

TECHNICAL GENOME REPORT

Genome identifier: id-1492
Isolate/laboratory identifier: M54
Year of isolation: 2020
Location: Vadodara, India
Source type: Human
Host tissue sampled: Urine

Accession number: Not defined
Genome report date: 2026-01-14
Sequencing technology: Illumina
Genome quality: Acceptable (detailed below)
Version control: Kleborate v3.2.4 analysis on 2025-11-12

Summary: *Klebsiella pneumoniae* with intrinsic ampicillin resistance. Note multidrug resistance - ESBL and CPE producing. One virulence factor present (yersiniabactin) and 7 plasmid types (Col(pHAD28), Col440II, ColKP3, IncFIA(HI1), IncFII, IncR, IncX3).

Organism: *Klebsiella pneumoniae*. *Species match:* strong

Antibiotic resistance determinants: Resistance determinants identified through Kleborate v3.2.4 analysis on 2025-11-12. Only determinants with >90% coverage and >90% identity shown, also those with imprecise protein matches or reduced coverage will be flagged. 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. † Macrolides and tetracycline lack breakpoints as not recommended for therapy, resistance determinants included here. 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 (3 rd 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.I36_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
†Macrolides	ereA2*;mphA*;ermB.v1*
†Tetracycline	None found

Bacterial typing: subspecies characterisation and classification to assess isolate similarity

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

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

Phylogroup: Kp1

Sublineage: SL17

Clonal group: CG16

cgST: 12601

LIN (Life Identification Number): 0_0_22_27_0_7_0_0_0_0

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

Confidence: Typeable

Problems: ?3

O type: O13

Confidence: Typeable

Problems: ?3!

Problems key:

- = the locus was in multiple pieces, possibly due to a poor match or discontiguous assembly. The number of pieces is indicated by the integer directly following the ? symbol.
- = genes expected in the locus were not found.
- = extra genes were found in the locus.
- = one or more expected genes was found but with translated identity below the minimum threshold.
- = one or more genes was found but truncated.

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

Plasmid Inc typing: These are identified using PlasmidFinder <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

Most isolates with identical LIN codes (all 10 thresholds) have <100 and often <25 single nucleotide differences, but further single nucleotide analysis may be required for these isolates in cluster/outbreak investigations.

QC status: based on KlebNet criteria.

Genome quality: Acceptable

Species match: strong [determined with Kleborate]

Genome size: 5,567,000 bp [accepted criteria 4,969,898; 6,132,846]

Contigs: 150 [accepted criteria <500]

%GC content: 57.23 [accepted criteria 56.35-57.98]