Draft Genome Sequence of Multidrug Resistant Klebsiella Pneumoniae Strain C43 Isolated from Environmental Water Sample

Poster designed by: Ng Kar Kwan Sandra Joanne, Wong Li Xin Hannah, Vikneshwaren s/o Senthamil Selvan

(Soon Keong Wee, Eric Peng Huat Yap, American Society for Microbiology, 11(9), 2022)

Abstract

We report the genome of ESBL-producing *Klebsiella pneumoniae* strain C43, which was isolated from an environmental water sample. The genome is 5,614,412 bp in size with GC content of 56.86% with multidrug antimicrobial resistance genes and several metal resistance gene operons.

Introduction

Klebsiella pneumoniae is a Gram-negative Enterobacteriaceae capable of causing urinary tract infection, pneumonia, and wound or soft tissue infections. Apart from being a hospital-acquired pathogen, *K. pneumoniae* can cause a range of community-acquired infections and be transmitted through food, animal, and environmental sources. Multidrug resistance (MDR) in *K. pneumoniae* can be disseminated through global MDR lineages, acquisition of plasmids, and mobilisation of antimicrobial resistance genes.

In light of the above, we investigate the genomic sequence of an environmental *Klebsiella pneumoniae* strain C43 that is resistant to multiple antimicrobials

Methods

Isolate

Klebsiella pneumoniae strain C43 was isolated and enriched overnight in lysogeny broth (LB) at 37˚C with aeration and subsequently plated and subcultured on LB agar.

Antibiotic susceptibility

Antibiotic susceptibility testing was performed by disk diffusion. (2)

Extraction and Sequencing

The cells were grown in LB broth for bacterial DNA extraction using Qiagen DNA Mini kit and sequenced with Nextera XT DNA library preparation kit (Illumina, USA)

Genome assembly, assessment and annotation

The Genome Was assembled de novo using Unicycler Galaxy version 0.4.6.0 (3)

Genome quality assessment was done using CheckM

Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline 4.9. (4)

Species identification

Species identification was confirmed using average nucleotide identity (ANI) calculator. (5)

Multilocus sequencing typing (MLST), strict core genome MLST (scgMLST), and wzi gene capsular polysaccharide characterization (K typing) were carried out using BIGSdb database v1.22.3.(6)

CRISPR, Resistance genes, Plasmids

Presence of clustered regularly interspaced short palindromic repeat (CRISPR) sequences was predicted using CRISPRCasFinder (7).

Antimicrobial and metal resistance genes were predicted using NCBI AMRFinderPlus 3.0 (8).

In-silico detection of plasmids was done using PlasmidFinder 2.0 (9), and prophage prediction was carried out using PHASTER (10).

Results & Discussion

The Genome was assembled de novo using Unicycler Galaxy version 0.4.6.0 and 298 contigs (45-fold coverage depth, N50 of 61,998 bp) were obtained. The virulence factors of *K. pneumoniae* strain C43 include mrkABCDFIJ Type 3 fimbriae for cell adherence and bio-film formation and hsp20 heat shock protein. K. pneumoniae strain C43 belongs to ST432, scgST108 with K39 capsule type and wzi 39 allele.

It harbors 23 antimicrobial resistance genes (ARGs) against 10 classes of antimicrobials as well as 24 metal resistance genes against 5 metals. It is phenotypically susceptible to amikacin and meropenem; intermediate resistant to piperacillin-tazobactam, doripenem, and imipenem; and resistant to ampicillin/sulbactam, ceftazidime, cefotaxime, gentamicin, tetracycline, ciprofloxacin, and trimethoprim/sulfamethoxazole antibiotics.

The presence of multidrug resistant *K. pneumoniae* strain C43 in the aquatic environment suggests the possibility of a non-hospital reservoir for the transmission of antimicrobial and metal resistance genes. It poses a risk of community-acquired infection and dissemination into other environmental reservoirs.

	Klebsiella pneumoniae strain C43	Median of other *Klebsiella pneumoniae* strains
Genome Size (Mb)	5.61 ^	5.60
GC content (%)	56.86	57.16
Protein-coding genes	5514	5301
ARGs	23	13

Figure 1: Comparison between K. *pnemoniae* C43 strain vs other strains

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