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Metabalomics Profiles of Ciproflaxacin Treated Staphylococcus aureus and Acinetobacter baumannii Biofilms

Many bacterial organisms have the ability to form complex conglomerations of cells known as biofilms. It is important to understand this stage of bacterial life because it facilitates colonization and persistence in environments not suitable for planktonic cells. For example, biofilm structures grant an inherent resistance to antibiotic agents, a trait that is particularly concerning for infectious bacteria such as Staphylococcus aureus and Acinetobacter baumannii. With bacterial organisms such as these displaying powerful resistance to antibiotics, it is becoming ever more critical to understand biofilm structures, along with the inherent antibiotic resistance that they provide. To begin to understand these structures, many researchers have turned to analysis of the metabolomic profiles of bacterial species, and how those profiles differ between planktonic cells and biofilm conglomerations. In this project, it is proposed that the metabolomic profiles of S. aureus and A. baumannii will differ significantly between not only their free floating and biofilm states, but also in their antibiotic treated biofilm states. As such, I will work to combine an external metabolite analysis conducted using gas chromatography mass spectrometry (GCMS), with an internal metabolite analysis conducted using liquid chromatography mass spectrometry (LCMS), to create metabolomic profiles of each variant of these bacteria listed above. With this data, it will be possible to elucidate the biochemical pathways critical to S. aureus and A. baumannii biofilm antibiotic resistance. On a larger scale, this information will be critical in the pursuit of sensitizing S. aureus and A. baumannii to modern antibiotics.

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