**Virulence factors of *Pseudomonas aeruginosa*: Investigating the differential expression of the *pyocyanin* pigment in a polymicrobial setting**

Bacteria almost always exist in polymicrobial communities where communication or quorum sensing between *intra-*species and *inter-*species is very important in regulating their virulence gene expression. The focus of our research is to understand the differential regulation of quorum sensing genes in the bacteria *Pseudomonas aeruginosa*. *P.aeruginosa* is an opportunistic bacterium that often results in serious infections in health-care settings especially in immune compromised patients. This nosocomial opportunistic pathogen produces many virulence factors which are under the regulation of the quorum sensing gene circuit. One of the very important virulence factors of *P.aeruginosa* is the production of the blue-green pigment *pyocyanin*. We are using the *pyocyanin* production of the bacteria as phenotype readout to understand how the bacterium responds and regulates the gene expression in a polymicrobial setting. We co-cultured *P.aeruginosa* with various strains of gram positive and gram negative bacteria (*Klebsiella pneumonia, Escherichia coli, Staphylococcus aureus, Enterococcus faecalis*) which again are commonly found in nosocomial infections. Our preliminary results indicate that the expression of *pyocyanin* by the bacteria *P.aeruginosa* is highly dependent on the specific bacterial population that *Pseudomonas* encounters. We are also working on generating the *P.aeruginosa* knockout strains for the *pyocyanin* production with a goal to compare the relative gene expression differences between the wild type and mutant strains. Our findings would help understand how several other virulence factors of P. aeruginosa are [co-regulated](https://www.ncbi.nlm.nih.gov/pubmed/17254955?dopt=Abstract) with *pyocyanin* production. This could eventually provide valuable insight on the surveillance mechanisms of quorum sensing for Pseudomonas in detection of its bacterial neighbors and response by producing antimicrobial factors. Our findings can also suggest novel therapeutic strategies for treating P. aeruginosa dominated polymicrobial infections.