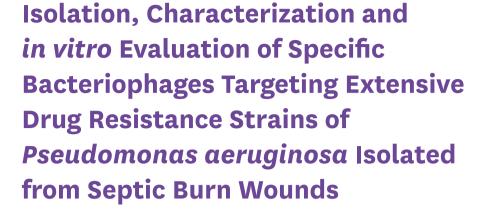


Original Article





Seyed Mahmoud Amin Marashi (b) 1, Farhad Nikkhahi (b) 1, Dariush Hamedi (b) 2, and Gholamhassan Shahbazi (b) 3,4

¹Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin, Iran ²Department of Molecular Medicine, Qazvin University of Medical Sciences, Qazvin, Iran ³Department of Microbiology and Immunology, Qazvin University of Medical Sciences, Qazvin, Iran ⁴Student Research Committee, Qazvin University of Medical Sciences, Qazvin, Iran

OPEN ACCESS

Received: Nov 20, 2021 Accepted: Mar 16, 2022 Published online: Mar 24, 2022

Corresponding Author: Gholamhassan Shahbazi, PhD

Department of Microbiology and Immunology, Qazvin University of Medical Sciences, Bahonar Blvd, Qazvin, Qazvin Province, Iran. Tel: +98-914-305-6243 Email: shahbazih90@gmail.com

Copyright © 2022 by The Korean Society of Infectious Diseases, Korean Society for Antimicrobial Therapy, and The Korean Society for AIDS

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (https://creativecommons.org/licenses/by-nc/4.0/) which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ORCID iDs

Seyed Mahmoud Amin Marashi https://orcid.org/0000-0003-2703-1715
Farhad Nikkhahi https://orcid.org/0000-0003-0369-8179
Dariush Hamedi https://orcid.org/0000-0002-2301-3213
Gholamhassan Shahbazi https://orcid.org/0000-0002-8042-0843

Funding

None.

Conflict of Interest

No conflict of interest.

ABSTRACT

Background: Antibiotic resistant bacteria and various infections caused by them especially extensive drug resistance (XDR) strains and worrying statistics of mortality due to these strains and also the lack of a clear vision for development and production of new effective antibiotics have made the necessity of using alternative therapies more apparent.

Materials and Methods: In this study, specific phages affecting the *Pseudomonas aeruginosa* XDR strain were extracted from hospital wastewater and their laboratory characteristics along with lysis effect on 40 XDR strains of *P. aeruginosa* were investigated.

Results: The results indicated that three isolated phages (PaB1, PaBa2 and PaBa3) belonged to the *Myoviridae* and *Pododoviridae* families and were specific to *Pseudomonas aeruginosa* strains. More than 98% of phages absorbed their host in less than 10 minutes (Adsorption time <10 min) and completed their lytic cycle after 40 minutes (latent time = 40 min). Burst size of PaBa1, PaBa2 and PaBa3 was 240, 250 and 220 pfu/cell, respectively. PaBa1 lysed 62.5% of the XDR strains with the highest efficiency. The three Phage cocktail was effective against 67.5% of the studied strains.

Conclusion: The results of this study indicate the significant potential of these phages for therapeutic use and prophylaxis of infections caused by this bacterium.

Keywords: Bacteriophage; Pseudomonas aeruginosa; Drug resistance; Antibiotic resistance

INTRODUCTION

Pseudomonas aeruginosa as an opportunistic bacterium can cause serious infections in people with deficient immune systems. This group of patients includes people with severe burn wounds, patients with cystic fibrosis, cancer patients and patients suffering from acquired immunodeficiency syndrome [1-3]. Various studies have reported a significant prevalence of