CLINICAL GENOME REPORT

Genome identifier: id-1492
Isolate/laboratory identifier: M54
Year of isolation: 2020
Location: Vadodara, India

Source type: Human
Host tissue sampled: Urine
Genome report date: 2025-11-20
Genome quality: Acceptable

Section 1: Clinical microbiology

Summary: *Klebsiella pneumoniae* with intrinsic ampicillin resistance. Note multidrug resistance - ESBL and CPE producing. ST-16 is recognised in hospital-acquired infection with genotypic and phenotypic carbapenem resistance.

Organism: *Klebsiella pneumoniae*

Bacterial typing: subspecies characterisation and classification to assess isolate similarity https://pubmlst.org/multilocus-sequence-typing

MLST (Multilocus sequence typing)
Sequence type (ST): 16

Profile:

gapA	infB	mdh	pgi	phoE	rpoB	tonB
2	1	2	1	4	4	4

Antibiotic resistance determinants: Genetically determined resistance mechanisms have been identified. Genetic variants (homologs) are highlighted *. "None found" means no resistance mechanisms have been identified in the antimicrobial resistance databases that exist at the time of reporting, correlate with phenotype. It is best practice to review these with the phenotypic antibiotic susceptibility profile. https://github.com/klebgenomics/Kleborate.

Drug class	Acquired genotypes
Penicillins (expected resistance due to blaSHV)	blaSHV-11^, blaCTX-M-15, blaNDM-5;OXA-181
+ β-lactamase inhibitor	None found
Cephalosporins (3rd gen)	blaCTX-M-15, blaNDM-5;OXA-181
+ β-lactamase inhibitor	None found
Carbapenems	blaNDM-5;OXA-181
Porin mutations (multiple drug classes)	OmpK36:p.136_137insThrAsp;OmpK35:p.Ile11fs
Aminoglycosides	aac(3)-IId^;aadA*;aadA2^;rmtB
Fluoroquinolones	qnrS1, GyrA:p.Ser83Phe;GyrA:p.Asp87Asn;ParC:p.Glu84Lys
Fosfomycin	None found
Phenicols	cmlA5
Polymixins	None found
Tigecycline	None found
Trimethoprim	dfrA12
+ Sulfonamides	sul1

Capsule and O typing: Polysaccharide K and lipopolysaccharide O serotypes as predicted by KL and O genotype https://github.com/klebgenomics/Kaptive.

K type: *K81*

O type: *O13*

Virulence factors: Factors that may lead to increased ability to cause invasive disease https://github.com/klebgenomics/Kleborate.

Virulence score: 1

Acquired siderophores:
Aerobactin ST: None
Salmochelin ST: None
Yersiniabactin ST: 384-2LV

Other factors:
Colibactin ST: None
Hypermucoidy: None

Section 2: Public health and Infection prevention and control

Summary: *Klebsiella pneumoniae* not known to be related to other isolates in the same geography. ST-16 is recognised in hospital-acquired infection with genotypic and phenotypic carbapenem resistance.

Bacterial typing: subspecies characterisation and classification to assess isolate similarity https://pubmlst.org/multilocus-sequence-typing

MLST (Multilocus sequence typing)
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Profile:

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Phylogroup: Kp1 Sublineage: SL17 Clonal group: CG16 cgST: 12601

LIN (Life Identification Number): 0_0_22_27_0_7_0_0_0_0

Plasmid Inc typing: Plasmid replicons that are extracted from short sequence read data may be less reliable than from long read data https://cge.food.dtu.dk/services/PlasmidFinder/
Plasmid type: Col(pHAD28), Col440II, ColKP3, IncFIA(HI1), IncFII, IncR, IncX3

Outbreak analysis: Identifying isolates that are genetically similar and maybe part of a transmission chain https://bigsdb.pasteur.fr/klebsiella/cgmlst-lincodes/.

Allele based:

LIN (Life Identification Number): 0_0_22_27_0_7_0_0_0_0
(based on cgMLST scheme with 629 genes)

There are 4 related isolates identified with the same LINcode prefix 0_0_22_27_0 (representing the 10 core genome MLST distance threshold) in the database.

id	isolate	country	year	LINcode
22874	NMI4821/11	Poland	2011	0_0_22_27_0_0_5_0_0_0
22876	NMI10734/11	Poland	2011	0_0_22_27_0_0_5_0_0_0
22877	NMI10898/11	Poland	2011	0_0_22_27_0_0_5_0_0_0
1495	MyNCGM268	Myanmar	2016	0_0_22_27_0_6_0_0_0_0
1492	M54	India	2020	0_0_22_27_0_7_0_0_0_0