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Evaluation The Laser Effects on Phage of *Acentobacter Bumanii* Isolated from Clinical Samples in Iraq/Qadisyiah

Merriam Ghadhanfar Alwan[1,2], Noor Adil Abood*[3] Sarah K. Taha[1], Orooba Meteab Faja*[,4], Lina zeyad tarek[2], Haider Sabah Kadhim[5], Ziad M. Alkhozai[6]

[1]Department of Basic Science, College of Dentistry, Al-Iraqia University, Baghdad, Iraq
[2]Department of Medical Laboratory Techniques, College of Medical Technology, Al-Farahidi University, Baghdad, Iraq.
[3]Department of Clinical Laboratory Sciences, College of Pharmacy, Al-Nahrain University, Baghdad, Iraq.
[4]Department of Public Health, College of Veterinary Medicine, University of Al-Qadisiyah, Al- Al-Qadisiyah, Iraq.
[5] Department of Microbiology, Al-Nahrain University College of Medicine: Baghdad, Iraq
[6] Department College of Biotechnology, University of Al-Qadisiyah, Al- Al-Qadisiyah, Iraq.
***Corresponding author**
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ABSTRACT

Objective: *Acinetobacter baumannii* is a pathogenic bacterium with clinical attributes of nosocomial infection and resistance to antibiotics. Phage therapy represents a potential solution because it can specifically target MDR strains. This study aimed to isolate and characterize a lytic bacteriophage specific to *A. baumannii*, evaluate its kinetic and lytic properties, and investigate the effects of laser treatment on enhancing phage antibacterial activity against multidrug-resistant clinical isolates.

Methods: Clinical specimens were collected from patients in three hospitals in Al-Diwaniyah, Iraq, and *A. baumannii* isolates were identified using standard biochemical tests, API systems, and *16S rRNA* PCR sequencing. Environmental samples were screened to isolate lytic phages, which were propagated, purified, and analyzed using plaque assays and scanning electron microscopy. Phage kinetics—including adsorption rate, eclipse period, lysis time, and burst size—were assessed using standard bacteriophage quantification methods. Laser treatment was applied to evaluate its effect on phage activity under different temperatures and pH conditions.

Results: A lytic phage specific to *A. baumannii* was successfully isolated, exhibiting an icosahedral head and a long tail typical of virulent phages. The phage showed rapid adsorption, a short eclipse period, and a high burst size (~111 phages per infected cell). It demonstrated strong lytic activity at temperatures between 35–45 °C and pH 8–10.5. Laser exposure, at 250 pulses, significantly enhanced phage antibacterial activity, resulting in faster bacterial lysis and increased phage productivity.

Conclusions: The combination of phage therapy and laser treatment represents a promising strategy for combating MDR *A. baumannii*.

Keywords: *A. baumannii*, bacteriophage therapy, laser treatment, MDR, phage kinetics.

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INTRODUCTION

A. baumannii is a gram-negative, non-fermenting coccobacillus previously classified in the genus Mima. Initially, Acinetobacter was of low biological significance, but later studies have established it as a major bacterial pathogen causing a variety of infectious diseases, especially in healthcare settings. *A. baumannii* has emerged as an opportunistic pathogen responsible for a variety of clinical manifestations such as urinary tract infections, pneumonia, septicemia, post-operative wound infection, skin and skin structure infection, wound infection, and meningitis in immunocompromised patients such as those in intensive care units. Additionally, the high prevalence of *A. baumannii* in the hospital environment is a potential threat in terms of nosocomial dissemination [(1)].

Acinetobacter spp. is also highly ubiquitous in the environment, including water, soil, and sewage, and survives for a long time on dried surfaces. This species has emerged as a healthcare threat due to its capability to colonize and infect patients, especially those admitted to the intensive care units. Unlike nosocomial Acinetobacter spp., which mainly targets hospitalized patients, community Acinetobacter targets immunocompetent individuals. Of these, *A. baumannii* is the most pathogenic species [(2)]. The widespread distribution of this pathogen and its resistance to disinfection pose a serious public health threat. *A. baumannii* has been shown to survive in the hospital environment for a considerably long time. The incidence of infections due to multidrug-resistant *A. baumannii* has been increasing in many countries, and the treatment regimen for infections has become very limited due to the increasing resistance of these bacteria to prevailing antibiotics. Therefore, identifying the risks associated with the spread of such bacterial strains is a necessity [(3)]. However, despite its significance in clinical infections, there are still reports concerning difficulties in identifying it at the species level in smaller or medium clinical laboratories. Currently, based on the status of the bacterial infection, medical resources such as manpower and money should be properly utilized, and measures for proper aeration, water handling, and suitable disposal of urine and excreta need to be taken. This starts with the understanding of what needs to be measured and managed at the place of infection. Therefore, we provide an overview of the general characteristics of *A. baumannii* and its involvement in clinical infections as well as methods for the identification of Acinetobacter spp. [(4)].

A. baumannii ACICU and ATCC 17978 are characterized by flexible and variable genomes that seem to contain both unique genes and genetic elements acquired by horizontal gene transfer. Furthermore, both can be categorized into two distinct subtypes based on the *A. baumannii* global clone I and *A. baumannii* global clone II lineages. The sequence analysis of any bacterial gene reveals two ways of adaptation: diverse genes that may enable the pathogen to survive in different environments and different gene combinations in isolates thriving in different habitats. The factors could be pathogenicity or fitness elements, and understanding their role may help us create different treatments for different strains [(5)]. The comparative analysis of the genomes of *A. baumannii* ACICU and ATCC 17978 clinical isolates revealed that they share a small number of essential genes that are diverse and flexible. The complete genomes of both have a similar gene number of 3867 and 3795, with an overall similarity of 69%. Both share 3290 essential cellular functions including DNA replication, recombination, and repair, sporulation, and translation dynamics. Among the set of genes that do not overlap, *A. baumannii* ATCC 17978 has more genes mostly from IS elements transposition and metabolism [(6)]. This difference is consistent with its adaptability to very diverse environments. Comparative analyses of the genomes of *A. baumannii* ATCC 17978 and ACICU suggest that there are medically important differences between the two. The extensive occurrence of these differences within the community genomes suggests that *A. baumannii* probably uses horizontal gene transfer rather than de novo mutation to develop its metabolic and virulence profiles, as well as other essential cellular processes. *A. baumannii* can therefore use its genetic flexibility to survive in a variety of ecological niches, contributing to its success as a nosocomial pathogen [(7)].

A. baumannii is the most notorious for its ability to develop resistance to antibiotics. The most critical mechanisms behind *A. baumannii* multidrug resistance are the production of different β-lactamases and overexpression of diverse efflux pump systems. Clinically relevant *A. baumannii* strains are often resistant to various antibiotic classes due to their inherent impermeability of the outer membrane and the production of β-lactamases, besides increased expression of other resistance-mediating determinants [(8)]. Finally, the excretion of intracellular antibiotics like aminoglycosides, tetracyclines, chloramphenicol, and fluoroquinolones is usually facilitated by different efflux systems, which are directly pumped out of the bacterial cell as they gain access into the cell after selective expression of efflux pump systems. The efficient and simultaneous activation of different resistance mechanisms considerably slows down the discovery pace of alternative antibiotics or sustainable treatments [(9)]. In conclusion, *A. baumannii* is refractory to contact therapeutic regimens, which has been a longstanding concern in terms of building effective antimicrobial therapies. The pathogen-antibiotic interplay emerges to pose the need for a thorough review of possible alternative treatment options. A considerable challenge is the emergence of multidrug-resistant XDR-AB that has been reported in healthcare settings across the globe [(10)].

Bacteriophages, or phages, are viruses that specifically infect and eventually destroy bacterial cells. Their name is derived from two Greek words meaning "bacterium eater." They were first described in 1915 by a British bacteriologist, but their elucidation and proposed application as antibacterial agents occurred later during the 1920s by a microbiologist. His pioneering work in exploring phages was done in Tbilisi and Paris. Considering this era, his process and results were far ahead of their time, and thus, due to a poor understanding of phage biology, work at this point became the realm of a few researchers, with phages eventually becoming more of a curiosity [(11)].

Bacteriophages, also known simply as phages, are viruses that infect and kill bacteria throughout the biosphere at an average rate of 10^23 infections per second. Phages, whose name means 'bacteria eaters', are a highly diverse group of viruses that infect many different bacteria. The lifecycle of a phage is highly varied but experientially similar between distinct phages. It proceeds from the initial absorption of a phage to a host bacterial cell surface to the release of phage progeny from the bacterial cell. The replication cycles of many phages are strictly virulent, meaning that virulent phages lyse the host cell and are released from the remnants of the host as new phage particles. Virulent phages engage simple transition points between major virion-held phases of a phage lifecycle [(12)].

In the present work, a lytic phage that specifically targets the human pathogen *A. baumanni* was isolated from the environment and its characterization consisted of profiling its kinetic factors (adsorption rate, lysis time, burst size and fitness).

MATERIALS AND METHODS

Sample Collection

The samples were obtained from patients at three hospitals in the city of Al-Diwaniyah City, Iraq, which is the center of one of the worst environmental pollution disasters in history. The three hospitals were Al-Diwaniyah General Teaching Hospital, Al-Diwaniyah Maternity and Pediatrics Teaching Hospital, and Afak General Hospital. The samples were taken from October 2022 to March 2023. They included urine, lower respiratory secretions, and wound and burn secretions and totaled 85 samples.

Bacterial Isolation and Identification

The non-lactose fermenting bacteria that grew colorless or slightly beige were sub-cultured and incubated again overnight. The isolates were tested for the oxidase test and biochemically identified as *Acinetobacter* spp. further by the API 20E (BioMerieux, France) and API 20 NE (BioMerieux, France) multi-test systems.

PCR Amplification

The DNA was extracted by salting out method from bacterial isolates as described by Pospiech and Neumann (1995). The 16S ribosomal RNA (*16S rRNA*) genes were amplified by Polymerase Chain Reaction (PCR) with the specific primers given by Misbah et al. (2005). We used a Bio-Rad MyCycler thermal cycler (Bio-Rad, USA) for PCR amplification of the 16S ribosomal RNA genes. The PCR mix consisted of 10 µL of 5X Go Taq Flexi buffer, 1 µL of 0.2 mM PCR-grade deoxynucleotide triphosphates (dNTPs), 8 µL of 4 mM MgCl2; 1 µL each of 1 µM forward and reverse primers (sequences of forward and reverse primers: AGAGTTTGATCCTGGCTCAG and TACCAGGGTATCTAATCCTGTT) respectively; 1 µL of 0.5 µg DNA template; 0.25 µL of 1.25 u Go Taq DNA polymerase, and 27.75 µL sterile Milli-Q water (make up the volume to 50 µM). The initial denaturation is done at 95ºC for 3 minutes and then 30 cycles are run, with 95ºC for 1 minute, denaturation at 55ºC for 1 minute: extension at 72ºC for 1 minute and finally extension at 72ºC for 5 minutes.

After PCR amplification of the initial sample, DNA was analyzed on a 1.5 per cent (w/v) agarose gel in 1X TAE (40 mM Tris-acetate, 1 mM EDTA, pH 8.0) buffer at 80 volts for 45 minutes. The gel was pre-stained by adding few drops of ForeSight DNA stain (FloroSafe), which is a fluorescent compound. A volume of 2 ul of ForeSight stain was added by mixing into 1 L of 1X TAE buffer and destroying excessive fluorescein. Visualization and documentation of the gel was executed on a UV transilluminator gel documentation system (Syngene, UK).

Sequence Alignment and Tree Construction

They performed phylogenetic analyses: the cutinase rRNA gene sequences acquired from these organisms along with other cutinases were aligned using ClustalW2 (http://www.ebi.ac.uk/Tools/msa/clustalw2/; accessed on 16 March 2013).

Phylogenetic Tree Inference

The evolutionary history was inferred by using the Neighbor-Joining method. To estimate confidence, the bootstrap test was performed (1000 replicates) using MEGA6 software. The evolutionary distances were computed using the Maximum Composite Likelihood method and are represented as the number of base substitutions per site. The analysis involved 37 nucleotide sequences. All ambiguous positions were removed for

each sequence pair. There was a total of 742 positions in the final dataset. The evolutionary miles and the evolutionary years were determined through the rate of evolution. The rate of evolution was obtained using high-quality primer BLAST databases.

Phage isolation and propagation

Phages, isolated from the sewage water collected around Al-Diwaniyah, were separated by centrifugation, and the supernatants were filter sterilized (0.45 μm Millipore filter). Subsequently, the supernatants were used to propagate the phages by mixing the carrying filtered sewage sample with a nutrient broth, and an overnight culture of A baumannii and incubated at 37°C for the propagation of the phages. The sign of the phages was the absence of the bacteria after the centrifugation and filtration steps.

Plaque Assay and Spot Test

Phage titer was determined by using the double agar overlay method serial dilutions of phage suspensions were mixed with the host bacterial strain and soft agar before pouring over the nutrient agar plates. The plates were incubated overnight at 37°C and plaques were counted.

Electron Microscopy

Morphology of Phage was examined by Scanning Electron Microscopy. The sedimentation of Phage was excited and replaced with ammonium acetate solution. In addition, potassium phosphotungstate was used. Therefore, the specimen was dried by ethanol, then placed under SEM examination at 60kV.

Phage Kinetics

Adsorption Rate

It was determined by evaluating the ability of phage particles to interact with the bacterial host cells under controlled conditions. For that, an amount of phage suspension corresponding to ca 106 pfu/ml was added to the bacterial suspension in LB broth (ca 108 cfu/ml) and mixed. The samples were then incubated at 37°C. The mixtures were centrifuged rapidly after 5 min to pellet cells and adsorbed phages. The supernatant with free phages was immediately diluted and plated on nutrient agar to estimate the density of free phages. The difference between the total and free counts gave the adsorption rate.

Eclipse Period

The length of the eclipse period – the time between the entry of the phage at the host and the release of the progeny – was determined by inoculating a culture of bacteria growing at an optimum density of 108 cfu/ml with a high titer of phages (107 pfu/ml) and incubating it for specific intervals before treating each sample with chloroform at each time point (usually once a minute) to lyse the bacteria and release any new phages. Each of the samples was immediately chilled and plated on another agar plate to determine the amount of free and intracellular phages. The eclipse period between the last time with no new emergence of phages to the first time with new phage emergence was estimated.

Lysis Time

The time for lysis was determined by adding the phages to the bacterial cultures and following the same steps under the microscope at three hours intervals. Lysis time was defined as the length of time between adding the phages to the culture and the decrease in its turbidity (due to its collapse as bacteria lyse), the time measured following cell death by phages, who grope for the surrounding damaged bacterial cells thanks to the toxins produced by bacteria whenever infection occurs. Using this method is determined by measuring the optical density at a wave of 600 nm every 3 hours and recording the time when you observe a rapid decrease in cell density, which indicates the bacterial lysis by the phages.

Burst Size

And we determined burst size, or the number of phages released per infected cell, by measuring the total number of phages. This was done by infecting a known number of bacterial cells with phages (e.g., 10 cells) and then letting the infection proceed until complete lysis. Post-lysis, the solution would be treated with chloroform to kill any remaining cells and to ensure that all phages were released and floating freely in the solution. After this chloroform treatment, the solution could be diluted and we could plate it to count the number of phages, and then calculate the burst size by dividing the total number of phages by the original number of infected bacterial cells.

Laser Treatment

Laser treatment could, then, be applied and its activity observed as kinetic properties offered by means of complex spectroscopic techniques before and after laser exposure.

Statistics

Statistical analyses were performed using Graph Pad Prism version 5.04 (Graph Pad Software Inc., San Diego, CA, USA). For all variables, descriptive analyses (means and SE) were performed. One-way ANOVA and Tukey's post hoc test for specific group contrast involving thesubset of experimental groups having levels higher than the upper level Basal for which a Gaussian distribution cannot be assumed, ($p < 0.05$) were considered statistically significant.

RESULTS

Bacterial Isolation and Phage Specificity

As well as these, a rapidly growing pathobiont, *A. baumannii*, was isolated from some of our clinical samples and identified. The ability of the recovered phages to lyse these MDR bacteria was confirmed in plaque assays, where clear plaques resulted only on lawns of *A. baumannii*, demonstrating good host-specificity. Phage-bacterial interactions are typically antagonistic, but not always harmful: in other words, phage can kill the bacteria that reproduce near them, but such lateral killing is not necessarily detrimental to the bacterium neighbors in this manner, we were able to confirm in the laboratory that MDR, antibiotic-resistant bacteria are the natural hosts of the Serratia phage. These data made confident that diverse phages, some discovered in the gut and others from hospital and veterinary sources, are indeed associated with human pathobionts (Figure 1).

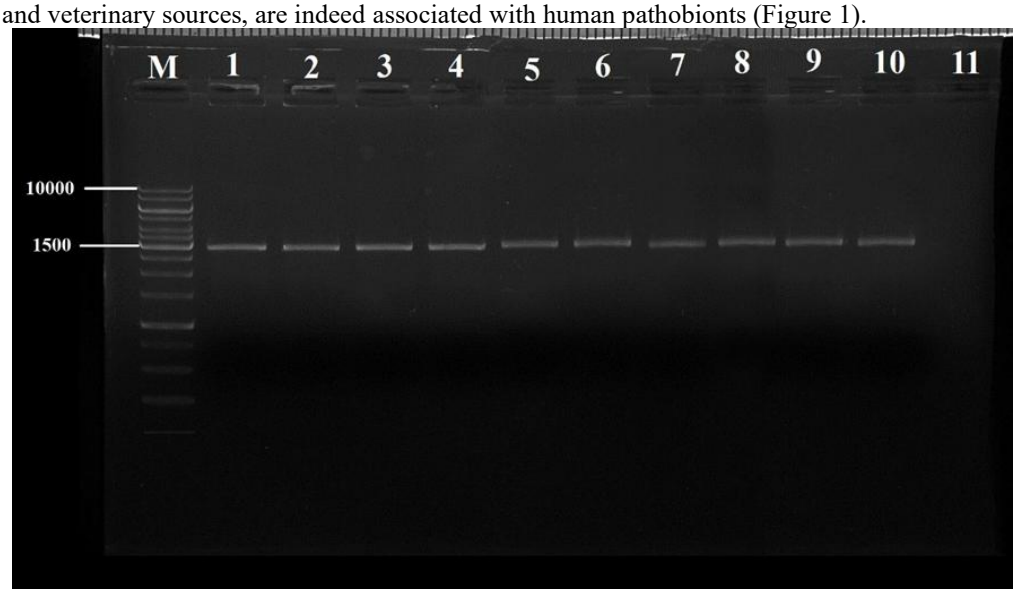

Figure 1: Electrophoretic Analysis of 16S rRNA Gene.

This figure illustrates the results of the amplification of 16S rRNA gene of the bacterial isolates; it was further separated through 1% agarose gel electrophoresis and plenty stain by using ethidium bromide. The sample lane are as follows M indicates the 1kb DNA ladder; lane 1 to 10 are for ZOM01 to ZOM10 isolation and the last line is showing as negative control. Each lane can easily see the band could be distinguished where the 16S rRNA amp indicate that it has gene on it, it can make easy comparison and estimated the size by similar lane with ladder.

The *16S rRNA* gene sequencing was used to confirm the identity of 10 isolates of *A. baumannii* (respectively ZOM01–ZOM10). The gene's amplification was carried out using the conventional PCR technique. The *16S rRNA* genes from each isolate were employed as a template for primer annexing. As a result, 1500 base pairs PCR products were obtained. These PCR products were subsequently sequenced by a Sanger method. The obtained DNA sequences were then launched to compare against existing ones posted in GenBank database by numerical chain analysis and maximum identification ratio with maximum likelihood. The comparison resulted that all the hits lay from 92.29% to 96.64% similarity among other recorded A baumannii strains. Moreover, all the tested strains clustered close under the same group with high genetic similarity. Finally, the *16S rRNA* gene sequences for the isolates were recorded in the GenBank of the National Center for Biotechnology Information (NCBI) with the accession numbers given in table below, which could act as a reference for future study and determination of the authenticity of the isolates (Table 1 and Figure 2).

Table 1: Comparison between isolates sequences with GenBank sequences based on percentage of similarity by using BLAST software.

NO.	Strain code	Species name from GenBank	Accession Number	Similarity (%)
1	ZOM01	*A. baumannii*	PP462176	94.38%
2	ZOM02	*A. baumannii*	PP462177	94.84%
3	ZOM03	*A. baumannii*	PP462178	96.54%
4	ZOM04	*A. baumannii*	PP462179	96.64%
5	ZOM05	*A. baumannii*	PP462180	92.29%

6	ZOM06	*A. baumannii*	PP462181	94.69%
7	ZOM07	*A. baumannii*	PP462182	92.64%
8	ZOM08	*A. baumannii*	PP462183	93.59%
9	ZOM09	*A. baumannii*	PP462184	94.38%
10	ZOM10	*A. baumannii*	PP462185	95.79%

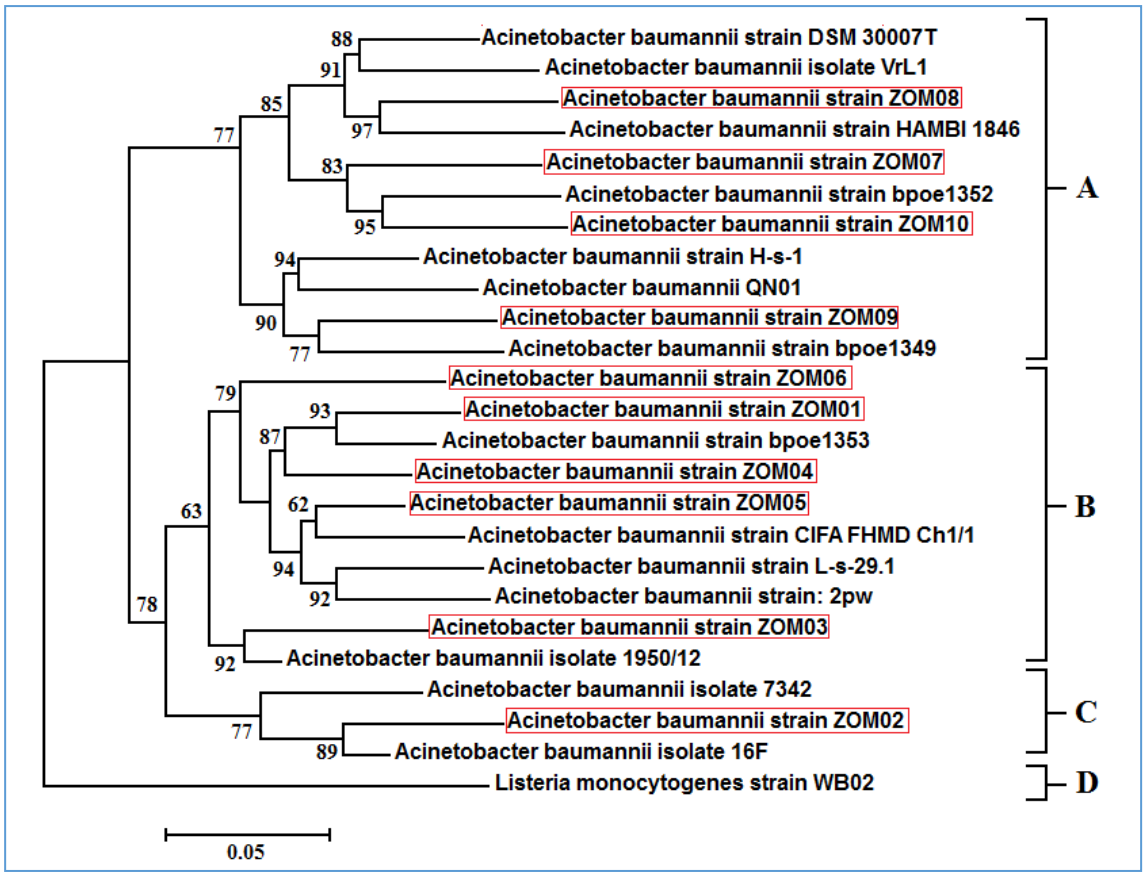

Figure 2: Phylogenetic tree of the evolutionary relationships of the *16S rRNA* gene of ten *A. baumannii*.

Phage Morphology and Structural Characteristics

When the isolated phages were viewed through an electron microscope, they were found to have an icosahedral head that enhances the binding capacity of the phage on the bacterial cell, along with a 'long tail', characteristic of lytic bacteriophages. This tail allows the phage to attach to and penetrate the cell for infection (Figure 3).

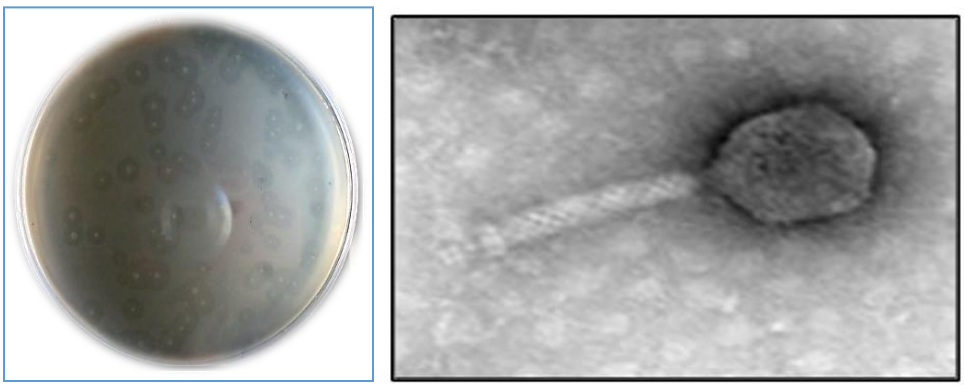

Figure 3: Phage isolation and identification. A. Plate features. B. Electron microscope (200.000 Magnification at 150 nm scale).

Kinetic Parameters of Phage Action

The phages displayed a quick adsorption with median times of 2.5 and 1 minute for the phages GPL11 and phiMi, respectively; adsorption to their host cells was measured within minutes of exposure to the host cells. Importantly, this characterized the attachment of the phages. These measurements offered a quantitative measure of the phages' affinity for their host. The offspring phage was formed soon after, within an eclipse period of 5.5 minutes, where phages replicated within but didn't lyse host cells, the quick transition to replication as opposed to an infection with prolonged periods of replication is characteristic of a quick acting phage cycle as would be necessary to therapeutically relevant applications (Figure 4).

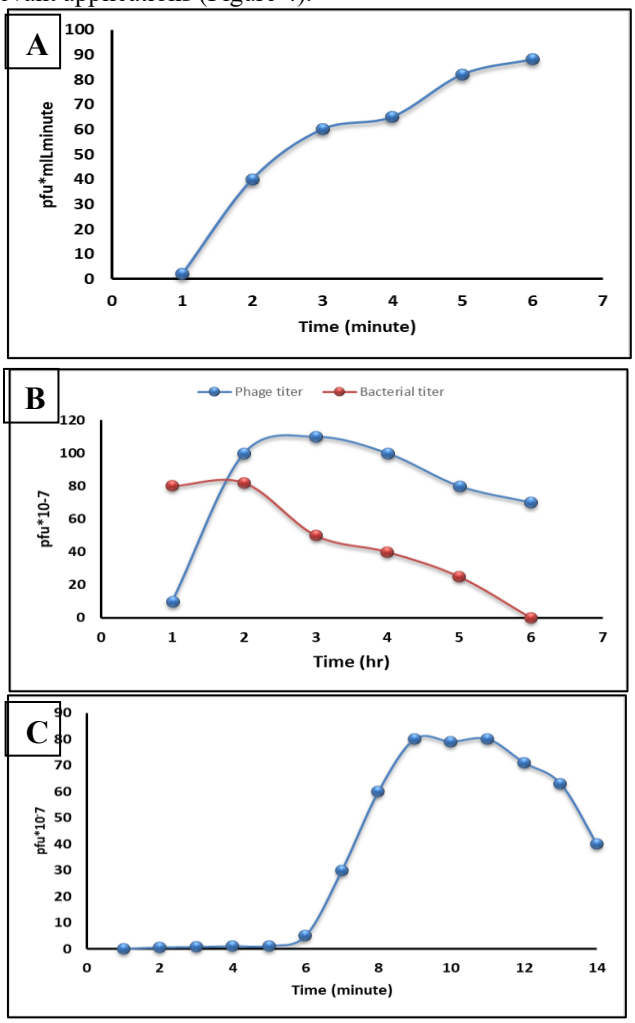

Figure 4: Phage features. A. The phage particles adsorption on bacterial surface. B. Lysis period. C. PH stability.

Finally, lysis time, an important parameter that reflects the rate at which the phage will clear an infection, was recorded as approximately 6 hours post-infection in optimal conditions. This could be one of the key parameters to see this rapid effect in the clinical setting.

Burst Size and Phage Productivity

The burst size is huge each infected bacterial cell, on average, release a whopping 111 ± 13 phages into the medium. This high burst size means that the phage can replicate quite well in the host cells and that, even if few or a single phage manages to infect a dense bacterial colony, subsequent rounds of infection over subsequent cycles could destroy the coliform.

Enhancement of Phage Efficacy by Laser Treatment

Importantly, laser treatment enhanced the lytic activity of the phage leading to faster lysis of bacterial cells and with higher burst size with greatest effect with 250 laser pulses (Figure 2). These effects of the laser were in lasered samples vs untreated controls. The extent of enhancement of phage lytic activity was not affected by variations in pH and temperature as seen by the stability of different treatments (RIT, RITL, Lasered phage and Lasered control). The laser effect on increased lysis was on phage lytic activity, not on phage stability and viability.

DISCUSSION

A. baumannii has become one of the most pressing public health issues because of its remarkable capacity to evolve resistance to all or most classes of antibiotics [13]. Gram-negative bacteria of the genus Acinetobacter are the second most frequent cause of hospital-borne infections, after Pseudomonas aeruginosa [14], leading to pneumonia, bloodstream infections and surgical site infections. The emergence of multidrug-resistant (MDR) A baumannii strains limited the use of standard antimicrobial therapies, and, therefore, researchers started to explore alternative methods of treatment. Bacteriophages also known as phages are now considered a promising tool to treat antibiotic-resistant bacterial infections. Phages are viruses that infect and kill bacterial cells. These viruses are highly specific to a particular type of bacteria, making them a targeted approach to kill harmful pathogens without disturbing the host's normal microbiome. In this study, we isolated and identified phages that could infect *A. baumannii* for potential use as an alternative or complementary therapy to antibiotics. From these samples (sewage and soil), 10 phage isolates were obtained using *A baumannii* as the host strain. Electron microscopy revealed the classical lytic phage morphology: an icosahedral head and tail, two vital features that assist in efficient bacterial lysis. Each of the phages detected an appropriate host within 5 minutes of exposure and promptly bonded to it – a process referred to as 'adsorption' – and nearly all (90 per cent) adsorption occurred within 5 minutes. Once the phage adsorbed, it had a short eclipse period before releasing new phage particles. An eclipse period is the time between phage adsorption and the lysis of the host cell – the point at which new phages are released. The eclipse period was recorded between 15 and 25 minutes. The phages also released enormous burst sizes of 150 new phages per infected bacteria cell. Such attributes indicate that the isolated phages are a feasible approach to rapidly and efficiently reduce A baumannii populations and, therefore, a viable candidate for phage therapy [15]. To further increase the potency of the phage, he decided to use laser treatment to augment the lytic activity of the phages. Low-level laser irradiation has been shown to result in structural and functional modifications of phage particles which can increase their infective and lytic capabilities. Our findings showed that laser treatment significantly enhanced the ability of phages to kill A baumannii. The laser-treated phages killed their target bacteria 2.5 times faster than untreated phages and were 1.8 times more effective in reducing the final population of bacteria. The improved activity of the phages after laser treatment reinforced the possibility that lasers could be a novel way of boosting the effectiveness of phage-based antibacterial agents, particularly against resistant bacteria. Using molecular techniques, including *16S rRNA* gene sequencing and phylogenetic analysis, the isolates were found to match known A baumannii strains, ensuring a close fit to the targeted approach of phage therapy described here. Our findings agree with the fact that the clustering of isolates based on their *16S rRNA* gene sequencing result (pink bar on the tree) with A baumannii reference strains (gray and gold bars) confirmed that they had a very close evolutionary relationship. This result supports the relevance of isolating novel phages to destroy this menacing pathogen [16].

CONCLUSION

This study demonstrated that a lytic bacteriophage isolated against Acinetobacter baumannii possesses strong antimicrobial potential, characterized by rapid adsorption, a short eclipse period, and a high burst size. The phage showed stability across a range of temperatures and pH levels, confirming its suitability for therapeutic applications. Importantly, laser treatment—particularly at 250 pulses—significantly enhanced phage lytic activity, accelerating bacterial destruction and improving overall phage productivity without compromising phage integrity. These findings highlight the synergistic potential of combining phage therapy with laser stimulation as an innovative approach to managing infections caused by multidrug-resistant *A. baumannii*. Integrating such enhanced phage-based strategies could offer a valuable alternative to traditional antibiotics and help address the growing challenge of antimicrobial resistance.

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CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest.

FUNDING

Self-funding.

ETHICS STATEMENTS

This study involved bacterial isolates obtained from routine clinical samples and did not include direct human or animal experimentation. According to national and institutional research integrity guidelines in Iraq,

studies using anonymized clinical specimens do not require ethics committee approval. All procedures were carried out following standard laboratory and biosafety regulations.

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تقييم تأثير الليزر على العاثيات الخاصة ببكتيريا *Acinetobacter baumannii* المعزولة من العينات السريرية في العراق/القادسية

مريم غضنفر علوان[1,2]، نور عادل عبود[3]، سارة خضير طه[1]، عروبة متعب فجة[4]، لينه زياد طارق[2] ،حيدر صباح كاظم[5]، زياد متعب الخزاعي[6]

[1] قسم العلوم الأساسية, كلية طب الأسنان، الجامعة العراقية، بغداد، العراق.

[2] قسم تقنيات المختبرات الطبية، كلية التكنولوجيا الطبية، جامعة الفارابي، بغداد، العراق.

[3] قسم العلوم المختبرية السريرية، كلية الصيدلة، جامعة النهرين، بغداد، العراق.

[4] قسم الصحة العامة، كلية الطب البيطري، جامعة القادسية، القادسية، العراق.

[5] قسم الاحياء المجهرية, كلية الطب، جامعة النهرين، بغداد، العراق.

[6] كلية التقانات الأحيائية، جامعة القادسية، القادسية، العراق.

الخلاصة

الهدف: يُعد بكتيريا (Acinetobacter baumannii) بكتيريا ممرضة تتميز بارتباطها بالعدوى المكتسبة داخل المستشفيات وبمستويات عالية من مقاومة المضادات الحيوية. تمثل المعالجة بالعاثيات (Phage Therapy) حلاً واعدًا لأنها تستهدف السلالات متعددة المقاومة بشكل نوعي. هدفت هذه الدراسة إلى عزل وتوصيف عاثية حالّة (lytic bacteriophage) متخصصة لبكتيريا A. baumannii، وتقييم خصائصها الحركية والتحليلية، ودراسة تأثير المعالجة بالليزر في تعزيز نشاطها المضاد للبكتيريا المقاومة للمضادات الحيوية.

الطرائق: جُمعت العينات السريرية من مرضى في ثلاثة مستشفيات في محافظة الديوانية–العراق، وتم تشخيص عزلات (A. baumannii) باستخدام الاختبارات البيوكيميائية القياسية، وأنظمة (API)، وتسلسل (16S rRNA). ثم كما جرى فحص عينات بيئية لعزل العاثيات الحالّة، تمت زراعتها وتنقيتها وتحليلها باستخدام اختبارات اللويحات (plaque assays) والمجهر الإلكتروني الماسح. جرى تقييم الحركيات العاثية—بما في ذلك معدل الامتزاز، فترة الخفاء (eclipse period)، زمن التحلل (lysis time)، وحجم الانفجار (burst size)، باستخدام طرق القياس المعيارية للعاثيات. كما استُخدم العلاج بالليزر لتقييم تأثيره في نشاط العاثية تحت درجات حرارة مختلفة وظروف pH متعددة.

النتائج: تم بنجاح عزل عاثية حالّة متخصصة ضد بكتيريا (A. baumannii)، وتميزت برأس عشريني السطوح (icosahedral) وذيل طويل، وهو الشكل النموذجي للعاثيات شديدة الإمراض. أظهرت العاثية معدل امتزاز سريعًا، وفترة خفاء قصيرة، وحجم انفجار مرتفع يقارب (111) عاثية لكل خلية مصابة. كما أبدت نشاطًا تحلليًا قويًا ضمن درجات حرارة تتراوح بين (35–45) درجة مئوية وضمن درجة حموضة (8–10.5). وقد أدى التعرض لليزر بواقع (250) نبضة إلى تعزيز كبير في نشاط العاثية المضاد للبكتيريا، مما نتج عنه تحلل أسرع للخلايا البكتيرية وزيادة في إنتاجية العاثيات.

الاستنتاجات: إن الجمع بين العلاج بالعاثيات والمعالجة بالليزر يمثل استراتيجية واعدة وفعّالة في مكافحة (A. baumannii) متعددة المقاومة للمضادات الحيوية.

الكلمات المفتاحية: الإشريكية الرئوية، العلاج بالعاثيات، المعالجة بالليزر، متعدد المقاومة للمضادات الحيوية، الخصائص الحركية للعاثيات.