

ASIAN CATFISH GENUS PANGASIUS: DIAGNOSIS AND DISTRIBUTION

Rudhy Gustiano*1, Vitas Atmadi Prakoso1 and M.H. Fariduddin Ath-thar1

¹Research Institute for Freshwater Aquaculture and Fisheries Extension, Jl. Sempur No 1, Bogor, West Java,16129, Indonesia Received; March 15-2018 Received in revised from July 30-2017; Accepted August 07-2018

ABSTRACT

Pangasiidae are economically important riverine catfishes that generally exist in freshwater from the Indian subcontinent to the Indonesian Archipelago. Among genera in Pangasiidae, genus Pangasius has numerous species. The objective of the present study is to describe all species of genus Pangasius with their diagnosis and natural distribution. Nine hundred and ninety nine specimens formed the core of the material examined in this study. All examined species were collected from Bangladesh, Vietnam, Cambodia, Thailand, Malaysia, and Indonesia. Additional samples including specimens of 49 previously described species housed in various museums were also examined. On each specimen, 35 point to point measurements covering the possible variation of the body conformation were taken using dial calipers. Measurements were logtransformed before the PCA was run on the covariance matrix. The first factor, considered as the size-factor was not taken into account to minimize the effects of size differences among samples. Allometry is indicated by unequal loading of variables on the first component and by biological interpretation of allometric data proceed using coefficients of the first components against the second components that was linear. An independent PCA was run on the correlation matrix from the untransformed count data. Finally, data analysis consisted in characterizing groups from scatter plots between pairs of structuring characters for subsequent use in generic identification keys. The results show Asian catfish genus Pangasius consist of 21 valid species. This paper describes the diagnosis and distribution of all valid species.

Keywords: Genetic; catfish; Pangasius; diagnosis; distribution

INTRODUCTION

Catfishes form a significant part of inland fisheries, where several species have been introduced in fish culture. Numerous species are of interest to the aquarium industry where they represent a substantial portion of the world trade (Teugels, 1996).

Considerable confusion has arisen in the systematics of this group of catfish. Most of the previous researchers described species without consulting existing type specimens. Almost all authors have problems recognizing juveniles of the larger species, and junior synonyms are often based on small sized specimens. In their revision of the family Pangasiidae, Roberts & Vidthayanon (1991) recognized only two genera with 21 species: *Pangasius* Valenciennes, 1840 (19 species) and *Helicophagus* Bleeker, 1858 (2 species) (see Blekeer, 1858a,b). Nevertheless, this work was not supported by any phylogenetic study. The monophyly of the genera or the species groups has not been

demonstrated yet. It should be noted too that their work was based on a limited number of specimens for many species and that only few morphometric variables were studied. Recently, seven new species were added to the genus Pangasius (Pouvaud et al., 1999; Roberts, 1999; Pouvaud and Teugels., 2000; Pouyaud et al., 2002; Gustiano et al., 2003) and one species was described in the genus Helicophagus (Ng & Kottelat, 2000). At present, the phylogenetic study on this family has been published by Gustiano (2003), Pouyaud et al. (2004), Gustiano & Pouyaud (2007), Karinthanyakit & Jondeung (2012), and Azlina et al. (2013), in which the phylogenetic interference based on molecular data provide support for the recognition of some of the Pangasius sub-genera and, or species groups as distinct genera. The phylogenetic analysis demonstrated the recognized genera and the genetic relationships among the species. Overall, trees from the osteological (Gustiano, 2003), molecular (Pouyaud et al., 2004) and biometric analyses (Gustiano & Pouyaud, 2005) show similar topologies and confirm the hypothesis

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derived from geological history, paleontology, and similar models in other taxa of fishes from the same area (Gustiano, 2003). The monophyly of the genus *Pangasius* is supported from above studies. The oldest genus may already existed when Asia mainland was still connected to the islands in the southern part about 20 million years ago (Pouyaud *et al.*, 2004).

After serial studies in the last decade, phylogenetic of the species belonging Pangasiidae have been revised. Nowadays, the status of systematic of this group is clearly identified. Following recent publication in restricted region such as Malaysian Peninsula (Azlina *et al.*, 2013; Haslawati *et al.*, 2014) and Thailand (Karinthanyakit & Jondeung, 2012), new information contributed additional data related to distribution. The objective of the present study is to determine all the species of the genus *Pangasius* with their diagnosis and natural distribution.

MATERIALS AND METHODS

All materials examined in this study were collected and delivered from Bangladesh, Vietnam, Cambodia, Thailand, Malaysia and Indonesia, the areas where the pangasiids catfishes exist. At amount of 49 recognized type specimens of pangasiids catfishes deposited at various museum in the world were also included in the analyses. The following measurement presented in Figure 1 was already described in the previous publications (Gustiano and Pouyaud, 2007; 2008).



Figure 1. Measurements taken on *Pangasius* specimens: 1. Standard length; 2. Head length; 3. Snout length; 3a. Anterior snout width; 3b. Posterior snout length; 4. Head depth; 5. Head width; 6. Predorsal length; 7. Caudal peduncle length; 8. Caudal peduncle depth; 9. Pectoral fin length; 10. Pectoral spine length; 11. Dorsal fin length; 12. Dorsal spine width; 13. Pelvic fin length; 14. Anal fin height; 15. Anal fin length; 16. Adipose fin height; 17. Adipose fin width; 18. Eye diameter; 19. Mouth width; 20. Lower jaw length; 21. Interorbital length; 22. Distance snout to ishtmush; 23. Postocular length; 24. Maxillary barbel length; 25. Mandibulary barbel length; 26. Body width; 27. Prepectoral length; 28. Prepelvic length; 29. Vomerine width; 30. Vomerine length; 31. Palatine length; 32. Palatine width; 33. Dorsal spine width.

Principal component analysis (PCA) was applied to recognize different species (Bookstein *et al.*, 1985). In order to avoid the effects of size variation among samples, the first factor of PCA was ignored. Unequal loading of variables on the first component showed allometry illustrated by linear line produced from the first components against the second components (PCII). An independent PCA was run on the correlation matrix from the untransformed count data. Finally, data analysis consisted in characterizing groups from scatter plots between pairs of structuring characters for subsequent use in generic identification keys.

RESULTS AND DISCUSSION Results

The first morphological observation enables to separate the examined specimens into two groups according to the vomerine toothplate: one group without additional toothplate of vomerine toothplate, while the other has an additional toothplate of the vomerine toothplate. The analysis with the group of specimens without additional toothplate of the vomerine tooth band showed that plot of PCII versus the third component (PCIII) of PCA taken enables to separate the specimens into four groups. Based on the type of species, they are recognized as *P*. humeralis Roberts, 1989, *P. lithostoma* Roberts, 1989, *P. kinabatanganensis* Roberts & Vidtahyanon, 1991, and *P. nieuwenhuisii* (Popta, 1904)(Fig. 2). Dominant factor loadings of PCA are shown in Table 1. Further analysis of the dominant characters showed that *P. kinabatangensis* is isolated by combination of high adipose fin height (5-6% SL) and narrow anterior part of snout width (22.7-27.2% HL); *P. lithosoma* by combination of long anal fin length (more than 31% SL) and short prepelvic length (less than 44% SL); *P. nieuwenhuisii* by combination of wide head (more than 13.5% SL) and slender dorsal spine (less than 7.7% HL); *P. humeralis* by combination of wide head (more than 13.5% SL) and robust dorsal spine (7.7-9.3% HL).



- Figure 2. Plot of PCII versus PCIII taken from a PCA of 27 log-transformed metric variables on 66 specimens.
 holotype of *P. humeralis*; specimens of *P. humeralis*; Φ holotype of *P. lithostoma*; ◊ specimens of *P. lithostoma*; = holotype of *P. kinabatanganensis*; □ specimens of *P. kinabatanganensis*; ▲ holotype of *P. nieuwenhuisii*; △ specimens of *P. nieuwenhuisii*.
- Tabel 1. The second and third factor score coefficients for the morphometric PCA taken from 27 logtransformed variables on 43 specimens.

Characters	PCII	PCIII
Log standard length	-0.074213	-0.072629
Log head length	-0.004096	-0.088260
Log snout length	-0.081877	0.063390
Log anterior width of snout	0.054046	0.164894
Log posterior width of snout	-0.071649	0.025953
Log head depth	-0.074797	0.017937
Log head width	0.163455	0.120141
Log predorsal length	-0.074570	-0.092814
Log caudal peduncle length	-0.077706	-0.063112
Log caudal peduncle depth	-0.183625	-0.159843
Log anal fin length	-0.433254	-0.080701
Log adifose fin height	0.367617	-0.377810
Log adipose fin width	0.598409	-0.201410
Log eye diameter	0.053713	0.428485

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Log width of mouth	0.060105	0.008129
Log lower jaw length	0.038685	-0.098521
Log interorbital distance	0.128928	0.055229
Log distance snout to isthmus	-0.204616	-0.037892
Log opercular length	0.029318	-0.165354
Log body width	0.075667	0.084995
Log prepectoral length	-0.166482	-0.003848
Log prepelvic length	0.157043	-0.026586
Log vomerine width	-0.171489	0.134252
Log vomerine length	-0.171494	-0.401107
Log dorsal spine width	0.014457	0.327869

The second observation, after removal of four recognized groups, is able to recognize another isolated group by their filamentous fins. A combined plot of PCIII and PCMI indicates two groups: the first one, including the type of *P. beani* Smith, 1931 lies in the negative sector of PCMI (Fig. 3). The second one is mostly located in the positive sector of PCIII together with the type of *P. taeniura* Fowler, 1935 and *P. burgini* Fowler, 1937. Further analysis of the dominant characters from the loading factors (Table 2 & 3) showed that a combination of head length (% SL) and body width could be used to distinguish two

different groups. These two different groups are also found when gill raker number is plotted with standard length; one group has higher gill raker number including the type of *P. beani* while the other group has a lower gill raker number and includes the type of *P. larnaudii* Bocourt, 1866; *P. taeniura* and *P. burgini*. The conclusion indicated the group of examined specimens with filamentous fins includes two valid species. The first one is *P. larnaudii* with its junior synonyms *P. taeniura* and *P. burgini*, and the second one is *P. sanitwongsei* with *P. beani* as its junior synonym.



Figure 3. Plot of PCIII taken from a PCA of 20 log-transformed metric variables on 31 specimens versus PCMI taken from a PCA of 5 counts on 30 specimens. ■ holotype of *P. burgini*; ▲ holotype of *P. taeniura*; △ paratype of *P. taeniura*; ○ specimens of *P. larnaudii*; * holotype of *P. beani*; ◇ specimens of *P. sanitwongsei*.

Tabel 2. The third factor score coefficients for the morphometric PCA taken from 20 log-transformed variables on 31 specimens.

Tabel 3. The first factor score coefficient for the meristic PCA using five counts for 30 specimens

Characters	РСМІ
Gill raker	-0.777741
Dorsal fin ray	0.580732
Pectoral ray	-0.652618
Pelvic fin ray	0.616285
Anal fin ray	0.658916

The third observation (after removal six recognized groups) revealed that one group in *Pangasius* has an extremely long barbel length (Fig. 4).

Further PCA showed that there is no plot of factor scores enabling to separate the examined specimens (Fig. 5). This group includes the holotype of *P. macronema*, types of *P. siamensis* and *P. aequilabialis*. In conclusion, *P. macronema* is a valid species with two synonyms, *P. siamensis* and *P. aequilabialis*. Concerning *P. delicatissimus* (Bleeker, 1862) recorded by Bleeker (1862) in a note on p. 73, Atlas Ichthyologique II, from Krawang, Java, nothing else is known besides his very short description after a drawing, made by artist of the former "commission for natural history research in Nederland India" (Weber & De Beaufort, 1913). "The pearly bandlet that starts on the muzzle rises up the temple and follows the curvature of the back until after the caudal fin" which distinguishes it according to Bleeker from all other species of *Pangasius*. However, the present observation agree with Weber & De Beaufort (1913) who mentioned that criteria also occurs in *P. macronema*, hence *P. delicatissimus* is a synonym of *P. macronema*.



Figure 4. Graphical representation of maxillary barbel length (% HL) in the remaining examined specimens (after removal six groups) of *Pangasius*. Medians are represented by line, distribution data by box, non-outlier data by tail, o outlier data.



Figure 5. Plot of PCII versus PCIII derived from a PCA of 25 log-transformed metric variables taken on 47 specimens. • holotype of *P. macronema*; • specimens of *P. macronema*; • syntype of *P. acronema*; • holotype of *P. acronema*; • syntype of *P. acronema*; • holotype of *P. acronema*; • syntype of *P. a*

siamensis, ◊ holotype of *P. aequilabialis*.

The fourth observation (after removal seven recognised groups) showed that one group has a very short predorsal length, less than 31.2% HL (Fig. 6). Further PCA analysis on the observed group showed a single group exists, no factor scores enabled to distinguish others. This group includes the type of *P. polyuranodon* Bleeker, 1852 and *P. juaro* Bleeker, 1852 (see Blekeer, 1852a,b). We,therefore, conclude that *P. polyuranodon* is valid species and *P. juaro* is its synonym.

The fifth observation of clearly defined characters on the remaining *Pangasius* specimens (after removal eight groups) showed one group isolated by a long caudal peduncle (17.6-21.4% SL) (Fig. 7). Further analysis using PCA revealed only a single group including the holotype and paratypes of *P. elongatus* Pouyaud *et al.* (2002). The analysis thus concludes that the group with long peduncle length is *P. elongatus*.



Figure 6. Graphical representation of predorsal length (% SL) in the remaining examined specimens of *Pangasius* (after removal seven groups). Median is represented by line, distribution data by box, non-outlier data by tail, o outlier data.



Figure 7. Graphical representation of predorsal length (% SL) in the remaining examined specimens of *Pangasius*. Median are represented by line, distribution data by box, non-outlier data by tail, o outlier data.

Further observation on the remaining *Pangasius* specimens showed that plot of eye diameter combined with predorsal length is able to distinguish one group with larger eye diameter (more than 22.8% HL) and short predorsal length (less than 33% SL) (Fig. 8). Detailed analysis of the isolated group revealed that the group includes all the types of *P. mahakamensis* Pouyaud *et al.*, 2002. It concludes that this group is *P. mahakamensis*.

The sixth observation of clearly defined characters on the remaining *Pangasius* specimens (after removal 10 groups) demonstrates groups with a short distance snout-isthmus (% SNL) (Fig. 9). A combined plot of PCMI from a PCA using five meristic and PCII showed that the groups consists of three different subgroups (Fig. 10). The first group is in the negative sector of PCMI and negative sector of PCII including the type of *P. sabahensis* Gustiano *et al.*, 2003. The second group is in the negative sector of PCMI and positive sector of PCII including type of *P. mekongensis* Gustiano *et al.*, 2003). The third one is in the positive sector of PCII; no type falls in this group because the type specimens with missing data are casewise deleted. Further analysis using characters with important factor loadings shows that the plot of

mandibular versus maxillary barbel length and snout length against dorsal spine width are able to distinguish *P. sabahensis* from the remaining specimens examined. On the other side, only gill raker number enable to separate *P. mekongensis* from *P. kunyit* Pouyaud *et al.*, 1999. Therefore, overall analyses conclude three valid species in the group, *P. sabahensis*, *P. mekongensis*, and *P. kunyit*.



Figure 8. Plot of eye diameter (% HL) versus predorsal length (% SL). ■ holotype of *P. mahakamensis*; □ paratypes of *P. mahakamensis*; △ specimens of *P. mahakamensis*; ○ remaining *Pangasius* specimens.



Figure 9. Graphical representation of distance snout-isthmus (% snout length) in the remaining examined specimens of *Pangasius* (after removal 10 groups). Median are represented by line, distribution data by box, non-outlier data by tail, o outlier data.





▲holotype of *P. sabahensis*; △paratypes of *P. sabahensis*; ■holotype of *P. mekongensis*; □ paratypes of *P. mekongensis*; ○ specimens of *P. kunyit*.

The next analysis shows that combination of posterior part of snout width and dorsal spine width (Fig. 11), predorsal length and snout length and

predorsal length and anterior part of snout width also distinguish a group recognized as *P. krempfi* Fang & Chaux, 1949 (in Chaux and Fang, 1949).



Figure 11. Plot of dorsal spine width against predorsal length. ▲holotype of *P. krempfi*; △ specimens of *P. krempfi*.

The combination of head length versus dorsal spine width (Fig. 12), dorsal spine width versus head width and dorsal spine width versus body width enable to recognize *P. rheophilus* (Pouyaud &Teugels, 2000).

The seventh observation on clearly defined characters on the remaining specimens (after removal 15 groups) demonstrates a group with high number of gill rakers on the first branchial arch (Fig. 13). The first group includes type of *P. bocourti* Sauvage, 1880 with 35-47 gill rakers, while the second group includes type of *P. djambal* (Bleeker, 1846) (with 27-39 gill rakers). Another character that can be useful to recognize between two species is anterior part of snout width: it is slightly wider in *P. djambal* than in *P. bocourti*. It also shows that *P. djambal* are together with the type of *P. bedado* Roberts, 1999. Further series analysis concludes that *P. bedado* is synonym of *P. djambal*.



Figure 12. Plot of head length against dorsal spine width. + holotype of *P. rheophilus*; Aparatype of *P. rheophilus*; o specimens of *P. rheophilus*.





 Φ holotype of *P. bocourti*; \Diamond specimens of *P. bocourti*.

The following analysis on the remaining examined specimens (after removal 17 groups) demonstrates that two groups are separated by the combination of head length and predorsal distance (Fig. 14). The first group showing a short head and a short predorsal includes the type of *P. myanmar* Roberts & Vidthayanon, 1991, syntype of *P. buchanani* Valenciennes, 1840, and the specimens identified following their museum identification as *P. pangasius* (Hamilton, 1822). The second one, with a long head and a long predorsal distance, consists of the paratypes of *P. conchophilus* (Roberts and Vidthayanon 1991), specimens of *P. conchophilus*,

the holotype of *P. nasutus* (Bleeker, 1863), and specimens of *P. nasutus*.

Next is the analysis on the group with short head and short predorsal distance. A plot of postocular length combined with dorsal spine width shows that the group contains two different species (Fig. 15). The first group, together with type of *P. myanmar* Roberts & Vidthayanon, 1991, has more robust dorsal spine width 8.1-8.9% SL, and the second one includes syntype of *P. buchanani*. In this plot, the specimens identified as *P. pangasius* clearly fall into two different groups. Six specimens are in the group of *P. myanmar*, and the other eight specimens are together with the syntype of *P. buchanani.* Therefore, it concludes the specimens previously identified as *P. pangasius* consists of two different species, and treat them with

different symbol for further analysis. The next analysis found that *P. myanmar* has shorter postocular length 28.6-33.3% HL.



Figure 14. Plot of head length (% SL) against predorsal length (% SL). * holotype of *Pangasius myanmar*, + paratype of *P. myanmar*, ● syntype of *P. buchanani*, ○ specimens identified as *P. pangasius*; ⊕ holotype of *P. nasutus*; ◊ specimens of *P. nasutus*; ▲ paratypes of *P.* conchophilus; △ specimens of *P. conchophilus*.



Figure 15. Plot of dorsal spine width against postocular length. * holotype of *Pangasius myanmar*, + paratype of *P. myanmar*, • syntype of *P. buchanani*; • specimens identified as *P. pangasius*.

The analysis on the remaining examined specimens with long head and long predorsal distance demonstrates that a plot of width of mouth versus vomerine toothplate width contains two different species (Fig. 16). The first one includes holotype of *P. nasutus* (Bleeker, 1863), all specimens known as *P. nasutus*, and the holotype of *P. ponderosus* Herre & Myers, 1937. This group has larger width of mouth

41.9-52.5% HL and bigger vomerine toothplate 21.9-30.7% HL. The second one includes the specimens and paratypes of *P. conchophilus* (Roberts & Vidthayanon, 1991) that has a narrower width of mouth (less than 41.9% HL) and smaller vomerine toothplate (less than 21.9% HL). Further analysis gives similar result when we combined width of mouth versus lower jaw length.



Figure 16. Plot of width of mouth against vomerine toothplate width. \blacktriangle paratypes of *P. conchophilus*; Δ

specimens of *P. conchophilus*; \Box holotype of *P. nasutus*; Φ holotype of *P. ponderosus*; \Diamond specimens of *P. nasutus*;

Based on the series analyses on the specimens belonging to genus *Pangasius*, the present study recognized 21 valid species. Keys identification are provided below and the species diagnosis together with distribution are provided in the following discussion section.

1.1 Key to species

- Vomerine toothplate without additional 1a. toothplate2 1b. Vomerine toothplate with additional toothplate5 2a. High adipose fin (5-6% SL) and narrow anterior part of snout width (22.7-27.2% HL)P. kinabatanganensis 2b. Low adipose fin (less than 5% SL) and large anterior part of snout width (25.5-35.5% HL) Anal fin length more than 31% SL and prepelvic За. length less than 44% SLP. lithostoma 3b. Anal fin length less than 31% SL and prepelvic length 42-52.9% SL4 Dorsal spine width more than 7.7-9.3% HL and 4a. head width more than 14.1-15.6% SLP. humeralis 4b. Dorsal spine width 5.5-7.6% HL and head width 13.8-16.4% SLP. nieuwenhuisii 5a. Filamentous fin rays6 5b. Non filamentous fin rays7 Body width 21.1-23.2% SL, head length 23.2-6a. 30.2% SL, gill rakers on the first branchial arch 17-26P. sanitwongsei
- Body width 16.9-21.9% SL, head length 20.3-28.3% SL, gill rakers on the first branchial arch 13-17*P. larnaudii*

- 9a. Long caudal peduncle (17.6-21.4% SL) and eve
- 10a. Eye diameter 22.8-29.4% HL and predorsal length 30.1-32.7% SL*P. mahakamensis*
- 10b. Eye diameter less than 22.8% HL and predorsal length more than 31.8% SL11
- 11a. Short distance snout isthmus (less than 110% SNL)12
- 11b. Long distance snout isthmus (more than 110% SNL)14
- Maxillary barbel length 79-97%; mandibular length 56-66% HL and dorsal spine width 4.4-5.7% HL *P. sabahensis*
- 12b. Maxillary barbel length less than 80.7% HL, mandibular barbel length less than 52% HL; dorsal spine width more than 6.5% HL13
 13a. Gill rakers on the first branchial arch 16-23
- P. mekongensis

- 13b. Gill rakers on the first branchial arch 24-32
- Predorsal length 31.8-35.3% SL, snout length 45.5-52.4% HL, anterior part of snout width 32.6-37.8% HL, posterior part of snout width 42.2-49.1% HL
- 15a. Dorsal spine width 4.7-6.2% HL, head length 19.6-23.2% SL, head width 11-14.2% SL, and body width 14.9-17% SL**P. rheophilus**
- Dorsal spine width 5.4-10.4% HL, head length 21.3-28.8% SL, head width 11.9-20.6% SL, body width 16.5-21.4% SL16
- 16a. Higher gill rakers number on the first branchial arch (more than 27)17
- 17a. 35-47 gill rakers on the first branchial arch, anterior part of snout width 26.4-31.1% HL
- 17b. 27-39 gill rakers on the first branchial arch, anterior part of snout width 29.3-36.6.5% HL
- 18b. Predorsal length 36.1-42.8% SL and head length 23.8-28.8% SL20

- 20b. Width of mouth 41.9-52.5% HL, vomerine toothplate width 21.9-30.7% HL, and lower jaw length 23.9-31.5% HL......*P. nasutus*

Discussion

Based on the analyses of 35 measured and five counted characters, the diagnosis of the family, the diagnosis of the genus, and the description of the valid species are given below. Morphologically, pangasiid catfishes are recognized by a laterally compressed body, the presence of two pairs of barbels (one pair of maxillary and one pair of mandibular), the relatively long anal fin, and short dorsal fin with two spines (first small and hidden under the skin), and adipose fin small with free posterior margin.

Pangasius Valenciennes, 1840

Diagnosis: six pelvic fin rays, short predorsal length (<37%), and robust dorsal spine width (>5% HL), robust of anterior part of snout length(>16.5%HL), posterior nostril close behind anterior ones and above imaginary line from anterior nostril and orbit, long and slender premaxillary toothplate, eyes varies from small to large, relatively long barbel length (192%ED), dorsal and pectoral fin robust, and adipose fin relatively robust.

Below, the distribution of different species of genus *Pangasius* are presented.

Pangasius kinabatanganensis Roberts & Vidthayanon, 1991

Pangasius kinabatanganensis is endemic to Kinabatangan River in North Borneo (Present Sabah), draining into the Sulu Sea, and flowing through falt alluvial plain with a few scattered, low hill (Inger & Chin, 1962).

Pangasius lithostoma Roberts, 1989

Pangasius lithostoma is only known from middle part of Kapuas, the biggest river in West Kalimantan. Kapuas River is the largest and probably has the richest ichthyofauna of any of the modern rivers derived from the Sunda drainage (Roberts, 1989).

Pangasius humeralis Roberts, 1989

Pangasius humeralis only occurs in the middle part of Kapuas River in West Kalimantan. This species occurs sympatrically with *P. lithostoma* (Roberts, 1989; pers. obs.). The local people differentiate between this species and *P. lithostoma* based on body coloration. They call *P. humeralis* 'black seladang' and *P. lithosoma* 'white seladang' in Kalimantan, Indonesia (Roberts & Vidthayanon, 1991).

Pangasius nieuwenhuisii (Popta, 1904)

Pangasius nieuwenhuisii is endemic to East Kalimantan (Indonesia) and only occurs in the Mahakam basin. The Mahakam River is the second largest river in Kalimantan, with a course of some 920 km and a drainage area of 77.700 km² (Christensen, 1992).

Pangasius larnaudii Bocourt, 1866

Pangasius larnaudii is known to occur in large rivers and floodplains of the Chao Phraya, Mekong. Migrates into floodplains and spawns at the beginning of flood season (Rainboth, 1996). Large schools of adults are often seen in some fishing refuge places together with *P. hypophthalmus* and other fishes. Reared in ponds as well as in weirs around the Great Lake in Cambodia.

Pangasius sanitwongsei Smith, 1931

This species occurs in the Chao Phraya and Mekong basins. However, the species seems to be no longer commonly found in the former river.

Pangasius macronema Bleeker, 1851

From all drainages in the Sundaic region, only a single fresh specimen was caught in our study from Barito River, Banjarmasin, South Kalimantan, Indonesia (see Bleekere 1851a). Of all specimens recorded in literature (see Blekeer, 1851 b), two were from Java (Eschmeyer, 1998). This species also occurs in the continent of Southeast Asia in the Mekong and Chao Phraya Rivers.

Pangasius polyuranodon Bleeker, 1852

Pangasius polyuranodon is presently known from the major drainages in Sumatra where it was observed in the Musi, Batang Hari, Indragiri and Way Rarem Rivers. *P. polyuranodon* is also present in southern and western Kalimantan, where it was found in the Barito River (same as type collection from Bleeker), in the Kapuas River and in the Batang Rajang River (Sarawak, Malaysia). The species was also recorded from North Borneo (Sabah, Malaysia) in the Kinabatangan River (Inger & Chin, 1962) but no specimens were available for the present study.

Pangasius elongatus Pouyaud, Gustiano & Teugels, 2002

Pangasius elongatus is presently known from most of the major rivers in Indochina, such as the Mekong (Thailand, Vietnam, Laos) and the Chao Phraya Basin (Thailand). At present, this species is considered close to extinction in Thailand (Vidthayanon, 2013).

Pangasius mahakamensis Pouyaud, Gustiano & Teugels, 2002

Pangasius mahakamensis is endemic to East Kalimantan, (Indonesia) and it is presently only known from the type locality, the Mahakam River. The Mahakam River is the second largest river in Kalimantan, with a course of some 920 km and a drainage area of 77.700 km² (Christensen, 1992). Specimens smaller than 150 mm were collected in brackish water in the delta of the river, while larger sized specimens were found in the upper part. Both environments have no vegetation on the banks, have a relatively strong current, and have deep but transparent water.

Pangasius sabahensis Gustiano, Teugels & Pouyaud, 2003

Pangasius sabahensis is endemic to northern Borneo and is presently known only from the type locality, the Kinabatangan River, Sabah State, Malaysia. This species is reported lives in estuarine areas.

Pangasius mekongensis Gustiano, Teugels & Pouyaud, 2003

Pangasius mekongensis is presently known only from the lower part of the Mekong River where it was usually identified as *P. djambal, P. bocourti* or *P. kunyit. Pangasius mekongensis* was collected in fresh and brackish waters in the Mekong Delta. This species is commonly caught with *P. krempfi*, a species also reported in seawater (Roberts & Vidthayanon, 1991).

Pangasius kunyit Pouyaud, Teugels & Legendre, 1999

Pangasius kunyit is known from most of the major drainages in Sumatra (Indonesia), where it was observed in the Musi River (Palembang), in the Batang Hari River (Jambi, Muara Jambi, and Muara Tebo), and in the Indragiri River (Rengat). *P. kunyit* is also present in Kalimantan where it was found in the Kapuas River (Pontianak, Kalimantan Barat, Indonesia), in the Barito River (Kuala Kapuas and Banjarmasin, Kalimantan Tengah, Indonesia), in the Mahakam River (Samarinda and Sangasanga (Kalimantan Timur, Indonesia). In Sumatra, *P. kunyit* was usually identified as *P. pangasius* or *P. djambal*.

Pangasius krempfi Fang & Chaux, 1949

The species occurs in the middle Mekong, Hue and Red Rivers, occasionally in the South China Sea, off Vietnam, and also has been reported in the southern China coast (Vidthayanon, 1993). In the Mekong River, the species occurs up to Nongkhai province, northeastern of Thailand. In the middle part of the river, specimens of *P. krempfi* were more than 50 cm SL.

Pangasius rheophilus Pouyaud & Teugels, 2000

Pangasius rheophilus is presently known from Kayan and Berau River in the Bulungan Regency, East Kalimantan (Indonesia). Pangasius rheophilus has been collected from freshwater near the mouth but also from the upper reaches of the two basins. In the lower reaches, the habitats consist of large pools near the sea, with deep and turbid waters. In the upper reaches, the habitats consist of big torrent characterized by turbulent and clear water (altitude 200-400 m).

Pangasius bocourti Sauvage, 1880

This species occurs in the Mekong and Chao Phraya basins.

Pangasius djambal Bleeker, 1846

Pangasius djambal is presently known from most major drainage of Sumatra, in the Musi, Batang Hari, and Indragiri Rivers. The species also occurs in Java: in the Brantas and Solo Rivers. In Kalimantan, they are in the Barito, Mendawai, and Kahayan Rivers. Although the type locality of *P. djambal* is Batavia (former name of Jakarta), nowadays the species seems to have disappeared from all rivers of West Java.

Pangasius myanmar Roberts & Vidthayanon, 1991

Known only from type locality, it is considered endemic to the Irrawadi River, Yangon, Myanmar.

Pangasius pangasius (Hamilton, 1822)

This species is distributed from the Indian subcontinent (Ganges basin, the Godavari, Krishna rivers; in Brahmaputra, it was reported by Motwani *et al.* (1962) to Irrawadi River in Myanmar).

Pangasius conchophilus Roberts & Vidthayanon, 1991

This species is found in large rivers of the Mekong and Chao Phraya Basins.

Pangasius nasutus (Bleeker, 1862)

Pangasius nasutus occurs in Sumatra: the Musi, Batang Hari and Indragiri Rivers, in Kalimantan:the Kapuas, Barito, Batang Rajang Rivers, and in Peninsula Malaysia: the Perak and Pahang Rivers.

CONCLUSION

Based on the present study, twenty one species are recognized as valid in the genus of *Pangasius*. The species are distributed from India in the southern part of Asian continent up to Indonesian Archipelago in Southeast Asia. Except *Pangasius sabahensis*, *P. mekongensis*, *P. kunyit*, *P. krempfi* and *P. rheophilus*, which have distribution up to estuarine, all other species live in the middle or upper part of the major rivers.

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