Syracuse University
SURFACE at Syracuse University

International Programs

International Programs

8-27-2024

Why is the Mycobacterium tuberculosis Beijing genotype so prevalent in Colón, Panama? Uncovering the risk factors of a dangerous strain

Daniela Candanedo

Follow this and additional works at: https://surface.syr.edu/eli

Part of the Education Commons

The views expressed in these works are entirely those of their authors and do not represent the views of the Fulbright Program, the U.S. Department of State, or any of its partner organizations.

Recommended Citation

Candanedo, Daniela, "Why is the Mycobacterium tuberculosis Beijing genotype so prevalent in Colón, Panama? Uncovering the risk factors of a dangerous strain" (2024). *International Programs*. 260. https://surface.syr.edu/eli/260

This Poster is brought to you for free and open access by the International Programs at SURFACE at Syracuse University. It has been accepted for inclusion in International Programs by an authorized administrator of SURFACE at Syracuse University. For more information, please contact surface@syr.edu.





Why is the *Mycobacterium tuberculosis* Beijing genotype so prevalent in Colón, Panama? Uncovering the risk factors of a dangerous strain

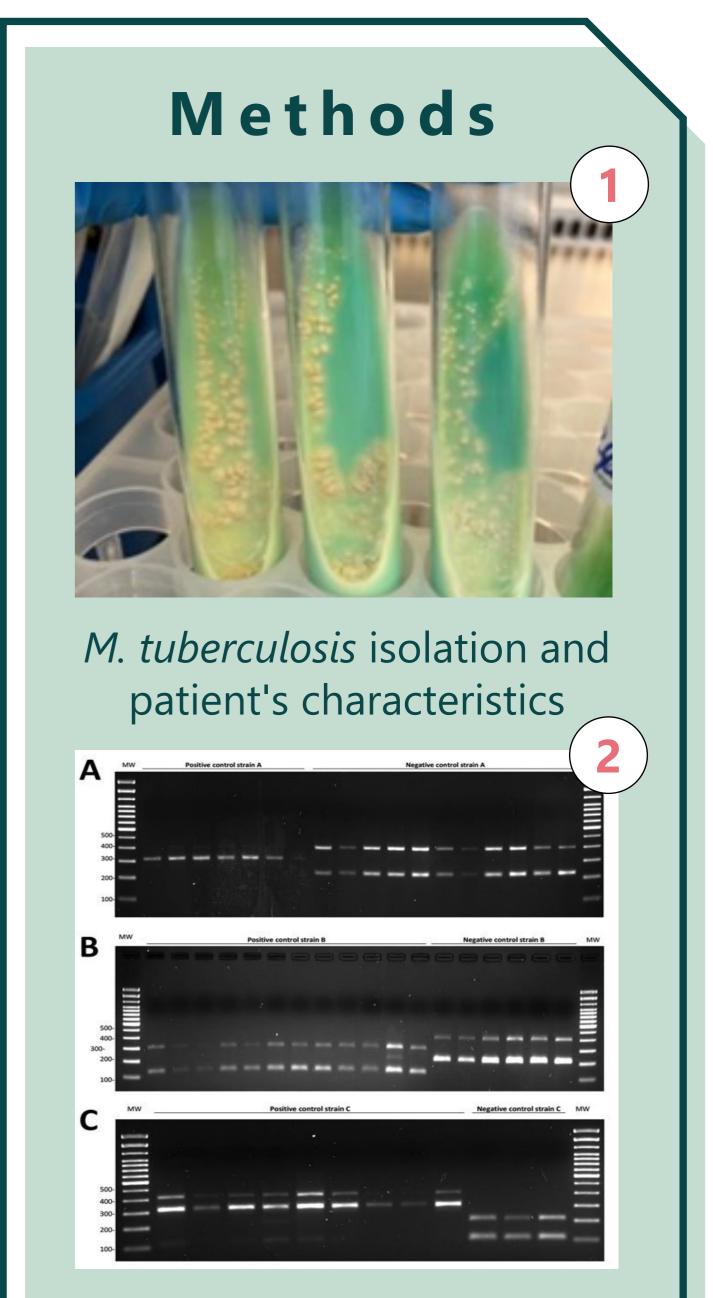
Daniela L. Candanedo Crespo

Introduction

Tuberculosis (TB) remains one of the leading causes of morbidity and mortality worldwide (WHO, 2021).

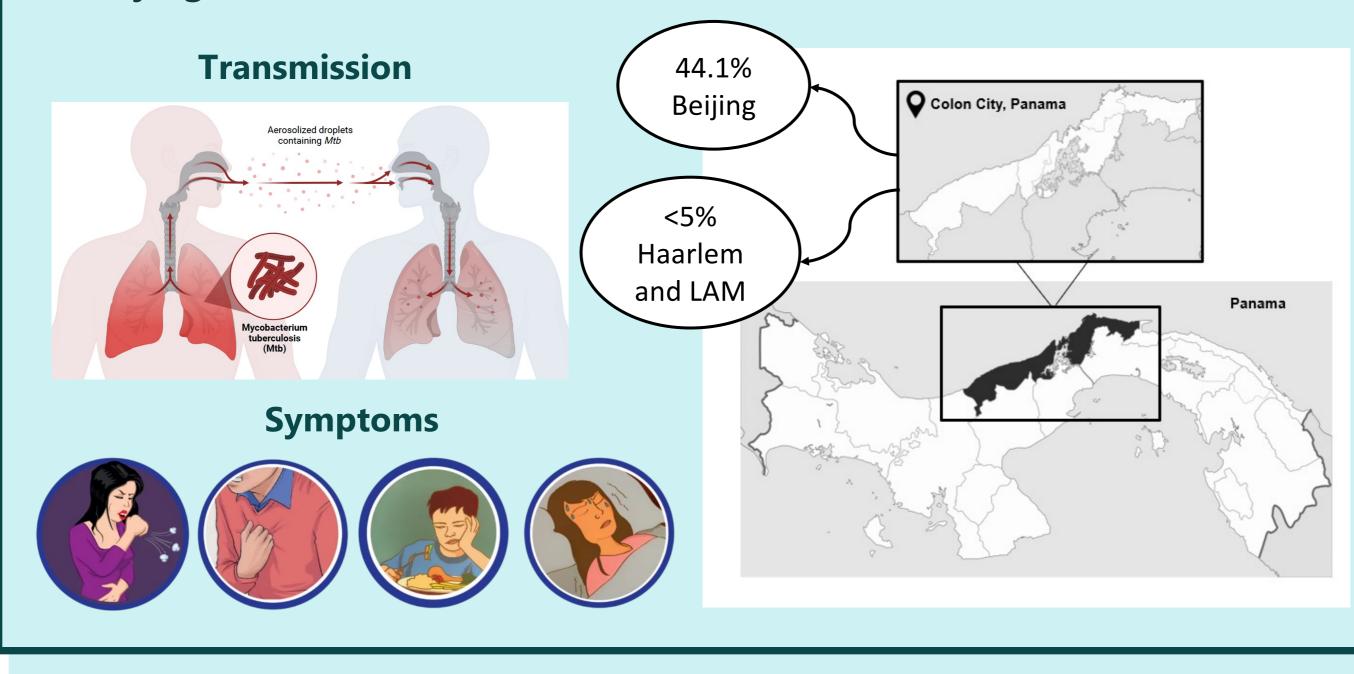
In Panama, TB incidence is 45.3 per 100,000 population, affecting underdeveloped areas like the Colón province (MINSA, 2023).

The Beijing genotype (Lineage 2), known for its high transmissibility and multidrug resistance, poses a significant challenge (Pérez-Lago ot al. 2019)



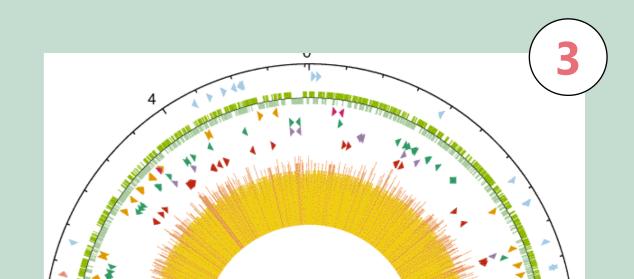
et al., 2019).

A novel molecular surveillance method using allele-specific oligonucleotide PCR (ASO-PCR) was developed to identify Beijing, Haarlem and LAM genotypes in Colón, Panama (Domínguez et al., 2019). This technique detected 44.1% of Beijing strain and <5% of Haarlem and LAM strains between 2018-2020 (Acosta et al., 2020). This method was also applied between 2021-2022, identifying 29.1% of Beijing strain (Candanedo et al., 2023).



Objective

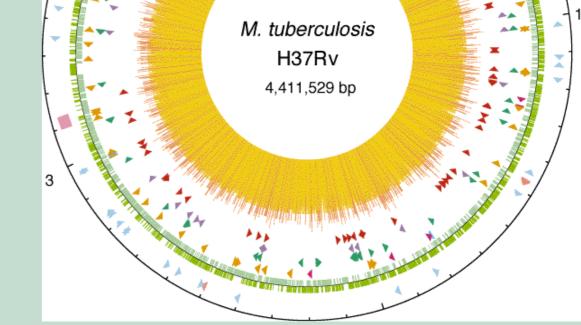
DNA extraction and ASO-PCR for Beijing strain



This study aims to identify and analyze the epidemiological risk factors associated with the Beijing strain infection in Colón, Panama between 2025-2026. Demographic, clinical, and geographic variables will be assessed to better understand the infection and transmission dynamics.

Study Importance

The findings will provide critical information to enhance TB control and prevention strategies in Colón, influence health policy formulation, and optimize resource allocation.



Whole-Genome Sequencing and Bioinformatics analysis

Data Analysis (R-Console)

	Phase	Activities	Period	
Ð	Preparation	Study design, grant approval, ethical a	approval acquisition. Month 1-2	
Timelin	Data Collection	Participant recruitment, structued surv and medical records review; and biolo collection and molecular testing		Γ
	Data Analysis	Data processing and coding; and resu	Its interpretation Month 3-12	
	Report Writing	Discussion and conclusions drafting; a scientific dissemination materials	and preparation of Month 13-15	
	Review and presentation	Publication in scientifics journals	Month 16-18	

References



Daniela Candanedo Biotechnologist

 \bowtie

danielacandanedo@gmail.com

<u>dcandane@syr.edu</u>



LinkedIn