



One Day One Genome

Klebsiella pneumoniae

A poorly understood gut microbe, primarily recognized as an opportunistic pathogen



Isolation

Stool sample from a TB patient after five months of anti-TB treatment



Genomics

Whole genome sequencing (WGS) to understand the genomic changes in response to prolonged antibiotic exposure



Insights

Isolate of sequence type (ST17), a globally recognized clone associated with multidrug-resistant (MDR) and hospital-acquired infections worldwide.



Translation

Crucial information for understanding how antimicrobial resistance develops in response to prolonged antibiotic treatment.

Quality of Genome Assembly and Annotation:

Results from indigenously developed **BHARAT** analysis pipeline:
(**B**acterial **H**ybrid genome **A**ssembly and **R**apid **A**nnotation **T**oolset)

Table 1: Assembly Details	
Contigs	99
GC Content	57.30
Contig L50	8
Genome length	5,482,745 bp
Contig N50	266,766

Table 2: Annotated Genome Features	
CDS	5,458
tRNA	79
Repeat Regions	0
rRNA	4

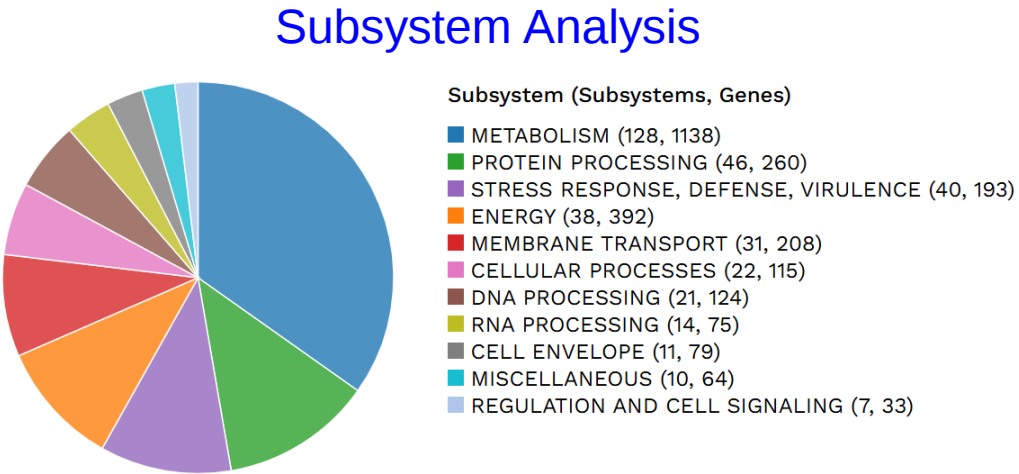


Table 3: Antimicrobial Resistance Genes	
AMR Mechanism	Genes
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, inhA, fabI, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Efflux pump conferring antibiotic resistance	AcrAB-TolC, AcrAD-TolC, AcrEF-TolC , AcrZ, EmrAB-TolC, EmrD, MacA, MacB, MdfA/Cmr, MdtABC-TolC, MdtL, MdtM, SugE, TolC/OpmH
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Antibiotic resistance gene cluster,cassette,or operon	MarA, MarB, MarR
Regulator modulating expression of antibiotic resistance genes	AcrAB-TolC, EmrAB-TolC, H-NS, OxyR

Genome Assembly

