.2	0
<i>Staphylococcus lugdunensis</i>	1	0.2	0

Species	Number	Proportion (%)	ESBL-producers
<i>Serratia marcescens</i>	1	0.2	0
<i>Staphylococcus patenkov</i>	1	0.2	0
<i>Neisseria subflava</i>	1	0.2	0
<i>Corynebacterium argentoratense</i>	1	0.2	0
<i>Streptococcus sinicus</i>	1	0.2	0
<i>Rothia dentocariosa</i>	1	0.2	0
<i>Ralstonia aeruginosa</i>	1	0.2	0

ESBL – extended spectrum beta-lactamases

Table SIII

The species, number and proportion of bacteria isolated in the sample after usual decontamination procedures.

Species	Number	Proportion (%)	ESBL-producers
<i>Streptococcus oralis</i>	2	15.4	0
<i>Neisseria mucosa</i>	2	15.4	0
<i>Staphylococcus epidermidis</i>	1	7.7	0
<i>Klebsiella aerogenes</i>	1	7.7	0
<i>Streptococcus pneumonia</i>	1	7.7	0
<i>Streptococcus crista</i>	1	7.7	0
<i>Ralstonia pickettii</i>	1	7.7	0
<i>Rhododendron kiwii</i>	1	7.7	0
<i>Rothia dentocariosa</i>	1	7.7	0
<i>Staphylococcus caprae</i>	1	7.7	0
<i>Streptococcus sanguis</i>	1	7.7	0