Pseudomonas aeruginosa is one of the leading nosocomial pathogens worldwide. Fifty pre-identified local isolates of *P. aeruginosa* were collected from major hospitals in Duhok and Erbil during the period from April 2015 to September 2015. The isolates were identified by classical biochemical methods and antibiotic sensitivity profiles were also obtained. Molecular investigation started with DNA extraction, confirmatory identification by the detection of 16S rRNA; PCR amplifications were applied to detect the presence of *oxa* 10 and *tox*A genes and then sequencing of the resulted PCR products was also performed. The results showed that all the fifty isolates had biochemical profiles characteristic of *P. aeruginosa* as it was also confirmed by the amplification band of 956 bp relevant to 16S rRNA; and that 50 % of the isolates revealed resistance to imipenem while 98 % of the isolates were resistant to cefepime. Furthermore, *oxa*10 gene was successfully detected by PCR in 92 % of the isolates with products bands of 760 bp while *tox*A gene was detected in 84 % of the isolates with an amplification bands of 396 bp. Then the PCR products of randomly selected ten samples (five for *oxa* 10 gene (designated A1through A5) and another five for *tox* A gene (designated B1 through B5) were purified by using a commercial PCR product purification kit and sequenced. The results of sequencing were analyzed in the University of Duhok/Scientific Research Center using DNASTAR/Laser Gene software. Regarding *oxa*10 gene, the results revealed that strains A4 and A5 are much more related when compared with the other strains. While the result of sequencing *tox* A gene indicated that isolates B2 and B5 are much more related in comparison with the other three isolates and isolate B1 was much more related to the positive control when all the isolates were compared.