



ABSTRACT

Pseudomonas aeruginosa is the most common and ubiquitous pulmonary pathogen of human beings which cause successfully unscrupulous infections in the patients with suppressed immune system of every age group and considered as the first or second key pathogen in supreme researches. Majority of the mortality and morbidity was caused by this pathogen every year globally due to several virulence factors and higher rates of significant infections. The most lethal and persistent pathogen that caused the acute ventilator acquired pneumonia (VAP) disease is *Pseudomonas aeruginosa*. The QS system is present in *Pseudomonas aeruginosa* which act as the regulator and regulates the expression of various virulence factors. The current study was established to detect the *lasR* gene associated with acute pulmonary infections in *Pseudomonas aeruginosa*. The samples include secretions (Endotracheal tract) and Blood samples from patients of acute Ventilator associated pneumonia (VAP) were provided by Microbiology lab of GCU Lahore. Total 5 strains of *P.aeruginosa* were selected as most virulent strains after confirmatory test of antibiotic sensitivity and virulence assays. Mutation was induced in these strains and virulence is compared in both wild and mutant strains of *Pseudomonas aeruginosa*. No prominent change of mutation was observed. These strains were then used for Ribotyping of 16SrRNA gene. PCR products results and sequence analysis results after BLAST at NCBI confirmed 100% presence of *Pseudomonas aeruginosa*. Later wild pathogenic strains of *P. aeruginosa* were used for Ribotyping of specific gene *lasR*. PCR products results and sequence analysis results after BLAST at NCBI confirmed 100% presence of *lasR* in the genome of *P. aeruginosa* strains which are involved in multiple virulence factors and responsible for acute pulmonary infections. In the recent study the contribution of *lasR* gene of pathogenic *P.aeruginosa* responsible for acute pulmonary infections was investigated.