

Quorum Sensing and Biofilm Production: Comparing the Efficiencies of AI-1 and AI-2

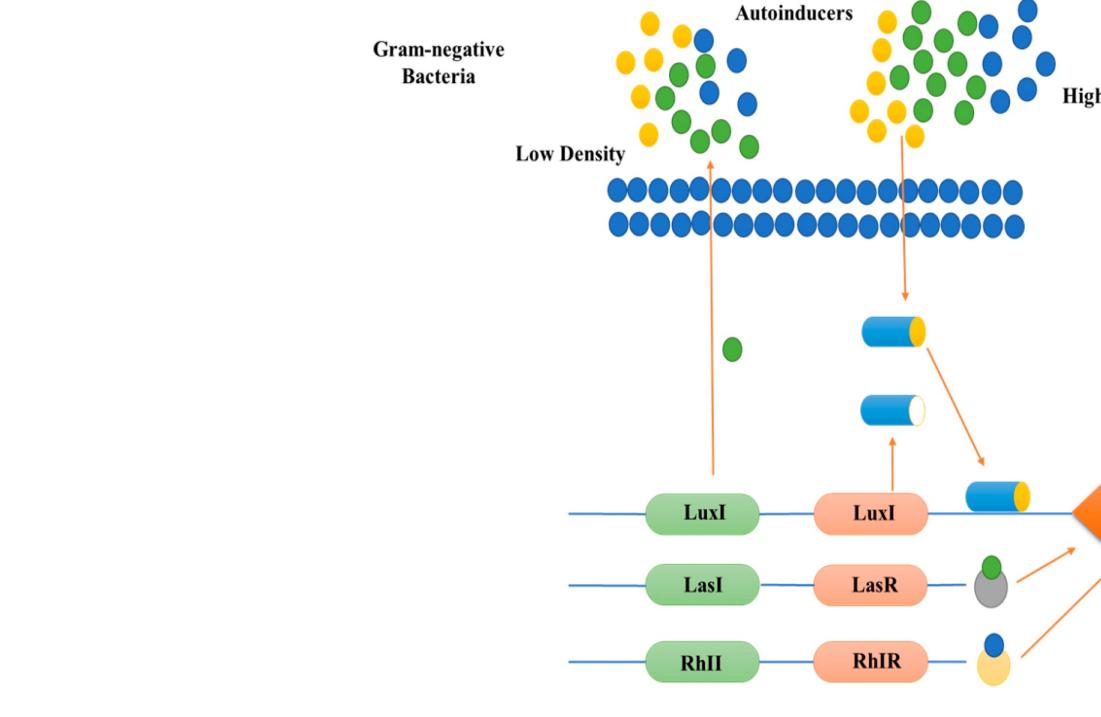
Ann-Marie Gilliam, Arin Matos, Dr. Marcos Vasconcelos — Department of Electrical and Computer Engineering,

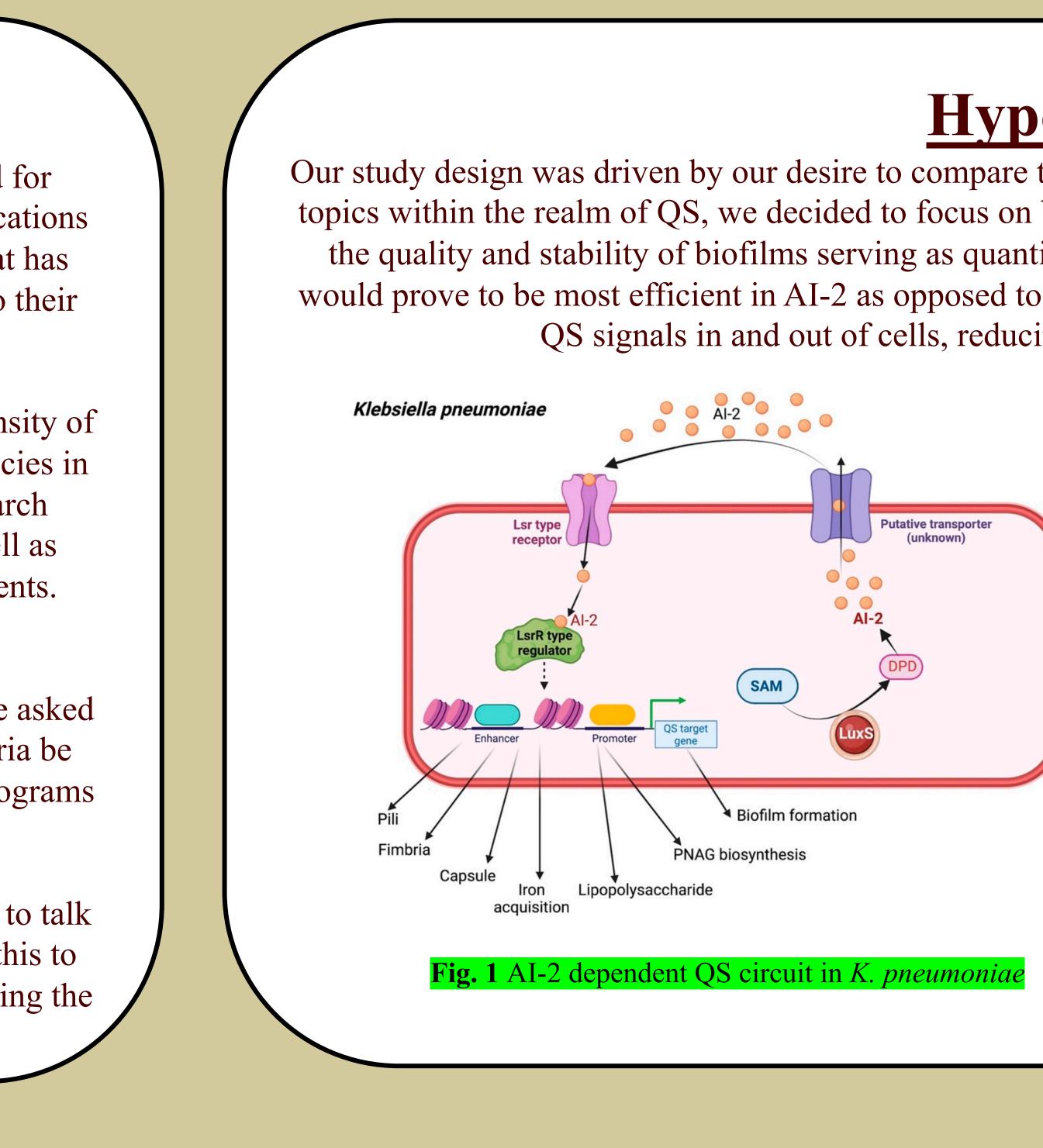
Motivation

- Bacterial Quorum Sensing has been studied and analyzed for decades. Nobel prizes have been one and hundreds of publications have been celebrated during that time. This mechanism that has been perfected by bacteria for millions of years is crucial to their survival.
- Bacteria employ certain signaling molecules to sense the density of the population of its friends to maintain longevity of the species in its given environment. Traditional Quorum Sensing research highlights different ways bacteria are ever evolving as well as continued embeddedness in diverse and hostile environments. However, what we plan to achieve is much deeper.
- As computer programs and artificial intelligence evolves, we asked ourselves how the mechanism of Quorum sensing in bacteria be extracted and implemented into the software of computer programs using a mathematical model.
- The goal is to use this data and software to allow computers to talk to each other and exchange data. In theory we hope to use this to further bridge the gap between mankind and technology, fusing the two with our research.

Background

- Quorum sensing (QS) is the mechanism where bacteria utilize their surroundings by means of cellular communication.
- During QS, chemical signal molecules called autoinducers (AIs) are released by bacteria and accumulate in accordance with increasing cell density.
- The extracellular accumulation of AIs allows bacteria to "sense" when the population is large enough to perform cooperative behaviors.
- Communal gene expression and behavior coordinated by signal relay mechanism.
- As bacteria population grows, cells secrete and detect chemical signals to coordinate functioning and form a biofilm, then "attack" the host when large enough.
- Communal gene expression and behavior coordinated by signal relay mechanisms and target genes, which are controlled by QS communication systems.
- Preliminary studies show a differences in signaling mechanisms and pathways in both gram positive and gram-negative bacteria.





AHL Receptor Other kinds of autoinducer Specific Receptor

Cell adhesive proteins Virulence Factor (Pyocyanin, Lectin, Toxins Proteases **Biofilm Formation**

• In bacterial quorum sensing, analyzing signaling molecules like acyl-homoserine lactones or peptides is essential for understanding microbial communication. Techniques such as LC-MS and HPLC allow precise identification and quantification of these molecules, offering insights into quorum sensing dynamics.

• Genetic and transcriptomic analyses, along with genetic manipulation, help correlate changes in gene expression with alterations in quorum sensing activity, unraveling individual contributions to overall efficiency.

• Additionally, live cell imaging techniques such as fluorescence microscopy and bioluminescence assays provide real-time visualization of quorum sensing dynamics within bacterial populations, offering a dynamic perspective on how communities coordinate behavior in response to environmental changes.

• Integration of computational modeling further aids in predicting quorum sensing outcomes under different scenarios, contributing to hypothesis formulation and experimental validation.

• Overall, a multifaceted approach combining chemical, molecular, and imaging techniques, complemented by computational tools, is crucial for a comprehensive understanding of bacterial quorum sensing, benefiting fields from microbiology to biotechnology and environmental science.

Florida State University, Tallahassee, Florida

Hypothesis

Our study design was driven by our desire to compare the functionality of AI-1 and AI-2. Due to the complexity of topics within the realm of QS, we decided to focus on biofilm formation as our singular application of study, with the quality and stability of biofilms serving as quantifiable variables. We hypothesized that biofilm formation would prove to be most efficient in AI-2 as opposed to AI-1, as AI-2 primarily relies on complex proteins to carry QS signals in and out of cells, reducing the prevalence of transcription errors.

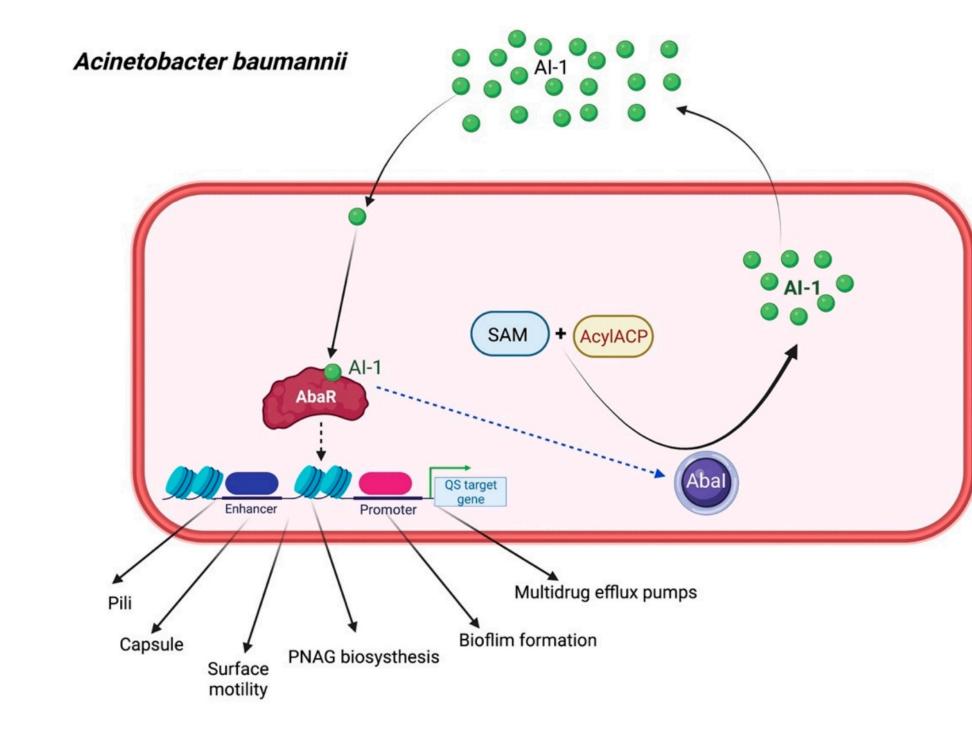


Fig. 1 AI-1 dependent QS circuit in A. baumanni

Methods



Discussion

- While formulating experimental model and pinpointing a topic of study, our team kept these aspects in mind:
- What areas within bacterial Quorum Sensing research do you believe warrant further exploration or innovation, and why?
- How do you think the findings and insights gained from studying bacterial quorum sensing could be translated into practical solutions for issues in healthcare, agriculture, or environmental conservation?
- What ethical considerations should researchers keep in mind when conducting experiments involving genetic manipulation of bacterial quorum sensing components?

Future Directions

- While our research is ongoing and has not yet reached a finalized result, significant progress has been made. We are actively developing and optimizing mathematical models to simulate quorum sensing dynamics within bacterial populations. Additionally, we are in the process of writing code to implement these models in Cello, enhancing our ability to engineer synthetic genetic circuits capable of quorum sensing.
- Moving forward, our focus will be on refining our mathematical models, validating their predictive accuracy through experimental validation, and exploring novel strategies to further quantify quorum sensing efficiency.
- By continuing to advance our understanding and manipulation of quorum sensing mechanisms, we aim to contribute to the development of innovative approaches for controlling bacterial behavior and combating infectious diseases.

References

• Bassler, Bonnie L, and Mellisa B Miller. "Quorum Sensing in Bacteria Annual Review of Microbiology." Quorum Sensing in Bacteria, Annual Reviews, Oct. 2001, www.annualreviews.org/doi/abs/10.1146/annurev.micro.55.1.165. • Santajit, Sirijan, et al. "Quorum Sensing in ESKAPE Bugs: A Target for Combating Antimicrobial Resistance and Bacterial Virulence." Biology, vol. 11, 6 Oct. 2022, p. 1466, https://doi.org/10.3390/biology11101466.

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