

Microbial and Physiochemical Analysis of Water From Semenggok Inland Fishery Centre, Kuching, Sarawak

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Abstract

Water quality is emphasized by the aquaculture sector as it affects the health and growth performance of aquaculture species. However, due to the outbreak of COVID-19 pandemic in Malaysia, various sectors including aquaculture sector, have been instructed to shut down as a lockdown alternative to control the spread of the disease. The total lockdown has made impossible to give proper management to the aquaculture ponds and indirectly led to the high mortality of aquaculture organisms. High mortality has led to rapid microbial growth, which affected the water quality and the balance in the aquaculture system.

The objective of this project was to examine the water quality of selected ponds at Semenggok Inland Fishery Centre via physiochemical and microbial analysis. This project also aimed to determine and identify the bacteria population in examined water samples. Lastly, this project sought to determine the antimicrobial susceptibility patterns of identified isolates.

In this study, the characteristics of aquaculture environmental samples were determined. Water and soil samples were collected from three randomly selected ponds in the Semenggok Inland Fishery Centre, Kuching, Sarawak and the physiochemical and biological parameters were analysed. Bacteria were isolated from both water and soil samples and then characterised. Boiling-centrifugation method with modifications were used for DNA extraction of the bacteria ^[1,2]. (GTG)₅-PCR was utilized to screen for clonal diversity among the isolates. A dendrogram was constructed using GelJ 1.0 software from the banding profile of (GTG)₅-PCR products ^[3]. Out of all the isolates analysed, 11 representative isolates were selected for 16S rRNA sequencing based on the grouping from the dendrogram. The 11 isolates were identified as *Brevundimonas* sp., *Staphylococcus* sp., *Pseudomonas* sp., *Escherichia* sp., *Ralstonia* sp., and *Exiguobacterium* sp. (Table 1).

Table 1: The isolation code, bacteria identity and similarity percentage of the isolate after BLAST analysis

Isolates Code	Bacteria Identity	Similarity Percentage
6	<i>Brevundimonas vancanneytii</i>	99.07%
7	<i>Ralstonia</i> sp.	99.19%
8	<i>Escherichia coli</i>	98.98%
12	<i>Ralstonia pickettii</i>	98.48%
20	<i>Ralstonia mannitolilytica</i>	99.60%
23	<i>Brevundimonas diminuta</i>	99.77%
29	<i>Staphylococcus</i> sp.	99.40%

33	<i>Staphylococcus warneri</i>	99.20%
37	<i>Brevundimonas faecalis</i>	99.31%
41	<i>Pseudomonas stutzeri</i>	97.13%
45	<i>Exiguobacterium aurantiacum</i>	99.61%

The isolates were tested for antibiotic resistance using the disc diffusion method. Most of the isolates tested were resistant to ampicillin (10 µg), penicillin (10 µg), and streptomycin (10 µg). The MAR index of isolates were calculated, ranged from 0.143 to 0.714, indicating high possibility of culturing fish in the contaminated water. This study revealed the risk of presence of multiple antibiotic resistance (MAR) bacteria in the fishery centre. Therefore, the fishery centre should improve the aquaculture system by constantly monitoring and also provide a proper management to the wastewater to minimise the distribution of MAR bacteria.

Keywords

Antimicrobial susceptibility testing, (GTG)₅-PCR, 16S rRNA sequencing

References

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