



## RESEARCH PAPER

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## Mitochondrial gene marker sequences reveal identities of gobies at Minalungao National Park, Nueva Ecija, Philippines

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### Abstract

Gobiidae is a rapidly growing family besides being the largest, with new species continuously discovered in all parts of the world, specifically in Asia and in the Philippines. Given this diversity, this study provides an initial identification and is the first report of gobies found at Minalungao National Park, a Key Biodiversity Area (KBA) in Central Luzon, Philippines. Goby species were identified molecularly using mitochondrial genes namely: CO1 (Cytochrome Oxidase 1), Control Region or D-Loop, and 16s rRNA. Samples were collected along Minalungao River. DNA was extracted from muscle tissues and gene markers were amplified using polymerase chain reaction. Sequences were subjected to BLAST for species identification. Results showed CO1 sequences ranging from 712-719 bp; D-Loop at 781-841 bp; and 559-592 bp in 16srRNA. BLAST sequences revealed four species of gobies belonging to 2 genera namely *Rhinogobius giurinus* (99% maximum identity using 16srRNA, 95% with D-Loop), *Rhinogobius brunneus* (97% matched using CO1), *Glossogobius bicirrhosus* (82% matched with D-Loop), and *Glossogobius giuris* (with 87% CO1 match).

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## Introduction

The Philippines is one of the mega diverse countries that holds around 80% of the world's biodiversity (Conservation International, 2006; DENR-PAWB, 2006) with the highest form of endemism in an area. While most fish biodiversity studies are focused on marine species, researches on inland or freshwater fishes are mostly focused on commercially important species. With more endemic species to be discovered, biodiversity and identification studies are warranted. Among these fishes are the gobies under the Family Gobiidae. It is largely marine though with fresh water representatives, with newer species continuously discovered and named, mostly in Asia and in the Philippines where approximately 146 species of Gobiidae are known to occur with seven (7) endemic species and around 68 species native to the Philippines.

Among the areas that needs to be assessed for gobies is the Minalungao National Park, a Key Biodiversity Area (KBA) in Central Luzon, Philippines. Through the efforts of the government to protect and conserve its natural resources, Minalungao forests was designated as a protected National Park. It covers 2,018 hectares of thick, unexplored forests and affluent rivers, and indeed, requires attention for conservation. Thus, a biodiversity assessment is imperative to help design better plans for its protection and conservation.

Accordingly, biodiversity assessment requires species identification. To accurately identify the species, molecular markers are employed. Mitochondrial markers are extensively used in identification and phylogenetic studies in fishes because of its rapid rate of evolution (Chauhan and Rajiv, 2010). Most molecular identification studies in fishes have relied on the analysis of mitochondrial DNA (mtDNA) sequence variation because of its maternal inheritance and high rate of mutation (Liu and Cordes, 2004; Angers and Bernatchez, 1998; Sato *et al.*, 2003). Among these markers are the CO1 (Cytochrome oxidase 1), used as a standard barcode marker in fishes (Ward *et al.*, 2005); the Control

Region or D-Loop, for studying genetic variation among closely related individuals because of its highly divergent sequences (Walberg and Clayton, 1981), high mutation accumulation (Xie *et al.*, 2006) and fastest mutation rate among the mitochondrial genes; and the 16s rRNA, a common molecular marker to identify commercial fish and seafood species (Rasmussen and Morrisey, 2008) routinely used for determining phylogeny in fishes. This study provides an initial inventory of Gobiidae at Minalungao National Park, Philippines.

## Materials and methods

### Sample collection

The fish samples were collected from three sites along Minalungao River (15°17'52.36" N). Samples chosen for molecular identification were based on phenotypes and overall appearance. Goby fishes were quickly identified based on the description of Herre (1927) by having a fused ventral fin, unstalked eyes, thick lips and laterally compressed belly. Muscle tissue samples were preserved in 95% ethanol and stored at -20°C prior to DNA extraction. Voucher specimens were preserved in formaldehyde.

### DNA extraction

Genomic DNA from muscle tissue was extracted using DNeasy Tissue Kit (Qiagen® Group, Hilden Germany) following the manufacturer's protocol. About 180 µl Buffer ATL and 20µl proteinase K were mixed to homogenized tissue before incubation at 56°C. About 200 µl buffer AL and 200 µl of 95% ethanol were then added and vortexed, and the samples pipetted to the DNeasy Mini Spin Column to centrifuge at 8000 rpm for 1 min. The supernatant was discarded and the DNeasy Mini Spin Column was transferred to a new 2 ml tube. Five hundred microliter (500 µl) Buffer AW1 was dispensed to the sample and was centrifuged for 3 min. The flow-through was discarded again and the DNeasy Mini Spin Column was placed in a new 1.5 ml tube. Buffer AE was directly pipetted to the DNeasy Mini Spin Column membrane before subjecting to final centrifugation.

### Polymerase chain reaction

The target regions of the mitochondria were amplified using the specific primer pairs: COI-F (GGTCAACAAATCATAAAGATATTGG) and COI-R (TAAACTTCAGGGTGACCAAAAAATCA); 16SH (5'-CCGGTCTGAACTCAGATCACGT-3') and 16SL (5'-GTTTACCAAAAACATGGCTTC-3') (Heralde III *et al.*, 2010); Ormt-449UP (5'-CTAACTCCCAAAGCTAGGATTCT-3') and Ore012S-L (5'-CCCAGTTTGTTCGCGAGCTTTCGT-3') (Samonte *et al.*, 2003). PCR amplification was performed using a final volume of 30 µl comprised of 19.1 µl sterile distilled water, 3.0 µl PCR Buffer, 3.0 µl MgCl<sub>2</sub>, 1.2 µl dNTP's, 1.2 µl forward primer, 1.2 µl reverse primer, 0.3 µl Taq Polymerase Recombinant and 1.0 µl DNA template. PCR reaction was performed in a 96 – well programmable thermal cycler (Veriti) with the following program: initial denaturation of 94°C for 5 minutes; 35 cycles of denaturation for 1 minute at 94°C; annealing for 90 secs at 50°C; extension for 90 secs at 72°C; and a final extension of 5 min at 72°C with a hold of 4°C.

### DNA sequencing

The PCR products were sent to the Philippine Genome Center at National Institute of Molecular Biology and Biotechnology in University of the Philippines-Diliman, Quezon City, Philippines for purification and sequencing. Sequences were assembled using the ChromasLite and were subjected to Basic Local Alignment Search Tool (BLAST, NCBI) for identification.

### Results and discussion

The range of the contiguous sequences generated for CO1 were at 712bp and 719 bp; the Control region (D-loop) at 781-841 bp; and 16S rRNA from 558 to 608 bp). Using NCBI BLAST, CO1 sequences revealed the identities of *Rhinogobius brunneus* (97%) and *Glossogobius giuris* (87%). 16s and D-Loop (Control Region) revealed *Rhinogobius giurinus* (99%) and *Glossogobius bicirrhosus* species (82%).

The identity match of the sequences to *Rhinogobius brunneus* using two gene markers were congruent to the occurrence and diversity of this species in the Philippines and in other Asian countries where it is widely distributed (Chen *et al.*, 1999; Suk &Choe 2002; Froese & Pauly, 2006) where adults are generally found in lakes and rivers. This identification could help contribute to a baseline data for its conservation as this species faces a number of potential threats such as pollution and hydrological projects like dams and water diversion projects (Devi & Boguskaya, 2009) as well as overfishing for food consumption. Given a wider sampling area and collection time, it is supposed that more variants can be characterized from this species as they are generally known with several phenotypes based on shape and coloration which tend to be isolated according to habitat (fishbase.org), of which molecular identification is particularly useful. This supposition is true with the identification of another *Rhinogobius* species, *R. giurinus* through two gene markers, 16s and D-Loop, which are more sensitive markers to delineate closely related species. This identification comes as no surprise considering that this species have a large distribution area and has no known major widespread threats and has been assessed with a status of Least Concern in the IUCN list (Huckstorf, 2012). It has a wide distribution in Asia, as well and originally distributed over China, Taiwan, Korean, Japan, Bonin Islands, Ryukyu Islands and from Red river basin and Viet Nam (Masuda *et al.*, 1984; Chen & Shao, 1996, Xie *et al.*, 2001; Ngyuen, 2005, Serov *et al.*, 2006). This identification may serve as initial data on this species, especially those inhabiting Minalungao National Park as there is no concrete information available on the species population yet but was reported to have been caught in small trap nets in rivers with less abundance (Masuda *et al.*, 1984). They are found from large rivers to streams and in shallow waters over sandy bottom (Serov *et al.*, 2006). They are also found both upstream and estuaries, are carnivorous and lay their eggs under stones in river shoals and the larvae travel in both river and the sea and return to rivers (Masuda *et al.* 1984).

All the three gene markers used provided the identity for the *Glossogobius* species. Two *Glossogobius* species were identified, *G. giuris* and *G. bicirrhosus*. For *G. bicirrhosus* no species identity matched with the sequences using 16sRNA. However, D-Loop provided species identification at 82%. Similar with the *Rhinogobius* species, its identification is consistent with its reported large distribution area with no known major widespread threats to the species (Larson, 2012), which are found mainly in streams or sand bottoms (Allen, 1991). It is predominantly distributed in Indonesia, Philippines, Taiwan and Japan and is also reported from Melanesia, north-eastern Australia and Papua New Guinea. (Talwar & Jhingran, 1991). This species has a status of Least Concern at the IUCN Red List (2018). Comparable with the collected samples, *G. giuris* is usually characterized phenotypically with a brownish-yellow body as well as rounded, dark spots on the sides. Other specimens display mimicked coloration of the substrates, hence, dark and ivory coloration are observed (Keith *et al.*, 1999).

This study confirms previous reports that diversity of gobies are mostly found along this part of Luzon (Herre, 1927). Herre (1927) particularly mentioned that it is only along the North of the Philippines that they occur in such enormous quantities that their capture and preservation form one of the chief resources of the region and one of the most valuable sources of income. Endemism of gobies to inland waters are due to the archipelagic nature of the Philippines that in turn, contains various flora and fauna in its landscapes and seascapes (Vedra *et al.*, 2013). Studies on this should be a priority for the reason that high level of endemism of these fishes is a significant indicator of the local biodiversity (Sanda & Kovacic, 2009; Bagorodsky *et al.*, 2010).

Few studies were conducted despite goby species diversity (UPLB Limnological Research Station, 2011) in the Philippines. These studies usually utilize morphological characters and morphometrics in identifying goby fishes (Akihito & Meguro, 1975; Kok

& Blaber, 1976; Miller & Wongrat, 1979; Parenti & Maciolek, 1993; Chen *et al.*, 1995; Chen *et al.*, 1997; Chen *et al.*, 1999; Chen & Kottelat, 2003; Chen & Tan, 2005; Chen & Fang, 2006; Huang & Chen, 2007; Shibukawa & Aonuma, 2007; Jaafar & Larson, 2008; Hossain *et al.*, 2009; Greenfield & Jewett, 2011; Myers *et al.*, 2012; Froese & Pauly 2012; Kannan *et al.*, 2013). This leaves molecular identification of goby fishes bare and sparse especially in the Philippines (Keith *et al.*, 2010). This molecular identification of gobies at Minalungao National Park serves as baseline information for the gobies present in the area which could help in their conservation and aid in the prevention of potential threats to these species.

### Conclusion

The mitochondrial markers were successful in the identification of gobies at Minalungao National Park. Four species belonging to two genera were identified: *Rhinogobius brunneus*, *Rhinogobius giurinus*, *Glossogobius giuris* and *Glossogobius bicirrhosus* species. While only 4 species were identified in this study, we hypothesize that a large number of gobies can still be discovered and named with improved collection, timing, and more robust technology, hence, identification of more species is recommended.

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