



Morphological and genetic identifications of *Spirulina* based on 16S rRNA gene

Bahana Safiria Dito*¹⁾, Sajidan²⁾, Ari Susilowati¹⁾, Yasir Sidiq³⁾

¹⁾Master's Program in Bioscience, Faculty of Mathematics and Natural Sciences, Sebelas Maret University, Surakarta 57126, Indonesia.

²⁾Department of Biology Education, Faculty of Teacher Training and Education, Sebelas Maret University, Surakarta 57126, Indonesia.

³⁾Department of Biology Education, Faculty of Teacher Training and Education, Universitas Muhammadiyah Surakarta, Kartasura 57102, Indonesia.

*Corresponding e-mail: sajidan@fkip.uns.ac.id

How to cite:

Dito, B. S., Sajidan, S., Susilowati, A., & Sidiq, Y. (2026). Morphological and Genetic Identifications of *Spirulina* based on 16S rRNA Gene. *Bioeksperimen: Jurnal Penelitian Biologi*, 12(1), 92–99. <https://doi.org/10.23917/bioeksperimen.v12i1.14879>.

Article info

Article History:

Received: 6 January 2026,
Revised: 21 January 2026,
Available Online: 31
March 2026

Keywords:

Arthrospira, phylogenetic,
morphology, molecular,
spirulina

©2026 Bioeksperimen. This work is licensed under a Creative Commons Attribution-NonCommercial 4.0 (CC-BY-NC) International (<https://creativecommons.org/licenses/by-nc/4.0/>).

Abstract

Spirulina is a microalga with spiral or linear trichome shapes that has potential in industrial and food sectors due to its rich nutritional content. *Spirulina* can live in various aquatic habitats with different environmental conditions. Differences in cultivation environments can affect the morphological characteristics of *Arthrospira* due to phenotypic plasticity, making morphology-based identification prone to errors. Therefore, molecular identification using the 16S rRNA gene for phylogenetic analysis is necessary. This study aims to identify and analyze the genetic relationships of *Spirulina* from freshwater and brackish water based on 16S rRNA gene sequences. Freshwater *Spirulina* samples were taken from Bogor (BGR) and Yogyakarta (MRP), while brackish water *Spirulina* was taken from Jepara (JPR). DNA extraction was performed using the Zymo Research Quick-DNA Fungal/Bacterial Miniprep Kit, amplification of the 16S rRNA gene was conducted through PCR, followed by DNA sequencing. Phylogenetic analysis was carried out using MEGA11 to construct the phylogenetic tree. The morphology of strains BGR and MRP showed straight and thin filaments, whereas JPR had spiral and relatively long filaments. Sequencing analysis results showed that strains JPR and MRP had the closest homology similarity to *Arthrospira* sp. IAQUASC-C0001 with percentages of 99.34% and 99.12%, respectively. Meanwhile, *Spirulina* from BGR had the closest homology similarity to *Arthrospira fusiformis* strain AICB 668 with a percentage of 99.78%. Phylogenetic analysis indicated that strains BGR, JPR, and MRP are more closely related to *Arthrospira* than to *Limnospira*.

Introduction

Spirulina is the commercial name for the genus *Arthrospira*, which is one of the genera in the phylum cyanobacteria (Furmaniak et al., 2017). *Spirulina* is a multicellular organism that has trichomes shaped like helices or spirals, and some are linear or straight. *Spirulina* typically has a diameter of 3–12 µm with a variable length (50–500 µm) (Wan et al., 2016). The color of *Spirulina* is blue-green, which comes from photosynthetic pigments called chlorophyll and phycocyanin. *Spirulina* can grow in freshwater, brackish, or marine environments and can also thrive in both warm and cold waters. It can live in tropical and subtropical waters with a high pH ranging from 8 to 11. The optimal growth temperature for *Spirulina* is between 25 °C and 35 °C (Mishra et al., 2022).

Global *Spirulina* production for human consumption reached 10,000 tons per year in 2021 and is estimated to increase to 68,025 tons by 2025. China is the largest *Spirulina* producer in the world, accounting



for 80% of the total global *Spirulina* production, followed by the United States, Taiwan, Thailand, and India (Selvendar, 2015; [Thevarajah et al., 2022](#); [Rilisa and Suantika, 2021](#)). Indonesia has the potential to be a *Spirulina* producer due to its supportive geographical conditions. Currently, many in Indonesia cultivate *Arthrospira* on both large and small scales, in both brackish and freshwater environments ([Buwono et al., 2018](#)). Differences in cultivation habitats (brackish and freshwater) can affect gene expression and the genetic diversity of *Spirulina* populations.

Environmental conditions such as light intensity, pH, salinity, and water nutrients usually influence morphological characteristics, including size and shape ([Lao & Edullantes, 2025](#)). Therefore, identification based solely on morphology can lead to misidentification due to phenotypic plasticity. Phenotypic plasticity is the ability of an organism to change its form and morphology in response to environmental conditions ([Susintowati et al., 2018](#)). A study by [Emam et al., \(2025\)](#) stated that *Spirulina* with different morphological forms actually have a high genetic similarity (95%) based on molecular markers. Thus, molecular identification is necessary to determine taxonomic identity more accurately.

Salinity is one of the key environmental factors influencing the adaptation of *Spirulina* to its habitat ([Lao & Edullantes, 2025](#)). Differences in salinity between brackish and freshwater environments act as selective pressures that affect osmotic balance, metabolic regulation and the stability of cellular structures ([Lestari & Pangastuti, 2025](#)). Over the long term, these condition may drive genetic differentiation and ecological adaptation in *Spirulina* populations inhabiting environments with contrasting salinity levels. Therefore, comparing *Spirulina* isolates from brackish waters and freshwater is relevant to test whether environmental differences are associated with morphological and molecular variation.

The molecular marker most widely used for cyanobacteria identification is the 16S rRNA gene. This gene is present in all prokaryotes. The presence of conserved and variable regions in the 16S rRNA gene allows the design of universal primers as well as taxonomic differentiation down to the genus and species levels, making the 16S rRNA gene suitable for identification and phylogenetic analysis ([Li et al., 2024](#)). In studies on *Spirulina* taxonomy and relationships, the 16S rRNA gene has been widely used to compare isolates from geographic locations with different habitat conditions ([Misztak et al., 2021](#); [Mishra et al., 2022](#); [Chotchindakun et al., 2024](#)). Sequencing the 16S rRNA gene enables the determination of genetic relationships among microorganisms, revealing differences that are not visible through phenotypic approaches. Identification methods usually begin with DNA extraction, target gene amplification using Polymerase Chain Reaction (PCR), followed by sequencing and bioinformatics analysis to determine genetic similarity levels and construct phylogenetic trees illustrating their relationships ([Karamalis et al., 2025](#)). Based on the above background, molecular identification of *Spirulina* from brackish and freshwater environments based on the 16S rRNA gene needs to be conducted.

Materials and methods

1. Materials

This study used three *Spirulina* isolates: the brackish-water strain JPR from Jepara, Central Java, and two freshwater strains, BGR from Bogor, West Java and MRP from the Merapi area, Special Region of Yogyakarta. The research was conducted in the Biology Laboratory, Faculty of Mathematics and Natural Sciences, Sebelas Maret University, Surakarta, Indonesia.

2. Procedures

Cultivation Sample

Spirulina samples from BGR, JPR, and MRP were cultivated by culturing 25 ml of sample in 500 ml of culture medium. The culture medium was made from 500 ml of distilled water, 1 ml of Walne fertilizer, 1 ml of CaCO₃, and NaCl was added to reach a salinity of 30 ppt, then sterilized. This maintenance was carried out using sunlight and aeration. Harvesting was done on the 5th day. This cultivation was carried out based on [Lestari & Pangastuti, \(2025\)](#), in which the optimal salinity used for *Spirulina* cultivation was 30 ppt, resulting in maximum biomass production, and the harvest time was set at day 5 because it represents the optimal growth phase.

Morphological Observation

This morphological characterization was conducted using a light microscope with 10x magnification. The characters used for comparison included color, shape, and cell size ([Zapata et al., 2021](#)).

Molecular Identification

A spirulina cell suspension (approximately 50 mg) was collected by centrifugation for 10 minutes at 10,000 x g. The genomic DNA from these cells was then extracted using the Quick-DNA™ Fungal/Bacterial Miniprep Kit (Zymo Research, D6005). Subsequently, the DNA concentration was measured using an Eppendorf biophotometer plus. The extracted DNA, if not used immediately, can be stored at -20 °C ([Balouch et al., 2023](#)). DNA amplification of Spirulina based on the 16S rRNA gene was carried out using custom designed primers with the following sequences (5'→3') forward ATAAGCCTCGGCTAACTCCG and reverse GGTAAGGTTCTTCGCGTTGC, producing a product length of 491 bp (Lach et al., 2024).

Each PCR reaction mixture of 50 µL contained 25 µL GoTaq Green Master Mix 2X, 19 µL Nuclease-Free Water (Promega, USA), 1 µL of each primer, and 1 µL of template DNA. DNA amplification was performed in stages: initial denaturation at 94 °C for 3 minutes, followed by 30 cycles of denaturation at 94 °C for 30 seconds, annealing at 52 °C for 30 seconds, extension at 72 °C for 30 seconds, and a final extension step at 72 °C for 7 minutes ([Ko et al., 2023](#)). DNA samples successfully amplified by PCR were then separated by electrophoresis on a 1% agarose gel at 80 V for 60 minutes. Samples showing DNA bands of the expected size were subsequently sent for sequencing at Genetika Science, Tangerang. The obtained DNA sequences were analyzed using MEGA11 to determine genetic distance and to construct a phylogenetic tree.

Results and discussion

1. Morphology of Spirulina

The morphology of spirulina can be seen in [Figure 1](#). Where images a (BGR) and c (MRP) are spirulina cultivated in fresh water, whereas image b (JPR) is spirulina cultivated in brackish water.

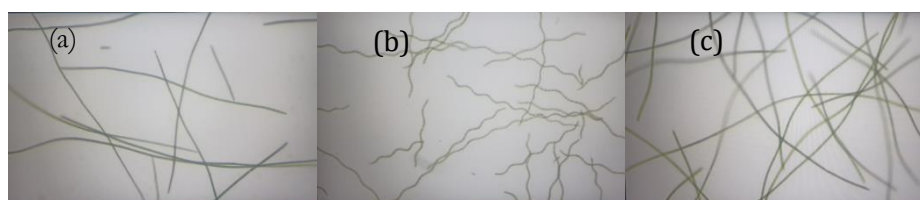


Figure 1. Morphology of the spirulina strain; (a) BGR, (b) JPR, dan (c) MRP observed at 10× magnification.

Observations show that there are differences between Spirulina strains living in freshwater and brackish water. The BGR and MRP strains have trichomes that tend to be linear with slight curves, whereas the JPR strain has more convoluted or spiral-shaped trichomes with relatively large spacing between the coils. This morphological difference is influenced by environmental conditions such as light intensity, pH, salinity, and aeration during cultivation ([Jung et al., 2021](#)). Freshwater has a salinity of less than 0.5 ppt, while brackish water tends to have higher salinity, less than 30 ppt ([Ujwala, 2025](#)). Freshwater has a more neutral pH compared to brackish water; freshwater pH is 7, while brackish water tends to be more alkaline, ranging from 7.7 to 9 ([Supriatna et al., 2020](#)). Consistent with the study by Hong et al. (2023), Spirulina exhibits a high adaptability, marked by morphological changes in response to salinity stress. Spirulina living in water with higher salinity experiences shorter trichomes due to fragmentation and looser spiral density. This also aligns with the research by [Nosratimovafagh et al. \(2023\)](#), which states that increased water salinity thickens the outer spiral sheath, reduces flexibility, and decreases the spiral diameter in Spirulina, thereby increasing the spacing between coils (screw pitch length). Besides the spiral form, Spirulina can undergo morphological conversion into linear filaments, usually influenced by environmental factors and nutrients ([Lijassi et al., 2024](#)).



2. Molecular Identification

a. DNA Extraction Results

The visualization results of *Spirulina* DNA extraction can be seen in [Figure 2](#).

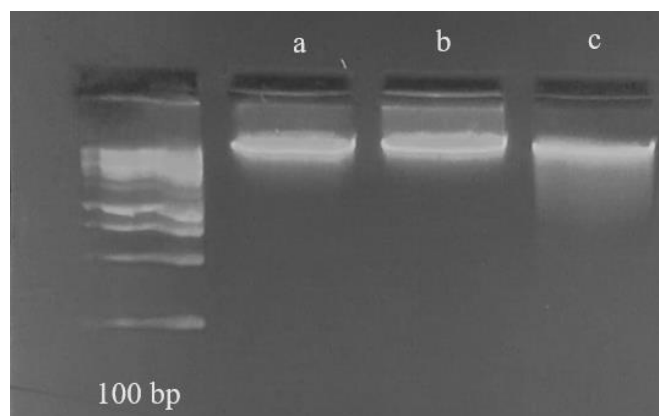


Figure 2. Visualization results of DNA extraction (a) BGR, (b) JPR, dan (c) MRP. The 16S rRNA gene was used as the DNA marker for molecular identification

Based on the results above, it is known that the three strains have fairly good genomic DNA bands. Strains BGR and JPR have relatively thick DNA bands, whereas strain MRP shows a slight smear on its DNA band. The thickness of the DNA bands indicates the concentration level of DNA in the sample; the thicker the DNA band, the higher the DNA concentration ([Alfaruqi, 2021](#)). The presence of smearing on the DNA band is caused by contaminants such as proteins and residual solution during the isolation process ([Iqbal et al., 2016](#)).

b. The results of DNA amplification

The results of the *Spirulina* DNA amplification can be seen in [Figure 3](#).

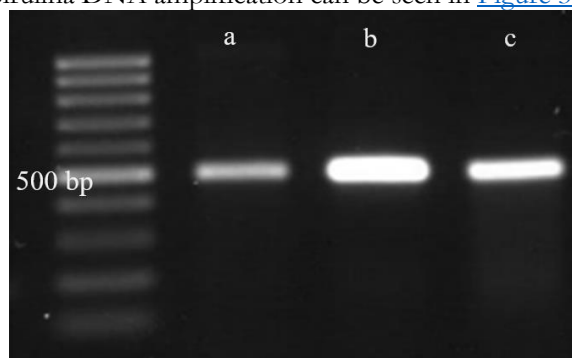


Figure 3. Visualization results of the 16S DNA amplicon (a) BGR, (b) JPR, dan (c) MRP. The 16S rRNA gene was used as the DNA marker for molecular identification

Based on electrophoresis, the PCR technique using the designed primers successfully amplified the 16S rRNA gene from *Spirulina*. The presence of a DNA band around 500 bp indicates that the genomic DNA of *Spirulina* was successfully extracted as a template. The study by [Johnson et al. \(2022\)](#) showed that amplification of the V1–V3 region of the 16S rRNA gene using primers 27F–519R produced fragments approximately 450–550 bp in size, which were effective for identifying and analyzing the phylogenetic relationships of cyanobacteria. The successful amplification of the 16S rRNA gene indicates that the primers used were specific to the target gene and that the PCR amplification proceeded well. Furthermore, no non-specific bands or signs of DNA degradation were found, demonstrating that the primers have high specificity for the conserved region of the 16S rRNA gene.

c. DNA Sequencing Results

The DNA band sequencing results were used to determine the DNA sequence, from which the identity of the spirulina strain could be identified through BLAST analysis. BLAST (Basic Local Alignment Search Tool) is a bioinformatics method used to compare nucleotide or protein sequences with sequences available in databases (Strover & Clavalcanti, 2017). BLAST enables the identification of bacterial species, genus, or phylum based on genetic sequence similarity, especially in gene markers such as the 16S rRNA gene. BLAST analysis of the spirulina strain showed a very high similarity level, with an identity percentage around 99%. The BLASTn analysis results of Spirulina are shown in Table 1.

Table 1. BLASTn Analysis Results

Sample	Similarity (%)	Homologue	GenBank accession number
BGR	99,78%	<i>Arthrospira fusiformis</i> strain AICB 668	AY672721.1
JPR	99,34%	<i>Arthrospira</i> sp. IAQUASC-C0001	MT160371.1
MRP	99,12%	<i>Arthrospira</i> sp. IAQUASC-C0001	MT160371.1

The results show that the *Arthrospira* JPR and MRP isolates have the closest homology similarity to the *Arthrospira* sp. IAQUASC-C0001 species, with percentages of 99.34% and 99.12%, respectively. Meanwhile, the *Arthrospira* BGR isolate has the closest homology similarity to *Arthrospira fusiformis* strain AICB 668 16S ribosomal RNA gene, partial sequence, with a similarity percentage of 99.78%. The high identity percentage (>99%) indicates a close phylogenetic relationship with the species found in the database (Aristya et al., 2025). The similarity percentage in this study is lower compared to the research by Szubert et al. (2021), which stated that spirulina found in the Baltic Sea with codes CCNP1310 and 06S082 showed 100% similarity with *S. subsalsa* PD2002/gca and *S. subsalsa* KD 01, indicating similarity above 97%. Lin et al. (2023) stated that bacterial identification at the species level using the 16S rRNA gene requires a higher sequence similarity threshold, namely above 99% or >99.5%. This is used to improve the accuracy of taxonomic determination.

d. Phylogenetic Analysis

The phylogenetic analysis can be seen in Figure 4.

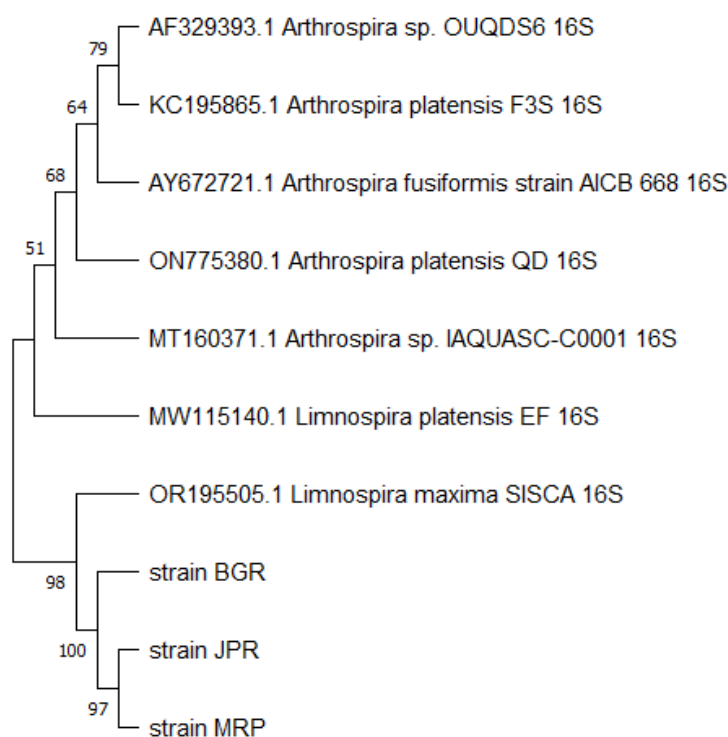


Figure 4. Phylogenetic tree based on the maximum-likelihood method

Based on [Figure 4](#), the 16S rRNA gene sequences show a phylogenetic relationship among three isolates, namely BGR, JPR, and MRP, with several *Arthrospira* and *Limnospira* species from GenBank. These three isolates form the same clade and are separated from the *Limnospira* group. The bootstrap values obtained are relatively high, ranging from 97 to 100, indicating strong confidence in this grouping. Such high bootstrap values suggest that the three isolates have a very close genetic relationship with each other. [Puspitasari et al. \(2025\)](#) state that the higher the bootstrap value, the greater the accuracy of the tree topology resulting from the reconstruction.

Strains BGR, JPR, and MRP show the highest phylogenetic closeness to *Arthrospira* sp. IAQUASC-C0001 and *Arthrospira fusiformis* strain AICB 668, consistent with the BLAST analysis results ([Table 1](#)), which show sequence similarity exceeding 99%. *Limnospira platensis* and *Limnospira maxima* are placed in a different clade, indicating taxonomic separation between the genera *Arthrospira* and *Limnospira*. Although BLASTn analysis ([Table 1](#)) shows the highest sequence similarity to *Arthrospira* species, the phylogenetic reconstruction ([Figure 4](#)) places all isolates within the *Limnospira* clade. This discrepancy is likely due to recent taxonomic revisions, where several species previously classified as *Arthrospira* are now assigned to the genus *Limnospira* ([Sinetova et al., 2024](#)). Therefore, based on phylogenetic inference, the isolates are more appropriately identified as *Limnospira*. This grouping pattern shows that the isolates studied are genetically more closely related to the genus *Arthrospira* than to *Limnospira*. This supports the identification of the isolates as members of the genus *Arthrospira*. This aligns with the research of [Zhang et al. \(2022\)](#), where BLAST results showed that the 16S rRNA sequence similarity of the study isolates with *Arthrospira* in GenBank was more than 99%, indicating that *Arthrospira* isolates have high genetic homology and form a single clade in phylogenetic analysis. This study shows that the observed morphological variation more likely reflects phenotypic responses to different environmental conditions rather than significant genetic differences. [Emam et al. \(2025\)](#) state that spirulina with diverse morphological forms still has a high genetic similarity of around 95%, based on molecular marker analysis

Conclusion

The conclusion obtained is that *Spirulina* has filamentous forms that vary, both spiral and linear, influenced by genetic and environmental factors. Based on homology similarity, the BGR strain has 99.78% similarity with *Arthrospira fusiformis* strain AICB 668, while JPR and MRP have 99.34% and 99.12% similarity with *Arthrospira* sp. IAQUASC-C0001, respectively. Based on genetic distance analysis, the BGR, JPR, and MRP strains have an evolutionary distance closer to *Arthrospira* than to *Limnospira*. High genetic similarity does not always correlate directly with morphological uniformity, as the phenotypic expression of an organism can be influenced by environmental factors and genetic regulatory mechanisms.

Author Statements

Acknowledgements and funding statements: This research is supported by the Universitas Sebelas Maret Research Grant with contract number PF (Fundamental Research): 369/UN27.22/PT.01.03/2025.

Competing of interest: The authors declare no competing interests

Author's contributions: Bahana Safiria Dito: research design, data collection, data analysis, and manuscript writing. Sajidan: conceptualization, critical revision of the manuscript, and final approval of the manuscript. Ari Susilowati and Yasir Sidiq: critical revision of the manuscript and literature review. All authors have read and approved the final version of the manuscript.

Generative AI: Not applicable

Data availability: The data supporting the findings of this study are available from the corresponding author upon reasonable request.

References

- Alfaruqi, H. Q. D. (2021). Kajian Molekuler Pada Probiotik Asal Air Susu Ibu Dalam sintesis eksopolisakarida (EPS). *Jurnal Bioteknologi dan Biosains Indonesia*, 8(1), 114-123. [10.29122/jbbi.v8i1.4554](https://doi.org/10.29122/jbbi.v8i1.4554)
- Aristya, G. R., Judith, T. P., Kasiamdari, R. S., Damaiyani, J., & Arif, M. F. (2025). Molecular identification and phylogenetic reconstruction of sugarcane (*Saccharum officinarum* L.) cultivars from Indonesia

- based on rbcL chloroplast gene. *Australian Journal of Crop Science*, 19(6), 620-632. <https://search.informit.org/doi/10.3316/informit.T2025072900005300939774002>
- Balouch, H., Zayadan, B.K., Sadvakasova, A.K., Kossalbayev, B.D., Bolatkhan, K., Gencer, D., Civelek, D., Demirbag, Z., Alharby, H.F. and Allakhverdiev, S.I., 2023. Prospecting the biofuel potential of new microalgae isolates. *International Journal of Hydrogen Energy*, 48(50), pp.19060-19073. <https://doi.org/10.1016/j.ijhydene.2023.02.028>
- Buddington, K.K., J.B. Donahoo, and R.K., Buddington. 2002. Dietary oligofructose and inulin protect mice from enteric and systemic pathogens and tumor inducers. *J. Nutr.* 132:472-477. <https://doi.org/10.1093/jn/132.3.472>
- Buwono, N. R., & Nurhasanah, R. Q. (2018). Studi Pertumbuhan Populasi Spirulina sp. pada Skala Kultur yang Berbeda [Study of Spirulina sp. Population Growth in The Different Culture Scale]. *Jurnal Ilmiah Perikanan dan Kelautan*, 10(1), 26-33. <https://doi.org/10.20473/jipk.v10i1.8516>
- Chotchindakun, K., Buddhasiri, S., & Kuntanawat, P. (2024). Enhanced Growth and Productivity of *Arthrospira platensis* H53 in a Nature-like Alkalophilic Environment and Its Implementation in Sustainable *Arthrospira* Cultivation. *Sustainability*, 16(19), 8627. <https://doi.org/10.3390/su16198627>
- Emam, H. A., Abdel-Sattar, E., Salama, M. M., Salem, M. A., & Hashem, M. M. (2025). Spirulina platensis: Unveiling phenotypic plasticity impact on its metabolic profile and bioactivity via chemometric analysis. *Food Bioscience*, 63, 105605. <https://doi.org/10.1016/j.fbio.2024.105605>
- Furmaniak, M. A., Misztak, A. E., Franczuk, M. D., Wilmotte, A., Waleron, M., & Waleron, K. F. (2017). Edible cyanobacterial genus *Arthrospira*: Actual state of the art in cultivation methods, genetics, and application in medicine. *Frontiers in Microbiology*, 8, 2541. <https://doi.org/10.3389/fmicb.2017.02541>
- Iqbal, M., Buwono, I. D., & Kurniawati, N. (2016). Analisis perbandingan metode isolasi DNA untuk deteksi White Spot Syndrome Virus (WSSV) pada udang Vaname (*Litopenaeus vannamei*). *Jurnal Perikanan Kelautan*, 7(1). <https://jurnal.unpad.ac.id/jpk/article/view/13941>
- Johnson, M. S., Burns, B. P., Herdean, A., Angeloski, A., Ralph, P., Morris, T., ... & Larkum, A. W. (2022). A cyanobacteria enriched layer of Shark Bay stromatolites reveals a new *Acaryochloris* strain living in near infrared light. *Microorganisms*, 10(5), 1035. <https://doi.org/10.3390/microorganisms10051035>
- Jung, C. H., Braune, S., Waldeck, P., Küpper, J. H., Petrick, I., & Jung, F. (2021). Morphology and growth of *Arthrospira platensis* during cultivation in a flat-type bioreactor. *Life*, 11(6), 536. <https://doi.org/10.3390/life11060536>
- Karamalis, C., Xirogianni, A., Simantirakis, S., Delegkou, M., Papandreou, A., & Tzanakaki, G. (2025). Molecular Identification of Meningitis/Septicemia Due to *Streptococcus* spp. in Greece (2015–2024). *Diagnostics*, 15(13), 1632. <https://doi.org/10.3390/diagnostics15131632>
- Ko, J. T., Li, Y. Y., Chen, P. Y., Liu, P. Y., & Ho, M. Y. (2024). Use of 16S rRNA gene sequences to identify cyanobacteria that can grow in far-red light. *Molecular Ecology Resources*, 24(1), e13871. <https://doi.org/10.1111/1755-0998.13871>
- Lach, L., Khomutovska, N., Kwiatowski, J., & Jasser, I. (2024). Testing 16S Primers for Proper Identification of Cyanobacterial Communities in Small Water Bodies. *Water*, 16(10), 1357. <https://doi.org/10.3390/w16101357>
- Lao, I. K. M., & Edullantes, B. (2025). Growth, Productivity, and Size Structure of Spirulina Strain Under Different Salinity Levels: Implications for Cultivation Optimization. *Phycology*, 5(3), 31. <https://doi.org/10.3390/phycolgy5030031>
- Lestari, M. D., & Pangastuti, A. (2025). Laju Pertumbuhan, Biomassa, dan Produksi Fikosianin *Arthrospira platensis* Perairan Pulau Jawa Pada Variasi Salinitas. *Bioscientist: Jurnal Ilmiah Biologi*, 13(4), 2848-2857. <https://doi.org/10.33394/bioscientist.v13i4.18387>
- Li, M. N., Han, Q., Wang, N., Wang, T., You, X. M., Zhang, S., ... & Zhang, G. F. (2024). 16S rRNA gene sequencing for bacterial identification and infectious disease diagnosis. *Biochemical and Biophysical Research Communications*, 739, 150974. <https://doi.org/10.1016/j.bbrc.2024.150974>
- Lijassi, I., Arahou, F., Mansouri, Z., Wahby, A., Rhazi, L., & Wahby, I. (2024). Comparative Analysis of Effect of Culture Conditions on Growth and C-Phycocyanin Production in Helical and Linear Spirulina. *Current Microbiology*, 81(6). <https://doi.org/10.1007/s00284-024-03684-y>



- Lin, J. N., Lai, C. H., Yang, C. H., & Huang, Y. H. (2023). Validation of 16S rRNA and complete rpoB gene sequence analysis for the identification of Elizabethkingia species. *International Journal of Molecular Sciences*, 24(16), 13007. <https://doi.org/10.3390/ijms241613007>
- Mishra, P., Mishra, R. R., Prasad, S. M., & Nath, G. (2022). Isolation and molecular characterization of nutritionally potent *Arthrospira maxima* from Indian paddy field. *Biocatalysis and Agricultural Biotechnology*, 42, 102338. <https://doi.org/10.1016/j.bcab.2022.102338>
- Misztak, A. E., Waleron, M., Furmaniak, M., Waleron, M. M., Bazhenova, O., Daroch, M., & Waleron, K. F. (2021). Comparative genomics and physiological investigation of a new *Arthrospira/Limnospira* strain O9. 13F isolated from an alkaline, winter freezing, Siberian lake. *Cells*, 10(12), 3411. <https://doi.org/10.3390/cells10123411>
- Nosratimovafagh, A., Esmaeili Fereidouni, A., & Kruczak, F. (2023). Effect of light spectrum, salinity, and glucose levels on *Spirulina* morphology. *Journal of the World Aquaculture Society*, 54(6), 1687-1701.
- Puspitasari, A., Budiarsa, I. M., Ashari, A., Dhafir, F., Windarsih, Y., & Trianto, M. (2025). Analisis Filogenetik Cryptic species *Apis cerana* Fabricius, 1793 Berdasarkan Gen 16S rRNA. *Bioscientist: Jurnal Ilmiah Biologi*, 13(1), 521-530. <https://doi.org/10.33394/bioscientist.v13i1.14967>
- Rilisa, C & Suantika, G. (2021). Biological, Technical, and Financial Feasibilities Study *Spirulina* sp. Biomass Production with Modified Commercial Medium in Indonesia, *3BIO: Journal of Biological Science, Technology and Management*, 3(2):67-76. <https://doi.org/10.5614/3bio.2021.3.2.2>
- Selvendran, D. (2015). Large scale algal biomass (*Spirulina*) production in India. In *Algal biorefinery: An integrated approach* (pp. 151-167). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-319-22813-6_7
- Sinetova, M. A., Kupriyanova, E. V., & Los, D. A. (2024). *Spirulina/Arthrospira/Limnospira*—Three names of the single organism. *Foods*, 13(17), 2762. <https://doi.org/10.3390/foods13172762>
- Stover, N. A., & Cavalcanti, A. R. (2017). Using NCBI BLAST. *Current Protocols Essential Laboratory Techniques*, 14(1), 11-1. <https://doi.org/10.1002/cpet.8>
- Supriatna, M., Mahmudi, M., & Musa, M. (2020). Model pH dan hubungannya dengan parameter kualitas air pada tambak intensif udang vaname (*Litopenaeus vannamei*) di Banyuwangi Jawa Timur. *JFMR (Journal of Fisheries and Marine Research)*, 4(3), 368-374. <https://doi.org/10.21776/ub.jfmr.2020.004.03.8>
- Susintowati, S. H., Puniawati, N., Poedjirahajoe, E., & Handayani, N. S. N. (2018, July). Plastisitas Fenotip Gastropoda Mangrove Taman Nasional Alas Purwo: Morfometri Cangkang Dan Operkulum. In *PROSIDING SEMINAR NASIONAL*. <https://ejournal.unisri.ac.id/index.php/prosemnas/article/view/2105>
- Szubert, K., Toruńska-Sitarz, A., Stoń-Egiert, J., Wiglusz, M. and Mazur-Marzec, H., 2021. Comparative characterization of two cyanobacteria strains of the order Spirulinales isolated from the Baltic Sea-polyphasic approach in practice. *Algal Research*, 55, p.102170. <https://doi.org/10.1016/j.algal.2020.102170>
- Thevarajah, B., Nishshanka, G. K. S. H., Premaratne, M., Nimarshana, P. H. V., Nagarajan, D., Chang, J. S., & Ariyadasa, T. U. (2022). Large-scale production of *Spirulina*-based proteins and c-phycoyanin: A biorefinery approach. *Biochemical Engineering Journal*, 185, 108541. <https://doi.org/10.1016/j.bej.2022.108541>
- Ujwala, et al. (2025). Life between Salt and Fresh: The Unique World of Brackish Water Habitats. *Journal of Marine Science: Research & Development*, 15(1), pp. 490. <https://www.omicsonline.org/open-access-pdfs/life-between-salt-and-fresh-the-unique-world-of-brackish-water-habitats.pdf>
- Wan, D., Wu, Q., & Kuča, K. (2016). *Spirulina*. In *Nutraceuticals* (pp. 569-583). Academic Press.
- Zapata, D., Arroyave, C., Cardona, L., Aristizábal, A., Poschenrieder, C., & Llugany, M. (2021). Phytohormone production and morphology of *Spirulina platensis* grown in dairy wastewaters. *Algal Research*, 59, 102469. <https://doi.org/10.1016/j.algal.2021.102469>
- Zhang, J., Xue, H., Yan, S., Shi, H., Du, L., Zhang, J., ... & Ma, C. (2022). Phylogenetic analysis of *Arthrospira* strains from Ordos based on 16S rRNA. *Scientific Reports*, 12(1), 14375. <https://doi.org/10.1038/s41598-022-18695-7>