Low Fluid Shear Culture of *Staphylococcus aureus* Represses *hfq* Expression and Induces an Attachment-Independent Biofilm Phenotype

Background: The opportunistic pathogen, Staphylococcus aureus, experiences fluctuations in fluid shear during infection and colonization of a human host. Colonization frequently occurs at mucus membrane sites such as in the gastrointestinal tract where the bacterium may experience low levels of fluid shear. The response of S. aureus to low fluid shear remains unclear. Methods: S. aureus was cultured to stationary phase using Rotating-Wall Vessel (RWV) bioreactors which produce a physiologically relevant low fluid shear environment. The bacterial aggregates that developed in the RWV were evaluated by electron microscopy as well as for antibiotic resistance and other virulence-associated stressors. Genetic expression profiles for the low-shear cultured S. aureus were determined by microarray analysis and quantitative real-time PCR. **Results:** Planktonic *S. aureus* cultures in the low-shear environment formed aggregates completely encased in high amounts of extracellular polymeric substances. In addition, these aggregates demonstrated increased antibiotic resistance indicating attachment-independent biofilm formation. Carotenoid production in the low-shear cultured S. aureus was significantly decreased, and these cultures displayed an increased susceptibility to oxidative stress and killing by whole blood. The *hfq* gene, associated with low-shear growth in Gram negative organisms, was also found to be down-regulated in S. aureus. Conclusions: Collectively, this data suggests that S. aureus decreases virulence characteristics in favor of a biofilm-dwelling colonization phenotype in response to a low fluid shear environment. Furthermore, the identification of an Hfg response to low-shear culture in S. aureus, in addition to the previously reported responses in Gram negative organisms, strongly suggests an evolutionarily conserved response to mechanical stimuli among structurally diverse prokaryotes.