

**P1098**

**Poster Session IV**

**Enterobacteriaceae: resistance and fitness**

**GENOMIC ANALYSIS OF NDM-1 PRODUCING MORGANELLA MORGANII THROUGH WHOLE-GENOME SEQUENCING**

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**Objectives:** *Morganella morganii* F675 is a multidrug resistant bacteria harboring New Delhi metallo-beta-lactamase 1 (NDM-1) gene, isolated from the biopsy of a patient with diabetic foot ulcer in Jerusalem, Israel. The aim of this study was to employ whole genome sequencing to decipher the pathogenicity and resistome of this bacterium.

**Methods:** Genomic DNA was isolated from *M. morganii* F675 by phenol-chloroform method and sequenced using both paired-end pyrosequencing strategy on the 454-Titanium instrument (454 Life Sciences) and SOLiD version 4 paired-end sequencing technology (Applied Biosystems). The reads generated were assembled using the Newbler assembler. Genomic analysis was done using various bioinformatic softwares including our newly developed program 'ARG-ANNOT '(Antibiotic Resistance Gene-ANNOTation) database and through comparative genomic analysis.

**Results:** The bacterial genome harbored a total of 13 antibiotic resistance (AR) genes belonging to six different antibiotic families including bla(NDM-1)(Table 1). Sixty one percent of the AR genes were located on plasmid, indicating the genetic plasticity of the isolate. Virulence genes detected in strain F657 genome include: O antigen gene cluster located between *cpxA* and *yibK* housekeeping genes similar to other proteae bacteria, urease gene cluster, flagellar gene cluster, haemolysin genes, all of which play important role in the bacterial pathogenicity.

**Conclusion:** Whole genome sequencing is becoming an invaluable technique in the study of bacterial pathogens. The high number of plasmid-borne AR genes including bla(NDM-1) detected in this intrinsically-colistin *M. morganii* F675 shows that most of the AR genes might have been acquired through horizontal transfer. More so, the various virulence genes detected in the bacterial genome further provides insight into the pathogenic properties usually observed in this bacterium.