



Article

Bacterial Community Composition and Prevalence of Aeromonas dhakensis in Four Tilapia Freshwater Aquaculture Systems in Malaysia

Sook Ling Lim ¹, Suat Moi Puah ^{1,*}, Siti Nursyuhada Baharudin ², Nur Insyirah Mohd Razalan ¹, Kieng Soon Hii ², Wei Ching Khor ³, Yen Ching Lim ³, Kyaw Thu Aung ^{3,4,5}, Kek Heng Chua ¹, Po Teen Lim ² and Chui Pin Leaw ^{2,*}

- Department of Biomedical Science, Faculty of Medicine, Universiti Malaya, Kuala Lumpur 50603, Malaysia; evanlim0516@um.edu.my (S.L.L.); 23099664@siswa.um.edu.my (N.I.M.R.); khchua@um.edu.my (K.H.C.)
- Bachok Marine Research Station, Institute of Ocean and Earth Sciences, Universiti Malaya, Bachok 16310, Kelantan, Malaysia; 22065965@siswa.um.edu.my (S.N.B.); hiiks@um.edu.my (K.S.H.); ptlim@um.edu.my (P.T.L.)
- National Centre for Food Science, Singapore Food Agency, 7 International Business Park, Singapore 609919, Singapore; khor_wei_ching@sfa.gov.sg (W.C.K.); lim_yen_ching@sfa.gov.sg (Y.C.L.); aung_kyaw_thu@sfa.gov.sg (K.T.A.)
- Department of Food Science and Technology, National University of Singapore, Science Drive 2, Singapore 117543, Singapore
- School of Biological Sciences, Nanyang Technological University, 60 Nanyang Dr, Singapore 637551, Singapore
- * Correspondence: suatmoi@um.edu.my (S.M.P.); cpleaw@um.edu.my (C.P.L.)

Abstract: The tilapia (*Oreochromis*) aquaculture industry in Malaysia has expanded rapidly to meet the increasing demand for animal protein. However, this growth is challenged by microbial infections, particularly those caused by the emerging pathogen Aeromonas dhakensis. This study aimed to investigate the microbial community composition across four distinct tilapia farming systems and assess associated water physicochemical parameters, with a focus on detecting the presence of A. dhakensis and elucidating its environmental associations. Water physicochemical parameters were measured to evaluate environmental conditions, microbial communities were characterized through 16S rDNA metabarcoding, and A. dhakensis was detected using both microbiological and molecular approaches. Principal component analysis (PCA) and canonical correspondence analysis (CCA) were employed to explore the influence of environmental variables and microbial community dynamics on pathogen occurrence. Our results indicated that floating cages exhibited higher levels of temperature, ammonium, and fecal coliform, while cement tanks showed signs of nutrient accumulation. PCA revealed that both systems were associated with degraded water quality. A total of 45 A. dhakensis strains with distinct fingerprints were isolated. The 16S metabarcoding revealed Proteobacteria, Actinobacteria, and Planctomycetota as the dominant phyla. Alpha diversity did not differ significantly among pond systems, while beta diversity revealed variations in microbial assemblages across aquaculture systems. CCA identified dissolved oxygen, temperature, macronutrients (phosphate, ammonium, nitrate, and nitrite), and turbidity as significant environmental drivers shaping the microbial community structure across the pond systems. In conclusion, this study highlights the importance of environmental factors, particularly dissolved oxygen, temperature, and nutrient levels, in shaping microbial community composition and potentially influencing the presence of pathogenic bacteria such as A. dhakensis. These findings underscore the need for improved environmental management in tilapia aquaculture to mitigate disease risks and support fish health.



Academic Editor: Jiong Chen

Received: 11 March 2025 Revised: 24 April 2025 Accepted: 28 April 2025 Published: 1 May 2025

Citation: Lim, S.L.; Puah, S.M.;
Baharudin, S.N.; Mohd Razalan, N.I.;
Hii, K.S.; Khor, W.C.; Lim, Y.C.; Aung,
K.T.; Chua, K.H.; Lim, P.T.; et al.
Bacterial Community Composition
and Prevalence of *Aeromonas dhakensis*in Four Tilapia Freshwater
Aquaculture Systems in Malaysia. *Fishes* 2025, 10, 204. https://doi.org/
10.3390/fishes10050204

Copyright: © 2025 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/ licenses/by/4.0/).