Summary

The present study was designed to investigate the role of genes responsible for multi-drug resistance phenomena of *Pseudomonas* spp. in neonates and infants hospital infections. A total of 288 hospitals samples(Clinical 134 and environmental 154) were collected from three Maternity and Pediatrics Teaching Hospitals(Ibn Al-Atheer , Al-Khansa′a and Al-Batool)in Al-Mosul city from February 2011till end June 2011.

The isolated bacteria were diagnosed phenotypically by using cultural, biochemical and Mini API 20NE system. The sensitivity of *Pseudomonas* isolates against antibiotics were also tested, *in vitro* .

Polymerase Chain Reaction was used to detect *16SrRNA* as a house keeping gene for detection of *Pseudomonas* isolates, in addition to *Opr-d-b*, *Opr-M, mexB* , *mexY* and *mexZ* as multi-drug resistance genes .

The results revealed that the percent of bacterial isolation from clinical samples was 90/134(67.1%) and environmental samples was 111 /154(72.1%).The classical diagnosis methods showed that *Staphylococcus* spp. was the most frequent Gram positive bacteria 57/296(19.25%) followed by *Streptococcus* spp. 29/296(9.79%) and *Enterococcus* spp. 11/296(3.72%), while *E. coli* was the most frequent Gram negative bacteria 69/296(23.3%)followed by *Klebsiella* spp. 53/296 (17.9%), *Pseudomonas* spp. 47/296 (15.88%), *Proteus* spp. 23/296 (7.7%), *Salmonella* spp. 5/296(1.69%) and *Acinetobacter* spp.2/296 (0.67%).

This study showed that the isolation of *Pseudomonas* spp. from environmental samples 30/47(63.8%)more than clinical samples 17/47 (36.1%). The high percent of *Pseudomonas* isolation in clinical samples occurred in throat swabs and tracheal aspirates 5/17(29.4%) followed by gastrointestinal tract samples 4/17(23.5%), whereas the percent of *Pseudomonas* isolation in environmental samples was showed in fluid sucker instruments 8/30(26.6%) followed by swabs of each of kitchen

and washing water of breast pumps 4/30(13.3%).Statistical analysis showed significant differences between clinical and environmental isolation .

PCR technique based on amplification of *16SrRNA* gene revealed that 21 strains of *Pseudomonas* isolates contain one distinct band with molecular weight approximately of 990-1Kb. when electrophorized on agarose gel, with high specificity (100%) in detecting *Pseudomonas* isolates in comparison with cultural, biochemical and Mini API 20NE system .

The antibiotics susceptibility test of *Pseudomonas* spp. showed that 19(90.4%)isolates were sensitive to azithromycin, ciprofloxacin, gentamicin and norfloxacin while 19(90.4%) isolates were resistant to ampicillin, amoxicillin, methicillin, ceftriaxone, cefotaxime, co-trimoxazol and chloramphenicol and the percent of resistance differed according to the types of other tested antibiotics.

According to PCR technique out of 21(100%)*Pseudomonas* isolates contained the multi-drug resistance genes, *Opr-d-b, Opr-M, mexB, mexY,* and *mexZ* . DNA amplification showed one distinct band with molecular weight : 200-220 bp., 290-310 bp., 250-270 bp., 530-560 bp. and 594 bp. respectively.

The relationship between the presence of multi-drug resistance gene in *Pseudomonas* isolates (by the role of efflux pump MexAB-OprM and MexXY in extrusion of antibiotics out of the cell) with increasing of resistance to many antibiotics was shown in this study, which led to emergence and prevalence of new multi-drug resistant strains of *Pseudomonas* isolates .