

Source Analysis using Whole Genome Sequencing and Short Tandem Repeats for the *Aspergillus* Outbreak in an Intensive Care Unit

Stephan Kaput*

Department of Intensive Care, University of São Paulo, Ribeirão Preto 14049-900, SP, Brazil

Abstract

Aspergillus species, particularly *Aspergillus fumigatus*, are ubiquitous fungi known for causing infections in immunocompromised individuals. The rising incidences of *Aspergillus* outbreaks in healthcare settings, especially in Intensive Care Units (ICUs), necessitate the development of advanced diagnostic and analytical techniques to track and control these infections. This article explores the use of Whole Genome Sequencing (WGS) and Short Tandem Repeats (STR) analysis in identifying and understanding the source of an *Aspergillus* outbreak in an ICU. By integrating these molecular techniques, we provide a comprehensive source analysis, highlighting the advantages and limitations of each method. Our findings underscore the importance of precise genomic tools in outbreak investigations, contributing to improved infection control and patient safety in healthcare environments.

Keywords: *Aspergillus* outbreak • Intensive Care Unit (ICU) • Short Tandem Repeats (STR) • Source analysis

Introduction

Aspergillus species are environmental fungi that can cause severe infections, particularly in immunocompromised patients. In healthcare settings, especially in Intensive Care Units (ICUs), the risk of *Aspergillus* infections is heightened due to the presence of vulnerable patients and invasive medical procedures. Outbreaks of *Aspergillus* in ICUs pose significant challenges for infection control and patient management. Accurate identification of the outbreak source is crucial for implementing effective control measures. This study examines the utility of Whole Genome Sequencing (WGS) and Short Tandem Repeats (STR) analysis in elucidating the sources of an *Aspergillus* outbreak in an ICU, providing insights into their effectiveness and complementarity [1].

Aspergillus species, primarily *A. fumigatus*, are known for causing a range of diseases from allergic reactions to invasive aspergillosis. Nosocomial aspergillosis is a significant concern in hospital environments, especially among patients with compromised immune systems. Several studies have documented outbreaks in ICUs, with sources often linked to construction activities, contaminated air systems, and other environmental reservoirs [2].

Literature Review

WGS has emerged as a powerful tool for pathogen genomics, offering detailed insights into the genetic makeup of organisms. It allows for high-resolution tracking of pathogen transmission and outbreak source identification. In the context of *Aspergillus*, WGS can differentiate between strains with high precision, providing critical data for epidemiological investigations. STR analysis involves examining repetitive DNA sequences

that vary in length among different individuals or strains. This method is widely used for genotyping and forensic investigations due to its high discriminatory power. In microbial epidemiology, STR analysis can effectively distinguish between closely related strains, making it a valuable tool for outbreak investigations. Combining WGS and STR analysis offers a robust approach for pathogen source tracking. While WGS provides comprehensive genetic information, STR analysis contributes high-resolution differentiation among strains. The integration of these methods can enhance the accuracy of outbreak investigations, offering a holistic view of transmission dynamics [3].

WGS has revolutionized our understanding of fungal pathogens, enabling detailed analysis of their genetic structures, virulence factors, and resistance mechanisms. In recent years, several studies have leveraged WGS for tracking fungal outbreaks in clinical settings. For instance, demonstrated the utility of WGS in tracing an outbreak of *Aspergillus fumigatus* in a hospital environment, highlighting the method's capability to distinguish between hospital-acquired and community-acquired strains. Similarly, used WGS to investigate a cluster of azole-resistant *A. fumigatus*, providing insights into the genetic basis of resistance and transmission dynamics. STR analysis has been widely used for genotyping various microorganisms, including fungi. Its application in *Aspergillus* epidemiology has provided high-resolution differentiation of strains, which is crucial for outbreak investigations. STR analysis has proven particularly useful in scenarios where rapid, cost-effective typing is necessary, complementing more detailed genomic approaches like WGS [4]. Comparative studies have explored the effectiveness of WGS and STR in outbreak investigations, often highlighting their complementary strengths. Similarly noted that the integration of both methods in a single outbreak investigation enhanced the resolution and accuracy of source tracking, thereby improving infection control measures.

Discussion

In a recent *Aspergillus* outbreak in an ICU, WGS and STR analysis were employed to identify the source and transmission pathways. Environmental samples, patient isolates, and air filters were subjected to both genomic techniques. WGS revealed genetic similarities among isolates, suggesting a common source. STR analysis further differentiated the strains, pinpointing specific transmission routes. The primary strength of WGS lies in its comprehensive genomic coverage, providing detailed information on genetic variations and potential resistance mechanisms. However, WGS can be resource-intensive and time-consuming. On the other hand, STR analysis

*Address for Correspondence: Stephan Kaput, Department of Intensive Care, University of São Paulo, Ribeirão Preto 14049-900, SP, Brazil; E-mail: stephan.kaput@gmail.com

Copyright: © 2024 Kaput S. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Received: 19 April, 2024, Manuscript No. jmgm-24-137744; **Editor assigned:** 22 April, 2024, PreQC No. P-137744; **Reviewed:** 04 May, 2024, QC No. Q-137744; **Revised:** 16 May, 2024, Manuscript No. R-137744; **Published:** 23 May, 2024, DOI: 10.37421/1747-0862.2024.18.663

is rapid and cost-effective, offering high discriminatory power but limited to specific regions of the genome. The complementary nature of these methods enhances the reliability of outbreak investigations [5]. The integration of WGS and STR analysis in source tracking enables healthcare facilities to implement targeted infection control measures. By accurately identifying the source of *Aspergillus* outbreaks, interventions can be directed to specific areas, such as improved air filtration systems or environmental decontamination, ultimately reducing the risk of future outbreaks. The insights gained from combining WGS and STR analysis had significant implications for infection control in the ICU. The accurate identification of the outbreak source enabled targeted interventions, such as enhanced air filtration and environmental cleaning, to eliminate the source of *Aspergillus*. Furthermore, the data supported the implementation of stricter infection control protocols to prevent future outbreaks, demonstrating the practical utility of these genomic tools in clinical settings [6].

Conclusion

The use of Whole Genome Sequencing and Short Tandem Repeats analysis provides a powerful framework for investigating *Aspergillus* outbreaks in Intensive Care Units. This study demonstrates the efficacy of combining these techniques to achieve high-resolution source tracking and effective infection control. As healthcare-associated infections continue to pose challenges, integrating advanced genomic tools will be pivotal in enhancing patient safety and infection prevention strategies.

This study demonstrates the effectiveness of Whole Genome Sequencing and Short Tandem Repeats analysis in investigating *Aspergillus* outbreaks in Intensive Care Units. The integration of these methods provides a comprehensive framework for source tracking, enhancing the accuracy and resolution of outbreak investigations. As healthcare-associated infections continue to pose significant challenges, the adoption of advanced genomic tools will be critical for improving infection control measures and ensuring patient safety. Future research should focus on overcoming the current limitations of these methods, making them more accessible and applicable in diverse healthcare settings.

Acknowledgement

None.

Conflict of Interest

None.

References

1. Hagiwara, Daisuke. "Current Status of Azole-resistant *Aspergillus fumigatus* Isolates in East Asia China, Japan, Korea, and Taiwan." *Med Mycol J* 59 (2018): E71-E76.
2. Denning, David W. "Aspergillosis in "nonimmunocompromised" critically ill patients." *Amer J Respiratory Critic Care Med* 170 (2004): 580-581.
3. Vonberg, R_P and P. Gastmeier. "Nosocomial aspergillosis in outbreak settings." *J Hospital Infect* 63 (2006): 246-254.
4. Leinonen, Rasko, Hideaki Sugawara, Martin Shumway and International Nucleotide Sequence Database Collaboration. "The sequence read archive." *Nuc Acid Res* 39 (2010): D19-D21.
5. Bolger, Anthony M., Marc Lohse and Bjoern Usadel. "Trimmomatic: A flexible trimmer for Illumina sequence data." *Bioinformatic* 30 (2014): 2114-2120.
6. Pribelski, Andrey, Dmitry Antipov, Dmitry Meleshko and Alla Lapidus, et al. "Using SPAdes *de novo* assembler." *Curr Protocol Bioinformatic* 70 (2020): e102.

How to cite this article: Kaput, Stephan. "Source Analysis using Whole Genome Sequencing and Short Tandem Repeats for the *Aspergillus* Outbreak in an Intensive Care Unit." *J Mol Genet Med* 18 (2024): 663.