

Genetic Diversity of the Endangered Mekong Giant Catfish, Striped Catfish, and Their Hybrids From Thailand

Authors: Phadphon, Poompat, Amontailak, Thitapa, Kotchantuek, Napatsakorn, Srithawong, Suparat, Kutanan, Wibhu, et al.

Source: Tropical Conservation Science, 12(1)

Published By: SAGE Publishing

URL: <https://doi.org/10.1177/1940082919869487>

The BioOne Digital Library (<https://bioone.org/>) provides worldwide distribution for more than 580 journals and eBooks from BioOne's community of over 150 nonprofit societies, research institutions, and university presses in the biological, ecological, and environmental sciences. The BioOne Digital Library encompasses the flagship aggregation BioOne Complete (<https://bioone.org/subscribe>), the BioOne Complete Archive (<https://bioone.org/archive>), and the BioOne eBooks program offerings ESA eBook Collection (<https://bioone.org/esa-ebooks>) and CSIRO Publishing BioSelect Collection (<https://bioone.org/csiro-ebooks>).

Your use of this PDF, the BioOne Digital Library, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at www.bioone.org/terms-of-use.

Usage of BioOne Digital Library content is strictly limited to personal, educational, and non-commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

BioOne is an innovative nonprofit that sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

Genetic Diversity of the Endangered Mekong Giant Catfish, Striped Catfish, and Their Hybrids From Thailand

Tropical Conservation Science
Volume 12: 1–9
© The Author(s) 2019
Article reuse guidelines:
sagepub.com/journals-permissions
DOI: 10.1177/1940082919869487
journals.sagepub.com/home/trc



Poompat Phadphon¹, Thitapa Amontailak¹,
Napatsakorn Kotchantuek², Suparat Srithawong¹,
Wibhu Kutanan¹ , and Chatmongkon Suwannapoom³

Abstract

Previous genetic investigations of the Mekong giant catfish (*Pangasianodon gigas* Chevey, 1913) and striped catfish (*Pangasianodon hypophthalmus* Sauvage, 1878) provided discordant results. Here, we sequenced mitochondrial (mt) DNA of the *cytochrome B* region, and a control region, to characterize the genetic variation of *P. gigas*, *P. hypophthalmus*, and hybrids of these two species. Among the three groups, *P. hypophthalmus* had the greatest diversity in both regions, yet all three studied groups showed lower genetic diversity compared to the results of previous studies. The Bayesian Skyline Plots showed a reduction in effective population sizes of the parental species. The hybrids were found to have a constant population size with a recent divergence time. As expected, the network and neighbor joining tree showed a close maternal genetic relationship between the hybrid and *P. hypophthalmus*, a reflection of the breeding between male *P. gigas* and female *P. hypophthalmus*. Our results provide genetic information on these endangered fish that will be useful for both conservation and commercial breeding programs.

Keywords

Mekong giant catfish, mitochondrial DNA, cytochrome B region, control region, Thailand

Introduction

The Mekong giant catfish (*Pangasianodon gigas* Chevey, 1913) and striped catfish (*Pangasianodon hypophthalmus* Sauvage, 1878) are 2 of the 11 *Pangasianodon* species found in Thailand (Roberts & Vidthayanon, 1991). Endemic to the Mekong River, *P. gigas* is one of the largest freshwater fish, measuring up to 3 m in length and weighing up to 300 kg (Hogan, Moyle, May, Zanden, & Baird, 2004). With a dramatic decrease in population size of up to 90% over three decades (Hogan et al., 2004), *P. gigas* was classified as a Critically Endangered A4abcd ver 3.1 on the IUCN Red List of Threatened Species (Hogan, 2013) and listed in Appendix I of the Convention on International Trade in Endangered Species of Wild Flora and Fauna (CITES). The decreasing number of *P. gigas* also led the Thai Department of Fisheries to initiate a captive breeding program, which, since 1985 has released thousands of *P. gigas* to the wild (Hogan, 2013).

In contrast, *P. hypophthalmus* (commonly known as “Sawai” across Thailand) is much smaller than *P. gigas*, weighing 2 to 10 kg. The species is also a commercially important freshwater fish, serving as a food source for mainland Southeast Asian countries, for example, Thailand, Laos, Cambodia, and Vietnam. Striped catfish significantly declined in Thailand from 1980 to 1990, and

¹Department of Biology, Faculty of Science, Khon Kaen University, Thailand

²Kaennakhon Witthayalai School, Khon Kaen, Thailand

³Department of Fishery, School of Agriculture and Natural Resources, University of Phayao, Thailand

Received 11 April 2019; Revised 23 July 2019; Accepted 23 July 2019

Corresponding Author:

Wibhu Kutanan, Department of Biology, Faculty of Science, Khon Kaen University, Khon Kaen 40002, Thailand.

Email: wibhu@kku.ac.th

Chatmongkon Suwannapoom, Department of Fishery, School of Agriculture and Natural Resources, University of Phayao, 40002, Thailand
Email: chatmongkonup@gmail.com



Creative Commons Non Commercial CC BY-NC: This article is distributed under the terms of the Creative Commons Attribution-NonCommercial 4.0 License (<http://www.creativecommons.org/licenses/by-nc/4.0/>) which permits non-commercial use, reproduction and distribution of the work without further permission provided the original work is attributed as specified on the SAGE and Open Access pages (<https://us.sagepub.com/en-us/nam/open-access-at-sage>)

in Cambodia in 2006; the declines led to it being classified as Endangered A2bd + 4bcd ver.3.1 on the IUCN species (The IUCN Red List of Threatened Species (Vidthayanon & Hogan, 2013). Intergenetic hybridization, or interspecies hybridization, has been used to create hybrids that receive a combination of beneficial parental characteristics, for example, hybrid vigor, fast development, and disease resistance (Burnside, 2004; Tave, 2003). Recently, interspecies hybridization between *P. gigas* and *P. hypophthalmus* has been initiated to counteract the economic disadvantages of both the giant and striped catfish; *P. gigas* grows slowly and is hard to rear, whereas *P. hypophthalmus* has an unpopular taste and yellow muscle color, making it unsuitable for export to western countries. The viable hybrid possesses commercially beneficial characteristics, for example, rapid development and the desired white muscle color (Panase, Amornlerdpison, & Mengumphan, 2013).

Previous genetic studies investigated *P. gigas* and its closely related species using mitochondrial (mt) DNA in the 16 rRNA region (Na-Nakorn et al., 2006) and in the mtDNA control region and autosomal microsatellites (Ngamsiri et al., 2007). The two studies provided discordant results in which the former stated that genetic variation in the Mekong giant catfish was commensurate with the other related species, including *P. hypophthalmus*, indicating that the Mekong giant catfish population might be more robust than currently thought and showed a genetic signature of the historically larger population due to wild origin. The latter study indicated low genetic variation in *P. gigas*, compared to other freshwater fish. However, to date, there have been no reports on the genetic variation and genetic sources of the hybrid species; in addition, no information has been published on the mtDNA of the *cytochrome B* (*cytB*) region of the parental species (*P. gigas* and *P. hypophthalmus*). Here, we report on sequencing data of the *cytB* and control regions from newly collected samples of *P. gigas* and *P. hypophthalmus* and their hybrids in Thailand, in order to provide a baseline for management strategies.

Materials and Methods

Sample Collection

We collected 117 tissue samples belonging to three fish groups, that is, (a) 48 samples of *P. gigas* from five farms: one from Sakon Nakhon Province (SK), in the north-east of Thailand, and four from Phayao Province (PY), Fisheries Stations at Chiang Rai Province (CR [FS]), Uttaradit Province (UT), and Chiang Rai Province (CR), in northern Thailand; (b) 44 wild samples of *P. hypophthalmus* from the Mun River, a tributary of Mekong River, in the Ubon Ratchathani Province (UB), north-eastern Thailand; and (c) 25

samples of hybrids from a farm in Chiang Mai Province (CM), northern Thailand (Figure 1; Table 1). All catfish were anesthetized with 0.1 mL/L Eugenol (in accordance with the EU Directive 2010/63/EU), and an approximately 1 cm² piece of anal fin or clip was collected and stored for around 1 year in absolute ethanol for further DNA extractions. Fish were then allowed to recover from the anesthetic and were released back into either the river (at the sampling site) or fish ponds.

In total, six farms were visited to collect captive samples (five for the *P. gigas* stock and one for the hybrid stock). The parent breeding stocks of *P. gigas* were from the Mekong River, whereas the parent breeding stocks for the hybrids were from different sources; the parental *P. gigas* group was from a farm in Chiang Rai Province, but the parental *P. hypophthalmus* was from an unknown origin in Ubon Ratchathani Province.

All samples were collected from 2016 to 2017 and were coded as PG for *P. gigas*, PH for *P. hypophthalmus* and HB for the hybrids. This research protocol was approved by the Laboratory Animal Research Centre, University of Phayao (No. UP-AE59-02-04-0005) and the Animal Ethics Committee of the Institute of Animals for Scientific Purpose Development of Thailand (No. U1-01205-2558).

DNA Extraction, Amplification, and Sequencing

We extracted genomic DNA using ZR Tissue & Insect DNA Mini PrepTM (Zymo Research Corp., USA). For the *cytB* region, 1,225 base pairs (bp) were amplified using modified primer pairs, that is, L14724 5'-GACTTGAAAAACCACCGTTG-3' and H15915 5'-CGATCTCCGGATTACAAGAC-3' (Xiao, Zhang, & Liu, 2001). For the control region, 855 to 859 bp were amplified using a modified primer pair, that is, L16007 5'-CCCAAAGCTAGGATTCTC-3' (Kocher et al., 1989) and a modified R-D loop: 5'-GTTTAG GGGTTTGACAGG-3' (Ngamsiri et al., 2007). A polymerase chain reaction (PCR) was performed with 38 to 40 cycles, each of which comprised a denaturation step at 94°C for 45 seconds; an annealing step at 58°C for the *cytochrome B*, and 56°C for the control region, for 45 seconds; and an extension at 72°C for 24 seconds. Each PCR reaction mixture had a total volume of 30 µL, including: 1 U *Taq* DNA polymerase, 0.1 mM dNTP, 1X buffer, 2.0 mM MgCl₂, 0.5 µM of each primer, and 50 ng DNA template. PCR amplicons were checked by electrophoresis using 1.5% agarose gel and then sent for sequencing at Macrogen Inc., South Korea. Both strands were sequenced with the same PCR primer pairs in both the *cytB* and control regions. An additional forward primer, namely L15519 5'-GGAGACCCAG AAAACTTTACCCC-3' (Xiao et al., 2001), was also used for *cytB* sequencing.

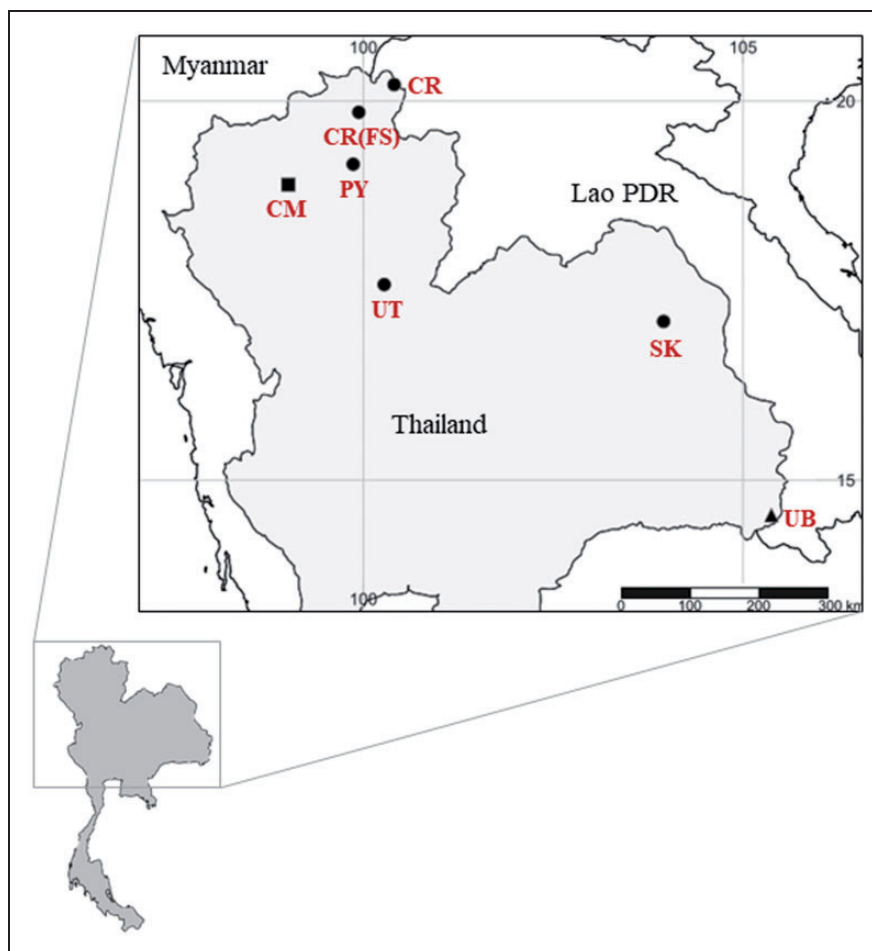


Figure 1. Locations where the samples were collected. Black circles (●) represent *P. gigas* samples. (PG_SK, PG_CR, PG_CR[FS]), PG_PY and PG_UT refer to *P. gigas* from Sakon Nakhon, Chiang Rai, Fisheries Station from Chiang Rai, Phayao and Uttaradit Provinces, respectively). Triangle (▲) represents *P. hypophthalmus* samples from Ubon Ratchathani Province (PH_UB). Square (■) represents hybrid samples from Chiang Mai Province (HB_CM). SK = Sakon Nakhon; PY = Phayao; CR (FS) = Fisheries station at Chiang Rai; UT = Uttaradit; CR = Chiang Rai; UB = Ubon Ratchathani; CM = Chiang Mai.

Table 1. Population Locations and Sizes of *P. gigas*, *P. hypophthalmus*, and Their Hybrids.

Species	Locations (population)	Code	Sample size	Latitude	Longitude
<i>P. gigas</i> (captive stock)	Sakon Nakhon Province	SK	11	17.092375	103.953983
	Phayao Province	PY	16	19.166961	99.866624
	Fisheries station at Chiang Rai Province	CR (FS)	2	19.851889	99.939976
	Uttaradit Province	UT	8	17.579447	100.275077
	Chiang Rai Province	CR	11	20.216885	100.406740
<i>P. hypophthalmus</i> (wild stock)	Ubon Ratchathani Province	UB	44	14.534353	105.374007
Hybrids (<i>P. gigas</i> × <i>P. hypophthalmus</i>) (captive stock)	Chiang Mai Province	CM	25	18.898045	99.012887

Statistical Analyses

The obtained sequences were edited and assembled using SeqScape software v2.7 (Applied Biosystem, USA). A multiple sequence alignment was executed with the reference sequences from Genbank—AY762971 for the

Mekong giant catfish (Jondeung, Sangthong, & Zardoya, 2007) and KC846907.1 for the striped catfish (Zhao, Kong, & Zhou, 2014)—using MAFFT 7.271 (Katoh & Standley, 2013). Sequences were manually checked again with Bioedit (www.mbio.ncsu.edu/BioEdit/bioedit.html).

Because the number of sequences on the *cytB* and control region were not equal (Table 2), separate analyses were conducted; Arlequin 3.5.1.3 (Excoffier & Lischer, 2010) was used to obtain the following summary statistics: number of haplotypes, haplotype diversity (h), nucleotide diversity (π), mean number of pairwise difference, and the neutrality estimators, that is, Fu's F_s (Fu, 1997) and Tajima's D (Tajima, 1989). Pairwise genetic distance (Φ_{st}) was also computed by Arlequin 3.5.1.3. A neighbor joining (NJ) tree (Saitou & Nei, 1987), with 1,000 bootstraps, was constructed with the software MEGA 7 (Kumar, Stecher, & Tamura, 2016). Median-joining networks (Bandelt, Forster, & Röhl, 1999), without pre- and postprocessing steps, were constructed with Network (www.fluxus-engineering.com).

For the control region, the Bayesian Skyline Plots (BSP), based on Bayesian Markov Chain Monte Carlo analyses, were created using BEAST 1.8.0. We did not perform BSP for *cytB* due to very low genetic variation. The jModel test 2.1.7 (Darriba, Taboada, Doallo, & Posada, 2012) was run in order to choose the most suitable models to create BEAST input files by BEAUTi v1.8.0 (Drummond, Suchard, Xie, & Rambaut, 2012). The HKY substitution model was used for the analyses of *P. gigas* and the hybrids, whereas the HKY+G model was used for *P. hypophthalmus*. The BSP calculations were executed with strict clocks and a mutation rate of 3.6×10^{-8} (Donaldson & Wilson, 1999). The analysis was run for 3×10^7 steps, sampling every 10^3 steps, under the piecewise-constant skyline model with a random starting tree. Tracer 1.6 was used to generate the BSP plot from the BEAST results.

Results

We generated a total of 107 sequences, each with a length of 637 bp (15714–16350), for the control region, and 86 sequences of 917 bp from 14474 to 15390 for the *cytB* region (GenBank accession numbers for *cytB* is MN027096-MN027181 and for control region is MN017599-MN017705). Genetic diversity values from both mtDNA segments were highest in *P. hypophthalmus* (Table 2), that is, haplotype diversity (h) = 0.8070 ± 0.0342 and nucleotide diversity (π) = 0.0171 ± 0.0088 for the control region; $h = 0.5376 \pm 0.0822$ and $\pi = 0.0007 \pm 0.0006$ for *cytB*. Although the hybrids were the group with the lowest sample size, their extremely low genetic diversity ($h = 0.1000 \pm 0.0880$ and $\pi = 0.0005 \pm 0.0006$ for the control region; $h = 0.1053 \pm 0.0920$ and $\pi = 0.0001 \pm 0.0002$ for *cytB*) did not differ much from that of *P. gigas* ($h = 0.6729 \pm 0.0202$ and $\pi = 0.0088 \pm 0.0048$ for the control region; $h = 0.0000 \pm 0.0000$ and $\pi = 0.0000 \pm 0.0000$ for *cytB*).

The nonsignificant p values of Fu's F_s and Tajima's D ($p > .01$) infer that there has been no previous

Table 2. Genetic Diversity Values.

	<i>cytB</i>			D-Loop		
	<i>P. gigas</i>	<i>P. hypophthalmus</i>	Hybrid	<i>P. gigas</i>	<i>P. hypophthalmus</i>	Hybrid
Sample size	36	31	19	48	39	20
Number of haplotypes	1	3	2	3	6	2
Haplotype diversity	0	0.5376 (0.0822)	0.1053 (0.092)	0.6729 (0.0202)	0.807 (0.0342)	0.1 (0.088)
Nucleotide diversity	0	0.000657 (0.000598)	0.000115 (0.000223)	0.008822 (0.004782)	0.017068 (0.008822)	0.000478 (0.000581)
Mean number of pairwise differences	0	0.602151 (0.492565)	0.105263 (0.182826)	5.619681 (2.744395)	10.701754 (4.978668)	0.3 (0.326275)
Segregating site	0	2	1	12	31	3
Tajima's D	0 (1)	0.41134 (0.709)	-1.1648 (0.145)	3.21227 (1)	1.59234 (0.969)	-1.72331 (0.017)
Fu's F_s test	0 (NA)	0.46237 (0.55)	-0.83782 (0.085)	12.8821 (0.996)	12.0008 (0.997)	0.5439 (0.395)

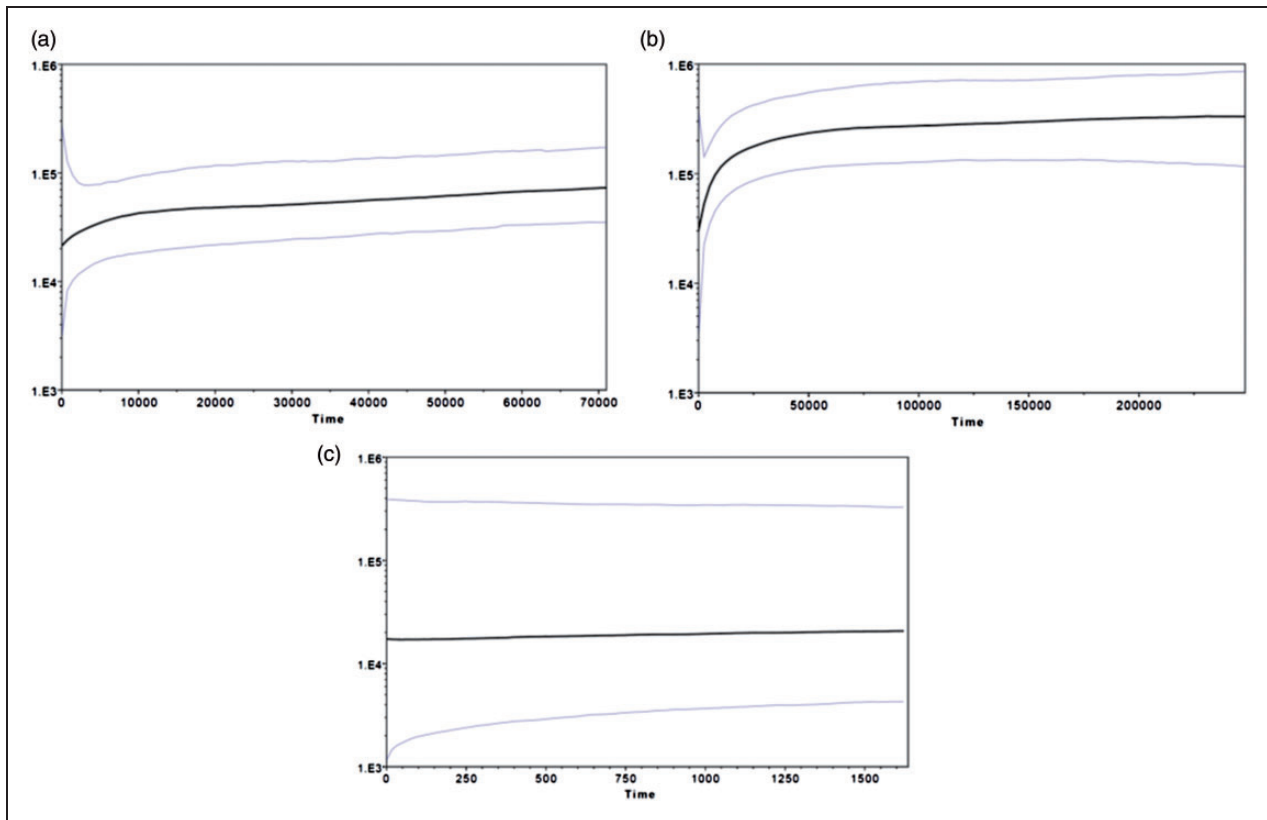


Figure 2. The Bayesian Skyline Plots based on mtDNA control regions showing the maternal effective population size changes of three populations, that is, *P. gigas* (a), *P. hypophthalmus* (b), and the hybrids (c). The maternal effective size and the time from present in years are shown in the y-axis and x-axis, respectively. The solid line indicates the median estimate and the thin lines are the 95% highest posterior density edge.

demographic expansion of these three groups. The BSP, based on the control region, showed population reduction in *P. gigas* and *P. hypophthalmus* (Figure 2(a) and (b)), whereas the hybrid group was found to have a relatively unchanged population size (Figure 2(c)). In addition, a short time of convergence indicated the recent origin of the hybrid group (Figure 2(c)).

As expected, analyses of the genetic relationships among the three fish groups indicated maternally genetic relatedness between the hybrid and *P. hypophthalmus*. The NJ tree and network showed the same clustering of the hybrid and *P. hypophthalmus* and a distinct clade of *P. gigas* (Figures 3 and 4). One shared haplotype between the hybrid and *P. hypophthalmus* was observed in both regions (Figures 3 and 4). Smaller values of pairwise genetic distances (Φ_{st}), with significant p value ($p < .01$), between the hybrid and *P. hypophthalmus* (0.3961 for the control region and 0.6941 for *cytB*) than the other two pairs ($\Phi_{st} > 0.9$) further supported a maternal genetic origin of the hybrid from *P. hypophthalmus*.

For the control region, three haplotypes of *P. gigas* are separated in different clusters in the NJ tree (Figure 3).

Networks show that the haplotype of *P. gigas* from Payao Province (red) had diverged from that from Chiang Rai (green) (Figure 4). In addition, the haplotype of fish from the north-eastern province of Sakon Nakhon is shared with those of the Uttaradit and Chiang Rai Provinces located in northern Thailand.

Discussion

Here, we reported our sequencing data of the *cytB* and control regions, from newly collected samples of *P. gigas* and *P. hypophthalmus* and their hybrids from Thailand. The hybrids were genetically closer to *P. hypophthalmus* than *P. gigas*, possibly due to the hybridization between female *P. hypophthalmus* and male *P. gigas*. The reciprocal cross between male *P. hypophthalmus* and female *P. gigas* might produce either unsuccessful cross breeding or a low survival rate of the offspring, as exemplified by previous studies (Panase et al., 2013; Sutthi, Amornlerdpisan, Chitmanat, & Mengumphan, 2014). Hybridization results between the two *Clarias* catfishes (*C. gariepinus* \times *C. batrachus*) showed that male *C. gariepinus* \times female *C. batrachus* could produce viable

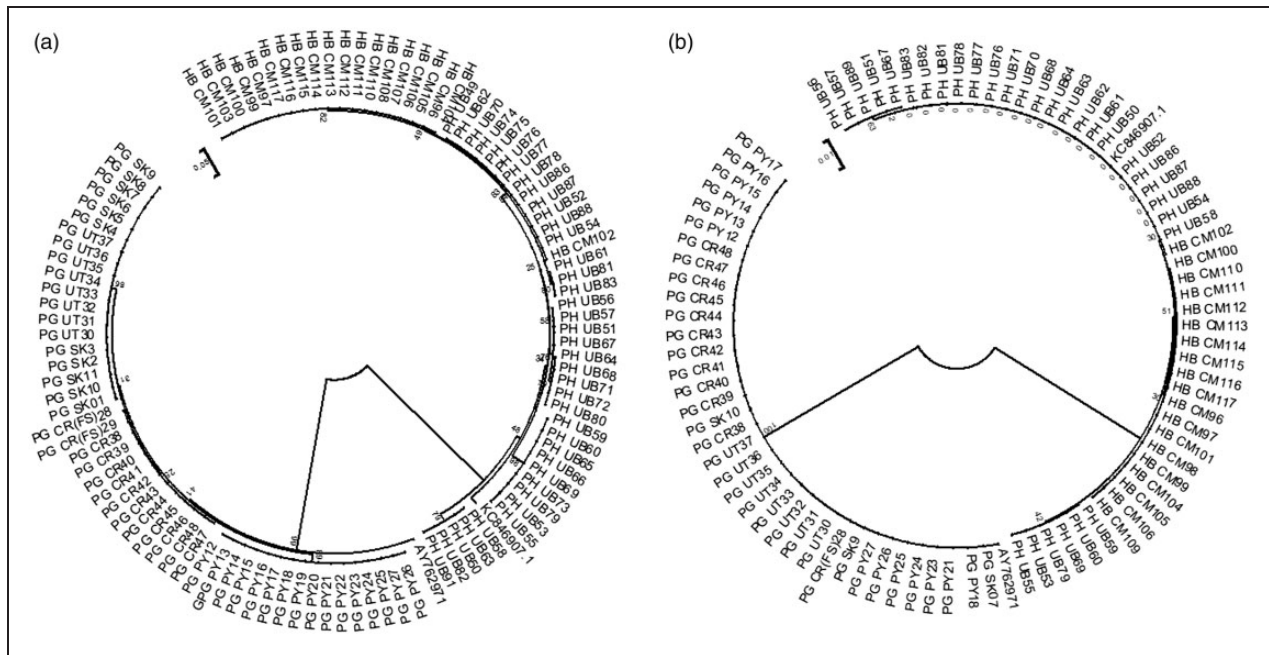


Figure 3. Neighbor joining tree of mtDNA sequences, based on the control region (a) and *cytB* (b). See population abbreviation in Figure 1.

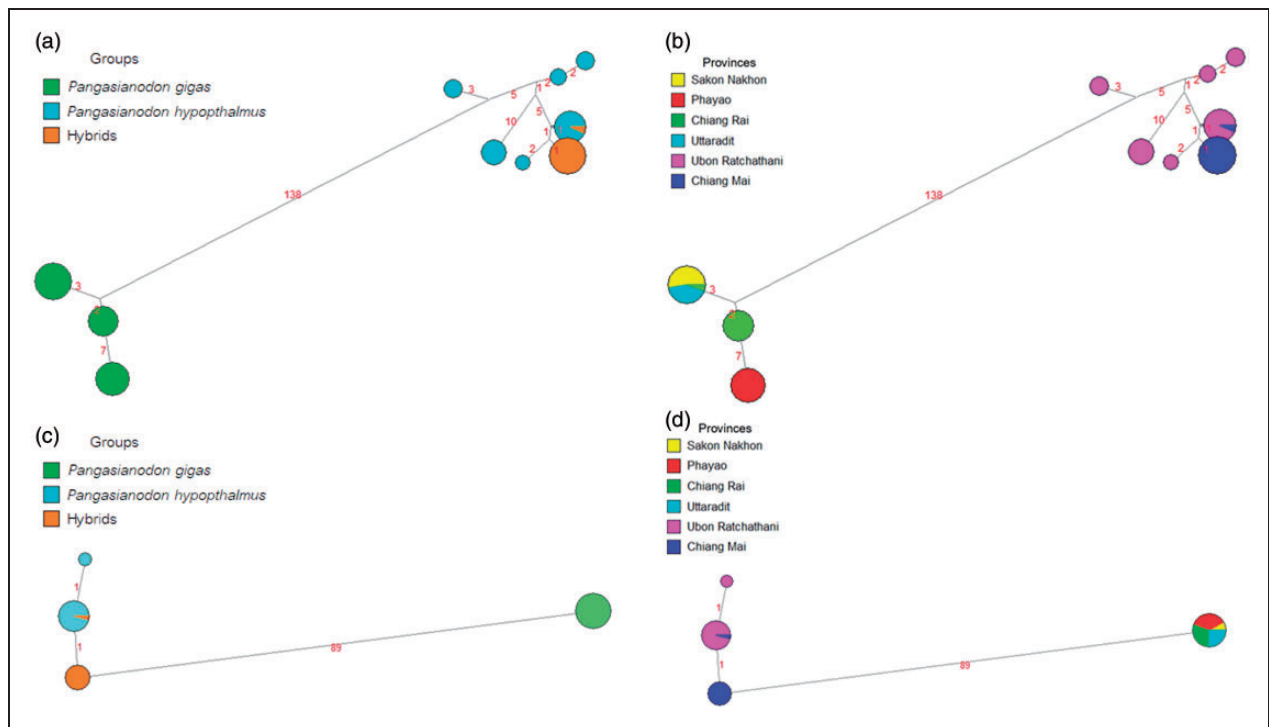


Figure 4. Networks of mtDNA sequences from the control region, based on groups (a) and geography (b) and from *cytB*, based on groups (c) and geography (d). Red numbers indicate number of base substitutions.

offspring, whereas all offspring from the reciprocal cross (female *C. gariepinus* × male *C. batrachus*) died within a few hours after hatching due to deformed morphology (Olufeagba & Okomoda, 2016). Another possible result

of a reciprocal cross between female *P. gigas* × male *P. hypophthalmus* was hybrids lacking commercially positive heterosis, or less effective hybrids, as demonstrated in hybrids of male channel catfish (*Ictalurus punctatus*) ×

female blue catfish (*I. furcatus*) (Masser & Dunham, 1998) and hybrids of male *P. hypophthalmus* × female *P. nasutus* (Hassan, Ambak, & Samad, 2011).

In general, the mtDNA diversities of all the fish groups were low; *P. hypophthalmus* showed highest genetic diversity in both mtDNA segments but, for *P. gigas*, genetic diversity in the control region (nucleotide diversity) was commensurate with that of a previous report (Ngamsiri et al., 2007); however, these values were higher than in the study by Na-Nakorn et al. (2006). The variation of the *cyt B* coding region showed extremely low genetic diversity in all groups. The very low internal diversity of *P. gigas* could be a result of captive stocks that were created from a limited number of founders, captured from the wild. However, we found a shared haplotype between *P. gigas* of the north and north-east of Thailand, indicating that geographic location had little influence on genetic diversity of wild *P. gigas* in the Mekong River, along the border of Thailand, before their use as a parent breeding stock.

The genetic diversity of *P. hypophthalmus* was greater than found in previous studies, in both regions (Na-Nakorn et al., 2006; So, Van Houdt, & Volkaert, 2006). This might be due to difference of mtDNA studied regions which higher mutation rate in this study than those previous reports (Nicolas et al., 2012). However, compared to other catfish (Nakagawa, Seki, Ishikawa, & Watanabe, 2016; Ochoa et al., 2015; Xu, Huang, Zeng, Li, & Peng, 2017; Zhong et al., 2013) and freshwater fish species (Hou et al., 2014; Kenthao, Wangsomnuk, & Jearanaiprepreme, 2016; Song, Hou, Zhang, Yue, & Song, 2014; Swain et al., 2014), *P. gigas*, *P. hypophthalmus*, and their hybrids exhibited lower genetic diversity, which was also lower than those of other endangered and critically endangered fish species (Alves, Coelho, Collares-Pereira, & Coelho, 2001; Mandal et al., 2012; Wang et al., 2016).

Being discordant with earlier results (Na-Nakorn et al., 2006), our BSP plots supported the absence of demographic expansion. This might be explained by a wild origin and wide distribution of samples of *P. gigas* in previous study (Na-Nakorn et al., 2006). We detected a population reduction in *P. gigas* and *P. hypophthalmus* (Figure 2(a) and (b)) which agrees with So et al. (2006). However, many discordant results on genetic diversity values in both fish species could be clarified by further extensive sampling and studying more variable markers. The declining number of *P. gigas* caught from the Mekong River over many years (Hogan et al., 2004) supported our findings of population size reduction in this endangered species. Over-fishing, habitat destruction, habitat isolation, and migration route blockage might be causing the low genetic diversity of *P. gigas* and *P. hypophthalmus* (Hogan, 2013). Moreover, improper hatchery practices, for example, a low

number of founders (founder effect), which promotes inbreeding; directional selection in breeding programs and the adaptation of reared populations to culture conditions could also lead to reduced genetic diversity (Cheng & Huang, 2013; Hsu, Takata, Onozato, & Gwo, 2015; Karlsson, Moen, & Hindar, 2010).

For captive fish, loss of genetic diversity within populations due to inbreeding might be minimized by introducing individuals from genetically distant wild stocks and carefully designing breeding programs based on cautious pedigree analysis (Vrijenhoek, 1998). Yet, due to the rarity of wild stocks of Mekong giant catfish, molecular relatedness estimators could be more feasible for conservation breeding schemes to avoid the mating of genetically close individuals (Fisch, Kozfkay, Ivy, Ryder, & Waples, 2015). If populations reared with high genetic homogeneity were released to the small natural populations, a decline of genetic diversity (Hsu et al., 2015; Karlsson et al., 2010; Yang et al., 2015) and reduction in population fitness (Vrijenhoek, 1998) might occur. Therefore, identifying population structure and genetic variation within and between populations were important for conservation program.

In summary, our results provided more genetic information on the hybrids of the endangered Mekong giant catfish (*P. gigas*) and striped catfish (*P. hypophthalmus*) in Thailand. We found low genetic diversity and a reduction in the effective population size in the parental species, as well as a constant population size of recent origin in the hybrid group.

Implications for Conservation

Our results support a decreased effective maternal population size with extremely low genetic diversity, which is putatively caused by several factors: inbreeding and improper hatchery practices for *P. gigas* and the hybrid species, and habitat destruction, habitat isolation, and migration route blockage for *P. hypophthalmus*. These results provide more mtDNA information not only for *P. gigas* but also for *P. hypophthalmus* and their hybrids, in Thailand. Our methods and results for the maternal genetic background of these catfish can be extended to further autosomal microsatellite studies and be applied to future farm and conservation management programs.

Acknowledgments

The authors would like to thank Unit of Excellence 2019 on Biodiversity and Natural Resources Management, University of Phayao, and the grant (nos. RD62018 and UoE62005) from University of Phayao. The authors would also like to thank the Laboratory Animal Research Centre, University of Phayao, and The Institute of Animal for Scientific Purposes Development, Thailand, for permission to work in the field.

Declaration of Conflicting Interests

The author(s) declared no potential conflicts of interests with respect to the research, authorship, and/or publication of this article.

Funding

The author(s) disclosed receipt of the following financial support for the research, authorship, and/or publication of this article: This study was supported by the Research and Academic Affairs Promotion Fund, Faculty of Science, Khon Kaen University, Fiscal year 2017 (RAAPF).

ORCID iD

Wibhu Kutanan  <https://orcid.org/0000-0001-7767-1644>

References

- Alves, M. J., Coelho, H., Collares-Pereira, M. J., & Coelho, M. M. (2001). Mitochondrial DNA variation in the highly endangered cyprinid fish *Anaocypris hispanica*: Importance for conservation. *Heredity*, *87*, 463–473.
- Bandelt, H. J., Forster, P., & Röhl, A. (1999). Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution*, *16*, 37–48.
- Burnside, E. B. (2004). To Successfully Crossbreed, It Is Essential to Utilize Breeds That is Competitive and Superior for Individual Trait. Article of Crossbreeding for Profit, November 2004, Twoplus, Norway.
- Cheng, Q., & Huang, N. (2013). Mitochondrial DNA variation in wild and hatchery populations of northern pike, *Esox lucius* L. *Iranian Journal of Fisheries Sciences*, *12*, 792–801.
- Darriba, D., Taboada, G. L., Doallo, R., & Posada, D. (2012). jModelTest 2: More models, new heuristics and parallel computing. *Nature Methods*, *9*, 772.
- Donaldson, K. A., & Wilson, R. R. (1999). Amphi-panamaic geminates of snook (Percoidei Centropomidae) provide a calibration of divergence rates in the mitochondrial DNA control region of fishes. *Molecular Phylogenetics and Evolution*, *13*, 208–213.
- Drummond, A. J., Suchard, M. A., Xie, D., & Rambaut, A. (2012). Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Molecular Biology and Evolution*, *29*, 1969–1973.
- Excoffier, L., & Lischer, H. (2010). Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources*, *10*, 564–567.
- Fisch, K. M., Kozfkay, C. C., Ivy, J. A., Ryder, O. A., & Waples, R. S. (2015). Fish hatchery genetic management techniques: Integrating theory with implementation. *North American Journal of Aquaculture*, *77*, 343–357.
- Fu, Y. X. (1997). Statistical tests of neutrality of mutations against population growth, hitchhiking and background selection. *Genetics*, *147*, 915–925.
- Hassan, A., Ambak, M. A., & Samad, A. P. A. (2011). Crossbreeding of *Pangasianodon hypophthalmus* (Sauvage, 1878) and *Pangasius nasutus* (Bleeker, 1863) and their larval development. *Journal of Sustainability Science and Management*, *6*, 28–35.
- Hogan, Z. (2013). *Pangasianodon gigas*. *The IUCN Red List of Threatened Species 2013*: e.T15944A5324699. Downloaded on 4 July 2019. <https://www.iucnredlist.org/species/15944/5324699>
- Hogan, Z., Moyle, P. B., May, B. P., Zanden, M. J. V., & Baird, I. G. (2004). The imperilled giants of the Mekong: Ecologists struggle to understand—and protect—Southeast Asia's large migratory catfish. *American Scientist*, *92*, 228–237.
- Hou, X., Zhu, F., Yin, S., Zhang, L., Hu, Y., Wang, Y., ... Li, L. (2014). Genetic diversity of *Odontobutis potamophila* from different geographic populations inferred from mtDNA control region. *Mitochondrial DNA*, *25*, 400–406.
- Hsu, T. H., Takata, K., Onozato, H., & Gwo, J. C. (2015). Causes of the drastic loss of genetic variation in the critically endangered Formosa landlocked salmon of Taiwan. *Endangered Species Research*, *27*, 277–287.
- Jondeung, A., Sangthong, P., & Zardoya, R. (2007). The complete mitochondrial DNA sequence of the Mekong giant catfish (*Pangasianodon gigas*), and the phylogenetic relationships among Siluriformes. *Gene*, *387*, 49–57.
- Karlsson, S., Moen, T., & Hindar, K. (2010). Contrasting patterns of gene diversity between microsatellites and mitochondrial SNPs in farm and wild Atlantic salmon. *Conservation Genetics*, *11*, 571–582.
- Katoh, K., & Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. *Molecular Biology and Evolution*, *30*, 772–780.
- Kenthao, A., Wangsomnuk, P. P., & Jeerranaiprepreme, P. (2016). Genetic variations and population structure in three populations of beardless barb, *Cyclocheilichthys apogon* (Valenciennes, 1842) inferred from mitochondrial cytochrome b sequences. *Mitochondrial DNA*, *29*, 82–90.
- Kocher, T. D., Thomas, W. K., Meyer, A., Edwards, S. V., Pääbo, S., Villablanca, F. X., & Wilson, A. C. (1989). Dynamics of mitochondrial DNA evolution in animals: Amplification and sequencing with conserved primers. *Proceedings of the National Academy of Sciences*, *86*, 6192–6200.
- Kumar, S., Stecher, G., & Tamura, K. (2016). MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*, *33*, 1870–1874.
- Mandal, A., Mohindra, V., Singh, R. K., Punia, P., Singh, A. K., & Lal, K. K. (2012). Mitochondrial DNA variation in natural populations of endangered Indian Feather-Back fish, *Chitala chitala*. *Molecular Biology Reports*, *39*, 1765–1775.
- Masser, M., & Dunham, R. (1998). Production of hybrid catfish. Southern Regional Aquaculture Center 190, Stoneville, MS.
- Nakagawa, H., Seki, S., Ishikawa, T., & Watanabe, K. (2016). Genetic population structure of the Japanese torrent catfish *Liobagrus reinii* (Amblycipitidae) inferred from mitochondrial cytochrome b variations. *Ichthyological Research*, *63*, 333–346.

- Na-Nakorn, U., Sukmanomon, S., Nakajima, M., Taniguchi, N., Kamonrat, W., Poompuang, S., & Nguyen, T. T. (2006). MtDNA diversity of the critically endangered Mekong giant catfish (*Pangasianodon gigas* Chevey, 1913) and closely related species: Implications for conservation. *Animal Conservation*, 9, 483–494.
- Ngamsiri, T., Nakajima, M., Sukmanomon, S., Sukumasavin, N., Kamonrat, W., Na-Nakorn, K., & Taniguchi, N. (2007). Genetic diversity of wild Mekong giant catfish *Pangasianodon gigas* collected from Thailand and Cambodia. *Fisheries Science*, 73, 792–799.
- Nicolas, V., Schaeffer, B., Missouf, A. D., Kennis, J., Colyn, M., Denys, C., ... Laredo, C. Assessment of three mitochondrial genes (16S, Cytb, CO1) for identifying species in the Praomyini tribe (Rodentia: Muridae). *PLoS One*, 7(5), e36586.
- Ochoa, L. E., Pereira, L. H. G., Costa-Silva, G. J., Roxo, F. F., Batista, J. S., Formiga, K., ... Oliveira, C. (2015). Genetic structure and historical diversification of catfish *Brachyplatystoma platynemum* (Siluriformes: Pimelodidae) in the Amazon basin with implications for its conservation. *Ecology and Evolution*, 5, 2005–2020.
- Olufeagba, S. O., & Okomoda, V. T. (2016). Parentage determination of the hybrid between *Clarias batrachus* and *Clarias gariepinus* using cytochrome b. *Banat's Journal of Biotechnology*, 7, 53–59.
- Panase, P., Amornlerdpisan, D., & Mengumphan, K. (2013). Sexual Maturity and Breeding Efficiency of 3 Catfish; *Pangasianodon gigas*, *Pangasianodon hypophthalmus*, Their Hybrid (Male *P. gigas* × Female *P. hypophthalmus*) and Hybrid Using Backcross Technique. *Journal of Fisheries Technology Research*, 7, 27–37.
- Roberts, T. R., & Vidthayanon, C. (1991). Systematic revision of the Asian Catfish Family Pangasiidae, with biological observations and descriptions of three new species. *Proceedings of the Academy of Natural Sciences of Philadelphia*, 143, 97–144.
- Saitou, N., & Nei, M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, 4, 406–425.
- So, N., Van Houdt, J. K. J., & Volkaert, F. (2006). Genetic diversity and population history of migratory catfishes *Pangasianodon hypophthalmus* and *pangasianodon bocourti* in the Cambodian Mekong River. *Fisheries Science*, 72, 469–476.
- Song, J., Hou, F., Zhang, X., Yue, B., & Song, Z. (2014). Mitochondrial genetic diversity and population structure of a vulnerable freshwater fish, rock carp (*Procypris rabaudi*) in upper Yangtze River drainage. *Biochemical Systematics and Ecology*, 55, 1–9.
- Sutthi, N., Amornlerdpisan, D., Chitmanat, C., & Mengumphan, K. (2014). Annual growth and reproductive performance in an F2 catfish hybrid. *Journal of Agricultural Science and Technology*, 1, 113–118.
- Swain, S. K., Bej, D., Das, S. P., Sahoo, L., Jayasankar, P., Das, P. C., & Das, P. (2014). Genetic variation in *Labeo fimbriatus* (Cypriniformes: Cyprinidae) populations as revealed by partial cytochrome b sequences of mitochondrial DNA. *Mitochondrial DNA*, 27, 1986–1990.
- Tajima, F. (1989). Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics*, 123, 585–595.
- Tave, D. (2003). Genetics and stock improvement. In J. S. Lucas & P. C. Southgate (Eds.), *Aquaculture farming aquatic animals and plants* (pp. 123–145). Oxford, England: Blackwell Publishing.
- Vidthayanon, C., & Hogan, Z. (2013). *Pangasianodon hypophthalmus*. *The IUCN Red List of Threatened Species 2013: e.T180689A7649971*. <https://www.iucnredlist.org/species/180689/7649971>
- Vrijenhoek, R. C. (1998). Conservation genetics of freshwater fish. *Journal of Fish Biology*, 53, 394–412.
- Wang, K., Zhang, S. H., Wang, D. Q., Wu, J. M., Wang, C. Y., & Wei, Q.-W. (2016). Conservation genetics assessment and phylogenetic relationships of critically endangered *Hucho bleekeri* in China. *Journal of Applied Ichthyology*, 32, 343–349.
- Xiao, W., Zhang, Y., & Liu, H. (2001). Molecular systematics of Xenocyprinae (Teleostei: Cyprinidae): Taxonomy, biogeography, and coevolution of a special group restricted in East Asia. *Molecular Phylogenetics and Evolution*, 18, 163–173.
- Xu, D., Huang, Y., Zeng, Q., Li, B., & Peng, Z. (2017). Genetic diversity and population history among geographic populations of *silurus asotus* in different water systems in China based on mtDNA Cytb gene sequences. *Journal of Fisheries of China*, 41, 1489–1499.
- Yang, M., Tian, C., Liang, X. F., Zheng, H., Zhao, C., & Zhu, K. (2015). Genetic structure and diversity in natural and stocked populations of the mandarin fish (*Siniperca chuatsi*) in China. *Genetics and Molecular Research*, 14, 5153–5160.
- Zhao, H., Kong, X., & Zhou, C. (2014). The mitogenome of *Pangasius sutchi* (Teleostei, Siluriformes: Pangasiidae). *Mitochondrial DNA*, 25, 342–344.
- Zhong, L., Song, C., Wang, M., Chen, Y., Qin, Q., Pan, J., & Chen, X. (2013). Genetic diversity and population structure of yellow catfish *Pelteobagrus fulvidraco* from five lakes in the middle and lower reaches of the Yangtze River, China, based on mitochondrial DNA control region. *Mitochondrial DNA*, 24, 552–558.