



Srinakharinwirot University Journal of Sciences and Technology

Volume 18, Issue 1, January - June 2026, Pages 1 – 12 ISSN 2985-2641 (Online)



Research Article

การประเมินกลุ่มประชากรแบคทีเรียในน้ำตัวอย่างจากป่าชายเลนที่ดูดซับด้วยการประยุกต์ใช้ชุดตรวจโควิด-19 โดยเทคโนโลยีเอ็นจีเอส

Assessment of Bacterial Communities in Water Samples from Mangrove Absorbed via COVID-19 Antigen Test Kits Using Next-Generation Sequencing Technology

กัญญาณัฐ ศิริพรหมพิศาล¹, ณัฐชานันท์ เบ้าคำ¹, ปาริชาติ อัมพูช¹, มณนิชา วงภูธร¹, ภัทรพงษ์ เกริกสกุล¹, ธนิณซ์พลสิทธิ์ แสงภักดี¹, วีรกรรณ ดวงใจ², พฤทธิ ราชรักษ์³, แพรพิไล มิตรารัตน์¹, อรินทม งามนิยม^{1*}

Kanyanat Siriphompisan¹, Natchanan Baowkum¹, Parichat Ampuch¹, Monnichha Wongputorn¹, Patarapong Kroeksakul¹, Thaninatphasit Sangpakdee¹, Wirongrong Duangjai², Phruet Racharak³, Praepilai Mittrarith¹, Arin Ngamniyom^{1*}

¹ภาควิชาสิ่งแวดล้อมและทรัพยากร คณะวัฒนธรรมสิ่งแวดล้อมและการท่องเที่ยวเชิงนิเวศ มหาวิทยาลัยศรีนครินทรวิโรฒ

¹Department of Environment and Resources, Faculty of Environmental Culture and Eco-tourism, Srinakharinwirot University.

²ภาควิชาวนวัฒนวิทยา คณะวนศาสตร์ มหาวิทยาลัยเกษตรศาสตร์

²Department of Silviculture, Faculty of Forestry, Kasetsart University.

³ภาควิชาชีววิทยาป่าไม้ คณะวนศาสตร์ มหาวิทยาลัยเกษตรศาสตร์

³Department of Forest Biology, Faculty of Forestry, Kasetsart University.

*Corresponding author, e-mail: arin@gs.swu.ac.th

Received: 31 March 2026; Revised: 18 May 2026; Accepted: 20 May 2026

บทคัดย่อ

การศึกษานี้มีวัตถุประสงค์เพื่อศึกษาประสิทธิภาพของแถบทดสอบแบบจุ่มดูดซับน้ำในการวิเคราะห์กลุ่มประชากรของแบคทีเรียโดยเทคโนโลยี Next-Generation Sequencing (NGS) ตัวอย่างน้ำถูกเก็บจากป่าชายเลนของจังหวัดสมุทรปราการ ซึ่งเป็นพื้นที่ที่มีความหลากหลายทางชีวภาพของจุลินทรีย์ ตัวอย่างน้ำถูกดูดซับโดยใช้ชุดตรวจโควิด-19 ดีเอ็นเอ

ถูกสกัดจากแถบทดสอบของชุดตรวจ (กลุ่ม A) และสกัดโดยตรงจากตัวอย่างน้ำ (กลุ่ม B ซึ่งเป็นกลุ่มควบคุม) โดยใช้ชุดสกัด DNA Extraction kit วิเคราะห์ลำดับพันธุกรรมของแบคทีเรียบริเวณ V3-V4 hypervariable ของ 16S rRNA ดำเนินการด้วย NGS ผลการศึกษาพบ Operational Taxonomic Units (OTUs) ที่พบร่วมกันระหว่างทั้งสองกลุ่มเท่ากับ 7,140 OTUs ในขณะที่ 867 OTUs พบเฉพาะในกลุ่ม A และ 1,148 OTUs พบเฉพาะในกลุ่ม B ใน กลุ่ม A พบ Proteobacteria เป็นหลัก ในขณะที่ Bacteroidota มีความอุดมสมบูรณ์สูงในกลุ่ม B แบคทีเรีย *PLTA13* มีมากในกลุ่ม A ส่วน *SBR1031* และ *A4b* พบได้มากในกลุ่ม B นอกจากนี้ยังพบความแตกต่างอย่างมีนัยสำคัญของ Shannon diversity index ระหว่างกลุ่ม ($p < 0.05$) จากผลการวิจัยนี้ชี้ให้เห็นถึงความแตกต่างในองค์ประกอบของกลุ่มประชากรแบคทีเรียบางส่วนและดัชนีความหลากหลายเมื่อเปรียบเทียบระหว่างวิธีใช้แถบทดสอบดูดซับกับวิธีเก็บตัวอย่างน้ำโดยตรง งานวิจัยนี้ยังได้อธิบายถึงกลุ่มแบคทีเรียหลักในป่าชายเลนจากตัวอย่างที่รวบรวมผ่านสองเทคนิคที่แตกต่างกัน นอกจากนี้ ยังเป็นข้อมูลพื้นฐานสำหรับการประยุกต์และปรับปรุงเทคนิคการวิเคราะห์ทางจุลชีววิทยาในสิ่งแวดล้อม

คำสำคัญ: ตำแหน่ง V3-4, จุลินทรีย์, ป่าชายเลน, แอนติเจน เทสต์ คิท, โควิด-19

Abstract

This study aimed to investigate the bacterial communities in water samples from mangroves absorbed via COVID-19 antigen test kits and next-generation sequencing (NGS) technology. The locality considered for water sampling was the mangrove area in Samut Prakan Province, which exhibits a high biodiversity of microorganisms. The water samples were absorbed using a COVID-19 antigen test kit. Total genomic DNA was extracted from the test strips of the test kit (Group A) and directly from the water samples (Group B as the control) using a DNA extraction Kit. Bacterial sequencing analysis targeting the V3-V4 hypervariable regions of the 16S rRNA gene was conducted using NGS. A substantial overlap in operational taxonomic units (OTUs) was observed, with 7,140 OTUs shared between the two groups. Specifically, 867 OTUs were exclusive to Group A, whereas 1,148 OTUs were unique to Group B. At the phylum level, Group A was dominated by Proteobacteria. The abundance of Bacteroidota was high in Group B. At the genus level, bacterial *PLTA13* was abundant in Group A, whereas bacterial *SBR1031* and *A4b* were predominant in Group B. Regarding alpha diversity, there was a significant difference in the Shannon diversity index between groups ($p < 0.05$). The results revealed slight differences in some bacterial community compositions and one diversity index when comparing the absorbed test strips with the direct samples. This study elucidated the core bacterial microbiomes of mangroves, based on samples collected using two different techniques. Moreover, it provides important data for the further adaptation and optimisation of microbial analysis techniques in aquatic environments.

Keywords: V3-4, microbes, mangrove forest, antigen test kits, COVID-19

Introduction

Microorganisms, including bacteria, archaea, fungi, and microalgae, play important roles in the biological foundation of mangrove forests (Allard et. al., 2020) [1]. They act as primary catalysts for biogeochemical cycling, breaking down vast amounts of organic matter and regulating the flow of energy and nutrients throughout the coastal food web (Meng et. al., 2022) [2]. Mangrove ecosystems are among the environments that harbour a high diversity of bacteria (Yao et. al., 2025) [3]. Many studies from various geographic regions have investigated the bacterial microbiota of mangrove ecosystems in relation to environmental factors, aiming to elucidate the complex interactions between microbes and their habitat (Tabugo, 2025) [4], (Wainwright et. al., 2023) [5], (Lin et. al., 2019) [6]. The collection of water and sediment samples from targeted environments is important for the successful isolation of total microbial genomic DNA (Hinlo et. al., 2017) [7], (Demkina et. al., 2023) [8].

Rapid antigen test kits such as the SARS-CoV-2 antigen test are inexpensive and easy to use for diagnosing SARS-CoV-2 infection (Toptan et. al., 2019) [9]. The test strips of the lateral-flow assay consist of a sample pad, reagent pad, nitrocellulose membrane, and water-absorbent pad (Martin et. al., 2022) [10]. The test pad allowed and controlled the absorption and transport of the sample flow along the end of the test strip (Omidfar et. al., 2023) [11]. However, the application use of SARS-CoV-2 antigen test kit to collect water samples containing microorganisms for subsequent nucleic acid extraction remains unknown.

As a potential technology for DNA sequencing analysis, next-generation sequencing (NGS) is a powerful technology that allows massive parallel sequencing and rapid simultaneous sequencing of millions of DNA fragments (McCombie et. al., 2019) [12]. NGS is frequently utilised in the field of genomics, such as for the analysis of microbiota composition in the environment (Claesson et. al., 2010) [13]. Therefore, in the present study, we aimed to assess the bacterial communities in water samples from mangroves absorbed via COVID-19 antigen test kits using NGS.

Objective

In this study, we examined bacterial communities in water samples from mangroves absorbed via COVID-19 antigen test kits using next-generation sequencing technology.

Methods

The study site selected for water sampling was located within the mangrove ecosystem of Samut Prakan Province during the dry season. High biodiversity of microorganisms has been reported (Nimnoi and Pongsilp, 2022) [14]. To set the same conditions, 45 mL of water samples were collected at a depth of 30 cm in the late morning, transferred into sterile 50-mL centrifuge tubes, and immediately stored on ice for genomic DNA isolation. Environmental parameters (temperature, pH, and salinity) were recorded on-site using a portable multi-parameter probe. One-litre water samples were collected in laboratory bottles with

aluminium foil-covered caps and stored on ice for mineral analyses (Cu, Fe, Mn, and Zn). Limits of detection (LOD) were 0.0005, 0.0010, 0.0005 and 0.0005 mg/L for Cu, Fe, Mn, and Zn, respectively. Minerals were analysed using inductively coupled plasma mass spectrometry. All experiments were repeated thrice.

For DNA isolation, 100 μ L of the water sample in 50-mL centrifuge tubes was absorbed using a COVID-19 antigen test kit. The company of test kit does not allow its brand name to be mentioned in the publication. The DNA extracted from the test strips of the test kit was designated as Group A. In the control group, total genomic DNA was directly extracted from an equal volume of water (100 μ L) in 50-mL centrifuge tubes and designated as Group B. Total genomic DNA was extracted using the soil DNA extraction mini kit according to the manufacturer's protocol.

To evaluate the bacterial diversity and community composition, hypervariable region of the 16S rRNA gene (V3-V4) from each sample was amplified using universal primers and DNA polymerase proofreading with PCR Master Mix.

PCR amplification was performed with a pre-denaturation step at 97 °C for 4 min followed by 30 cycles for denaturation at 96 °C for 1 min, annealing at 57 °C for 36 s, and extension at 70 °C for 2 min. The final extension step was performed at 70 °C for 10 min. The amplicon size (~600bp) was verified using 1% agarose gel electrophoresis, and the DNA was subsequently purified using the QIAquick Gel Extraction Kit. Purified products were quantified using a Qubit dsDNA HS assay kit prior to library construction using a MetaVx Library Preparation kit. Sequencing was conducted on an Illumina MiSeq/NovaSeq platform to generate data for the operational taxonomic unit (OTU) analysis.

OTUs were analysed using USEARCH and a Naïve Bayesian classifier. Taxonomic assignments were performed using Greengenes and Ribosomal Database Project reference databases. Data visualisations, including Venn diagrams, and heat maps, were generated using R (v3.4.10). Furthermore, the relative abundances across taxonomic ranks and an unweighted pair group method with arithmetic mean (UPGMA) clustering tree were constructed using R (v3.1.1). Alpha diversity was evaluated by calculating the ACE, Chao1, and Shannon diversity indices. A *t*-test was used to determine the statistical significance of the differences between the means of the two groups ($p < 0.05$). Maximum-likelihood phylogenetic trees were constructed from the aligned OTU sequences using MEGA11. Principal component analysis (PCA) was used to visualise beta diversity based on the OTU abundance across samples. LEfSe (Linear discriminant analysis Effect Size) was employed to identify distinguishing biomarkers and characterize significant variations in taxonomic composition between groups.

Results

In records of general environmental factors, the values of temperature, pH, and salinity were 29.18 ± 1.65 (mean $\pm$ standard deviation, $n = 3$) °C, 7.18 ± 0.16 and 3.51 ± 0.11 ppt, respectively. The concentrations of Cu, Fe, Mn, and Zn were 0.0017 ± 0.0002 , 0.0140 ± 0.0064 , 0.0120 ± 0.0040 and 0.0690 ± 0.0110 ppm, respectively.

Analysis of the bacterial communities revealed 867 OTUs unique to Group A and 1,148 unique to Group B. Additionally, 7,140 OTUs were shared between the two groups (Figure 1a). In taxonomic profiling at the phylum level across samples, the number of bacterial phyla identified ranged from 60 to 63 in Group A and from 62 to 64 in Group B. Proteobacteria constituted the most dominant phylum in both Groups A and B. Group B exhibited a higher relative abundance of Chloroflexi and Bacteroidota compared with Group A. Conversely, the relative abundance of Desulfobacterota was slightly lower in Group B than in Group A (Figure 1b).

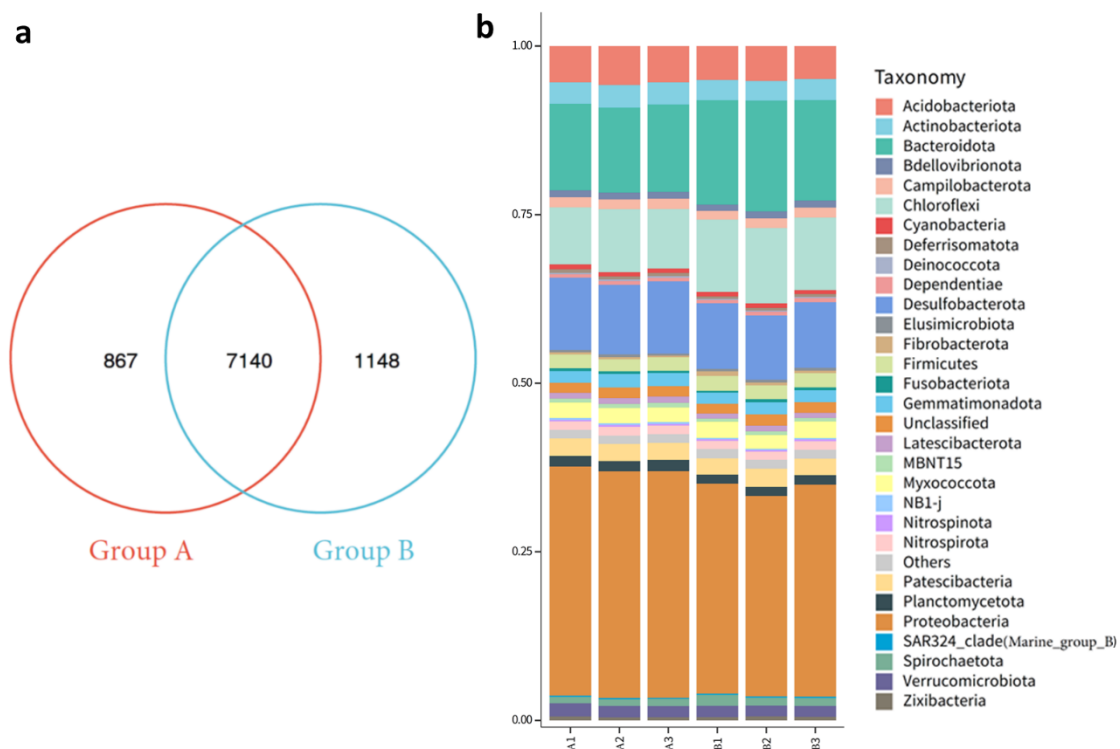


Figure 1. A Venn diagram of the bacterial OTUs from Groups A and B (a). Stacked bar represents the relative abundances of bacterial phyla in Group A (A1–A3) and Group B (B1–B3) (b).

At the genus level, the analysis revealed that the number of bacterial genera ranged between 957 and 973 in Group A and between 965 and 986 in Group B. The community was predominantly characterised by a large proportion of taxa of “Others,” which constituted more than half of the total relative abundance in every sample. Bacterial *PLTA13* was highly abundant in Group A, while bacterial *SBR1031* and *A4b* were predominant in Group B. Additionally, there was assigned to various “Unclassified”. Among the minor but identifiable components of the bacteria, genera such as *Altererythrobacter*, *Candidatus Kaiserbacteria*, *Ilumatobacter*, *Robiginitalea*, and *Sulfuricurvum* were consistently detected at low relative abundances across both experimental groups (Figure 2).

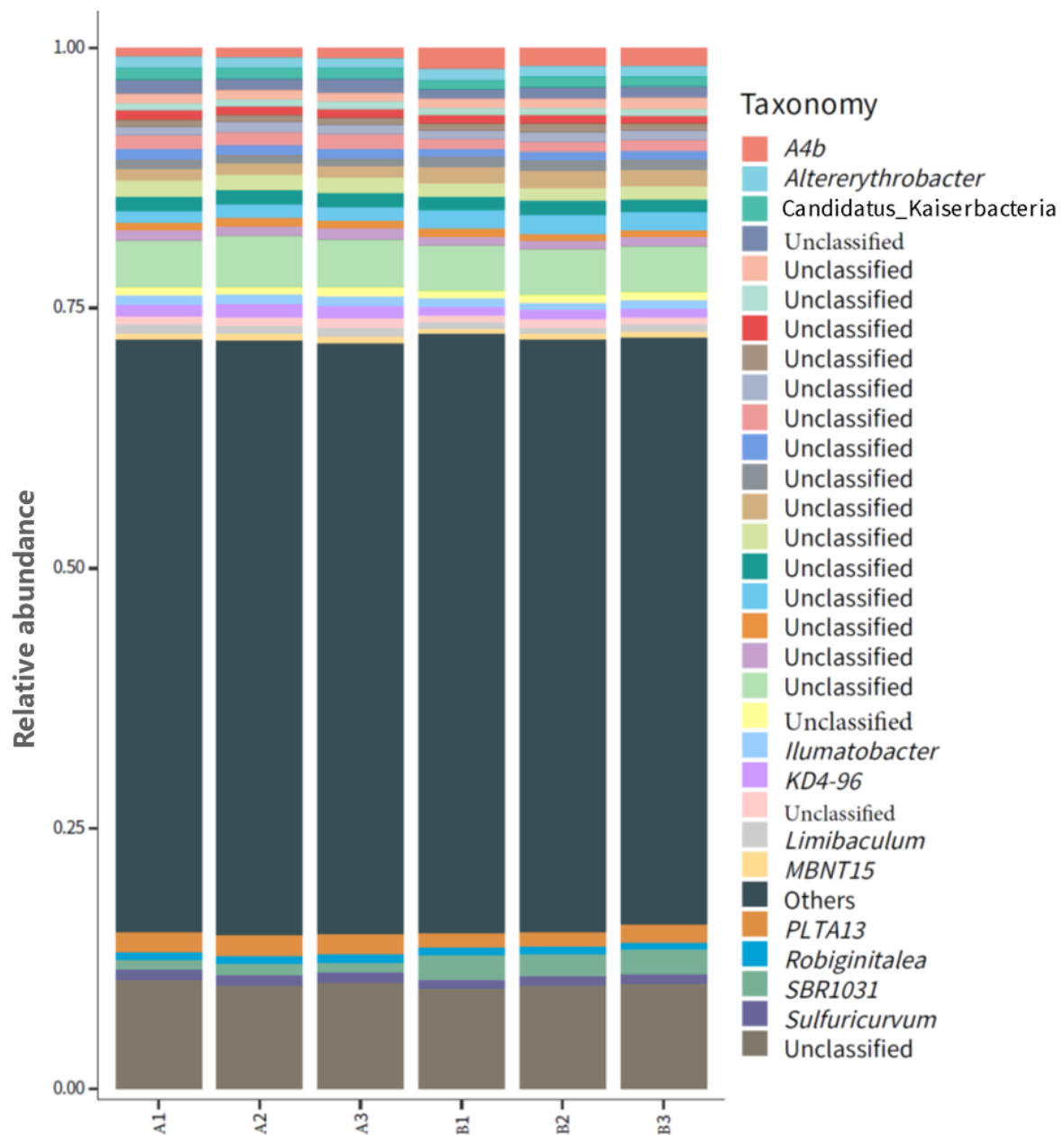


Figure 2. Stacked bars represent the relative abundance of bacterial genera in Groups A (A1–A3) and B (B1–B3).

The resulting phylogenetic tree clearly shows evolutionary clustering corresponding to the major taxonomic lineages. Notably, a prominent clade was formed by members of the phylum Proteobacteria, which included lineages such as *Azoarcus*, *Sulfurifustis*, and *Altererythrobacter*. Further branching revealed discrete monophyletic groups representing a wide array of other phyla, including Chloroflexi, Bacteroidota, and Desulfobacterota, highlighting the broad evolutionary divergence among the identified microbial populations (Figure 3).

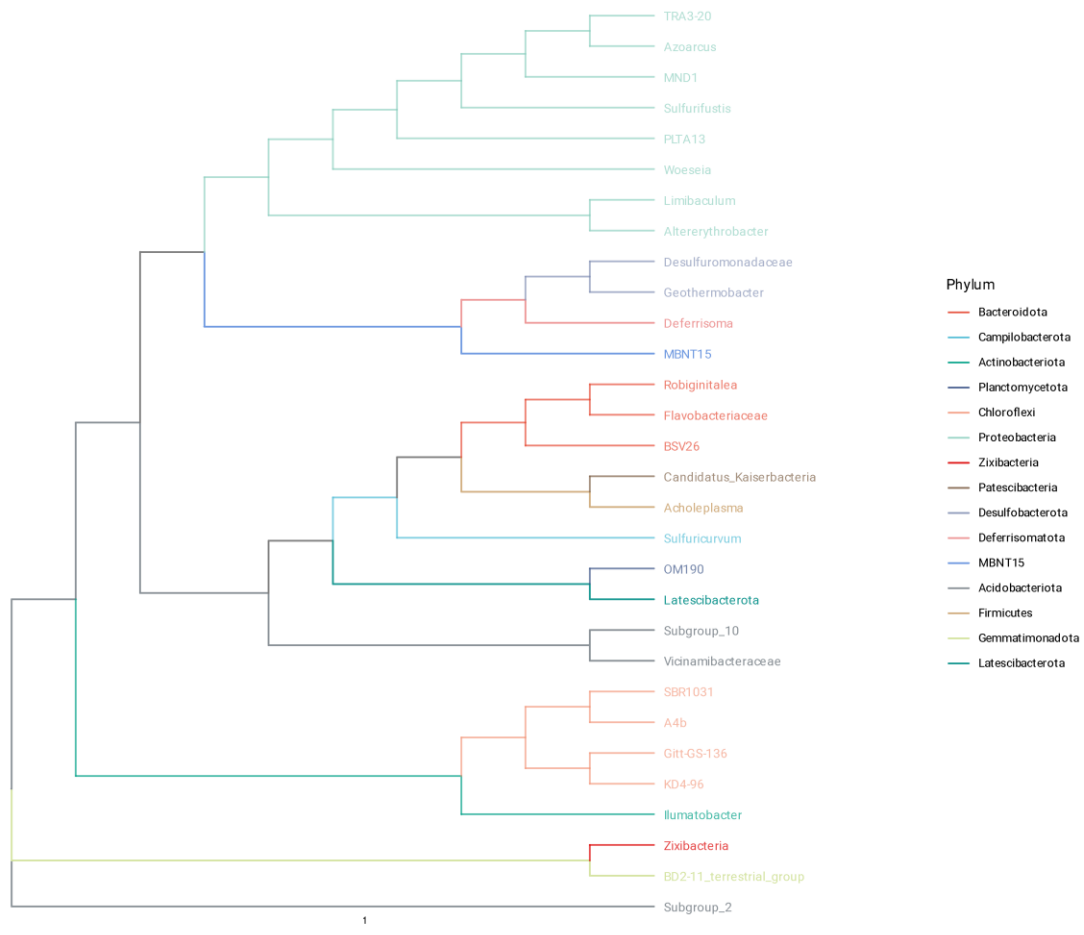


Figure 3. Phylogenetic tree of the genus based on operational taxonomic unit (OTU) sequences. Branch colours indicate the corresponding phyla.

In alpha diversity, ACE, Chao1, and Shannon diversity indices in Group A were 6678.06 ± 64.15 , 6682.72 ± 51.87 and 11.03 ± 0.02 , respectively. ACE, Chao1, and Shannon diversity indices in Group B were 7025.10 ± 250.43 , 6985.97 ± 210.83 , and 11.19 ± 0.02 , respectively. The Shannon diversity index was significantly different between groups. The Group B was higher than that of Group A ($P < 0.05$). Hierarchical clustering analysis using the UPGMA algorithm revealed a clear separation between the bacterial communities in the two groups. The PCA results showed that the first and second principal components were PC1 (23.29%) and PC2 (20.11%) (Figure 4a). The UPGMA tree bifurcated into two distinct primary clades, with all biological replicates from Group A (A1–A3) clustering independently of those in Group B (B1–B3) (Figure 4b). LefSe with the LDA value represented taxonomic categories and biomarkers with significant differences in abundance between the groups. Proteobacteria were significantly more abundant in Group A, and Chloroflexi, Bacteroidota, *SBR1031* and *A4b* were significantly more abundant in Group B (Figure 5).

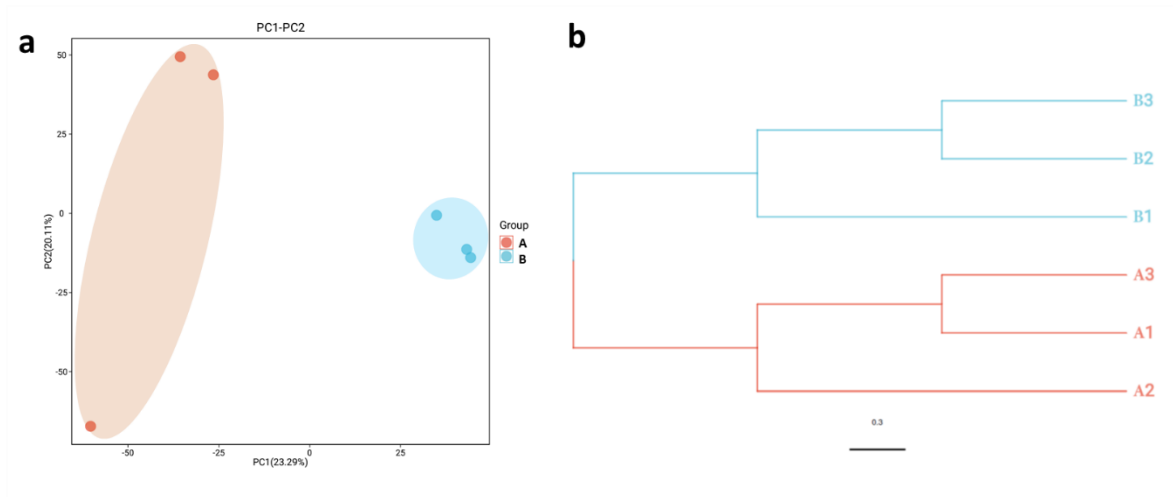


Figure 4. PCA revealed the principal components, PC1 and PC2, of Groups A and B (a). UPGMA tree of Groups A (A1–A3) and B (B1–B3) (b).

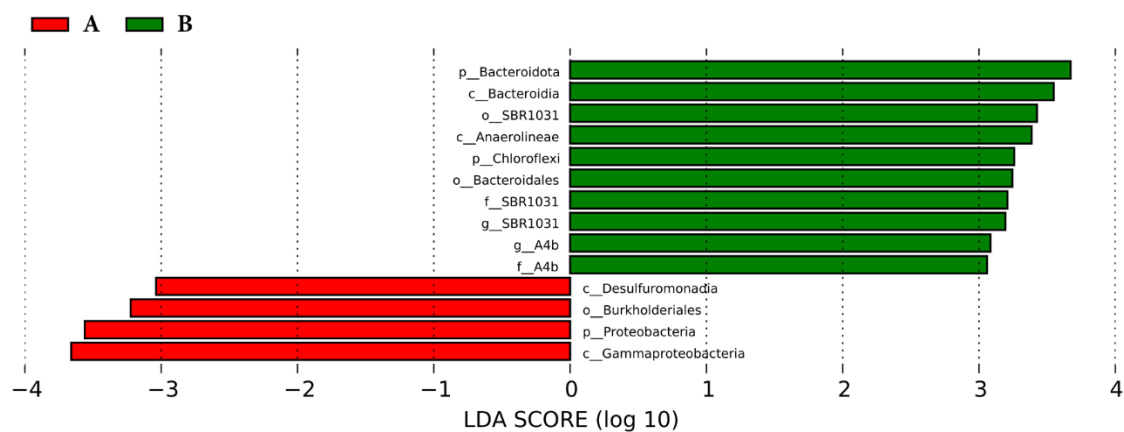


Figure 5. LefSe with the LDA score represents taxonomic categories and biomarkers with significant differences in abundance between Groups A and B.

Conclusions and Discussion

Before comparing the microbiota from mangrove water via test kits and those obtained through direct sampling, this study provided the bacterial groups in order to evaluate the efficiency of the methods used in Groups A and B. The concentrations of Cu, Fe, and Mn were found to be low, but concentration of Zn was slightly elevated (National Environment Board, 2021, Announcement of the National Environment Board on the Determination of Sea Water Quality Standards, Thailand). Moreover, there also discussed the overall bacterial diversity within the mangrove environment as database for experiment. The results of this study are consistent with those of previous reports, demonstrating that bacterial communities in mangrove forests were predominantly composed of the phyla Proteobacteria, Chloroflexi, and Firmicutes (Nimnoi and Pongsilp, 2022) [14], (Ghosh et. al., 2025) [15], (Chithira et. al., 2022) [16]. This suggests that bacterial

communities are common phyla in tropical mangrove ecosystems. Abiotic factors influence the relative abundances of microorganisms (Nimnoi and Pongsilp, 2022) [14], (Zhao et. al., 2025) [17]. *Bacillus* and *Clostridium* are the dominant bacterial genera in mangroves and play major roles in nutrient cycling. (Haldar and Nazareth, et. al., 2018) [18], (Jiang et. al., 2021) [19]. However, the prominent bacterial genera identified in these studies differed, which may have been influenced by environmental factors.

Many studies have reported the application of novel methods for water sampling to extract total genomic DNA from environments. Majaneva et al. (2018) [20] demonstrated the filter materials used for environmental DNA filtration techniques in NGS results. Cruaud et al. (2017) [21] reported how utilised Sterivex filters for DNA extraction from marine environments. Abdel-Hady et al. (2024) [22] described sampling techniques using liquids and filters for the recovery of bacteria from environmental water. Considering the diversity indices, the values in Group B were higher than those in Group A, suggesting that direct extraction from water samples was more efficient than extraction via test strips. There was little difference in the bacterial microbiota components between the two methods. Some phyla and genera differed between Groups A and B. It is assumed that Proteobacteria may be biomarkers for extraction from test strips, whereas Bacteroidota, genus *SBR1031* and genus *A4b* may be biomarkers for the extraction of water samples from mangroves. However, DNA extracted from water absorbed via test strips may not be sufficient to isolate some communities of bacteria in mangrove.

In addition, Yahaya et al. (2019) [23] demonstrated the impact of nitrocellulose membrane pore size on lateral flow immunoassay sensitivity for bacterial detection. Pore sizes of nitrocellulose membrane were below 12 μm (Koczula et al., 2016) [24]. Then, the pore sizes of test strip components may affect DNA extraction from samples. Low et al. (2013) [25] demonstrated that electrophoretic and hydrophobic interactions within nitrocellulose membranes were influenced by pore morphology and pH conditions. These conditions should be incorporated into the method proposed by Group A. However, it is so far to discuss the interaction between bacteria and test strips of the test kit. As suggested in the discussion, further data such as bacterial membrane structures and other parameters are required to ensure precision and accuracy.

In conclusion, the present study shows that the strips of the COVID-19 antigen test kit can absorb water samples containing environmental DNA for microbial analysis. This may have introduced specific taxonomic biases into diversity profiles. Consequently, utilising such materials for environmental biomonitoring requires careful methodological calibration to account for the preferential absorption of certain bacterial taxa. Upcycling or rapid biomonitoring that may be low-cost, and space-saving for sample storage, or for urgent on-site fieldwork focusing on an overview of the core microbiome prior to applying specific standard methods. In addition, this study emphasised data concerning the core bacterial microbiota in mangrove ecosystems from the collection site.

Acknowledgements

This work was funded by grants from the National Commission on Science, Research, and Innovation Promotion and the National Science, Research, and Innovation Fund (No. 019/2565, 023/2568).

References

- [1] Allard, S. M., Costa, M. T., Bulseco, A. N., Helfer, V., Wilkins, L. G. E., Hassenrück, C., Zengler, K., Zimmer, M., Erazo, N., Mazza, Rodrigues, J. L., Duke, N., Melo, V. M. M., Vanwonderghem, I., Junca, H., Makonde, H. M., Jiménez, D. J., Tavares, T. C. L., Fusi, M., Daffonchio, D., Duarte, C. M., Peixoto, R. S., Rosado, A. S., Gilbert, J. A., and Bowman, J. (2020). Introducing the mangrove microbiome initiative: Identifying microbial research priorities and approaches to better understand, protect, and rehabilitate mangrove ecosystems. *mSystems*, 5(5), Article e00658-20.
- [2] Meng, S., Peng, T., Liu, X., Wang, H., Huang, T., Gu, J. D., and Hu, Z. (2022). Ecological role of bacteria involved in the biogeochemical cycles of mangroves based on functional genes detected through geochip 5.0. *mSphere*, 7(1), Article e0093621.
- [3] Yao, L., He, M., Jiang, S., Li, X., and Shui, B. (2025). Spatiotemporal characteristics of bacterial communities in estuarine mangrove sediments in Zhejiang Province, China. *Microorganisms*, 13(4), Article 859.
- [4] Tabugo, S. R. (2025). Mangrove microbiomes as hidden ecological gatekeepers. *Trends in microbiology*, 33(12), 1254-1256.
- [5] Wainwright, B. J., Millar, T., Bowen, L., Semon, L., Hickman, K. J. E., Lee, J. N., Yeo, Z. Y., and Zahn, G. (2023). The core mangrove microbiome reveals shared taxa potentially involved in nutrient cycling and promoting host survival. *Environmental Microbiome*, 18(1), Article 47.
- [6] Lin, X., Hetharua, B., Lin, L., Xu, H., Zheng, T., He, Z., and Tian, Y. (2019). Mangrove sediment microbiome: Adaptive microbial assemblages and their routed biogeochemical processes in yunxiao mangrove national nature reserve, China. *Microbial Ecology*, 78(1), 57-69.
- [7] Hinlo, R., Gleeson, D., Lintermans, M., and Furlan, E. (2017). Methods to maximise recovery of environmental DNA from water samples. *PloS One*, 12(6), Article e0179251.
- [8] Demkina, A., Slonova, D., Mamontov, V., Konovalova, O., Yurikova, D., Rogozhin, V., Belova, V., Korostin, D., Sutormin, D., Severinov, K., and Isaev, A. (2023). Benchmarking DNA isolation methods for marine metagenomics. *Scientific Reports*, 13(1), Article 22138.
- [9] Toptan, T., Eckermann, L., Pfeiffer, A. E., Hoehl, S., Ciesek, S., Drosten, C., and Corman, V. M. (2021). Evaluation of a SARS-CoV-2 rapid antigen test: Potential to help reduce community spread?. *Journal of Clinical Virology*, 135, Article 104713.
- [10] Martin, S., Kohn, M. A., Bollyky, J., and Parsonnet, J. (2022). Validity of at-home rapid antigen lateral flow assay and artificial intelligence read to detect SARS-CoV-2. *Diagnostic Microbiology and Infectious Disease*, 104(3), Article 115763.

- [11] Omidfar, K., Riahi, F., and Kashanian, S. (2023). Lateral flow assay: A summary of recent progress for improving assay performance. *Biosensors*, 13(9), Article 837.
- [12] McCombie, W. R., McPherson, J. D., and Mardis, E. R. (2019). Next-Generation sequencing technologies. *Cold Spring Harbor Perspectives in Medicine*, 9(11), Article a036798.
- [13] Claesson, M. J., Wang, Q., O'Sullivan, O., Greene-Diniz, R., Cole, J. R., Ross, R. P., and O' Toole, P. W. (2010). Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. *Nucleic Acids Research*, 38(22), Article e200.
- [14] Nimnoi, P., and Pongsilp, N. (2022). Insights into bacterial communities and diversity of mangrove forest soils along the upper gulf of Thailand in response to environmental factors. *Biology*, 11(12), Article 1787.
- [15] Ghosh, A., Maile, A., and Nagarajaram, H.A. (2025). Prokaryotic co-occurrence patterns in diverse Indian mangrove ecosystems. *Scientific Reports*, 15(1), Article 38283.
- [16] Chithira, M.S., Aishwarya, P., Mohan, A.S., and Antony, S.P. (2021). Profiling bacteriome associated with the sediments of a mangrove ecosystem in Kerala, India, *Ecological Genetics and Genomics*, 21, Article 100103.
- [17] Zhao, H., Zhang, S., Yang, W., Xia, F., Ma, X., Tan, Q. (2025). Sources and distribution of soil organic matter in mangrove wetland of Qi'ao Island: Insights from stable isotope composition and fluorescence spectroscopy, *Ecological Indicators*, 177, Article 113772.
- [18] Haldar, S., and Nazareth, S.W. (2018). Taxonomic diversity of bacteria from mangrove sediments of Goa: metagenomic and functional analysis. *3 Biotech*, 8(10), Article 436.
- [19] Jiang, C., Diao, X., Wang, H., and Ma, S. (2021). Diverse and abundant antibiotic resistance genes in mangrove area and their relationship with bacterial communities - A study in Hainan Island, China. *Environmental Pollution*, 276, Article 116704.
- [20] Majaneva, M., Diserud, O. H., Eagle, S. H. C., Boström, E., Hajibabaei, M., and Ekrem, T. (2018). Environmental DNA filtration techniques affect recovered biodiversity. *Scientific Reports*, 8(1), Article 4682.
- [21] Cruaud, P., Vigneron, A., Fradette, M.-S., Charette, S. J., Rodriguez, M. J., Dorea, C. C., and Culley, A. I. (2017). Open the Sterivex™ casing: An easy and effective way to improve DNA extraction yields. *Limnology and Oceanography: Methods*, 15(12), 1015-1020. <https://doi.org/10.1002/lom3.10221>
- [22] Abdel-Hady, A., Monge, M., Aslett, D., Mikelonis, A., Touati, A., and Ratliff, K. (2024). Comparison of liquid and filter sampling techniques for recovery of *Bacillus* spores and *Escherichia coli* from environmental water. *Journal of Environmental Management*, 370, Article 122711.
- [23] Yahaya, M. L., Zakaria, N. D., Noordin, R., and Razak, K. A. (2019). The effect of nitrocellulose membrane pore size of lateral flow immunoassay on sensitivity for detection of *Shigella* sp. In milk sample. *Materials Today: Proceedings*, 17(3), 878-883.

[24] Koczula, K. M., and Gallotta, A. (2016). Lateral flow assays. *Essays in Biochemistry*, 60(1), 111-120.

[25] Low, S. C., Shaimi, R., Thandaithabany, Y., Lim, J. K., Ahmad, A. L., and Ismail, A. (2013).

Electrophoretic interactions between nitrocellulose membranes and proteins: Biointerface analysis and protein adhesion properties. *Colloids and Surfaces. B, Biointerfaces*, 110, 248-253.