

Comparative Transcriptomic Analysis of Antibiotic resistant and susceptible *Klebsiella pneumoniae* Biofilms

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INTRODUCTION. Bacterial infectious diseases have been presented as a threat for the world community, causing profound damages to public health. Usually, these microorganisms were frequently found in complex associations with high resistance to antibiotics known as biofilms, a bacterial aggregate enclosed in a matrix of polysaccharide, extracellular DNA and proteins; that can form through bacterial attachment to solid surfaces or through bacterial aggregation on liquid culture. **OBJECTIVE:** This work intends to evaluate interspecific interactions existing on resistant and non-resistant (carbapenemase positive) strains of Klebsiella pneumoniae biofilms formation by using transcriptomic approach. MATERIAL AND **METHODS:** Planktonic cells were grown in LB media in a 24 well-plates, 37°C, 50 rpm during 8:30 h for determination of optimum growth rate. Biofilms cultures were grown in LB media in a 24 well-plates, 37°C, 50 rpm during 48 h. RNA extraction was performed by using the Pure Link RNA Mini kit and further treated with DNAse I. Quantification was performed by using Qubit equipment and the integrity confirmed by 1% agarose gel. RNA quality and integrity was also confirmed at Bioanalyzer 2100 software. High-throughput sequencing was performed by using Illumina MiSeq facility. **DISCUSSION AND RESULTS:** A transcriptional profile of both resistant and non-resistant strains of K. pneumoniae were performed. Growth conditions were established for both planktonic cells and biofilms cultures. Optimum growth time (reaching log growth time) was determined for planktonic cells and the point of major biofilm mass formation was settled using Pseudomonas aeruginosa as biofilm formation control. cDNA libraries were sequenced and mapped at a K. pneumoniae reference map. The unmapped transcripts were assembled by using de novo approach. This study will provide new insights into the probable adaptative mechanisms by which K. pneumoniae proceed to biofilm formation.

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