Understanding the Interaction between Nontuberculous Mycobacteria and the Host in Cystic Fibrosis

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Abstract

Nontuberculous mycobacteria (NTM) are environmental bacteria and can be found in soil, water, and dusts. However, they can cause lung diseases in certain populations with pre-existing lung conditions such as cystic fibrosis and chronic obstructive pulmonary disease (COPD). NTM employs a variety of mechanisms for their survival in the host, such as arresting phagolysosome maturation, cell wall component alteration, and attenuating T cell activation to interfere with the host's protective immune response. Host pathogen interaction first starts to occur when a pathogenic infection begins and the "innate immune systems respond to pathogen-associated molecular patterns and activate immediate host inflammatory and antimicrobial responses (Jo,1)." In this study, I am working with the senior lab members to understand the mechanism by which *Mycobacterium abscessus (M. abcessus)* , one type of NTM strains, causes active lung infections in cystic fibrosis patients. We hope that our research can aid in the medical approach and treatment plans of NTM infections.

Objective

The overall objective of this project is to identify Cystic Fibrosis mice and once identified, we aim to understand how *M. abcessus* infection leads to a dysregulated immune response in our cystic fibrosis mouse model.

Materials and Methods

To begin, we isolated the genomic DNA from the mouse ear-snip pieces using the HotShot technique. We then used the isolated DNA fragments to conduct a polymerase chain reaction (PCR) in order to amplify the specific DNA fragment that work as a biomarker for mouse genotypes. The PCR program used is shown in Figure 1. Following this, we stored the extracted DNA at -20 degrees Celsius until further use.

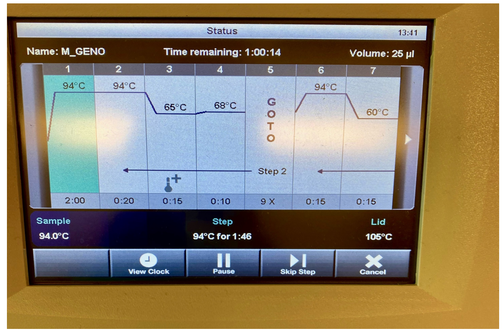

Figure 1: PCR protocol used.

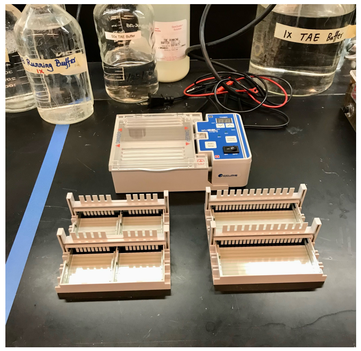

Figure 2: Gel Electrophoresis machine used

After PCR, we performed an agarose gel electrophoresis assay to separate the DNA fragments by size ranging from 100 bp to 20 kb. Once the electrophoresis has begun, the DNA fragments were attracted to the negatively charged end of the gel electrophoresis instrument. When the gel has finished its run, we imaged it using the Bio-Rad ChemiDoc XRS+ system to decipher which DNA samples have the cystic fibrosis gene and which do not. These results will then be used for further research in our lab.

Results

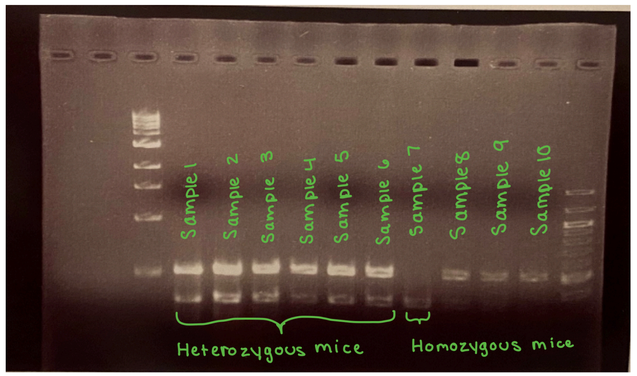

Figure 3: Mouse Genotyping (CFTR Gene)

As shown in Figure 3, we have identified both the heterozygous mice and the homozygous mice (one band). Homozygous mice can be said to have cystic fibrosis. Identifying these gene types is important because it enables us to continue our research and conduct more tests. These tests include tissue culturing and other models to help us to better understand the pathogenic influence of the gene in question.

Implications

Being able to understand the interaction between *M.abcessus* and the host in patients with cystic fibrosis will help to improve current treatments and enable improvement in future treatments, medications, and possible cures for those affected individuals. By investigating this topic, we stand to improve the health of a worldwide population and can change the way certain medical situations are approached.

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References

Jo, Eun-Kyeong. "Interplay between Host and Pathogen: Immune Defense and Beyond." *Nature News*, Nature Publishing Group, 11 Dec. 2019, https://www.nature.com/articles/s12276-019-0281-8.