

KLEBSIELLA SPECIES GENOME SEQUENCE REPORT

Level 3: Genomic epidemiologist use

Database identifier: 9439
Isolate identifier: CriePir26
Date entered: 2019-08-06
Location: Moscow, Russia
Host: Human

Genome report date: 2023-12-15
Genome quality: Marginal

Organism: *Klebsiella pneumoniae*

Bacterial typing: subspecies classifications to assess isolate similarity

MLST (Multilocus sequence typing)
Sequence type (ST): 377
Clonal group: CG377

Profile:

gapA	infB	mdh	pgi	phoE	rpoB	tonB
10	20	2	1	9	11	12

Life Identification Number: 0_0_152_1_0_0_0_2_0_0

Antibiotic susceptibility: Resistance mechanisms identified are used to predict antimicrobial susceptibility.

Drug class	Resistance determinants	Drug class	Resistance determinants
Aminoglycocides	aac(3)-IIa;aac(6')-Ib-cr;aadA;aph(3')-VIa (homolog);strA	Penicillins	OXA-1,SHV-110
Carbapenems	OXA-48,OmpK35-90%;OmpK36GD	Penicillins + β -lactamase inhibitors	
Cephalosporins (3rd gen)	CTX-M-15	Phenicols	CatB4 (fragment);catA1 (homolog)
Cephalosporins (3rd gen.) + β -lactamase inhibitors		Sulfonamides	sul1 (homolog, fragment);sul2
Colistin		Tetracycline	
Fluoroquinolones	GyrA-83Y;GyrA-87A;ParC-80I	Tigecycline	
Fosfomycin		Trimethoprim	dfrA15

Capsular typing: Polysaccharide K and lipopolysaccharide O types as predicted by KL and O genotype

K type: unknown (KL102)

O type: O2afg

Virulence factors: Factors that may lead to increased ability to cause invasive disease

Virulence score: 0

Hypermucoidy: None

Yersiniabactin ST: None

Aerobactin ST: None

Colibactin ST: None

Salmochelins ST: None

Related isolates

There are 4 related isolates identified with the same LINcode prefix [0_0_152_1_0](#) (representing the 10 core locus threshold) in the database.

id	isolate	country	year	LINcode
9439	CriePir26	Russia	2017	0_0_152_1_0_0_0_2_0_0
9440	CriePir28	Russia	2017	0_0_152_1_0_0_0_2_0_0
9441	CriePir152	Russia	2017	0_0_152_1_0_0_0_2_0_0
21806	CRE113	USA	2017	0_0_152_1_0_0_9_0_0_0
13189	SPARK_144_C1	Italy	2017	0_0_152_1_0_0_9_1_0_0