

## **Genomic studies of HLA region gene expression during *Pseudomonas aeruginosa* infection**

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The human leukocyte antigen (HLA) complex is an extensively studied region of genes that been found to have an immunoregulatory function. *Pseudomonas aeruginosa*, a pathogen commonly found in the environment, is capable of infecting individuals with weakened immune systems, and is considered the bacterium associated with the highest mortality rate. Previous genetic studies of the HLA region have found correlations between bacterial infection and its effect on regulating HLA genes' expression to establish their infection. In this project we will analyze the expression classical HLA loci (A, B, C, DRA/B1-3-5, DQA1/B1) in human lung epithelial cells and human macrophage cells during the infection of several virulent strains of *P. aeruginosa*. To achieve this, macrophage, human lung epithelial cells, and antigen presenting cells will be cultured and infected with different virulent, and heat-killed strains of *P. aeruginosa* for different time periods. The mRNA will be extracted and converted into cDNA followed by real-time quantitative PCR to determine the expression of the targeted HLA genes. Expression of these genes in the treated cells will be analyzed using Lyvak method. Results will be corroborated using the Western Blot technique to identify the cell surface expression of targeted HLA proteins. This study will help to understand the differential control of *P. aeruginosa* infection towards the immune response related genes in human host, which will provide a new insight to the pathogenic activities of *P. aeruginosa*. We expect to see changes in the gene expression patterns of the targeted HLA genes upon infection with *P. aeruginosa*, compared to the expression of the control.