Edubiotik : Jurnal Pendidikan, Biologi dan Terapan
ISSN 2528-679X (print), ISSN 2597-9833 (online)
Vol. 10, No. 02, Month 2025, pp. 540 – 549

Available online at:
https://ejurnal.uibu.ac.id/index.php/edubiotik

Research Article

OPEN ACCESS

Phage cocktails as a new antibiotic for combating bacteria consortium in foodborne disease

Salsabila Jahroh Marzuqi [1,a], Adelia Meita Putri [1,b], Martinus Effand Pratama Purwanto [2,c], Ahmad Hibban Murtadho [2,d], Amanda Claudia Ayuning Grahita [1,e], Erlia Narulita [1,f,*]

[1] Study Program of Biology Education, University of Jember, Jember, Indonesia
[2] Study Program of Medical Education, University of Jember, Jember, Indonesia
Email: salsabilajahroh@gmail.com [1,a], adeliameitaputri@gmail.com [1,b], martinuseffand1st@gmail.com [2,c], ahmad.hibban.murtadho@gmail.com [2,d], amandaclaudia376@gmail.com [1,e], erlia.fkip@unej.ac.id [1,f,*]
* Corresponding author

Article Information

Article History:
Submitted: 2025-10-11
Revised: 2026-01-10
Accepted: 2026-01-11
Published: 2026-01-28

Keywords:
Foodborne pathogens;
phage cocktails;
resistance;
spot assay

ABSTRACT

Foodborne diseases pose a critical global health threat, exacerbated by the alarming rise of multidrug-resistant (MDR) bacterial strains like Staphylococcus aureus, Escherichia coli, and Salmonella typhi. Conventional antibiotics are increasingly ineffective, necessitating the development of alternative therapeutic and biocontrol strategies. This study aims to evaluate the efficacy and stability of a bacteriophage cocktail as a potential non-antibiotic alternative for controlling a consortium of foodborne pathogenic bacteria. The research employed an experimental design using revived cultures of the three bacterial species and three phage isolates (ϕSZUT-01, ϕSZIP-01, ϕSZIP-02) as research samples. Data collected included bacterial growth kinetics, observation of lysis zones, and phage stability at various pH levels and storage temperatures. Data analysis was conducted descriptively, followed by one-way ANOVA at a 95% confidence level to determine differences among treatments. Three two-phage cocktails were formulated and tested, with all treatments consistently demonstrating strong lytic activity, evidenced by large and clear plaques. Lysis kinetics, monitored through OD600 measurements, confirmed rapid bacterial elimination beginning approximately 180 minutes post-infection. Notably, the bacterial consortium exhibited resistance to the positive control (Chloramphenicol), reinforcing the need for alternative interventions. Additionally, the phage cocktail demonstrated excellent stability, maintaining infectious titers across a broad pH range and during storage at both refrigerated (4°C) and room temperatures (21°C). This high stability supports its potential applicability in food safety systems and resilience in gastrointestinal environments. Overall, the bacteriophage cocktail demonstrated effective antibacterial activity against a consortium of foodborne pathogenic bacteria, as evidenced by the formation of clear lysis zones and exhibited high stability, supporting its potential application as a non-antibiotic alternative for controlling foodborne diseases.

Publisher

Biology Education Department
Universitas Insan Budi Utomo,
Malang, Indonesia

How to Cite

Marzuqi, S. J., Putri, A. M., Purwanto, M. E. P., Murtadho, A. H., Grahita, A. . C. A., & Narulita, E. (2026). Phage cocktails as a new antibiotic for combating bacteria consortium in foodborne disease. *Edubiotik : Jurnal Pendidikan, Biologi Dan Terapan, 10*(02), 540–549. https://doi.org/10.33503/ebio.v10i02.2394

INTRODUCTION

Foodborne diseases (FBDs) represent a continuing global public health threat. According to the World Health Organization (WHO), an estimated 600 million individuals suffer from FBDs annually, with 420,000 deaths and 125,000 fatalities occurring among children under the age of five (World Health Organization, 2020). This means that approximately one in ten people worldwide is affected by unsafe food each year, with the highest burden observed in the African and South-East Asian regions. In Indonesia, food poisoning remains a persistent concern, with 76 extraordinary foodborne outbreaks (KLB) recorded in 2021, affecting more than 3,000 people (Kementerian Kesehatan Republik Indonesia, 2021).

A wide range of bacteria are commonly implicated in FBDs, including *Salmonella, Campylobacter, Shigella, E. coli, Vibrio, Yersinia, Staphylococcus*, and *Listeria* (Muna & Khariri, 2020). However, a significant challenge emerges due to escalating antibiotic resistance, with multiple pathogens showing multi-drug resistant (MDR) profiles. For instance, *Salmonella enterica serovar Typhi, E. coli,* and *Staphylococcus aureus* have shown resistance to amikacin and ceftriaxone, *Shigella* spp. exhibit resistance to β-lactam antibiotics, and Acinetobacter baumannii displays resistance to piperacillin and imipenem (Kurnianto & Syahbanu, 2023). The rapid spread of antimicrobial resistance (AMR) is strongly linked to inappropriate and excessive antibiotic use in the health sector and agricultural industries (Antimicrobial Resistance Collaborators, 2022).

Among these pathogens, *Escherichia coli* serves as a key indicator organism of fecal contamination in food, water, and milk products (Istiani & Agustiani, 2021). Shiga toxin-producing *E. coli* (STEC) can cause life-threatening illnesses such as hemorrhagic colitis and hemolytic uremic syndrome (Scallan et al., 2020). Similarly, *Salmonella* is frequently associated with powdered milk, peanut butter, chocolate, infant formula, and cereal-based foods (Parra-Flores et al., 2024), while *Staphylococcus aureus*, commonly found in poultry products including eggs, contributes to foodborne toxic shock syndrome (Thaha et al., 2024). These pathogens contribute not only to gastrointestinal diseases but also to long-term nutritional consequences such as malnutrition (Scallan et al., 2020; Une et al., 2022).

Bacteriophages (phages) have emerged as a promising biocontrol strategy against foodborne bacterial pathogens due to their bacterial specificity and minimal off-target effects on human or environmental microbiota. Experimental studies demonstrate their safety and therapeutic potential. Bao et al. (2019) successfully applied the Salmonella phage vB_SenM-PA13076 in a murine model, while Iqbal et al. (2020) isolated three active phages capable of inhibiting *Salmonella* spp., *S. aureus*, and *E. coli*. Moreover, certain Salmonella-infecting phages have shown cross-infectivity against *Shigella* and *E. coli*, providing both narrow and broad host range capabilities (Narulita et al., 2020).

Given the wide bacterial diversity involved in foodborne contamination, the application of phage cocktails offers broader and more effective control than single-phage preparations by expanding host range and reducing the likelihood of bacterial resistance development (Abedon et al., 2021; Chen et al., 2024; Chen et al., 2022). However, most existing studies have predominantly focused on single-pathogen models, clinical isolates, or mechanistic analyses such as biofilm disruption, with limited relevance to real food systems and food-derived bacterial populations (Bao et al., 2019; Iqbal et al., 2020; Vashisth et al., 2022). In particular, investigations addressing phage cocktail performance against multiple dominant foodborne pathogens simultaneously remain scarce, despite the fact that food contamination in real settings commonly involves mixed bacterial populations rather than a single species. This limitation highlights a significant research gap in the development of phage cocktail formulations capable of effectively controlling major foodborne bacteria within practical food safety contexts.

Unlike most previous studies that primarily investigated bacteriophage efficacy against single bacterial species or individual isolates, the present study differs in its experimental scope and design. Earlier research commonly evaluated phage activity under simplified laboratory conditions, focusing on isolated host–phage interactions, biofilm disruption, or therapeutic efficacy without incorporating mixed bacterial populations or food-relevant environmental parameters. In contrast, this study evaluates phage cocktail performance against a mixed consortium of dominant foodborne pathogens while simultaneously assessing antibacterial efficacy, comparison with conventional antibiotics, and physicochemical stability under pH and temperature conditions relevant to food safety applications. This integrated approach provides a more realistic representation of food contamination scenarios and constitutes a methodological novelty compared to previous single-pathogen or single- variable studies.

The present study was therefore designed to address this gap by formulating and evaluating a bacteriophage cocktail targeting *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella enterica*, three pathogens to represent distinct yet complementary contamination pathways commonly encountered in food systems. While previous studies have largely examined these pathogens individually, their combined evaluation in this study reflects real-world foodborne contamination involving fecal contamination (*Escherichia coli*), *Salmonella enterica* remains a leading cause of foodborne outbreaks, and *Staphylococcus aureus* is strongly associated with toxin-mediated food poisoning and post-processing contamination. By targeting this combination of pathogens, the study provides a more realistic representation of foodborne microbial consortia than previous single-pathogen approaches.

Accordingly, this research aims to evaluate the antibacterial efficacy of bacteriophage cocktails against a mixed bacterial consortium, compare the inhibitory performance of phage cocktails with conventional antibiotic treatment, and to assess the stability of the phage cocktails under various pH conditions and storage temperatures relevant to food safety applications. Through this integrated approach, the study seeks to generate robust experimental evidence supporting the use of phage cocktails as a stable, effective, and practical biocontrol strategy for mitigating multidrug-resistant foodborne bacteria and enhancing food safety.

RESEARCH METHODS

This study used a laboratory experimental approach designed to test the lytic activity and stability of phage cocktails against a consortium of pathogenic bacteria. The experimental design was controlled by applying several phage treatment groups along with positive and negative control groups to enable reliable comparisons of bacterial responses. All experimental procedures were conducted under aseptic conditions to ensure the validity of the results. Observations were made periodically at fixed intervals to ensure that the dynamics of phage-bacteria interactions could be recorded in detail. This design provided quantitative data on bacterial growth inhibition and lytic activity, as well as qualitative information on phage stability under different environmental conditions.

The study population consisted of three clinically relevant pathogenic bacteria, namely *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella typhi*, obtained from the Molecular Medicine Laboratory, University of Jember. Three bacteriophage isolates (ϕSZUT-01, ϕSZIP-01, and ϕSZIP-02) were used and combined into several phage cocktail treatments. LB broth and LB agar were employed as growth media, while top agar containing 0.45% agar was used to support plaque formation. All materials were prepared following laboratory sterility standards to prevent contamination.

The independent variables included the type and combination of bacteriophages in the phage cocktail, storage temperature (4±1°C and 21±1°C), pH conditions (3, 5, 9, and 11), and treatment type (phage cocktail, chloramphenicol as a positive control, and SM buffer as a negative control). The dependent variables comprised bacterial growth inhibition indicated by changes in optical density at 600 nm (OD600), plaque or lysis zone formation characteristics, and the ability of phage cocktail to maintain infectivity under different environmental conditions. Control variables included bacterial species, initial bacterial density (1×10^6 CFU/mL), phage concentration (1×10^6 PFU/mL), growth media composition (LB broth, LB agar, and top agar with 0.45% agar), incubation temperature (37°C) and duration, sample volumes, experimental procedures, and laboratory sterility conditions to ensure data consistency.

This study employed a controlled laboratory experimental design adapted from established bacteriophage propagation and lytic activity assays, as described by Narulita et al. (2020) and Vashisth et al. (2022), with minor modifications to suit the research objectives. The research began with the revitalization of bacterial culture using LB broth as a growth medium, followed by incubation at 37°C until reaching the log phase in approximately four hours. The bacterial suspension was then used for phage propagation using the double-layer agar technique. At this stage, instruments such as sterile micropipettes, microtubes, vortex mixers, petri dishes, and refrigerated centrifuges were used to mix the bacterial suspension with top agar, phage, and SM buffer before pouring it onto the surface of LB agar. After 24 hours of incubation, the formed plaques were harvested using SM buffer, then the suspension was centrifuged at 12,000 rpm for 10 minutes, and the clear supernatant was filtered with a 0.20 µm membrane to obtain pure phage lysate (Narulita et al., 2020). The effectiveness testing stage was carried out by mixing 100 µL of a bacterial culture with a density of 1×10^6 CFU/mL with warm top agar, then adding 100 µL of a phage cocktail with a concentration of 1×10^6 PFU/mL and incubating it in a shaker incubator at 37°C. Lytic activity was monitored using a spectrophotometer at OD600 every 15 minutes for 10 hours (Vashisth et al., 2022). At this stage, five treatment groups with four replicates per treatment were applied, consisting of three bacteriophage cocktail combinations, a positive control (chloramphenicol), and a negative control (SM buffer), as summarized in Table 1. The experiment was conducted under controlled laboratory conditions to minimize variability; therefore, four replicates per treatment were considered adequate for statistical analysis. The phage stability test was continued by storing the lysate at 4±1°C and 21±1°C and adjusting the pH to 7, 3, and 5 for acid treatment, and pH 9 and 11 for alkaline treatment. Each pH-adjusted sample will be incubated for 60 minutes, then plated to observe the plaque formation response.

Table 1. Experimental Treatment Design

Group	Treatment Category	Replicates (N)			
		N1	N2	N3	N4
T1	Phage cocktail combination of ϕSZUT-01 and ϕSZIP-01	T1N1	T1N2	T1N3	T1N4
T2	Phage cocktail combination of ϕSZUT-01 and ϕSZIP-02	T2N1	T2N2	T2N3	T1N4
T3	Phage cocktail combination of ϕSZIP-01 and ϕSZIP-02	T3N1	T3N2	T3N3	T1N4
T4	Positive control (Chloramphenicol)	T4N1	T4N2	T4N3	T1N4
T5	Negative control (SM buffer)	T5N1	T5N2	T5N3	T1N4

Research data was obtained through measurements of bacterial suspension turbidity and observation of the ability of phages to maintain lytic activity after temperature and pH treatment based on the formation of lysis zones in the spot assay test. A spectrophotometer was used as the main instrument in determining the OD600 value, which reflects the level of bacterial growth throughout its interaction with the phage. Lytic activity was evaluated by visual observation of clear lysis zones formed in the spot assay

after incubation to assess the consistency of bacteriophage activity in each treatment. In addition, an inhibition zone observation sheet was used to record plaque diameter (mm). The ability of the phages to maintain infectivity after temperature and pH treatments was assessed qualitatively based on the presence or absence of lysis zones.

All research data were analyzed descriptively to describe changes in turbidity, patterns of lysis zone formation, and phage responses to different temperature and pH conditions. Each experimental unit consisted of one petri dish containing two technical spots, and the mean value of the two spots was used for statistical analysis. The mean lysis zone diameter was analyzed using one-way ANOVA to determine significant differences among treatments at a 95% confidence level ($p < 0.05$). Phage effectiveness was then interpreted based on the reduction in OD600 values and the formation of clear lysis zones observed in the spot assay.

FINDING AND DISCUSSION

The results of the study were first obtained from the spot assay, and these findings are presented in Figure 1. Figure 1 explains that 1= P1 (ϕSZUT-01+ϕSZIP-01), 2=P2 (ϕSZUT-01+ϕSZIP-02), 3=P3 (ϕSZIP-01+ϕSZIP-02), 4=P4 (Chloramphenicol), 5=P5 (SM Buffer). Furthermore, Bacteria consortiums contain *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella typhi*. The plaques produced by the three phage cocktails (T1, T2, and T3) were clear and well-defined, indicating strong lytic activity against the bacterial consortium. The clarity of the plaques demonstrates effective adsorption and replication, which are characteristics expected from highly virulent lytic phages. These data confirm that all three cocktails successfully lysed *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella typhi*, showing broader host activity compared to the antibiotic control. Similar findings have been reported by Glonti et al. (2022), who observed that phages with high burst sizes typically form large and clear plaques. The weak inhibitory zone observed in the chloramphenicol control aligns with published data showing high MDR rates among Gram-negative foodborne pathogens, emphasizing the limitations of antibiotic therapy and supporting the urgency of alternative biocontrol strategies.

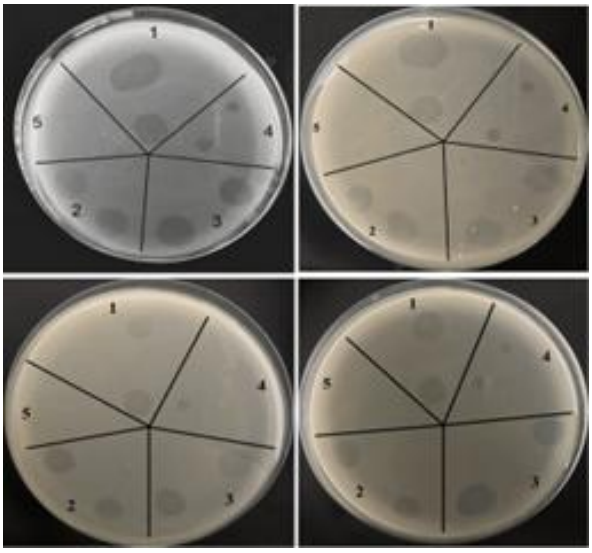

Figure 1. Bacteria Consortiums Lysis by Using the Spot Test

Further findings are presented in Figure 2, which shows the lysis kinetics based on OD600 measurements over ten hours. All phage cocktails produced a sharp decline in OD600 starting at

approximately the third hour, indicating the transition from the latent phase to massive bacterial lysis. This pattern shows that the phages replicated efficiently and continued suppressing bacterial growth throughout the observation period. Such rapid lytic kinetics are essential for food safety applications that require immediate bacterial inactivation to prevent toxin accumulation and the emergence of resistant subpopulations. These results are consistent with Gliźniewicz et al. (2024), who demonstrated that phage replication enables sustained antibacterial effects compared with static antibiotic action. The consistent OD600 reduction across treatments also aligns with Igler & Brockhurst (2023), who highlight the advantage of phage propagation in maintaining long-term lytic pressure on bacterial hosts. These findings support the concept proposed by Haines et al. (2021) that the effectiveness of phage cocktails is not solely determined by the number of phages but by the biological compatibility between phages in infecting the same host. Thus, the effectiveness of the cocktail in this study likely reflects synergistic interactions that overcome the limitations of single phages and antagonistic combinations.

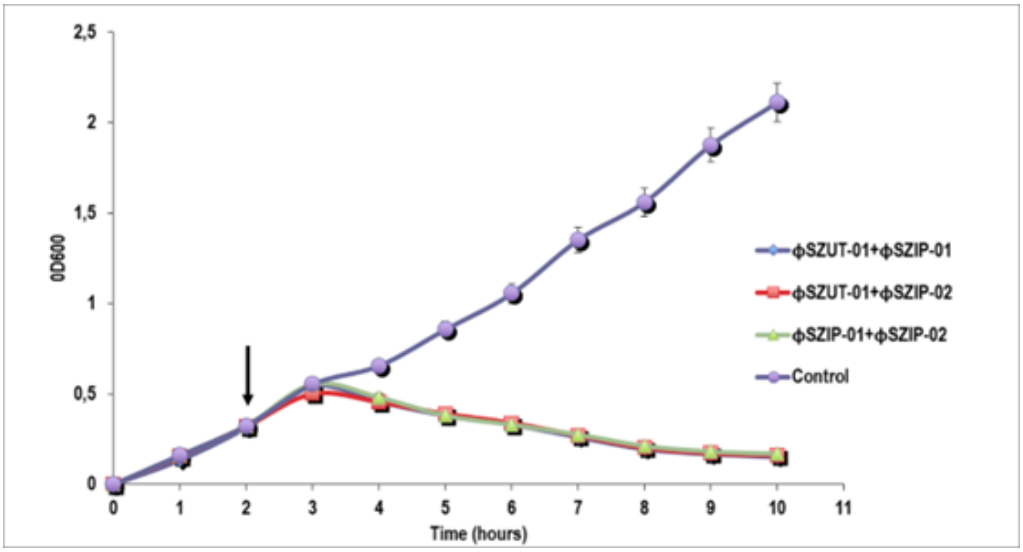

Figure 2. Lysis Effectiveness of each Phage Cocktails

In stark contrast, the positive control using chloramphenicol (T4) showed only a small zone of inhibition, confirming that the bacterial consortium exhibited a multi- drug resistant (MDR) phenotype. This finding aligns with regional reports of high AMR rates in Gram-negative pathogens and *Salmonella* strains and highlights the urgent need for non-antibiotic alternatives (Antimicrobial Resistance Collaborators, 2022). The demonstrated efficacy of the phage cocktails against this antibiotic-resistant consortium strongly positions phage therapy as a vital intervention in the face of the growing AMR crisis.

The results of the phage cocktail stability tests showed remarkable resilience. The cocktail proved stable across a wide range of pH conditions, from acidic to alkaline, and stable titers were confirmed under both refrigerated conditions (4±1°C) and moderate room temperature (21±1°C) (Figure 3). Stability across a broad pH range, especially against acidic pH, is a critical functional attribute that overcomes a major pharmacokinetic (PK) barrier in phage therapy development (Wdowiak et al., 2024). Phages are susceptible to inactivation in the harsh acidic environment of the stomach, which often impedes oral phage therapy. The cocktail's resilience suggests it can survive the gastrointestinal (GI) tract to target GI pathogens. This intrinsic pH stability, which can sometimes span from pH 2 to 13 for lytic phages, is also highly relevant for food safety biocontrol, enabling effective application on food surfaces that may have low pH (Skaradzińska et al., 2025).

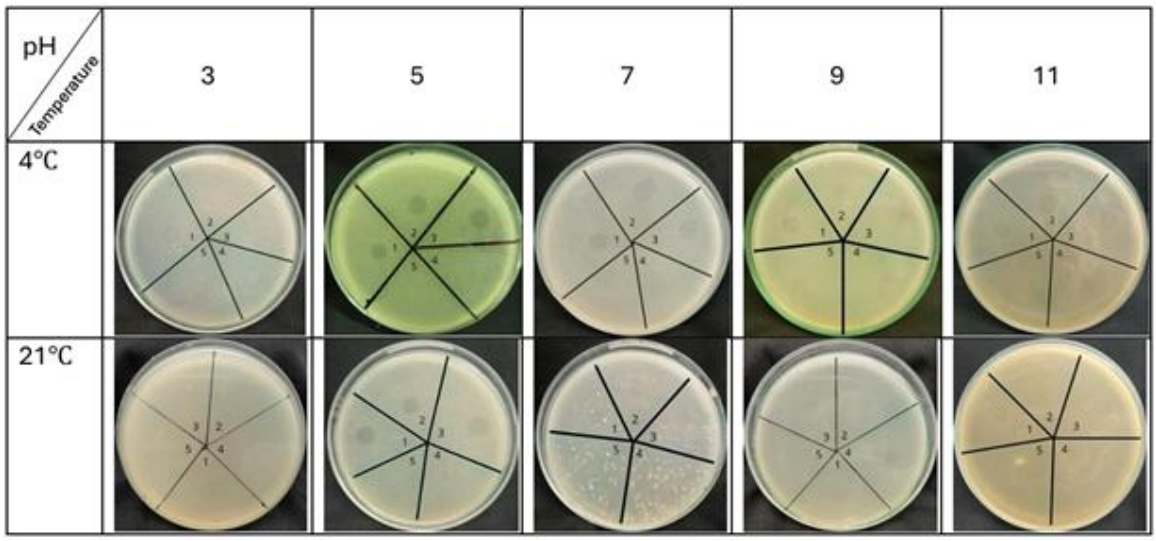

Figure 3. Stability of Bacteriophage Cocktails at Different pH (3, 5, 7, 9, and 11) and Temperatures (4 °C and 21 °C)

Bacteriophages exhibit stability that is strongly influenced by environmental conditions, particularly pH and temperature, as both factors play critical roles in phage adsorption, penetration, and replication processes (Sarkar et al., 2018). Phage activity is generally optimal only within specific pH and temperature ranges, whereas extreme conditions, such as pH <6 or >8 and temperatures <21 °C or >45 °C, can result in phage inactivation or loss of viability. Extreme temperatures have also been reported to reduce the number of replicating phages or prolong the latent period, thereby delaying the release of progeny phage particles (Pradeep et al., 2022). Although phages are generally more resilient to variations in pH and temperature than their bacterial hosts, this stability still has clearly defined tolerance limits (Shende et al., 2017). In this context, the use of phage cocktails represents a superior strategy compared to single-phage applications, as combining multiple phages provides more consistent and sustained antibacterial activity under fluctuating environmental conditions. Previous studies have demonstrated that both two- and three-phage cocktails can reduce bacterial populations more rapidly and maintain growth suppression for longer periods than single phages, even when partial bacterial regrowth occurs at later incubation stages (Thanki et al., 2022). Mean inhibition zone diameter (mm) of phage cocktail treatments can be seen in Table 2.

Table 2. Mean Inhibition Zone Diameter (mm) of Phage Cocktail Treatments

Treatment	Mean ± SD (mm)
T1 (ϕSZUT-01 + ϕSZIP-01)	10.14 ± 0.98
T2 (ϕSZUT-01 + ϕSZIP-02)	9.37 ± 0.78
T3 (ϕSZIP-01 + ϕSZIP-02)	10.61 ± 2.87
T4 (Chloramphenicol)	3.79 ± 0.58
T5 (SM buffer)	0.00 ± 0.00

In line with this concept, Figure 3 presents the phage cocktail stability under various pH and temperature treatments. The phages remained infective from pH 3 to 11 and were stable at both 4 ± 1 °C and 21 ± 1 °C, as evidenced by the presence of clear plaques in all tested conditions. Although this assessment was qualitative, the consistent formation of clear plaques across all tested conditions suggests that the phage cocktail retained lytic activity under a broad range of environmental stresses. Stability under acidic conditions is particularly important for oral phage therapy because gastric acidity often inactivates many phage types; therefore, the resilience observed in this study demonstrates a critical

advantage for therapeutic use (Wdowiak et al., 2024). The thermal stability results indicate that the cocktails can be stored effectively under refrigeration and can tolerate moderate room temperatures, which simplifies transportation and reduces dependency on cold-chain logistics. Thermally stable phages offer wider applicability for distribution and product storage. One-way ANOVA results for diameter can be seen in Table 3. Post hoc Tukey HSD (Honestly Significant Difference) results are shown in Table 4.

Table 3. One-way ANOVA Results for Diameter

Source	Sum of Squares	df	Mean Square	F	p-value
Between Groups	120.460	3	40.153	15.840	< 0.001
Within Groups	30.418	12	2.535		
Total	150.878	15			

Table 4. Post hoc Tukey HSD (Honestly Significant Difference)

Treatment	N	1	2
4.00	4	3.7850	
2.00	4		9.3725
1.00	4		10.1413
3.00	4		10.6050
Sig.		1.000	.699

The assumptions for parametric analysis were satisfied, as the Shapiro–Wilk normality test showed no significant deviation from normality across treatments ($p > 0.05$), and Levene's test confirmed homogeneity of variances ($p = 0.065$). Based on these assumptions, one-way ANOVA revealed a significant difference among treatments in terms of inhibition zone diameter ($F(3,12) = 15.840$; $p < 0.001$). Statistical analysis was conducted on treatments T1–T4 only, as treatment T5 consistently showed zero inhibition zone diameters across all replicates and was therefore excluded from the ANOVA due to the absence of variance. Post hoc Tukey HSD analysis demonstrated that treatments T1, T2, and T3 did not differ significantly from each other ($p > 0.05$), indicating comparable inhibitory effectiveness, whereas all three treatments produced significantly larger mean inhibition zone diameters compared to T4 ($p < 0.05$), which generated only a small lysis zone (mean = 3.79). Treatment T5, included solely in descriptive analysis as a negative control, did not produce any inhibition zone (mean = 0), confirming the absence of inhibitory activity against the target pathogen and supporting the validity of the experimental system.

The overall performance of cocktails T1, T2, and T3 shows that combining phages reduces the likelihood of phage-insensitive mutant (PIM) development. In this study, the stable OD600 decline and the consistent plaque formation under all conditions confirm that the cocktails successfully suppressed the bacterial population throughout the experiment. This supports previous findings by Gliźniewicz et al. (2024) and Wdowiak et al. (2024), who reported that phage cocktails impose multiple selective pressures that minimize bacterial escape. The poor performance of the antibiotic control further confirms the MDR profile of the bacterial consortium, matching reports of resistant *Salmonella* and Gram-negative strains in Southeast Asia. These findings strongly indicate that the phage cocktails formulated in this study have high potential for implementation in food biocontrol, MDR infection treatment, and future product development for safer and more effective antimicrobial alternatives.

CONCLUSION

This study demonstrated that the formulated bacteriophage cocktails are both effective and stable as a potential non-antibiotic alternative for controlling a consortium of foodborne pathogenic bacteria. The

phage cocktails exhibited strong antibacterial efficacy against *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella typhi*, as evidenced by clear lytic activity and significant bacterial reduction. Moreover, the cocktails maintained infectivity across a broad range of pH conditions and remained stable under both refrigerated and room temperature storage. Collectively, these findings directly address the research objective by confirming that the phage cocktail possesses both effective antibacterial activity and sufficient physicochemical stability, supporting its potential application in food safety control and further development as an alternative antimicrobial strategy.

ACKNOWLEDGMENT

This research was supported by a grant of Program Kreativitas Mahasiswa 2025 (no. 1995/B2/DT.01.00/2025) from the Ministry of Higher Education, Science, and Technology.

REFERENCES

Abedon, S. T., Danis-Wlodarczyk, K. M., & Wozniak, D. J. (2021). Phage cocktail development for bacteriophage therapy: Toward improving spectrum of activity breadth and depth. *Pharmaceuticals, 14*(1019), 1–25. https://doi.org/10.3390/ph14101019

Antimicrobial Resistance Collaborators. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *The Lancet, 399*(10325), 629–655. https://doi.org/10.1016/S0140-6736(21)02724-0

Bao, A., Burritt, D. J., Chen, H., Zhou, X., Cao, D., & Tran, L. S. P. (2019). The CRISPR/Cas9 system and its applications in crop genome editing. *Critical Reviews in Biotechnology, 39*(3), 321–336. https://doi.org/10.1080/07388551.2018.1554621

Chen, H., Liu, H., Gong, Y., Dunstan, R. A., Ma, Z., Zhou, C., Zhao, D., Tang, M., Lithgow, T., & Zhou, T. (2024). A Klebsiella-phage cocktail to broaden the host range and delay bacteriophage resistance both in vitro and in vivo. *Biofilms and Microbiomes, 10*(127), 1–17. https://doi.org/10.1038/s41522-024-00603-8

Chen, Q., Dharmaraj, T., Cai, P. C., Burgener, E. B., Haddock, N. L., Spakowitz, A. J., & Bollyky, P. L. (2022). Bacteriophage and bacterial susceptibility, resistance, and tolerance to antibiotics. *Pharmaceutics, 14*(7), 1425. https://doi.org/10.3390/pharmaceutics14071425

Gliźniewicz, M., Miłek, D., Olszewska, P., Czajkowski, A., Serwin, N., Cecerska-Heryć, E., Dołęgowska, B., & Grygorcewicz, B. (2024). Advances in bacteriophage- mediated strategies for combating polymicrobial biofilms. *Frontiers in Microbiology, 14*, 1320345. https://doi.org/10.3389/fmicb.2023.1320345

Glonti, T., & Pirnay, J.-P. (2022). In vitro techniques and measurements of phage characteristics that are important for phage therapy success. *Viruses, 14*(7), 1490. https://doi.org/10.3390/v14071490

Igler, C., & Brockhurst, M. (2023). Bacteriophage ecology: Getting a head start on genomic competitors. Current Biology. https://doi.org/10.1016/j.cub.2023.08.077

Iqbal, M., Narulita, E., Zahra, F., & Murdiyah, S. (2020). Effect of phage-antibiotic synergism (PAS) in increasing antibiotic inhibition of bacteria causing foodborne. *The Journal of Infection in Developing Countries, 14*(5), 488–493. https://doi.org/10.3855/jidc.12094

Haines, M. E. K., Hodges, F. E., Nale, J. Y., Mahony, J., Van Sinderen, D., Kaczorowska, J., Alrashid, B., Akter, M., Brown, N., Sauvageau, D., Sicheritz- Pontén, T., Thanki, A. M., Millard, A. D., Galyov, E. E., & Clokie, M. R. J. (2021). Analysis of selection methods to develop novel phage therapy cocktails against antimicrobial resistant clinical isolates of bacteria. *Frontiers in Microbiology, 12*, 613529. https://doi.org/10.3389/fmicb.2021.613529

Istiani, H. G., & Agustiani, E. (2021). Higiene penjamah, sanitasi pengolahan makanan, dan penyajian makanan berhubungan dengan keberadaan bakteri Escherichia coli pada makanan jajanan anak

sekolah. *Jurnal Kesehatan Pertiwi, 3*(1), 173–178. https://journals.poltekesbph.ac.id/index.php/pertiwi/article/view/47/29

Kementerian Kesehatan Republik Indonesia. (2021). Kejadian luar biasa (KLB)–Keracunan di Manggarai Timur, Nusa Tenggara Timur. Pusat Krisis Kesehatan Kemenkes RI. https://pusatkrisis.kemkes.go.id

Kurnianto, M. A., & Syahbanu, F. (2023). Resistensi antibiotik pada rantai pasok pangan: Tren, mekanisme resistensi, dan langkah pencegahan. *Agrointek, 17*(3), 608–621. https://doi.org/10.21107/agrointek.v17i3.14771

Muna, F., & Khariri. (2020). Bakteri patogen penyebab foodborne diseases. Prosiding Seminar Nasional Biologi, 6(1), 74–79. https://journal.uin-alauddin.ac.id/index.php/psb/article/view/15374

Narulita, E., Aji, G. P., Wahono, B., Murdiyah, S., & Yulian, R. (2020). Synergism of phage ϕPT1b and antibiotics for reducing infection of Escherichia coli. *Biogenesis, 8*(1), 22–28. https://doi.org/10.24252/bio.v8i1.11280

Parra-Flores, J., Cruz-Córdova, A., Acuña-Nelson, S. M., Aguirre-García, J., Holý, O., Cabal Rosel, A., & Ruppitsch, W. (2024). Enterobacteriaceae in powdered infant formula. In Powdered Infant Formula (Chapter). https://doi.org/10.1016/b978-0-12-822521-9.00182-9

Pradeep, A. N., Ramasamy, S., Veniemilda, J. K., & Vinod Kumar, C. S. (2022). Effect of pH and temperature variations on phage stability: A crucial prerequisite for successful phage therapy. *International Journal of Pharmaceutical Sciences and Research (IJPSR), 13*(12), 5178-5182. http://dx.doi.org/10.13040/IJPSR.0975-8232.13(12).5178-82

Sarkar, S., Das, M., Bhowmick, T. S., Koley, H., Atterbury, R., Chakrabarti, A. K., & Sarkar, B. L. (2018). Isolation and characterization of novel broad host range bacteriophages of Vibrio cholerae O1 from Bengal. *Journal of Global Infectious Diseases, 10*, 84–88. https://doi.org/10.4103/jgid.jgid_37_17

Scallan, E., Hoekstra, R. M., Angulo, F. J., Tauxe, R. V., Widdowson, M.-A., Roy, S. L., & Griffin, P. M. (2011). Foodborne illness acquired in the United States: Major pathogens. *Emerging Infectious Diseases, 17*(1), 7–15. https://doi.org/10.3201/eid1701.P11101

Shende, R. K., Hirpurkar, S. D., & Sannat, C. (2017). Isolation and characterization of bacteriophages with lytic activity against common bacterial pathogens. *Veterinary World, 10*, 973–978. https://doi.org/10.14202/vetworld.2017.973-978

Skaradzińska, A., Grygorcewicz, B., Śliwka, P., & Czajkowski, R. (2025). Phage-based strategies for foodborne pathogen mitigation. *Frontiers in Microbiology, 16*, 1-3. https://doi.org/10.3389/fmicb.2025.1649376

Thanki, A. M., Clavijo, V., Healy, K., Wilkinson, R. C., Sicheritz-Pontén, T., Millard, A. D., & Clokie, M. R. J. (2022). Development of a phage cocktail to target Salmonella strains associated with swine. *Pharmaceuticals, 15*(1), 58. https://doi.org/10.3390/ph15010058

Thaha, A. H., Malaka, R., Hatta, W., & Maruddin, F. (2024). Staphylococcus aureus as a foodborne pathogen in eggs and egg products. *International Journal of One Health, 10*(1), 141–147. https://doi.org/10.14202/IJOH.2024.141-147

Une, S., Riska, R., Mustofa, P. I. N., & Listiana, E. (2022). Cemaran Salmonella sp pada produk tahu di Pasar Liluwo, Kelurahan Liluwo, Kota Tengah, Gorontalo. *Prosiding Seminar Nasional Mini Riset Mahasiswa, 1*(2), 114–121. https://ejurnal.ung.ac.id/index.php/semasetwa/article/view/17824

Vashisth, M., Jaglan, A. B., & Yashveer, S. (2022). Development and evaluation of a bacteriophage cocktail to eradicate biofilms. *Viruses, 15*(427), 1–19. https://doi.org/10.3390/v15020427

Wdowiak, M., Paczesny, J., & Raza, S. (2022). Enhancing the stability of bacteriophages using physical, chemical, and nano-based approaches: A review. Pharmaceutics, 14(9), 1936. https://doi.org/10.3390/pharmaceutics14091936

World Health Organization. (2020). WHO estimates of the global burden of foodborne diseases. World Health Organization. https://www.who.int/activities/estimating-the-burden-of-foodborne-diseases