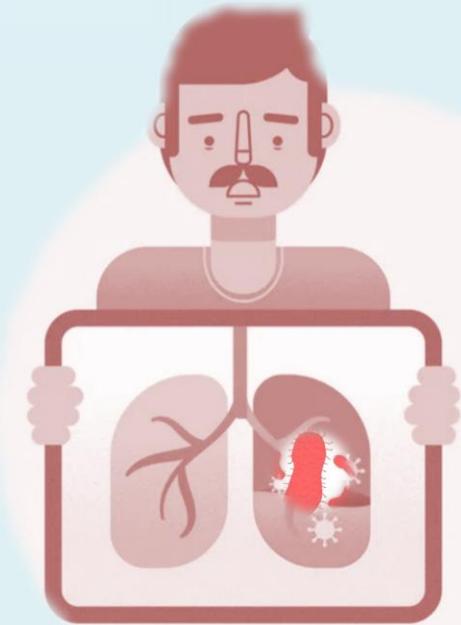
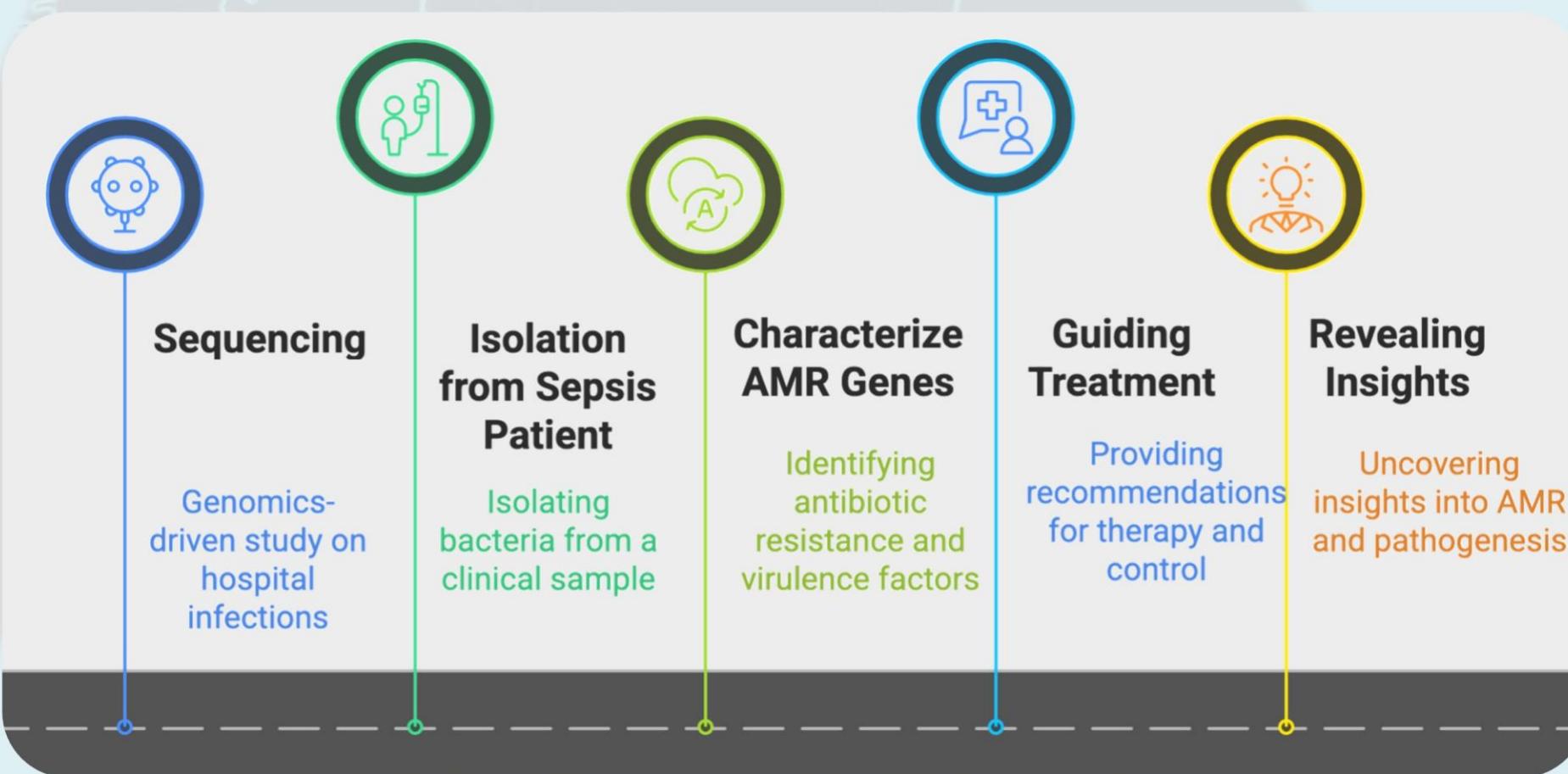




#OneDayOneGenomeInitiative

Klebsiella pneumoniae (CDFD_ODOG_Kleb_1)



Quality of Genome Assembly and Annotation:

Results from indigenously developed **BHARAT** analysis pipeline: (Bacterial Hybrid genome Assembly and Rapid Annotation Toolset)

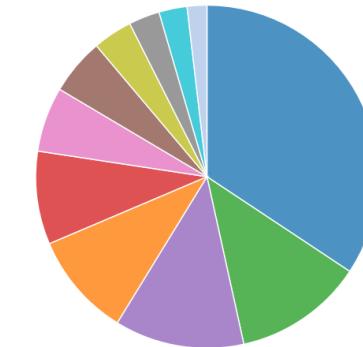
Table 1: Assembly Details

| | |
|---------------|--------------|
| Contigs | 102 |
| GC Content | 57.05 |
| Contig L50 | 11 |
| Genome length | 5,610,593 bp |
| Contig N50 | 195,347 |

Table 2: Annotated Genome Features

| | |
|----------------|-------|
| CDS | 5,498 |
| tRNA | 78 |
| rRNA | 3 |
| Repeat Regions | 11 |

Subsystem Analysis



Subsystem (Subsystems, Genes)

| | |
|-------------------------------------|-------------|
| METABOLISM | (129, 1163) |
| PROTEIN PROCESSING | (46, 260) |
| STRESS RESPONSE, DEFENSE, VIRULENCE | (46, 210) |
| ENERGY | (37, 376) |
| MEMBRANE TRANSPORT | (33, 252) |
| CELLULAR PROCESSES | (23, 118) |
| DNA PROCESSING | (20, 122) |
| RNA PROCESSING | (14, 77) |
| CELL ENVELOPE | (11, 77) |
| MISCELLANEOUS | (10, 40) |
| REGULATION AND CELL SIGNALING | (7, 34) |

Table 3: Antimicrobial Resistance Genes

| AMR Mechanism | Genes |
|--|---|
| Antibiotic inactivation enzyme | AAC(6')-Ib/AAC(6')-II, CatB family, CTX-M family, Mph(A) family, NDM family, SHV family, TEM family |
| Antibiotic resistance gene cluster,cassette,or operon | MarA, MarB, MarR |
| 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, QacE, SugE, TolC/OpmH |
| Protein altering cell wall charge conferring antibiotic resistance | GdpD, PgsA |
| Protein modulating permeability to antibiotic | OccD6/OprQ, OprB |

Genome Assembly

