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RESEARCH ARTICLE

Morphometric variations of the Genus *Barbonymus* (Pisces, Cyprinidae) harvested from Aceh Waters, Indonesia

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Abstract. The objective of the present study was to analyze the morphometric variations of the three presumed taxa within the *Barbonymus* group, namely *B. gonionotus*, referred to locally as naleh; *B. schwanenfeldii*, referred to locally as lampam-A; and *Barbonymus* sp. referred to locally as lampam-B. The naleh samples were collected from Nagan Raya District, while lampam-A and lampam-B were collected from Aceh Tamiang District, Indonesia. Traditional morphometric characters were measured in 150 fish samples (50 individuals of every taxon). The results of univariate (ANOVA) and multivariate (Discriminant function analysis, DFA) analyses showed that lampam-A and lampam-B have overlapping morphological characteristics, whereas naleh were distinctly different. Therefore, it is presumed that lampan A and lampan B are the same species of *B. schwanenfeldii*. It was concluded that the morphometric data indicated that there are two species of *Barbonymus* in Aceh waters, i.e., *B. schwanenfeldii* and *B. gonionotus.*

Keywords: morphometric, discriminant function analysis, naleh, lampam

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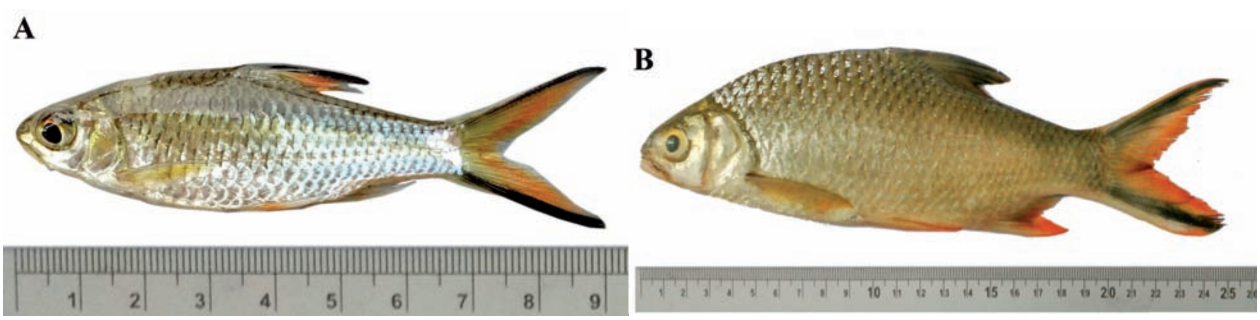
Introduction

Barbonymus belongs to the Cyprinidae family, and this species is a true freshwater fish that is omnivorous but tends to be herbivorous (Ahammad et al. 2009). According to Kottelat (2001), the genus *Barbonymus* is distributed throughout southeast Asian countries, such as Indonesia, Malaysia, Thailand, Vietnam, Laos, and Cambodia. In addition to consumption, *Barbonymus* species are also popular ornamental fish because of their dazzling coloring and behavior (Cheng et al. 2004, Gante et al. 2008, Eslamloo et al. 2012, Isa et al. 2012, Muchlisin et al. 2015). Several species within the genus *Barbonymus,* for example *B. schwanenfeldii* and *B. gonionotus*, are listed on the IUCN red list in the Least Concern (LC) category (Allen 2012, Thinh et al. 2012). On the other hand, the threats on these species in particular and freshwater fishes in general have been increasing over the last decade.

Several studies have been conducted on *Barbonymus* fishes, for example, Kamarudin and Esa (2009) studied the phylogeny and phylogeography of *B. schwanenfeldii* from Malaysian waters using the cytochrome b mtDNA gene. Mansour et al. (2017) studied feeding fry diets with different protein contents, and Isa et al. (2012) examined the population dynamics of the tinfoil barb, *B. schwanenfeldii*, in Pedu Reservoir, Malaysia. Pannusa et al. (2015) studied genetic and morphometric variations among hatchery stocks of *B. gonionotus* in Thailand. Akter et al. (2010) did a genetic characterization of *B. gonionotus* (Bleeker) from Bangladesh using the DNA fingerprinting technique, while Ahammad et al. (2009) reported on nursery rearing *B. gonionotus* larvae using three different supplementary feeds. However, no study has been conducted to date on morphometric variations within the genus *Barbonymus*.

Based on direct morphological observations, it was presumed that three taxa of *Barbonymus* occurred in the waters of Aceh, Indonesia. The first taxon is referred to locally as naleh (Fig. 1a), and this species is found in the Nagan Raya District. The second and third taxa are referred to locally as lampam and are found in Aceh Tamiang waters (Muchlisin and Siti-Azizah 2009, Muchlisin et al. 2015). Identification based on fish sample morphology and meristic characters indicated that naleh is *B. gonionotus*, while lampan-A is *B. schwanenfeldii* and lampam-B is *Barbonymus* sp., or a cryptic species. The differences between lampam-A and lampam-B refer to the shape of the snout and body depth; lampam-A (Fig. 1b) has a blunt snout and greater body depth compared to lampam-B (Fig. 1c). Nevertheless, no comprehensive examination on the morphological variations was conducted previously.

Morphometric characters are one of the important keys in systematic studies in ichthyology. This data is useful for examining and graphically displaying differences in shape (Ibańez et al. 2007, Mojekwu and Anumudu 2015), and it is also very valuable for estimating growth variability in ontogenetic traits and population variations. Therefore, morphometric data is valuable for discriminating among fish species, as was done in the current study. The objective of the present study was to characterize the morphometric variations within the three presumed groups of *Barbonymus* caught in Aceh waters.



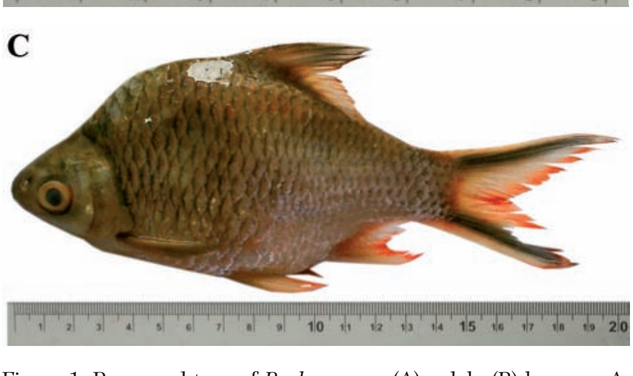


Figure 1. Presumed taxa of *Barbonymus*, (A) naleh, (B) lampam-A, (C) lampam-B.

Materials and methods

Study area

The study was conducted from July to September 2016. The samples were collected from Nagan Raya and Aceh Tamiang districts. The samples of naleh fish were collected from the Nagan River in Nagan Raya District (4°16’25.25"N and 96°24’22.34"E;

Table 1
The description of traditional morphometric characters measured in the study

No.	Characters	Code	Descriptions
1.	TL	Total length	Distance from the left foremost tip of the snout to the posterior edge of the forked portion of the caudal fin
2.	SL	Standard length	Distance from the left foremost tip of the snout to the end of caudal peduncle
3.	HL	Head length	Distance from the tip of the snout to the posterior edge of the operculum
4.	CPL	Caudal peduncle length	Distance between the end of the dorsal base and the origin of the caudal fin
5.	SNL	Snout length	Distance from tip of the snout in the middle of the upper lip to the anterior orbital rim
6.	DFD	Dorsal fin depth	Length of the longest simple dorsal ray
7.	DFBL	Dorsal fin base length	Base length between the first and the last ray of the dorsal fin
8.	ED	Eye diameter	Distance between the anterior and posterior edge of the eyeball
9.	CPD	Caudal peduncle depth	Depth at the narrowest part of the peduncle
10.	BD	Body depth	Distance between the origin of the dorsal fin and the pelvic fin
11.	PFL	Pectoral fin length	Distance from the origin of the pectoral fin to the tip of the longest pectoral fin ray
12.	VFL	Pelvic fin length	Distance from the origin of the pelvic fin to the tip of the longest pelvic fin ray

4°17’4.73"N and 96°25’56.83"E; 4°16’48.49"N and 96°27’8.50"E), while samples of lampam (two taxa) were collected from the Tamiang River in Aceh Tamiang District (4°16’43.75"N and 98° 0’10.20"E; 4°17’48.32"N and 97°59’36.19"E; 4°16’41.68"N and 97°58’57.15"E). The sampling sites were determined based on information from local fishermen. The samples were examined in the Laboratory of Ichthyology of Syiah Kuala University, Banda Aceh, Indonesia.

Sampling procedure

The fish were caught using casting nets (mesh size 12.5 and 25 mm), gillnets (mesh size 38 and 50 mm), and hooks. The fish were measured for total and standard length and body weight using digital calipers (Mitutoyo CD-6CS; standard error = 0.01 mm) and a digital scale (Toledo AB-204; standard error = 0.01 g). The samples were photographed for documentation, and then the fish were preserved in 10% formalin.

Morphometric measurement

A total of 150 fish samples of *Barbonymus* (50 samples of each taxa) were subjected to morphometric analysis. A total of 12 traditional morphometric characters were measured using a digital caliper (Mitutoyo CD-6CS; standard error = 0.01 mm). Morphometric characters were determined based on Muchlisin (2013) as presented in Fig. 2 and Table 1. The characters measured were transformed using the equation proposed by Schindler and Schmidt (2006) as follows: M_{trans} = (M x 100)/ TL where, M_{trans} = transformed data, M = direct measured data, TL= total length.

Data analysis

The morphometric data were subjected to univariate analysis (one-way ANOVA) followed by the Duncans multi-range test and multivariate Discriminant Function Analysis (DFA) using SPSS ver. 22.0 (Ibańez et al. 2007, Park et al. 2015).

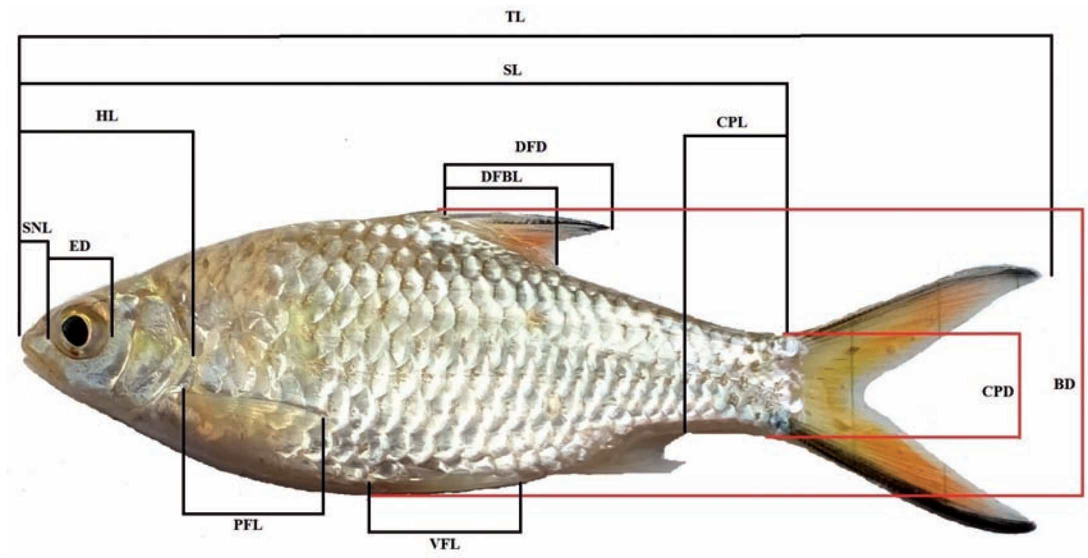


Figure 2. Traditional morphometric characters of the fish samples.

Results

The one-way ANOVA test revealed that all characters were significantly different at a 95% confidence level among the three groups ($P < 0.05$) except for head length (HL) ($P > 0.05$). This means that the three presumed taxa have a similar head length. However, lampam-A and lampam-B had higher similarity in almost all characters i.e., DFD, DFBL, ED, BD, PFL, and VFL, while only four characters were significantly different among these taxa, i.e., SL, CPL, SNL, and CPD (Table 2). In addition, most characters of naleh were significantly different from the other taxa (lampam-A and lampam-B), whereas only two

Table 2
The mean transformed values of traditional morphometric characters according to presumed taxa. Values in the same row followed by different superscripts are significantly different ($P < 0.05$)

		Presumed Taxa		
No.	Characters (code)	Naleh (n= 50)	Lampam-A (n=50)	Lampam-B (n=50)
1.	Standard length (SL)	71.02 ± 0.21^a	77.67 ± 2.69^b	72.04 ± 0.50^a
2.	Head length (HL)	18.11 ± 0.22^a	17.78 ± 0.18^a	18.15 ± 0.20^a
3.	Caudal Peduncle length (CPL)	4.82 ± 0.10^a	4.96 ± 0.08^a	5.39 ± 0.10^b
4.	Snout length (SNL)	3.92 ± 0.10^a	5.98 ± 0.10^b	6.40 ± 0.13^c
5.	Dorsal fin depth (DFD)	11.58 ± 0.24^a	21.28 ± 0.28^b	21.63 ± 0.28^b
6.	Dorsal finbase length (DFBL)	19.1 ± 0.17^a	22.08 ± 0.6^b	22.43 ± 0.60^b
7.	Eye diameter (ED)	5.66 ± 0.07^b	3.93 ± 0.18^a	4.37 ± 0.21^a
8.	Caudal Peduncle depth (CPD)	9.61 ± 0.06^a	11.17 ± 0.11^b	11.57 ± 0.13^c
9.	Body depth (BD)	24.46 ± 0.20^a	33.13 ± 0.34^b	33.56 ± 0.41^b
10.	Pectoral fin length (PFL)	15.1 ± 0.14^a	17.04 ± 0.20^b	17.41 ± 0.20^b
11.	Ventral fin length (VFL)	13.68 ± 0.13^a	16.9 ± 0.18^b	17.27 ± 0.17^b

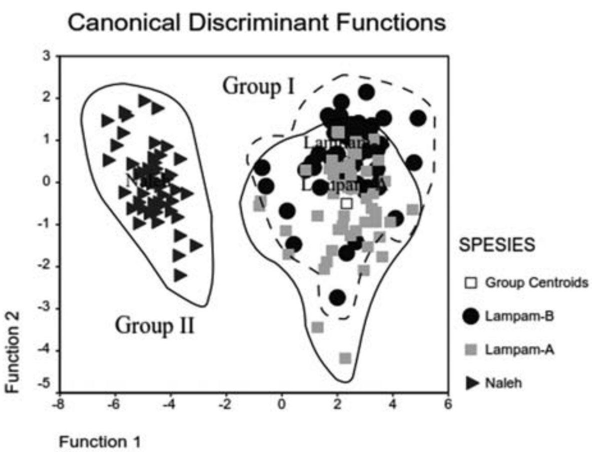


Figure 3. Scatter plot of traditional morphometric characters of three presumed taxa of *Barbonymus*.

characters of naleh were not significantly different from lampam-A, i.e., HL and CPL, and two characters from lampam-B, i.e., SL and HL (Table 2).

Discriminant function analysis (DFA) showed that the three presumed taxa were discriminated into two different groups; lampam-A and lampam-B were grouped into the same group (Group I) and naleh was discriminated into a different group (Group II) (Fig. 3). The DFA analysis resulted in two functions, where function 1 had an eigenvalue of 11.19 that explained 98.5% of the total variation, and function 2 had an eigenvalue of 0.17 that explained 1.5% of the variation (Table 3). In addition, function 1 had higher loading for four characters, i.e., DFD, BD, VFL, and PFL, whereas function 2 had higher loading for two characters, i.e., ED and CPL (Table 3).

The scatter plot (Figure 3) shows that Function 1 successfully discriminated the individuals into two separate groups, where the lampam-A group overlapped with the lampam-B group, and there was a negative relationship between the characters of the groups. Moreover, Function 2 also successfully discriminated the individuals into two different groups, where lampam-A and lampam-B overlapped between these characters (group I) and naleh was grouped separately (group II), and there was a positive relationship between the characters of group I and group II (Fig. 3).

Discussion

A total of 11 morphometric characters were included in multivariate analysis, and there were higher similarity characters between *B. schwanenfeldii* (lampam-A) and *Barbonymus* sp. (lampam-B), and only four characters were significantly different, i.e., SL, CPL, SNL, and CPD. On the other hand, there were very significant difference in morphometrics between the naleh group and lampam group with nine characters being significantly different.

The study shows that the quantitative morphological methods differentiated the three presumed taxa of *Barbonymus* into two separate groups. The lampam-A and lampam-B showed a considerably higher degree of overlap in traditional morphometric characters, while naleh was more distant. On the other hand, the naleh formed a distinct group. There

Table 3
Eigenvalues, % variance, and matrix structure of traditional morphometric characters

	Discriminant functions	
Discriminant variables	1	2
Eigenvalues	11.19	0.17
Cumulative % of variance	98.5	1.5
Canonical correlation	0.96	0.38
Dorsal fin depth (DFD)	0.749	0.166
Body depth (BD)	0.544	0.168
Ventral fin length (VFL)	0.414	0.308
Eye diameter (ED)	-0.355	0.218
Dorsal fin base length (DFBL)	0.174	-0.025
Pectoral fin length (PFL)	0.168	0.086
Caudal peduncle length (CPL)	0.078	0.646
Snout length (SNL)	0.425	0.545
Standard length (SL)	0.048	-0.504
Head length (HL)	-0.014	0.260
Caudal peduncle depth (CPD)	0.220	0.249

are some differences in morphology between lampam-A and lampam-B in caudal peduncle length (CPL), caudal peduncle depth (CDP), and snout length (SNL). However, the DFA scatter plot showed that the individual samples were overlapping between these two species, and this is an initial indication that the two taxa can be presumed to be the same species of *B. schwanenfeldii*. Therefore, further study on genetic data analysis is crucial to validate the precise taxonomic status of *Barbonymus* in Aceh waters.

In general, morphometric variations are influenced by genetic diversity (Hebert et al. 2003a, 2003b). Beside the morphological aspects, variations are also influenced by geographical or habitat aggregation factors (Elliott et al. 1995) and feeding habits (Cavalcanti et al. 1999). In addition, sex differentiation, population, geography distribution, physiology, and food sources are also the important factors affecting morphometric diversity (Aktas et al. 2006, Khan et al. 2012). Moreover, the feed niche and water depth are also crucial factors in differentiating variation in fish morphology (Clabaut et al. 2007). Therefore, there is a strong relationship between the morphology, genetics, and ecology of fishes (Cavalcanti et al. 1999).

Conclusions

The univariate and multivariate analysis of morphometric characters showed that lampam-A and lampam-B have higher biometric similarity, and they can be considered to be the same species, while naleh was discriminated separately. Therefore, it was concluded that there are two species of *Barbonymus* in Aceh waters; i.e., *B. Schwanenfeldii* and *B. gonionotus*. Nevertheless, further studies based on genetic analysis is needed to validate the taxonomic status of the *Barbonymus* in Aceh waters.

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