P1240
Poster Session V
Global epidemiology and molecular typing

DECIPHERING EVOLUTIONARY EVENTS AND PRESENCE OF RESISTANCE GENES BY FULL DE NOVO GENOME SEQUENCING OF CLONALLY RELATED MULTI-DRUG RESISTANT OXA-48 KLEBSIELLA PNEUMONIAE ST11 ISOLATES

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Objectives

The whole genomes from 6 clinical isolates of ST11 *Klebsiella pneumoniae* with positive screening tests for carbapenemase production recovered from March-2012 to November 2013 at the Ramon y Cajal Hospital were sequenced to investigate:

- Evolutionary events involved in the emergence of OXA-48 carbapenemase producing strains in our institution

- Clonal diversification

- Antibiotic resistance acquisition mechanisms

Methods

Sequencing: The six genomes were sequenced using illumina technology and adding PacBio sequence for one of them.

Assembly and Annotation: illumina sequences were assembled with velvet and spades. PacBio reads were used for scaffolding of the illumina contigs using AG7. Gene prediction and Functional annotation based on protein similarity was done with BG7.

Comparative genomics:

- Single Nucleotide Variants (SNV) were detected in the core genome mapping to the assembly of the reference K. pneumonieae ST11genome F64.

- We used the program Differences to detect insertions and deletions in their genomic context to evaluate their possible implications in phenotypic changes or in epidemiological identification.

- Orthologous table. All the different proteins encoded by all genes of the 6 genomes were clustered to build a 'pangenome'. An orthologous table for the 6 genomes was generated using the 'pangenome' proteins as reference

Results

The isolates under this study were obtained from an outbreak of *Klebsiella pneumonia* ST11 OXA-48 carbapenemase producing strains with a profile of antibiotic multiresistance. This profile was experimentally tested. The analysis of these 6 genomes has allowed investigating the possible genes responsible for this resistance profiles and the possible genetic and evolutionary mechanisms affecting antibiotic resistance acquisition.

The functional annotation with BG7 was especially designed to detect antibiotic resistance genes including in the annotation a set of 44900 reference proteins from bacteria related with antibiotic resistance.

All the genes with functional annotations related to antibiotic resistance were studied in the 6 genomes and their genetic context was analyzed trying to decipher antibiotic resistance acquisition and transference. The allocation in plasmids, phages, transpososns and the relationships with mobile elements were analyzed for these antibiotic resistance genes. The evolutionary relationships between the 6 genomes were analyzed to show the intra-clonal diversity and the types of changes that suffered this kind of genes involved in resistance.

Conclusions

The analysis of antibiotic resistance at the whole genome level offers a new global perspective with the possibility of analysing the genetic context of each target gene. The analysis of a set of related genomes using bioinformatics comparative genomics approaches open new possibilities for the study of evolutionary mechanisms involved in antibiotic acquisition within a specific pathogenic strain responsible of an outbreak.

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