

Evaluation of the Antimicrobial Activity of Simplicia Prepared from Wild and Cultivated *Phallus indusiatus*

Hikmah Zikriyani¹, Mutimanda Dwisatyadini¹, Inggit Winarni¹, Na'ilah Insani Alifiyah¹, Arie Aryanto¹, Primasari Pertiwi², Dwimaskurniawan¹

¹Biology Study Program, Faculty of Science and Technology, Universitas Terbuka, South Tangerang, Indonesia;

²Biology Study Program, Faculty of Mathematics and Sciences, Universitas Lampung, Bandar Lampung, Indonesia;

Article History

Received : June 07th, 2026

Revised : June 24th, 2026

Accepted : July 04th, 2026

*Corresponding Author: **Hikmah Zikriyani**, Biology Study Program, Faculty of Science and Technology, Universitas Terbuka, South Tangerang, Indonesia;
Email: hikmah.zikriyani@ecampus.ut.ac.id

Abstract: *Phallus indusiatus* is a macrofungus that has attracted attention because of its nutritional value and reported biological activities, including antimicrobial properties. This study evaluated the antimicrobial activity of wild and cultivated *P. indusiatus* against *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans* using the disc diffusion method. Wild samples were collected from Central Java, Indonesia, whereas cultivated samples were obtained from Hong Kong. Simplicia suspensions were prepared in sterile distilled water at a concentration of 100 mg/mL and tested against the selected microorganisms. No inhibition zones were observed in any treatment, indicating that the tested samples did not exhibit detectable antimicrobial activity under the conditions applied in this study. The positive control produced a mean inhibition zone of 32 mm, while no inhibition was observed in the negative control. Gene annotation data from previously generated whole-genome sequencing (WGS) of the wild sample were also reviewed to support the interpretation of the results. The selected annotated genes were mainly associated with cellular metabolism, transcriptional regulation, respiration, and metabolite transport. However, the genomic analysis was limited to a small number of annotated genes and was used only as supporting information. Overall, the findings suggest that aqueous suspensions of *P. indusiatus* simplicia did not show detectable antimicrobial activity against the tested microorganisms under the experimental conditions employed.

Keywords: Antimicrobial activity; Macrofungi; *Phallus indusiatus*; Whole Genome Sequencing (WGS).

Introduction

Indonesia is recognized as one of the world's megabiodiversity countries, harboring approximately 25% of global species across its diverse ecosystems (Risalba I, 2024). Its tropical climate, characterized by high temperatures, abundant rainfall, and high humidity, supports a remarkable diversity of organisms, including fungi. As an important component of biodiversity, fungi contribute substantially to ecosystem functioning through their roles in organic matter decomposition, nutrient cycling, and symbiotic interactions with other organisms. Fungi are heterotrophic eukaryotic organisms that commonly reproduce through spores (Nurhayat OD et al.,

2021; Suryani Y et al., 2020). The wide range of habitats found throughout Indonesia provides favorable conditions for the growth and distribution of numerous fungal species, particularly macrofungi.

Many macrofungi contain bioactive compounds and have long been utilized as food sources, such as oyster mushrooms (*Pleurotus ostreatus*) and wood ear mushrooms (*Auricularia auricula*). Nevertheless, several other macrofungal species remain underexplored, including bridal veil mushrooms (*Phallus* sp.).

The genus *Phallus* is distinguished by its unique morphology, particularly the bell-shaped cap covered with dark brown gelatinous exudate. In Indonesia, species belonging to this

genus have been reported from various regions, including Sumatra, Kalimantan, Java, and Papua (Zikriyani *et al.*, 2026). Despite its broad distribution, scientific studies focusing on the biological potential of this genus are still limited. In contrast, studies from other countries have reported that one species, *Phallus indusiatus*, contains bioactive compounds with possible antibacterial and therapeutic properties (Habtemariam, 2019).

Research on the antimicrobial potential of *P. indusiatus* has become increasingly relevant due to the growing global concern regarding microbial resistance to existing antimicrobial agents. Several pathogenic microorganisms, including *Staphylococcus aureus*, have developed multiple resistance mechanisms, such as the *mecA*-encoded penicillin-binding protein 2a (PBP2a), which reduces β -lactam affinity and enables bacterial survival under inhibitory antibiotic concentrations (Hasugian & Zikriyani, 2025). However, studies evaluating the antimicrobial activity of this mushroom in Indonesia remain scarce, particularly those comparing wild specimens collected from natural habitats with cultivated specimens.

Environmental conditions may influence the production of secondary metabolites, including antimicrobial compounds, which could lead to differences in biological activity between wild and cultivated samples. Furthermore, the integration of phenotypic antimicrobial assays with genomic data has not yet been explored. Genomic approaches based on whole genome sequencing can provide insights into genes potentially associated with strong or weak antimicrobial activity. Therefore, this study was conducted to evaluate the antimicrobial activity of wild and cultivated *Phallus indusiatus*. The findings are expected to provide preliminary information regarding its antimicrobial potential and serve as preliminary evidence for future extract-based antimicrobial, metabolomic, and secondary-metabolite gene-cluster studies.

Materials and Methods

Materials and Sample Sources

Two *Phallus indusiatus* samples from different origins were used in this study. Wild specimens were collected from Mirit District, Kebumen Regency, Central Java, Indonesia

(Figure 1), where the mushrooms were growing on decomposing organic matter in a humid terrestrial environment. Several mature fruiting bodies were collected and combined to obtain sufficient material for simplicia preparation and antimicrobial testing. A cultivated *P. indusiatus* sample was purchased from Hong Kong in dried form because commercial cultivation of this species is not yet available in Indonesia.

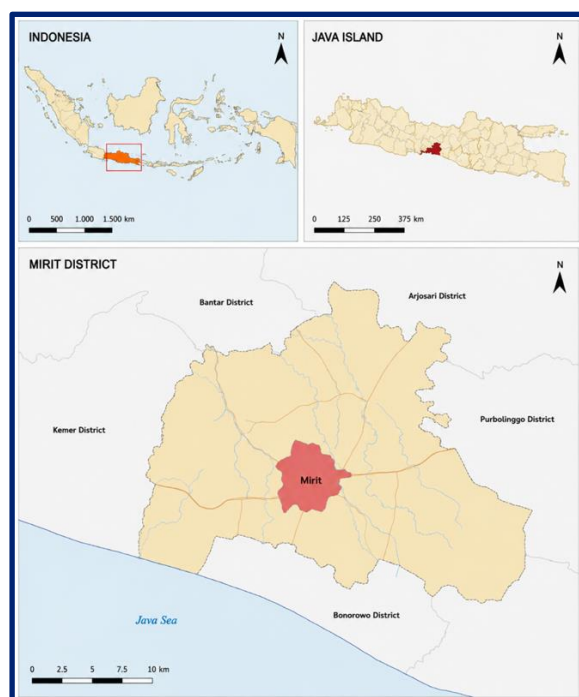


Figure 1. Sampling Location of Wild *Phallus indusiatus* Collected from Mirit District, Kebumen Regency, Central Java, Indonesia

The identity of the wild sample was verified through morphological observation and supported by previously generated whole-genome sequencing (WGS) annotation data. The cultivated sample was identified based on supplier information and morphological characteristics consistent with *P. indusiatus*. As this work was intended as a preliminary comparison between samples of different origins, one pooled sample from each source was analyzed.

Fresh wild fruiting bodies were washed with running water and dried under indirect sunlight to reduce possible degradation of bioactive compounds. After drying, the material was ground into powder using a blender (Prehatin *et al.*, 2025). The cultivated sample underwent the same grinding procedure. Both samples were subsequently used as dried simplicia for antimicrobial testing. The test microorganisms

were *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans*. All strains were obtained from the Integrated Research and Testing Laboratory (LPPT), Universitas Gadjah Mada (UGM), and were refreshed prior to use.

Preparation of Test Microorganisms

The test microorganisms used in this study were *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans*. Prior to antimicrobial testing, each microorganism was refreshed by subculturing in Nutrient Broth medium and incubated at $35 \pm 1^\circ\text{C}$ for 18–24 h. The resulting cultures were suspended in sterile 0.9% NaCl solution and adjusted to a density of approximately 10^8 CFU/mL, corresponding to a 0.5 McFarland standard ($\text{OD} \approx 0.1$ at 600 nm).

Preparation of Mushroom Samples

Wild and cultivated *Phallus indusiatus* simplicia powders were suspended in sterile distilled water at a concentration of 100 mg/mL. The suspensions were homogenized thoroughly before use and applied directly in the antimicrobial assay without further extraction, filtration, or sterilization. Sterile distilled water was used as the solvent control. The concentration of 100 mg/mL was selected because it represented the highest concentration that could be uniformly dispersed under the experimental conditions.

Antimicrobial Activity Assay

Antimicrobial activity was evaluated using the disc diffusion method. A volume of 1000 μL microbial suspension was aseptically transferred into a sterile Petri dish, followed by the addition of 15 mL Mueller–Hinton Agar (MHA) maintained at $45 \pm 1^\circ\text{C}$. After the medium solidified, sterile paper discs were placed on the agar surface and loaded with 25 μL of the mushroom suspension. Discs containing 0.5% chloramphenicol and sterile distilled water served as positive and negative controls, respectively. The plates were incubated at $35\text{--}37^\circ\text{C}$ for 18–24 h. Following incubation, inhibition zone diameters around the paper discs were measured using a caliper. All treatments were performed in triplicate.

Supporting Genomic Information

To provide additional context for interpreting the antimicrobial assay results, gene annotation data previously generated from whole-genome sequencing (WGS) of the wild *P. indusiatus* sample were reviewed descriptively. The annotation dataset, provided by a commercial sequencing service, contained functionally annotated genes identified from the assembled genome. Ten annotated genes representing cellular metabolism, regulation, respiration, and metabolite transport functions were selected as illustrative examples for discussion. No additional genome assembly, re-annotation, comparative genomic analysis, or biosynthetic gene cluster screening was conducted in the present study. Consequently, the genomic information was considered supplementary and was used only to support interpretation of the antimicrobial assay results rather than to comprehensively assess the antimicrobial biosynthetic potential of *P. indusiatus*.

Data Analysis

All antimicrobial assays were conducted in triplicate. Inhibition zone diameters were recorded in millimeters and expressed as mean $\pm$ standard deviation (SD). Antimicrobial activity was assessed descriptively by comparing inhibition zone measurements of wild and cultivated *P. indusiatus* simplicia with those of the positive and negative controls. The presence or absence of inhibition zones was used as an indicator of antimicrobial activity under the experimental conditions employed in this study.

Results and Discussion

Result

The antimicrobial activity assay using *Phallus indusiatus* simplicia from both wild and cultivated habitats did not produce inhibition zones against the three tested microorganisms, namely *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans* (Figures 2 and 3). At a concentration of 100 mg/mL, all triplicate treatments showed an inhibition zone diameter of 0.0 mm. In comparison, the positive control using chloramphenicol produced a strong inhibition zone, according to Rahman *et al.* (2022), with an average diameter of 32 mm, whereas the negative control using distilled water showed no inhibition zone (0.0 mm).

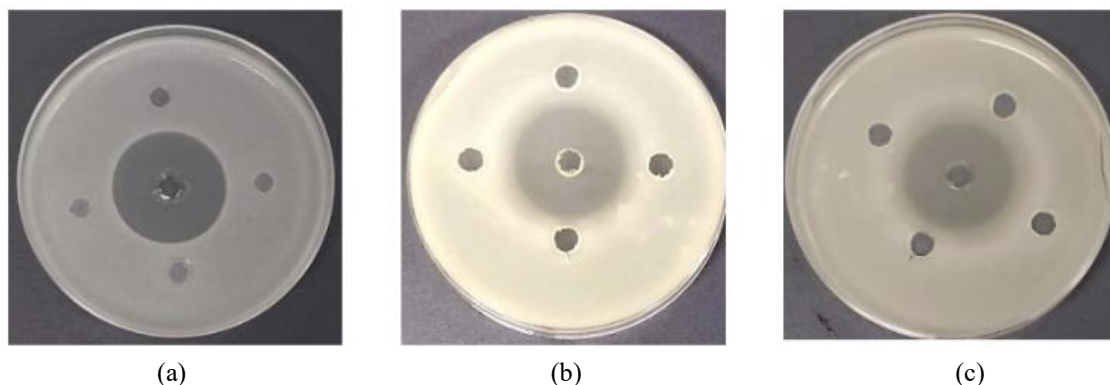


Figure 2. Antimicrobial activity assay of wild *Phallus indusiatus* against (a) *Candida albicans*, (b) *Escherichia coli*, and (c) *Staphylococcus aureus*, showing the absence of inhibition zones in all treatments

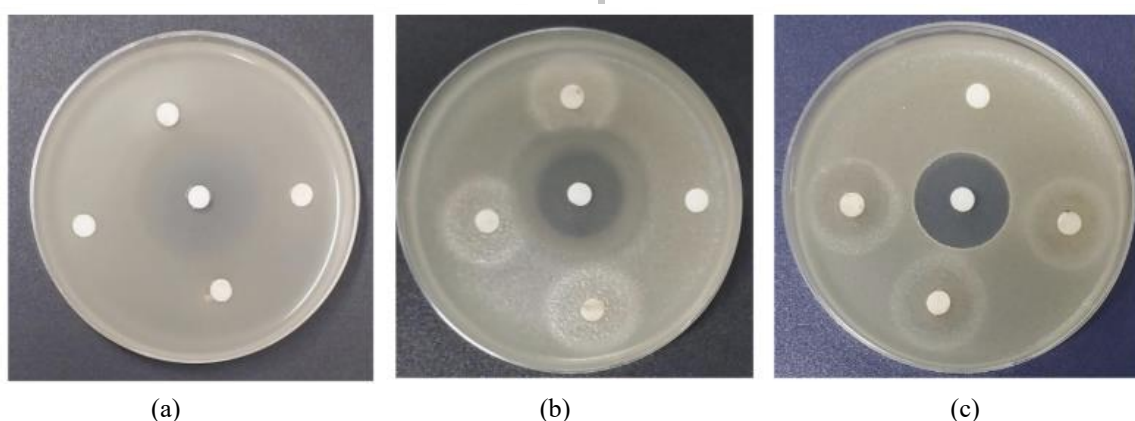


Figure 3. Antimicrobial activity assay of cultivated *Phallus indusiatus* against (a) *Candida albicans*, (b) *Staphylococcus aureus*, and (c) *Escherichia coli*, showing the absence of inhibition zones in all treatments

The absence of inhibition zones observed in this study may be influenced by the characteristics of the sample preparation method and the bioactive compounds present in *Phallus indusiatus* simplicia. Previous studies commonly utilized organic solvent extracts that may facilitate the recovery of specific secondary metabolites, whereas the present study evaluated the mushroom in simplicia form. In addition, bioactive compounds with non-polar or semi-polar characteristics may exhibit limited diffusion in agar media, which can affect their detectability using the diffusion assay method. The relatively low abundance of naturally occurring antimicrobial compounds in the fruiting body may also contribute to the observed results under the experimental conditions used in this study.

To provide additional context for the antimicrobial assay results, gene annotation data previously generated from whole-genome

sequencing (WGS) of the wild *Phallus indusiatus* sample were reviewed (Table 1). Ten annotated genes representing cellular metabolism, regulation, respiration, and metabolite transport functions were selected as illustrative examples. Genes such as ZWF1, IDH2, Hexokinase, and ATP7 were associated with primary metabolic processes and energy production, whereas FRS1, FRS2, TAF9, APR1, and ubc8 were related to cellular regulation and metabolic adaptation. These annotations provide supplementary genomic information that may assist in interpreting the antimicrobial assay results. However, because only selected annotated genes were examined and no comprehensive biosynthetic gene cluster analysis was carried out, the data should not be interpreted as evidence for the presence or absence of antimicrobial biosynthetic pathways in *P. indusiatus*.

Table 1. Selected Gene Annotations from the Whole-Genome Sequencing Dataset of *Phallus indusiatus*

No.	Gene Code (Query)	COG Category	Gene/Enzyme Name	Predicted Function	Potential Relationship to the Absence of Detectable Antimicrobial Activity	References
1.	NODE_1_lengt h_879780_cov _54.74.g33	G	ZWF1	Involved in the pentose phosphate pathway (PPP) and NADPH production	Indicates the predominance of primary metabolism through the PPP pathway rather than antimicrobial metabolite biosynthesis	(Yadav et al., 2021; Zhu et al., 2021)
2.	NODE_1_lengt h_879780_cov _54.74.g66	C	IDH2	TCA cycle enzyme involved in cellular energy metabolism	Indicates the predominance of energy metabolism and cellular respiration over antimicrobial metabolite biosynthesis	(Venkateswara Prasad et al., 2014)
3.	NODE_1_lengt h_879780_cov _54.74.g55	G	ATP7	Mitochondrial ATP synthase involved in ATP production through cellular respiration	The involvement of ATP7 in cellular energy metabolism is suggested to influence metabolic resource allocation, thereby reducing the predominance of antimicrobial compound biosynthesis pathways	(White et al., 2009)
4.	NODE_1_lengt h_879780_cov _54.74.g27	E	Hexokinase	Key enzyme in the early stage of glycolysis involved in glucose metabolism and cellular energy production	The predominance of glycolytic activity and energy metabolism is suggested to direct cellular metabolism toward primary processes rather than antimicrobial metabolite biosynthesis	(Wolf et al., 2016)
5.	NODE_1_lengt h_879780_cov _54.74.g41	J	FRS1	Transcription factor involved in the regulation of growth, oxidative stress responses, and cellular metabolism FAR1-RELATED SEQUENCE (FRS)	Indicates the involvement of metabolic regulation and general cellular responses rather than specific antimicrobial metabolite biosynthesis	(Ma & Li, 2018)
6.	NODE_1_lengt h_879780_cov _54.74.g21	J	FRS2	family protein involved in transcriptional regulation, oxidative stress response, and cellular metabolism	Indicates the predominance of physiological regulation and cellular stress responses over specific antimicrobial metabolite biosynthesis	(Ma & Li, 2018)
7.	NODE_1_lengt h_879780_cov _54.74.g47	J	MFS general substrate transporter	Membrane transporter belonging to the Major Facilitator Superfamily (MFS) involved in the transport of various cellular substrates	Suggested to be involved in metabolite efflux mechanisms, potentially preventing the optimal accumulation of antimicrobial compounds	(Pasqua et al., 2021)
8.	NODE_1_lengt h_879780_cov _54.74.g20	K	TAF9	Transcription factor involved in the TFIID complex and regulation of gene transcription processes	Indicates the predominance of transcriptional regulation and basic cellular physiological functions over specific antimicrobial metabolite biosynthesis	(Frontini et al., 2005)
9.	NODE_1_lengt h_879780_cov _54.74.g28	O	APR1	AraC/XylS family transcriptional regulator associated with metabolic gene regulation and	Suggested to direct cellular metabolic regulation toward degradation and substrate utilization pathways rather than antimicrobial metabolite	(Chen et al., 2025)

No.	Gene Code (Query)	COG Category	Gene/Enzyme Name	Predicted Function	Potential Relationship to the Absence of Detectable Antimicrobial Activity	References
10.	NODE_1_lengt h_879780_cov _54.74.g32	O	ubc8	adaptive cellular responses Ubiquitin-conjugating enzyme involved in protein degradation and cellular metabolic remodeling	biosynthesis Suggested to be involved in cellular metabolic reprogramming and protein degradation, thereby reducing the predominance of antimicrobial metabolite biosynthesis pathways	(Rödl et al., 2023)

Discussion

The absence of inhibition zones against all tested microorganisms differed from several previous studies reporting the antimicrobial potential of *Phallus indusiatus*. According to Kumar and Xu (2025), *Dictyophora indusiata* or *Phallus indusiatus* has been utilized not only as an edible mushroom but also for various biological activities, including antitumor, cardiovascular-protective, antioxidant, immunomodulatory, and antibacterial properties. One of the bioactive compounds identified from the dried fruiting body of this mushroom is albaflavenone, a sesquiterpene compound with natural antimicrobial potential, although it is present at a relatively low concentration of approximately 0.0063% (Habtemariam, 2019).

The absence of detectable antimicrobial activity in the present study may be associated with both the sample preparation method, and the physicochemical properties of bioactive compounds present in *Phallus indusiatus*. Previous studies reporting antimicrobial activity in *P. indusiatus* and other medicinal mushrooms commonly employed organic solvent extraction, including methanol, ethanol, ethyl acetate, or other solvents capable of extracting a broader range of secondary metabolites. In contrast, the present study evaluated aqueous suspensions of mushroom simplicia without prior extraction. Consequently, compounds with limited water solubility may not have been efficiently recovered and therefore may not have been available for antimicrobial activity testing.

In addition to extraction efficiency, the agar diffusion method itself may underestimate the activity of non-polar or poorly water-soluble compounds. Antimicrobial compounds must diffuse through the agar matrix to produce measurable inhibition zones. However, hydrophobic metabolites generally exhibit limited diffusion in aqueous agar media, which can result

in small or undetectable inhibition zones despite possessing biological activity. Therefore, the absence of inhibition zones observed in this study should be interpreted cautiously and does not necessarily indicate the complete absence of antimicrobial compounds in *P. indusiatus*. The naturally low abundance of bioactive metabolites in fruiting bodies, combined with the use of aqueous simplicia suspensions and the diffusion limitations of the assay, may have contributed to the negative results obtained under the experimental conditions employed.

To provide additional context for the antimicrobial assay results, gene annotation data obtained from previously generated whole-genome sequencing (WGS) of wild *P. indusiatus* collected from Kebumen District, Central Java, Indonesia, were reviewed (Figure 1). Several selected genes, including ZWF1, IDH2, ATP7, and Hexokinase, were annotated as being involved in primary metabolic processes such as the pentose phosphate pathway, glycolysis, cellular respiration, and the tricarboxylic acid cycle (Venkateswara Prasad et al., 2014; White et al., 2009; Wolf et al., 2016; Yadav et al., 2021; Zhu et al., 2021). Other selected genes were associated with transcriptional regulation, cellular adaptation, and metabolite transport. These annotations indicate that the selected genes are primarily related to general cellular functions. However, because only a limited subset of annotated genes was examined and no comprehensive biosynthetic gene cluster analysis was performed, the genomic information should be interpreted as supplementary evidence and not as a definitive assessment of the antimicrobial biosynthetic potential of *P. indusiatus*.

In addition, FRS1, FRS2, and TAF9 were associated with transcriptional regulation, oxidative stress responses, and general cellular metabolic regulation (Frontini et al., 2005; Ma & Li, 2018). The presence of these regulatory genes indicates that the physiological activities of *P.*

indusiatus under the tested conditions were more closely related to cellular adaptation and metabolic stability than to the activation of specific bioactive metabolite pathways. This observation further supports the possibility that antimicrobial metabolites were either present at low concentrations or not optimally expressed in the simplicia form used in this study.

The presence of the MFS general substrate transporter gene may also contribute to the absence of detectable antimicrobial activity. This gene encodes a membrane transporter belonging to the Major Facilitator Superfamily (MFS), which is associated with metabolite efflux mechanisms (Pasqua *et al.*, 2021). Such mechanisms may prevent the optimal accumulation of certain compounds, thereby limiting their detectable biological activity in agar diffusion assays. Furthermore, APR1 and *ubc8* were associated with metabolic regulation, protein degradation, and cellular metabolic remodeling (Chen *et al.*, 2025; Rödl *et al.*, 2023). Ubiquitin-conjugating enzymes are also known to play important roles in stress responses, cellular adaptation, and regulatory pathways related to environmental changes (Gao *et al.*, 2024). These functions suggest that the physiological activities of *P. indusiatus* under the tested conditions may have been more strongly directed toward cellular maintenance and metabolic adaptation rather than antimicrobial secondary metabolite biosynthesis.

Although the gene annotation data were available only for the wild *P. indusiatus* sample, both wild and cultivated samples produced similar antimicrobial assay results, with no detectable inhibition zones against *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans*. The consistency of these findings suggests that the tested aqueous simplicia preparations did not exhibit measurable antimicrobial activity under the experimental conditions employed in this study. The selected gene annotations provide supplementary genomic context for interpreting these results; however, they should not be considered definitive evidence regarding the antimicrobial biosynthetic potential of *P. indusiatus*.

A limitation of the present study is that antimicrobial activity was evaluated using aqueous simplicia suspensions and the disc diffusion method, which may not adequately recover or detect poorly water-soluble bioactive compounds. In addition, the comparison was conducted using pooled samples representing

wild and cultivated origins and therefore may not fully capture the biological variability within natural and cultivated populations of *P. indusiatus*. The genomic information included in this study was used solely as supporting evidence and did not involve comprehensive biosynthetic gene cluster analyses. Future studies should investigate organic solvent extracts, perform minimum inhibitory concentration (MIC) assays, and characterize secondary metabolites using metabolomic approaches. Increasing the number of samples from different habitats and cultivation systems would also provide a more comprehensive understanding of the antimicrobial potential and chemical diversity of *P. indusiatus*.

Conclusion

Under the tested simplicia-based disc diffusion conditions, neither wild nor cultivated *Phallus indusiatus* exhibited detectable antimicrobial activity against *Staphylococcus aureus*, *Escherichia coli*, or *Candida albicans*. Aqueous suspensions of *P. indusiatus* simplicia at a concentration of 100 mg/mL did not produce measurable inhibition zones under the experimental conditions employed in this study. These findings should be interpreted within the limitations of the extraction and assay methods used, particularly the use of aqueous simplicia suspensions and agar diffusion testing. Future studies should investigate organic solvent extracts, fractionated samples, and broth dilution assays to further evaluate the antimicrobial potential of *P. indusiatus* and characterize its bioactive compounds.

Acknowledgments

The authors would like to express their sincere gratitude to the Institute for Research and Community Service (Lembaga Penelitian dan Pengabdian kepada Masyarakat/LPPM), Universitas Terbuka, for funding this research through the 2025 Competitive Beginner Lecturer Research Grant scheme.

References

- Amir, N., Kabir, T., Opsory, M. H., Nafisa, N. J. & Turna, N. I. (2025). Phytochemical profiling, antioxidant potential, and antimicrobial assessment of the essential

- oil extracted from *Moringa oleifera*. Undergraduate thesis. Department of Mathematics and Natural Sciences, BRAC University.
- Aryanto Rahman, C., Santosa, D. & Kimia, K. (2022). Aktivitas rimpang temulawak sebagai antibakteri berdasarkan lokasi tumbuhnya: Narrative review. *Jurnal Pharmascience*, 9 (2).
- Chen, S., Cao, L., Lv, T., Liu, J., Gao, G., Li, M., Sun, L., Tian, W., Tian, Y., Li, G. & Ma, T. (2025). Regulation mechanism of the long-chain n-alkane monooxygenase gene *almA* in *Acinetobacter venetianus* RAG-1. *Applied and Environmental Microbiology*, 91 (1). DOI: <https://doi.org/10.1128/aem.02050-24>
- Frontini, M., Soutoglou, E., Argentini, M., Bole-Feysot, C., Jost, B., Scheer, E. & Tora, L. (2005). TAF9b (formerly TAF9L) is a bona fide TAF that has unique and overlapping roles with TAF9. *Molecular and Cellular Biology*, 25 (11): 4638–4649. DOI: <https://doi.org/10.1128/MCB.25.11.4638-4649.2005>
- Gao, W., Zhang, L., Zhang, Y., et al. (2024). Genome-wide identification and expression analysis of the UBC gene family in wheat (*Triticum aestivum* L.). *BMC Plant Biology*, 24: 341. DOI: <https://doi.org/10.1186/s12870-024-05042-3>
- Habtemariam, S. (2019). The chemistry, pharmacology and therapeutic potential of the edible mushroom *Dictyophora indusiata* (Vent ex. Pers.) Fischer (syn. *Phallus indusiatus*). *Biomedicines*, 7 (4): 98. DOI: <https://doi.org/10.3390/biomedicines7040098>
- Hasugian, I. A. & Zikriyani, H. (2025). Literature review on the therapeutic potential of bacteriophages against resistant *Staphylococcus aureus*. *Jurnal Biologi Tropis*, 25 (4): 4869–4879. DOI: <https://doi.org/10.29303/jbt.v25i4.9938>
- Kumar, Y. & Xu, B. (2025). New insights into chemical profiles and health-promoting effects of edible mushroom *Dictyophora indusiata* (Vent ex. Pers.) Fischer: A review. *Journal of Fungi*, 11 (1): 75. DOI: <https://doi.org/10.3390/jof11010075>
- Lingga, R., Dalimunthe, N. P., Afriyansyah, B., Irwanto, R., Henri, H., Januardi, E., Marinah, M. & Safitri, S. (2021). Keanekaragaman jamur makroskopik di Hutan Wisata Desa Tiang Tarah Kabupaten Bangka. *Bioma: Jurnal Ilmiah Biologi*, 10 (2): 180–200. DOI: <https://doi.org/10.26877/bioma.v10i2.7920>
- Ma, L. & Li, G. (2018). FAR1-RELATED SEQUENCE (FRS) and FRS-RELATED FACTOR (FRF) family proteins in *Arabidopsis* growth and development. *Frontiers in Plant Science*, 9: 692. DOI: <https://doi.org/10.3389/fpls.2018.00692>
- Nurhayat, O. D., Putra, I. P., Anita, S. & Yanto, D. H. Y. (2021). Notes on some macro fungi from Taman Eden 100, Kawasan Toba, Sumatera Utara, Indonesia: *Description and its potency*. *Bioeduscience*, 5 (1): 30–39.
- Pasqua, M., Bonaccorsi di Patti, M. C., Fanelli, G., Utsumi, R., Eguchi, Y., Trirocco, R., Prosseda, G., Grossi, M. & Colonna, B. (2021). Host-bacterial pathogen communication: The wily role of the multidrug efflux pumps of the MFS family. *Frontiers in Molecular Biosciences*, 8: 723274. DOI: <https://doi.org/10.3389/fmolb.2021.723274>
- Prehatin, C., Butarbutar, M. E. T., Sianturi, S. & Fernandes, A. (2025). Formulasi dan evaluasi krim ekstrak jamur sawit (*Volvariella* sp.) sebagai tabir surya dengan variasi konsentrasi basis lemak tengkawang dan lemak coklat. *Majalah Farmasetika*, 10 (1): 69–89. DOI: <https://doi.org/10.24198/mfarmasetika.v10i1.60520>
- Risalba, I. (2024). KOBİ successfully collected 11,137 data on Indonesian biodiversity. Faculty of Biology, Universitas Gadjah Mada.
- Rödl, S., den Brave, F., Räsche, M., Kizmaz, B., Lenhard, S., Groh, C., Becker, H., Zimmermann, J., Morgan, B., Richling, E., Becker, T. & Herrmann, J. M. (2023). The metabolite-controlled ubiquitin conjugase Ubc8 promotes mitochondrial protein import. *Life Science Alliance*, 6 (1). DOI: <https://doi.org/10.26508/lsa.202201526>

- Suryani, Y., Taupiqurrahman, O. & Kulsum, Y. (2020). Mikologi. PT. Freeline Cipta Granesia.
- Venkateswara Prasad, U., Swarupa, V., Yeswanth, S., Santhosh Kumar, P., Siva Kumar, E., Mahesh Kumar Reddy, K., Nanda Kumar, Y., Jhansi Rani, V., Chaudhary, A. & Venkata Gurunadha Krishna Sarma, P. (2014). Structural and functional analysis of *Staphylococcus aureus* NADP-dependent IDH and its comparison with bacterial and human NADP-dependent IDH. *Hypothesis*, 10 (2).
- White, C., Lee, J., Kambe, T., Fritsche, K. & Petris, M. J. (2009). A role for the ATP7A copper-transporting ATPase in macrophage bactericidal activity. *Journal of Biological Chemistry*, 284 (49): 33949–33956. DOI: <https://doi.org/10.1074/jbc.M109.070201>
- Wolf, A. J., Reyes, C. N., Liang, W., Becker, C., Shimada, K., Wheeler, M. L., Cho, H. C., Popescu, N. I., Coggeshall, K. M., Arditi, M. & Underhill, D. M. (2016). Hexokinase is an innate immune receptor for the detection of bacterial peptidoglycan. *Cell*, 166 (3): 624–636. DOI: <https://doi.org/10.1016/j.cell.2016.05.076>
- Yadav, P., Kim, N., Kumari, M., Verma, S., Sharma, T. K., Yadav, V. & Kumar, A. (2021). G-quadruplex structures in bacteria: Biological relevance and potential as an antimicrobial target. *Journal of Bacteriology*, 203 (13). DOI: <https://doi.org/10.1128/JB.00577-20>
- Zhu, X., Guo, Y., Liu, Z., Yang, J., Tang, H. & Wang, Y. (2021). Itaconic acid exerts anti-inflammatory and antibacterial effects via promoting pentose phosphate pathway to produce ROS. *Scientific Reports*, 11 (1). DOI: <https://doi.org/10.1038/s41598-021-97352-x>
- Zikriyani, H., Aryanto, A., Na'ilah, D. & Alifiyah, I. (2026). Tinjauan kuantitatif terhadap distribusi dan faktor lingkungan jamur *Phallus* sp. di Indonesia berdasarkan literatur. *Jurnal Penelitian Sains*, 28 (1D): 28. DOI: <https://doi.org/10.56064/jps.v28i1.1201>