



## Article DNA Barcoding and Phylogenetics Relationship of Pangasiid Catfishes in Peninsular Malaysia Revealed the Impacts of Aquaculture on the Native Species Conservation

Baharuddin Haslawati<sup>1,\*</sup>, Md Ali Amatul-Samahah<sup>1</sup>, Mohammed Rizman-Idid<sup>2</sup> and Sekaran Muniandy<sup>3</sup>

- <sup>1</sup> Fisheries Research Institute, Glami Lemi, Titi Jelebu 71660, Negeri Sembilan, Malaysia; amatul@dof.gov.my
- <sup>2</sup> Institute of Ocean and Earth Sciences, Universiti Malaya, Kuala Lumpur 50603, Malaysia
- <sup>3</sup> Faculty of Medicine, MAHSA University, Bandar Saujana Putra, Jenjarom 42610, Selangor, Malaysia
- \* Correspondence: haslawati@dof.gov.my

Abstract: Pangasiids are an economically significant group of catfish, and many pangasiids are threatened in the wild from anthropogenic pressures, including increases in fishing pressure, habitat degradation, and improperly managed aquaculture practices. This study demonstrates the usage of DNA barcoding of the Cytochrome Oxidase subunit I (COI) gene as an identification tool in detecting potentially threatening invasive pangasiid species by establishing the diversity and phylogenetic relationship of Pangasiidae catfishes in Peninsular Malaysia. A neighbour-joining (NJ) dendrogram (Kimura-2-parameter model) generated five clades to represent distinct genera. Pangasius was further subdivided into two clades (Clade A: Pangasius bocourti-P. djambal and Clade B: P. nasutus-P. conchophilus). Given the marginal genetic divergence, indigenous and non-native species should be treated cautiously in allopatrically distributed species. The analysis used Automatic Barcode Gap Discovery (ABGD) and revealed barcode gaps between the intraspecific and interspecific distances. The sequences were partitioned into five groupings, corresponding with the species delineation based on the distribution of pairwise differences, which could not be differentiated using the NJ dendrogram. ABGD allows the recognition of one or two additional species using the recursive approach, but other taxonomic methods should be considered for a solid conclusion. DNA barcoding demonstrates the identification of closely related species, thus justifying its application towards the conservation of these fish.

Keywords: DNA barcoding; catfish; native species; taxonomy; aquaculture

## 1. Introduction

Fish of the family Pangasiidae are medium- to large-sized catfish with diverse morphologies and ecologies [1]. Adults range from 20 to 300 cm in length, but most species are larger than 50 cm. Pangasiids are generally found in freshwater areas; however, some species can be found in brackish and marine environments [2,3]. Pangasiid catfish are widely distributed throughout Asia, ranging from the Indian subcontinent, the Indo-Malayan Archipelago [3], and China [4]. Kottelat (2013) catalogued four valid genera: *Helicophagus* Bleeker, 1858; *Pangasianodon* Chevey, 1930; *Pangasius* Valenciennes, in Cuvier & Valenciennes, 1840; and *Pseudolais*, Vaillant, 1902 [5,6], which comprises 30 species [7]. Several taxonomic ambiguities were encountered with respect to this group within these genera due to the morphological variations between conspecifics found on the Asian Mainland and the Indo-Malayan Archipelago [3]. These included morphologically disparate life stages [8], species complexes [6,9], and local-scale ecological variations in morphology [1,3,6,7,10].

Pangasiids are highly valued in aquaculture, and the demand for these fish is rapidly increasing. The major markets include the European and Asian countries, Mexico, Australia, the USA, the Middle East, and Russia [11,12]. The most commercially farmed Pangasius species are *Pangasius bocourti* and *Pangasianodon hypophthalmus* (also known as 'iridescent



Citation: Haslawati, B.; Amatul-Samahah, M.A.; Rizman-Idid, M.; Muniandy, S. DNA Barcoding and Phylogenetics Relationship of Pangasiid Catfishes in Peninsular Malaysia Revealed the Impacts of Aquaculture on the Native Species Conservation. *Hydrobiology* 2023, 2, 431–445. https://doi.org/ 10.3390/hydrobiology2020028

Academic Editor: Constanze Pietsch

Received: 9 April 2023 Revised: 20 May 2023 Accepted: 24 May 2023 Published: 20 June 2023



**Copyright:** © 2023 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/).