

THE 67<sup>TH</sup> INTERNATIONAL



# OPEN READINGS

CONFERENCE FOR STUDENTS OF PHYSICS AND NATURAL SCIENCES

**BOOK OF  
ABSTRACTS** | **2024**



Vilnius  
University

VILNIUS UNIVERSITY PRESS

Editors:

Martynas Keršys  
Rimantas Naina  
Vincentas Adomaitis  
Emilijus Maskvytis

Cover and Interior Design:

Goda Grybauskaitė

Vilnius University Press  
9 Saulėtekio Av., III Building, LT-10222 Vilnius  
info@leidykla.vu.lt, [www.leidykla.vu.lt/en/](http://www.leidykla.vu.lt/en/)  
[www.knygynas.vu.lt](http://www.knygynas.vu.lt), [www.journals.vu.lt](http://www.journals.vu.lt)

Bibliographic information is available  
on the Lithuanian Integral Library Information System (LIBIS) portal [www.ibiblioteka.lt](http://www.ibiblioteka.lt)  
ISBN 978-609-07-1051-7 (PDF)

© Vilnius University, 2024

# ANALYSIS OF VIRULENCE FACTORS IN ISOLATES OF OPPORTUNISTIC PATHOGEN *STENOTROPHOMONAS MALTOPHILIA*

Radvilė Drevinskaitė<sup>1</sup>, Laurita Klimkaitė<sup>1</sup>, Jūratė Skerniškytė<sup>1</sup>, Julija Armalytė<sup>1</sup>

<sup>1</sup>Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, Lithuania  
[radvile.drevinskaite@gmc.stud.vu.lt](mailto:radvile.drevinskaite@gmc.stud.vu.lt)

*Stenotrophomonas maltophilia* is an aerobic gram-negative bacterium that is widespread in the natural environment including soil, plants, and water sources. This bacterium of environmental origin is becoming an important opportunistic, nosocomial, multidrug-resistant pathogen associated with respiratory, bloodstream and urinary tract infections. Due to *S. maltophilia* innate resistance to various classes of antibiotics infections caused by this bacterium are difficult to treat and have high mortality rates of up to 69% [1]. Despite the wide range of clinical diseases associated with *S. maltophilia*, little information is available on the virulence factors of this bacterium. In addition to antibiotic resistance, the biofilm formation is considered a key virulence factor for *S. maltophilia* [2]. Secreted enzymes such as proteases, lipases and nucleases are thought to play an important role in *S. maltophilia* virulence, contributing to its ability to invade host tissues and degrade host components [3].

The aim of this study was to investigate the presence of genes encoding selected virulence determinants in 34 clinical and 43 natural isolates of *Stenotrophomonas maltophilia* from Lithuania. All clinical isolates were isolated from patients. Environmental isolates were isolated from various sources such as soil, water bodies and fish gut.

Genes encoding extracellular enzymes, toxins, components of secretion systems and iron uptake systems were selected for the detection of virulence factors. The analysis showed that the prevalence of most of the genes studied is similar in *S. maltophilia* isolates of natural and clinical origin. However, genes *stmPr1*, *afaD* and *zot*, encoding putative protease, adhesin and toxin respectively, were found to be exclusively present in isolates of clinical origin. The higher prevalence of virulence genes detected in clinical *S. maltophilia* isolates may be related to their importance in contributing to the ability of the bacterium to infect the host, to degrade various host components and to survive in clinical settings.

**Acknowledgements:** This research has received funding from the Research Council of Lithuania (LMTLT), project registration no. P-SV-23-156.

[1] Brooke JS. *Stenotrophomonas maltophilia*: an emerging global opportunistic pathogen. Clin Microbiol Rev. 2012 Jan;25(1):2-41.

[2] McCutcheon JG, Dennis JJ. The Potential of Phage Therapy against the Emerging Opportunistic Pathogen *Stenotrophomonas maltophilia*. Viruses. 2021 Jun 3;13(6):1057.

[3] Brooke JS. Advances in the microbiology of *Stenotrophomonas maltophilia*. Clin Microbiol Rev. 2021 May;34:e00030-19.