

# 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:** 2025-11-20  
**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 <sup>rd</sup> 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/>.

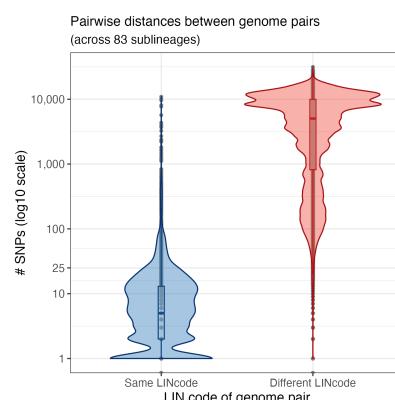
#### Allele based:

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
<a href="#">22874</a>	NMI4821/11	Poland	2011	0_0_22_27_0_0_5_0_0_0
<a href="#">22876</a>	NMI10734/11	Poland	2011	0_0_22_27_0_0_5_0_0_0
<a href="#">22877</a>	NMI10898/11	Poland	2011	0_0_22_27_0_0_5_0_0_0
<a href="#">1495</a>	MyNCGM268	Myanmar	2016	0_0_22_27_0_6_0_0_0_0
<a href="#">1492</a>	M54	India	2020	0_0_22_27_0_7_0_0_0_0



**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]