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: 2024-01-23

Genome quality: Marginal

Organism: Klebsiella pneumoniae

Bacterial typing: subspecies classifications to assess isolate similarity

MLST (Multilocus sequence typing) Profile:

Sequence type (ST): 377

Clonal group: CG377

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
Aminoglycosides	oglycosides aac(3)-IIa;aac(6')-Ib-cr;aadA;aph(3')- VIa (homolog);strA		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 Salmochelin ST: None

Related isolates

There are 4 related isolates identified with the same LINcode prefix $0_0_{152}_{10}$ (representing the 10 core genome MLST distance threshold) in the database.

	id	isolate	country	year	LINcode
	9439	CriePir26	Russia	2017	0_0_152_1_0_0_0_2_0_0
	<u>9440</u>	CriePir28	Russia	2017	0_0_152_1_0_0_0_2_0_0
	<u>9441</u>	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
	<u>13189</u>	SPARK_144_C1	Italy	2017	0_0_152_1_0_0_9_1_0_0