TRANSCRIPTIONAL FUSION STUDIES OF THE DNR PROMOTER IN PSEUDOMONAS AERUGINOSA

Mentor: Michael J. Schurr Ph.D. Dept. of Microbiology & Immunology Program in Molecular Pathogenesis and Immunity 1430 Tulane Avenue, New Orleans, LA 70112 (504) 988-4607 E-mail: mschurr@tulane.edu

Description:

Pseudomonas aeruginosa is a Gram negative opportunistic pathogen capable of many different types of infection. *P. aeruginosa* is capable of both acute and chronic infections. Acute infection sites may be ocular, aural, epithelial or blood-borne and are usually the result of a breach in the primary host defense system. The most notorious chronic infection caused by *P. aeruginosa* is located in the respiratory tracts of Cystic Fibrosis (CF) patients. *P. aeruginosa* CF isolates are characterized by an alginate overproducing phenotype described as mucoid. The main regulatory mechanism for the conversion of *P. aeruginosa* to a mucoid phenotype involves activation of the stress sigma factor AlgU (AlgT) through acquired mutations in the *mucA* gene, which encodes an anti-sigma factor. Another regulatory factor that is required for the expression of alginate is the response regulator AlgR. AlgR also controls an apparently unrelated process of twitching motility in *P. aeruginosa*. The mechanism for this is currently unknown. Additionally, we have recently shown that AlgR is required for *P. aeruginosa* virulence in a murine septicemia infection model. The previous roles for AlgR described all indicate that it is acting as a transcriptional activator of the processes described.

Recently, evidence indicates that *P. aeruginosa* may be utilizing anaerobic metabolism as one of the mechanisms to maintain a chronic infection in the CF lung environment. Two transcriptional regulators in *P. aeruginosa*, ANR and DNR have been shown necessary for denitrification, a process that occurs in an environment of low oxygen concentration. Our preliminary data using Affymetrix GeneChip technology indicate that AlgR is repressing anaerobic metabolism genes, as well as the transcriptional regulator *dnr* under mid-logarithmic growth and aerobic conditions.

Transcriptional fusion studies will determine if AlgR is directly or indirectly controlling transcription of the *dnr* gene.

Objective:

Measure the *dnr* promoter activity in *P. aeruginosa* under aerobic and anaerobic growth conditions.

Prerequisites:

No experience is required.