NIH Award from the National Institute of Allergy and Infectious Diseases

Principal investigator: Nicholas Cianciotto, microbiology-immunology
Feinberg School of Medicine

- **Project**: Virulence Factors of Stenotrophomonas Maltophilia
- **Start Date**: July 22, 2009
- **Total Award Amount**: $76,250

**How the results of this project will benefit society:**
Stenotrophomonas maltophilia is an environmental bacterium that has been implicated in an increasing spectrum of human infections, including infections of the lung, blood, heart, urinary tract, central nervous system, eyes, skin, and soft tissue. The respiratory tract is the most common locale for S. maltophilia, with approximately 5 percent of nosocomial pneumonias being associated with the organism. However, very little is known about the way in which S. maltophilia infects the lung.

**The problem the project is trying to solve:**
It is the intent of this proposed research to identify S. maltophilia factors that promote lung infection with a focus on the organism's type IV pili and the proteins secreted via the type II secretion system. Work from our lab and others has determined that type II protein secretion (T2S) is a major facilitator of virulence in lung pathogens, including Pseudomonas aeruginosa and Legionella pneumophila. Proteins secreted by T2S usually include toxins and tissue-degrading enzymes. Thus, we hypothesize that T2S is critical in S. maltophilia pathogenesis.

**How this project will work:**
To test this, we will mutagenize genes encoding the T2S apparatus that have been revealed by the sequencing of the S. maltophilia genome and then examine the mutants in the murine model of S. maltophilia lung infection. A reduction in the capacity of the mutants to infect and/or damage the lung would trigger the future pursuit of effectors. Other past work has shown that type IV pili (T4P) promote lung infection, and recent sequencing has also shown that S. maltophilia encodes this type of surface appendage. Thus, we posit that the T4P of S. maltophilia is another facilitator of disease. To address this, we will test T4P mutants of S. maltophilia for their behavior in the murine lung. The data obtained have the potential to lead to new forms of infectious disease diagnosis, treatment, or prevention.

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