

# Potential Student Colonization by Bacterial Pathogens in the Department of Medical Laboratory Sciences

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## Abstract

Studies evaluating the body's microbiome for differences amongst bacterial composition are at the forefront of microbiological studies. The nasal microbiome is the microorganisms that live within the nares and nasal passageways and differs based on a plethora of conditions, such as disease and exposures. The nasal microbiome has been shown to have been colonized by pathogens, such as Methicillin-resistant *Staphylococcus aureus* in established healthcare professionals; this suggests that those in healthcare are exposed to pathogens that can lead to species specific changes of the nasal microbiome. Nasal microbiomes of first year and last year Medical Laboratory Science students will be evaluated using DNA sequencing of the bacterial genomes within the nasal microbiome; thus, giving an insight into how the nasal microbiome of college medical laboratory students changes with exposure to potential pathogens and other bacterial species in the laboratory. DNA extracted from nasal swabs using the QIAamp DNA mini kit will be sequenced using Nanopore Technology and then compared between the two groups for differences in the microbiomes in association with program year. We saw a that relative number of species was the same for both groups, and a higher percentage of potential pathogens in last year students than first year students.

## Introduction

The nasal microbiome has been shown to have been colonized by pathogens such as Methicillin-resistant *Staphylococcus aureus* in established healthcare professionals, particularly nursing professionals and surgical ward employees (CDC, 2000); this suggests that those in healthcare are exposed to pathogens that can lead to species specific changes in the nasal microbiome of these healthcare professionals. Pathogen colonization of the nares of healthcare professionals creates resounding issues in patient care, as it leads to hospital acquired pathogenic infections (Legese et al., 2018).

Studies evaluating the body's microbiome for differences amongst bacterial composition based on specific aspects are at the forefront of microbiological studies. The nasal microbiome is the microorganisms that live within the nares and nasal passageways and differs based on a plethora of conditions, such as disease and exposures. The pertinence of studies regarding the nasal microbiome is the understanding of the benefits or consequences that are associated with the presence of certain bacterial species and pathogens.

The goal of this project is to understand whether college laboratory professional students experience similar pathogenic colonization rates as other healthcare professionals, and if their nasal microbiome changes significantly as they progress through the MLS program and are exposed to more pathogens in the clinical laboratory. To evaluate these differences, the nasal microbiomes of first year and last year Medical Laboratory Science students were evaluated using DNA sequencing of the bacterial genomes within the nasal microbiome; thus, giving an insight into how the nasal microbiome of college medical laboratory students changes with exposure to pathogens and other bacterial species in the laboratory.



<https://nanoporetech.com/products/minion>

## Acknowledgments

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## Results

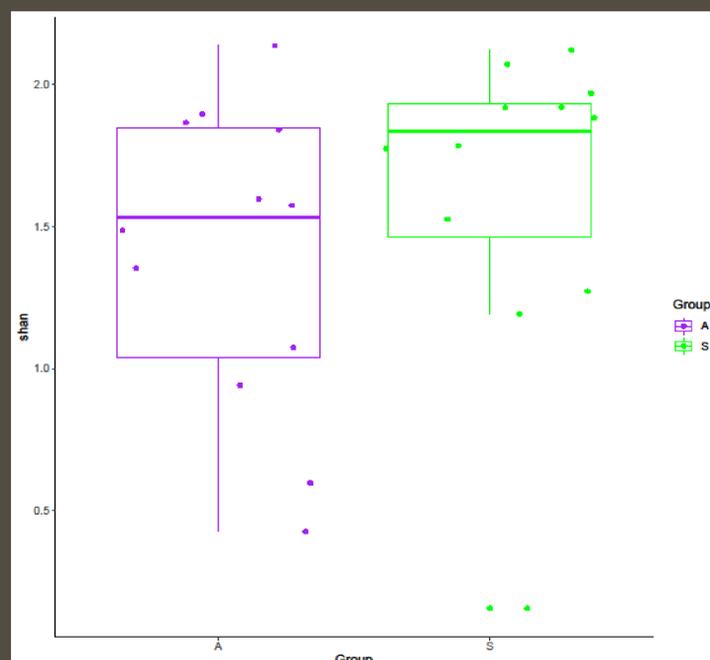
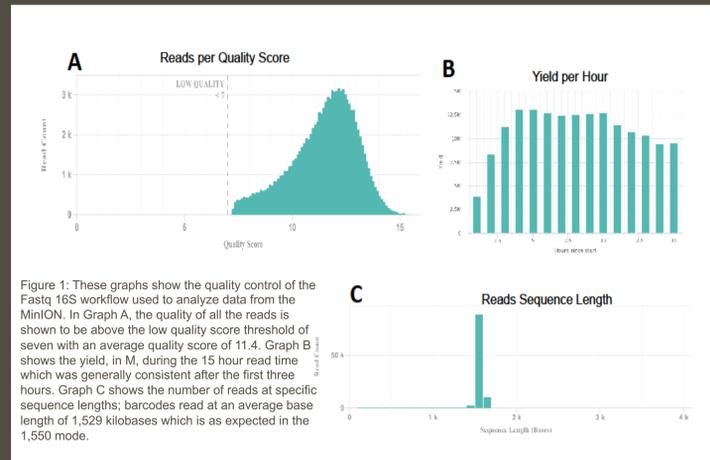


Figure 2: Box plot of Shannon diversity between applicants (purple) and seniors (green). The mean Shannon Diversity for applicants was 1.40, while the mean Shannon Diversity for seniors was 1.63. Using a Welch Two Sample T test to compare, we got a p-value of 0.35, meaning the difference among means is not statistically significant. This shows that the seniors do not have a higher microbial diversity compared to applicants.

Table 1. Demographic Data and <i>S. aureus</i> presence of groups		
	Senior (N=12)	Applicant (N=12)
Mean Age(years)	25.58	21.45
Medication Use	0.42	0.17
Other Lab Work	0.83	0.58
Mean Hospitalization (months)	0.42*	0.37*
<i>S. aureus</i> Present	4	2
<i>S. aureus</i> Not Present	8	10

Medication Use and Other Lab Work presented as frequencies within each group. Medication Use defined as taking any medication that is not antibiotics, Other Lab Work defined as laboratory work outside of the MLS student laboratories, and Mean Hospitalization is defined as being inpatient. ♦ Senior mean increased due to one senior spending five months in the hospital, the rest of the group spent little to no time in the hospital as an inpatient. ★ Applicant mean increased due to one applicant spending four months in the hospital, the rest of the group spent little to no time in the hospital as an inpatient. Presence of *S. aureus* between seniors and applicants. Seniors had twice the amount of *S. aureus* compared to applicants.

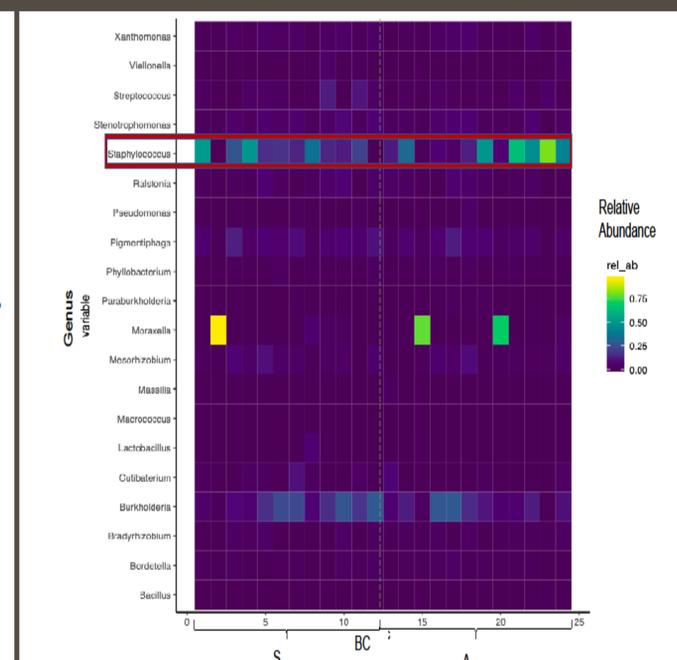


Figure 3: Relative abundance of top 10 Genera between seniors (S) and applicants (A). *Staphylococcus* is seen in a greater overall abundance in applicants compared to seniors.

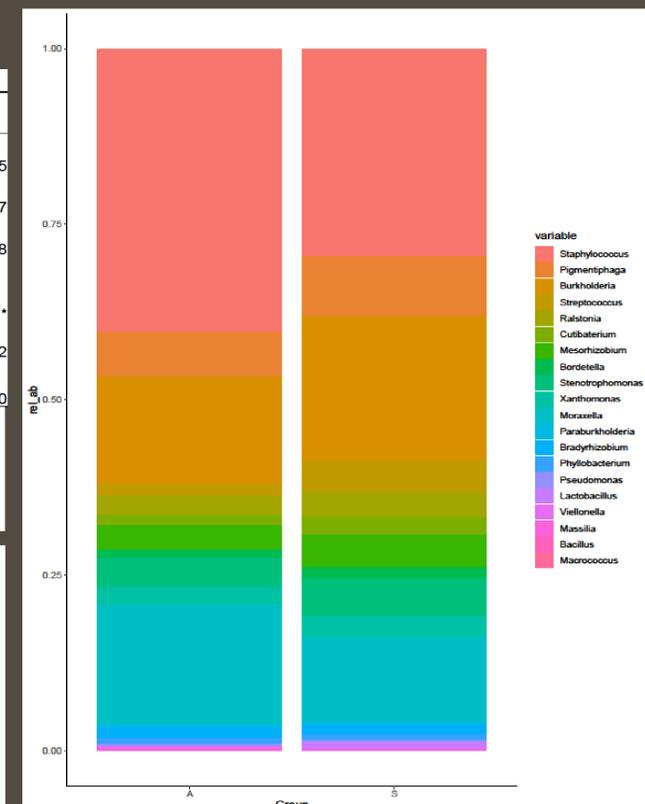


Figure 4: Relative abundance of top 20 Genera between seniors (S) and applicants (A). We see a greater abundance of *Pigmentphaga* and *Burkholderia* in seniors, and a greater abundance of *Staphylococcus* and *Moraxella* in applicants.

## Materials and Methods

### Population Selection

- First year students, enrolled in MLS 1113 or 1114; composed of 12 students
- Last year students, within a year of graduating with a bachelor's degree in MLS; composed of 12 students
- Candidates who were on antibiotics in the last 3 months or who have ever been diagnosed as immunocompromised were excluded from this study.

### Sample Collection and DNA Extraction

- Samples were collected with a DACRON swab approximately 2 cm up the nasal cavity and swirling for 3 seconds and placed in 1.5 mL Eppendorf tube to be refrigerated until extraction.
- DNA was extracted using a Qiagen QIAamp DNA mini kits per product protocol.

### Sequencing

- Extracted DNA was assigned a 16S barcode label
- Barcoded DNA underwent PCR for 30 cycles to amplify DNA.
- Amplified DNA was purified using AMPure beads.
- Samples were then loaded onto MinION nanopore sequencer for microbial species identification
- Using EPIME 16S bioinformatics tools, QC plots and taxa calls were generated from sequenced run.
- Sequenced data was then analyzed using R studio.

## Conclusion

- Seniors matriculated into the Medical Laboratory Science Program do not have a greater taxonomic richness than applicants not yet accepted into the program.
- Seniors are more likely to be colonized with bacterial pathogens, such as *S. aureus*, than applicants

## Discussion

- The alpha diversity was only slightly increased with seniors, with a mean of 1.63 in seniors compared to 1.40 in applicants.
- There was an outlier (figure 2) that could have brought down the mean for the alpha diversity of seniors.
- The similarities in alpha diversity between groups could be due to the groups being similar in age and sharing similar environments.
- One third of the seniors were carriers of *S. aureus*, while only one fifth of the applicants were carriers.
- An odds ratio was used to determine that seniors were 2.5 times more likely to acquire *S. aureus* than applicants
- The increase of *S. aureus* could be caused by seniors working with the microorganism in courses like Clinical Microbiology.

## Limitations

- Limited funding
- Small sample size
- Limited experience running the Nanopore sequencer
- To better understand and reduce these limitations, a longitudinal study has been set up to follow the applicants in this study each year of the program to see if their nasal microbiome shifts or changes in any way.