

Implications of antibiotic resistance caused by interspecies bacteria interactions.

A Thesis Prospectus

In STS 4600

Presented to

The Faculty of the
School of Engineering
University of Virginia

In Partial Fulfillment of the Requirements for the Degree
Bachelor of Science in Biomedical Engineering

By

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2024

Introduction

Antibiotic resistance has emerged as a growing global concern, posing significant challenges to public health systems worldwide. The traditional view of antibiotic resistance has primarily focused on the direct interactions between antibiotics and bacteria. However, recent research has shed light on the complex and dynamic nature of microbial communities, highlighting the crucial role of bacteria-to-bacteria microbiological interactions in the development and spread of antibiotic resistance (Bottery et. al, 2020). This comprehensive problem frame aims to explore the extent to which these interactions contribute to antibiotic resistance and the implications they have for human health.

The interactions between bacteria, collectively known as the bacterial microbiome, play a fundamental role in various ecological processes, including nutrient cycling, host-microbe interactions, and disease development. Recent studies have revealed that bacteria-to-bacteria interactions within the microbiome can significantly influence the acquisition and dissemination of antibiotic resistance genes (Crits-Christoph et. al, 2022). These interactions occur through horizontal gene transfer, where genetic material encoding resistance traits is exchanged between bacterial species.

One particular aspect of this problem frame involves understanding the implications of bacteria-to-bacteria interactions on antibiotic resistance and human health. The rise of antibiotic-resistant pathogens poses a serious threat to the effectiveness of antibiotic treatments, leading to increased morbidity, mortality rates, and healthcare costs. Unraveling the extent to which bacteria-to-bacteria microbiological

interactions contribute to antibiotic resistance is essential for devising effective strategies to combat the spread of resistant infections.

In this context, it is crucial to highlight the role of the Altered Schaefer Flora (ASF) in the dynamics of antibiotic resistance. The ASF refers to the collective microbial communities residing in the gastrointestinal tract, which are altered due to antibiotic exposure (Brand et. al, 2015). Antibiotics can disrupt the natural balance of the gut microbiota, leading to changes in the composition and function of the ASF. Such alterations can create favorable conditions for the emergence and dissemination of antibiotic resistance genes within the gut microbial community. The implications of ASF alterations extend beyond the gut, as the gut microbiota plays a crucial role in various physiological processes, including immune system development, metabolism, and protection against pathogens. Therefore, understanding how bacteria-to-bacteria interactions within the ASF contribute to antibiotic resistance is vital for comprehending the intricate relationships between microbial communities, antibiotic use, and human health.

This comprehensive problem frame aims to investigate the unknown knowledge surrounding the extent to which bacteria-to-bacteria microbiological interactions contribute to antibiotic resistance and its implications for human health. The role of the ASF in these dynamics is particularly crucial, as alterations in gut microbial communities can significantly impact antibiotic resistance development and spread. By gaining a deeper understanding of these interactions, we can develop targeted interventions and strategies to mitigate the emergence and dissemination of antibiotic resistance, ultimately safeguarding human health and improving the efficacy of antibiotic therapies.

Technical Topic

To effectively combat this growing problem, it is crucial to gain a comprehensive understanding of the intricate mechanisms underlying antibiotic resistance development. Measuring the growth rate of ASF bacteria can contribute to advancing microbiological understanding of the role that bacteria-bacteria interactions play in antibiotic resistance.

By measuring the growth rate of ASF bacteria, researchers can gain valuable insights into the dynamics of bacterial populations within this complex microbial community. This information can provide critical data on how bacteria-bacteria interactions contribute to the acquisition and spread of antibiotic resistance. The growth rate serves as an essential indicator of microbial fitness and can shed light on the competitive advantage of antibiotic-resistant strains within the ASF (Proctor et. al, 2022).

Understanding the growth dynamics of ASF bacteria can help explain the mechanisms by which antibiotic resistance genes are acquired and disseminated. Bacteria-bacteria interactions, such as horizontal gene transfer, play a crucial role in the transfer of resistance traits between different bacterial species (Bello-Lopez et. al, 2019). Measuring the growth rate allows researchers to assess the fitness cost associated with acquiring and maintaining antibiotic resistance genes. By comparing the growth rates of antibiotic-resistant strains to their susceptible counterparts, we can determine the selective pressures acting on these bacteria and better understand the dynamics of antibiotic resistance within the ASF.

Furthermore, studying the growth rate of ASF bacteria can provide insights into the impact of antibiotics on the overall structure and function of microbial communities. Antibiotic exposure can disrupt the delicate balance of the ASF, leading to changes in species composition and diversity (Raymann et. al, 2017). Measuring the growth rate allows researchers to assess the resilience and stability of microbial communities in the face of antibiotic pressure. Understanding how antibiotics affect the growth dynamics of ASF bacteria can help identify potential strategies to mitigate the development and spread of antibiotic resistance.

Measuring the growth rate of ASF bacteria can also contribute to the development of novel therapeutic interventions. By characterizing the growth dynamics of antibiotic-resistant strains within the ASF, researchers can identify potential vulnerabilities that can be targeted to disrupt the spread of resistance. Additionally, understanding the growth rates of different ASF bacteria can aid in the design of probiotics or other microbial-based therapies to restore balance to the gut microbiota and enhance resistance against antibiotic-resistant pathogens (Biggs et. al, 2017).

Moreover, the growth rate of ASF bacteria can serve as a valuable parameter for predicting the emergence and spread of antibiotic resistance. By monitoring changes in growth rates over time, researchers can identify shifts in microbial communities that may indicate the development of antibiotic resistance. This early detection can help inform public health strategies, such as implementing infection control measures or adjusting antibiotic prescribing practices, to prevent the further spread of resistant infections.

This approach offers valuable insights into the dynamics of microbial communities within the ASF and their response to antibiotic exposure. By characterizing the growth dynamics of ASF bacteria, researchers can better comprehend the acquisition and dissemination of antibiotic resistance genes and identify potential targets for intervention. Ultimately, this knowledge can inform the development of strategies to combat antibiotic resistance, safeguard human health, and preserve the efficacy of antibiotic therapies.

STS Topic

The emergence and spread of antibiotic resistance have profound implications for human health. While the direct impact of antibiotics on bacteria has long been recognized, recent research has shed light on the critical role of bacteria-bacteria interactions in the development and dissemination of antibiotic resistance (Habboush & Guzman, 2023). Understanding the implications of this phenomenon is crucial for devising effective strategies to mitigate the impact of antibiotic resistance on human health.

One of the primary implications of antibiotic resistance arising from bacteria-bacteria interactions is the limited treatment options available for infectious diseases. Antibiotics have long been the cornerstone of infectious disease management, but the increasing prevalence of antibiotic-resistant bacteria poses a significant challenge (Cave et. al, 2021). Bacteria that acquire resistance genes through horizontal gene transfer can rapidly spread these genes to other bacterial species, limiting the effectiveness of antibiotics across a wide range of pathogens. This can lead to

increased morbidity, mortality, and healthcare costs, as infections become more difficult to treat and require more potent and expensive antibiotics.

The implications of antibiotic resistance extend beyond the direct impact on treatment outcomes. Antibiotics disrupt the natural balance of microbial communities within the human body, particularly in the gut microbiota (Patangia et. al, 2022). The gut microbiota plays a crucial role in various physiological processes, including digestion, metabolism, and immune system development. Disruption of this delicate ecosystem can have long-term consequences for human health. Bacteria-bacteria interactions within the gut microbiota contribute to the acquisition and spread of antibiotic resistance genes, further exacerbating the impact of antibiotic resistance on human health.

Moreover, antibiotic resistance resulting from bacteria-bacteria interactions can have far-reaching effects on public health. Resistant bacteria can spread within healthcare settings, leading to healthcare-associated infections that are challenging to control (Dalton et. al, 2020). The transmission of antibiotic-resistant bacteria between individuals can occur through direct contact or indirect modes such as contaminated surfaces or healthcare personnel. This can result in outbreaks and the rapid dissemination of resistant strains within communities. The implications of these outbreaks include increased hospitalization rates, prolonged illnesses, and the potential for the emergence of multidrug-resistant pathogens that are resistant to multiple classes of antibiotics.

Another significant implication of antibiotic resistance arising from bacteria-bacteria interactions is the potential for the spread of resistance genes beyond the initial bacterial host. Horizontal gene transfer allows resistance genes to move between

bacterial species, including those that are pathogenic to humans. This transfer can occur within the human body or in the environment, further amplifying the spread of resistance. The implications of this phenomenon include the emergence of pan-resistant or extensively drug-resistant strains that are resistant to nearly all available antibiotics. This poses a grave threat to human health, as it leaves healthcare providers with limited or no treatment options for severe infections.

Furthermore, the implications of antibiotic resistance extend beyond the individual level to societal and economic impacts. The burden of antibiotic-resistant infections places a significant strain on healthcare systems, with increased hospitalizations, longer durations of illness, and the need for more costly interventions. The economic costs associated with antibiotic resistance are substantial, encompassing healthcare expenditures, productivity losses, and the expense of developing new antibiotics (Dadgostar, 2019). The limited pipeline of novel antibiotics compounds this issue, as the development of new drugs is slow and resource-intensive. The implications of antibiotic resistance on society include reduced productivity, increased healthcare costs, and potential disruptions to healthcare systems.

The limited treatment options, disrupted microbial ecosystems, increased risk of healthcare-associated infections, and the potential for the spread of resistance genes all contribute to the significant challenges posed by antibiotic resistance. Addressing these implications requires a multifaceted approach, including improved antibiotic stewardship, infection control measures, and the development of alternative strategies to combat bacterial infections. By understanding the implications of antibiotic resistance arising from bacteria-bacteria interactions, we can work towards the preservation of

effective antibiotics, the prevention of resistant infections, and the safeguarding of human health.

Research Question and Methods

To gain a better understanding of the intricate dynamics of bacteria-bacteria interactions in antibiotic resistance, measuring the growth rate of ASF bacteria can provide invaluable insights. This research question aims to explore the relationship between ASF growth rate and the acquisition and spread of antibiotic resistance genes, ultimately shedding light on the role of bacteria-bacteria interactions in antibiotic resistance. Additionally, this research question seeks to investigate how R programming can be utilized for the analysis and interpretation of the data obtained from measuring ASF growth rates.

The first component of the research question involves measuring the growth rate of ASF bacteria. This can be achieved through culturing ASF bacteria in the presence of antibiotics and monitoring their growth over time. By tracking the growth rate, researchers can assess the fitness and competitive advantage of antibiotic-resistant strains within the ASF (Watterson et. al, 2020). This information provides critical insights into how bacteria-bacteria interactions contribute to the acquisition and dissemination of antibiotic resistance genes.

The second component of the research question pertains to analyzing and interpreting the data obtained from measuring ASF growth rates. R programming, a powerful statistical and data analysis tool, can be utilized for this purpose. R programming provides a wide range of packages and functions specifically designed for data analysis, making it an ideal choice for investigating the relationship between ASF

growth rate and antibiotic resistance. Researchers can use R to perform statistical analyses, visualize the data, and explore trends and patterns within the dataset.

To analyze the data, researchers can employ various statistical techniques, such as regression analysis, to examine the relationship between ASF growth rate and antibiotic resistance. Additionally, R programming allows for the integration of other relevant variables, such as antibiotic concentrations or bacterial species composition, to further elucidate the underlying mechanisms driving bacteria-bacteria interactions in antibiotic resistance. By utilizing R programming, researchers can conduct robust statistical analyses, quantify the strength of associations, and uncover important insights from the data.

Furthermore, R programming facilitates data visualization, which is crucial for interpreting the results of the analysis. Researchers can create plots, charts, and graphs to visually represent the relationship between ASF growth rate and antibiotic resistance. These visualizations can help identify trends, patterns, and potential outliers within the data. They also aid in communicating the research findings effectively, allowing for a clearer understanding of the implications of bacteria-bacteria interactions in antibiotic resistance. All in all, the utilization of R programming provides a powerful tool for statistical analysis and data visualization, enabling researchers to extract meaningful information and enhance our understanding of the implications of bacteria-bacteria interactions in antibiotic resistance.

Conclusion

In conclusion, measuring the growth rate of ASF bacteria provides a valuable approach to understanding the impact of bacteria-bacteria interactions on antibiotic

resistance. By investigating the dynamics of bacterial populations within the ASF, we can gain insights into the acquisition and spread of antibiotic resistance genes. This knowledge is crucial for devising strategies to mitigate the development and dissemination of antibiotic resistance, safeguard human health, and preserve the efficacy of antibiotic therapies.

Additionally, exploring the implications of antibiotic resistance on human health is essential for addressing the challenges posed by resistant infections. Understanding the consequences of antibiotic resistance, such as limited treatment options, disrupted microbial ecosystems, and increased healthcare-associated infections, can inform public health interventions and guide the development of alternative strategies to combat bacterial infections.

By combining the research on measuring ASF growth rate and investigating the implications of antibiotic resistance on human health, we can advance our understanding of the intricate mechanisms underlying antibiotic resistance development and dissemination. This knowledge can contribute to the development of effective interventions, such as improved antibiotic stewardship, infection control measures, and the design of targeted therapies to combat antibiotic-resistant pathogens. Ultimately, these combined efforts can help mitigate the impact of antibiotic resistance, safeguard human health, and ensure the long-term effectiveness of antibiotic therapies.

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