## PHYLOGENETIC RELATIONSHIPS AMONG PANGASIID CATFISH SPECIES (SILURIFORMES, PANGASIIDAE) AND NEW INSIGHTS ON THEIR ZOOGEOGRAPHY

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#### Abstract

With the aim of detecting phylogenetic relationships among Pangasiidae catfishes, 23 enzyme loci were studied on 18 nominal species of the genera *Pangasius* and *Helicophagus* (Roberts & Vidthayanon, 1991). In order to assess the taxonomic position of *Laides* genus in the Schilbeidae or in the Pangasiidae, 2 species belonging to the genus *Laides* and 1 species of the genus *Pseudeutropius* (Siluriformes, Schilbeidae) were added in the study.

The results indicate that the species Laides hexanema and Laides sinensis appear to be genetically related with the Pangasiidae. The phylogenetic tree obtained shows a clustering of species which validate the genus Helicophagus but indicates that the genus Pangasius is polyphyletic.

The genus *Pangasius* is composed of 3 genetic differentiated groups. Group 1 is composed by 3 species belonging to two different morphological entities validated by Roberts and Vidthayanon (1991) as possible subgenus. *Pangasius hypophthalmus* and *P. gigas* which share common genetic characters validate the subgenus *Pangasianodon*. The possession of many private alleles by *P. pleurotaenia* confirms the morphological originality of this species which was therefore considered to belong to the monotypic subgenus *Pteropangasius*. The second group consists of *P. micronema*, *P. macronema*, *P. lithostoma* and *P. polyuranodon* and the last group represents all the other species of the genus *Pangasius*. By contrast *Neopangasius* considered as a possible subgenus by Roberts and Vidthayanon (1991) is polyphyletic. Although relative genetic similarities were found between *P. humeralis* and *P. nieuwenhuisii* which are located in group 3, the species *P. lithostoma* appears to be more closely related to species belonging to the group 2. By reference to the *Helicophagus* genus, the genetic distances estimated between these genetic distance between groups 2 and 3 lead us to maintain species of both groups in the genus *Pangasius*. In the same way the genus *Laides* could be placed in Pangasiidae as proposed by Roberts (1989). The results also confirm the nominal species revision proposed by Roberts and Vidthayanon (1991).

New insights are given in this paper, like the presence of *Pangasius djambal* in all major basins of Sumatra and the fact that, contrarily to previous statements, this species was never utilised for aquaculture in Indonesia so far. *Helicophagus typus* is not extinct, three specimens were caught in the Batang Hari river (Sumatra) in February 1997 and two specimens in the Kapuas river (West Kalimantan) in June 1997. Two possible new species were discovered, the first one (ref. sp1) occurring in Sumatra (Musi, Batang Hari and Indragiri rivers), in Kalimantan (Mahakam River) and in Vietnam (Mekong delta), the second one (ref. sp2) was observed in East Kalimantan (Berau River). The taxon sp1 shares several characteristics with *Pangasius pangasius*. However this latter species is not supposed to be represented in the Mekong River nor in Indonesian waters.

#### INTRODUCTION

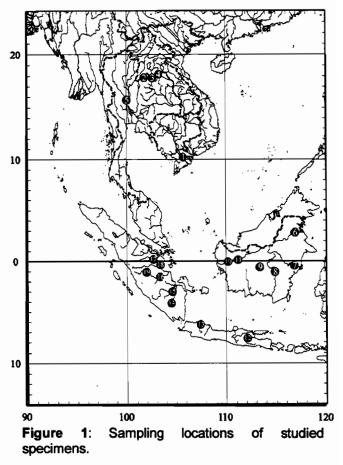
The tropical Asian catfish family Pangasiidae is characterised by a noticeable ecological and morphological diversity. In term of distribution, some species are endemic like *P. gigas* in the Mekong river, other have disjunctive distribution like *P. macronema* which occurs in mainland Asia only in the Mekong and Chao Phraya basins, while in the Indonesian archipelago, it is known only from southern Kalimantan and Java. Finally many species have a wide distribution like *P. micronema* and *P. polyuranodon* which are reported from most of the basins of south-east Asia. The Pangasiidae are freshwater fishes, with the exceptions of *P. pangasius*, *P. polyuranodon* and *P. krempfi* which can enter in saline waters. Concerning maximum size and growth rate, the situation is also contrasted. Some species, as *P. macronema* never grow longer than 200 mm SL while *P. gigas* can reach over 3 m for more than 300 kg body weight. These species exhibit a wide range of feeding behaviours.

With these considerations, it is noteworthy that phylogenetic relationships among populations of Pangasiidae remain problematic. Large distribution which leads in many cases to significant population differentiation and difficulty to access to comparative material in foreigner museums were responsible of many misidentifications. Before the systematic revision of Roberts & Vidthayanon (1991), a particular confusion prevailed. These authors studied type specimens and other material of Pangasiidae on 39 nominal species or subspecies, resulting to the recognition of 18 previously described species as valid. Three new species were also described bringing to 21 the total number of species recognised in Pangasiidae. They subdivided Pangasiidae in two genera, Pangasius Valencienne, 1840 and Helicophagus Bleeker, 1858. Neopangasius Popta, 1904. Pangasianodon Chevey, 1930 and Pteropangasius Fowler, 1937 were recognised by Roberts & Vidthayanon (1991) as possible subgenus of Pangasius. Two species have been placed in the genus Laides Jordan, 1919 and their position in Schilbeidae or in Pangasiidae is subject to controversy.

On the basis of the systematic revision of Roberts & Vidthayanon (1991) and in order to assess the phylogenetic relationships among Pangasiid catfish species, 23 enzyme loci were studied on 18 species of the genera *Pangasius* and *Helicophagus*. One species of the genus *Pseudeutropius* (Siluriformes, Schilbeidae) and two species of the genus *Laides* were also characterised at 19 enzyme loci in order to precise the taxonomic position of the genus *Laides*.

#### MATERIALS AND METHODS

216 individuals belonging to 62 populations of four genera (*Pangasius*, *Helicophagus*, *Laides*, *Pseudeutropius*) were analysed. The geographic origin (river system and location) and size of the samples are indicated in Figure 1 and table 1.



Captured specimens were dissected and the tissue samples were stored in liquid nitrogen for transfer to the laboratory. They were then stored at  $-20^{\circ}$  C for several months pending analysis. Two eyes and 2 cm<sup>3</sup> of muscle and liver were removed from each individual. To obtain optimal results, the samples were homogenised several hours before analysis. Each specimen was identified with key available in Roberts & Vidthayanon (1991) and stored in formalin for further examination.

The methods of starch gel electrophoresis were adapted from Pouyaud & Agnèse (1995). Table 2 shows the enzyme systems and the buffers used as well as the organs in which the different loci were expressed. The nomenclature is that proposed by Shaklee *et al.* (1990).

Species	CL	Sampling origin	Abbrev.	N	(Hobs)	<b>(P95</b> )
Pangasius Hypophthalmus	5	Tchao Prava Nakhom Sawan Thailand	HYP THA 2	3	0.0725	0.1739
Pangasius Hypophthalmus	1	Mekong Can Tho Viet Nam	HYP VIE 1	6	0.0870	0.3478
Pangasius Hypophthalmus	2	Mekong Thabo Thailand	HYP THA 1	6	0.0290	0.1304
Pangasius Hypophthalmus	13	CRIFFI Strain Sukamandi Indonesia	HYP JAV 2	3	0.0725	0.1739
Pangasius macronema	5	Tchao Praya Nakhom Sawan Thailand	MAC THA 2	5	0.1826	0.3478
Pangasius macronema	3	Mekong Nong Khai Thailand	MAC THA 1	4	0.1196	0.2174
Pangasius macronema	1	Mekong Can Tho Viet Nam	MAC VIE 1	5	0.0696	0.1739
Pangasius pleurotaenia	5	Tchao Praya Nakhom Sawan Thailand	PLE THA 2	5	0.0348	0.1304
Pangasius pleurotaenia	4	Mekong Bung Kan Thailand	PLE THA 1	1	0.0435	0.0435
Pangasius pleurotaenia	1	Mekong Can Tho Viet Nam	PLE VIE 1	1	0.0000	0.0000
Pangasius larnaudii	5	Tchao Praya Nakhom Sawan Thailand	LAR THA 2	4	0.0978	0.2174
Pangasius larnaudii	3	Mekong Nong Khai Thailand	LAR THA 1	1	0.0000	0.0000
Pangasius larnaudii	1	Mekong Can Tho Viet Nam	LAR VIE 1	1	0.0000	0.0000
Pangasius conchophilus	1	Mekong Can Tho Viet Nam	CON VIE 1	5	0.0609	0.1304
Pangasius conchophilus	2	Mekong Thabo Thailand	CON THA 1	3	0.0580	0.0870
Pangasius conchophilus	5	Tchao Praya Nakhom Sawan Thailand	CON THA 2	4	0.0326	0.0435
Pangasius sanitwongsei	4	Mekong Bung Kan Thailand	SAN THA 1	3 3	0.0000	0.0000
Pangasius krempfi	1	Mekong Can Tho Viet Nam	KRE VIE 1 GIG THA 1	2	0.0290	0.0870 0.1304
Pangasius gigas	3	Mekong Nong Khai Thailand	WAN THA 1	4	0.0652 0.0326	0.1739
Helicophagus waandersii	4	Mekong Bung Kan Thailand	WAN SUM 3	2	0.0000	0.0000
Helicophagus waandersii	16 5	Batang Hari Jambi Sumatra Indonesia Tchao Praya Nakhom Sawan Thailand	WAN THA 2	3	0.0000	0.0000
Helicophagus waandersii	16	Batang Hari Jambi Sumatra Indonesia	TYP SUM 3	3	0.0290	0.0870
Helicophagus typus Pangasius djambal	16	Batang Hari Jambi Sumatra Indonesia	DJA SUM 3	7	0.0230	0.1739
Pangasius ajambal Pangasius djambal	15	Musi Palembang Sumatra Indonesia	DJA SUM 2	4	0.0435	0.0870
Pangasius djambal	13	Brantas Jombang Java Indonesia	DJA JAV 1	10	0.0739	0.2609
Pangasius djambal	8	Barito Muara Tewe Kalimantan Indonesia	DJA KAL 3	1	0.0000	0.0000
Pangasius djambal	17	Indragiri Rengat Sumatra Indonesia	DJA SUM 4	7	0.0435	0.1304
Pangasius bocourti	1	Mekong Can Tho Viet Nam	BOC VIE 1	7	0.0807	0.3043
Pangasius bocourti	4	Mekong Bung Kan Thailand	BOC THA 1	4	0.0471	0.1739
Pangasius spl	15	Musi Palembang Sumatra Indonesia	SP1 SUM 2	5	0.0435	0.0435
Pangasius spl	7	Mahakam Samarinda Kalimantan Indonesia	SP1 KAL 2	4	0.0543	0.2174
Pangasius sp l	1	Mekong Can Tho Viet Nam	SP1 VIE 1	3	0.0870	0.1304
Pangasius micronema	17	Indragiri Rengat Sumatra Indonesia	MIC SUM 4	5	0.0783	0.2174
Pangasius micronema	10	Kapuas Sanggau Kalimantan Indonesia	MIC KAL 5	4	0.1196	0.2174
Pangasius micronema	12	Brantas Dam Karet Java Indonesia	MIC JAV 1	5	0.0783	0.2609
Pangasius micronema	18	Indragiri Teluk Kuantan Sumatra Indonesia	MIC SUM 5	3	0.1014	0.2174
Pangasius micronema	14	Tulang Bawang Kotabumi Sumatra Indonesia	MIC SUM 1	3	0.0725	0.1739
Pangasius micronema	8	Barito Muara Tewe Kalimantan Indonesia	MIC KAL 3	2	0.1522	0.3043
Pangasius sp2	6	Berau Tanjung Redeb Kalimantan Indonesia	SP2 KAL 1	3	0.0145	0.0435
Pangasius nasutus	9	Kayanan Palangkaraya Kalimantan Indonesia	NAS KAL 4	3	0.0290	0.0870
Pangasius nasutus	10	Kapuas Sanggau Kalimantan Indonesia	NAS KAL 5	2	0.0435	0.0435
Pangasius nasutus	8	Barito Muara Tewe Kalimantan Indonesia	NAS KAL 3	1	0.0435	0.0435
Pangasius nasutus	16	Batang Hari Jambi Sumatra Indonesia	NAS SUM 3	3	0.0000	0.0435
Pangasius nasutus	15	Musi Palembang Sumatra Indonesia	NAS SUM 2	3	0.0000	0.0435
Pangasius nasutus	17	Indragiri Rengat Sumatra Indonesia	NAS SUM 4	1	0.0435	0.0435
Pangasius nieuwenhuisii	7	Mahakam Samarinda Kalimantan Indonesia	NIE KAL 2	4	0.0761	0.1739
Pangasius lithostoma	11	Kapuas Sintang Kalimantan Indonesia Kapuas Sintang Kalimantan Indonesia	LIT KAL 6	1 1	0.0000 0.0000	0.0000 0.0000
Pangasius humeralis	11 17	Indragiri Rengat Sumatra Indonesia	HUM KAL 6 POL SUM 4	8	0.1087	0.2609
Pangasius polyuranodon	8	Barito Muara Tewe Kalimantan Indonesia	POL KAL 3	4	0.0435	0.1304
Pangasius polyuranodon Pangasius polyuranodon	<b>o</b> 1	Mekong Can Tho Viet Nam	POL VIE 1	6	0.0435	0.2174
Pangasius polyuranodon Pangasius polyuranodon	5	Tchao Praya Ayuttaya Thailand	POL THA 2	1	0.1304	0.1304
Pangasius polyuranodon Pangasius polyuranodon	10	Kapuas Sanggau Kalimantan Indonesia	POL KAL 5	1	0.0870	0.0870
Pangasius polyuranodon Pangasius polyuranodon	15	Musi Palembang Sumatra Indonesia	POL SUM 2	3	0.1739	0.2609
Pangasius polyuranodon Pangasius polyuranodon	15	Batang Hari Jambi Sumatra Indonesia	POL SUM 2	3	0.1159	0.1739
Pangasius polyuranodon Pangasius polyuranodon	14	Tulang Bawang Kotabumi Sumatra Indonesia	POL SUM 1	3	0.0725	0.1739
Laides hexanema	5	Tchao Praya Nackom Sawan Thailand	HEX THA 2	2	0.0263	0.0526
Laides hexanema	19	Batang Hari Muara Bungo Sumatra Indonesia	HEX SUM 6	3	0.0175	0.0530
Laides hexanema	4	Mekong Bung Kan Thailand	HEX THA 1	2	0.0263	0.0526
Laides sinensis	4	Mekong Bung Kan Thailand	SIN THA 1	2	0.0000	0.0000
Pseudeutropius brachypoptes	19	Batang Hari Muara Bungo Sumatra Indonesia	BRA SUM 6	3	0.0000	0.0000

**Table 1**: Species identification, code of sampling origin (CL, *cf.* Fig. 1), sampling origin, species abbreviations (Abbrev.), size of samples (N), observed heterozygosity ( $H_{obs}$ ) and polymorphic loci indices ( $P^{95}$ ).

Mean observed heterozygosities  $(H_{obs.})$  and polymorphic  $(P^{95})$  indices were computed using the GENETIX package (Belkhir et al., 1996). Standard genetic distances were estimated using the Nei's formula (1978). Phenograms were generated from distance matrix by Fitch cluster analysis using the PHYLIP package (Felsenstein, 1989). The robustness of the data set was tested by a resampling method such as bootstrapping (SEQBOOT in PHYLIP). This method is well developed by Felsenstein (1985) and involves the creation of new data set by sampling N characters randomly with replacement, so that the resulting data set has the same size as the original, but some characters have been left out and others are duplicated. The random variation of the results from analysing these bootstrapped data sets can be shown statistically to be typical of the variation that we would get from collecting new data sets. Bootstrap values were computed over 500 replications of resampled distances matrix.

A multivariate analysis (factor analysis of correspondence) was performed using the BIOMECO program (Lebreton *et al.*, 1990) from a matrix of alleles coded in presence or absence for each individual and each locus from raw electrophoresis data. This statistical analysis method was used with the goal to assess the genetic relatedness of species belonging to genus Laides.

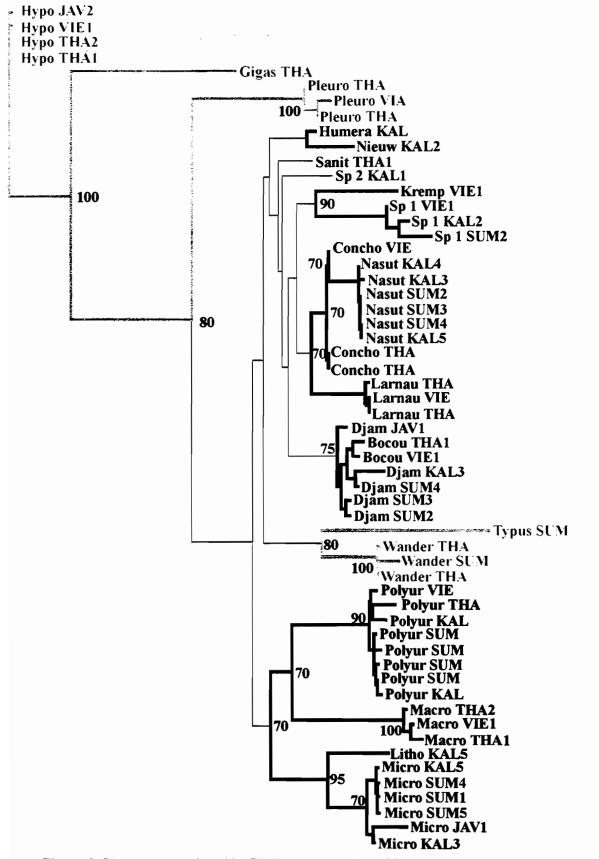
### RESULTS

The study concerned 23 loci (Table 2) excepting for species belonging to Laides and Pseudeutropius genera for which loci Sod-3, Sod-4. Adh and Sdh were not considered due to difficulty of interpretation. Analysis of the zymograms showed considerable polymorphism at the loci studied with a total of 199 alleles evidenced for all species. Only the locus Ldh-1 was monomorphic for the same allele in all the samples. The average rate of observed heterozygosity (Hobs.) for all loci per population was between 0.000 and 0.1826 and the average rate of polymorphism (P<sup>95%</sup>) between 0.000 and 0.3478.

A phylogenetic tree (Fig. 2) was obtained from the matrix of pairwises Nei's genetic distances between all pair of taxa. The results confirm all nominal species proposed by Roberts and Vidthayanon (1991). Bootstrap tests validated four genetic differentiated groups. Within these groups, 7 significant clusters were observed, in which occurrence probability was above 0.70. However internal topology of the genetic network was not

Enzyme system	Abbreviation	Locus	Tissue source	Electrode buffer
Aspartate aminotransferase	AAT	Aat	Liver	TEB
Alcohol dehydrogenase	ADH	Adh	Liver	POULIK ½
Creatine kinase	CK	Ck-1	Eyes	MC 2
		Ck-2	Eyes	MC 2
Fructose biphosphatase	FBP	Fbp	Liver	MC 2
Glucosephosphate isomerase	GPI	Gpi-1	Muscle Eyes	RW
		Gpi-2	Muscle Eyes	RW
Isocitrate dehydrogenase	IDHP	Idhp-1	Muscle	MC 2
		Idhp-2	Liver	MC 2
Lactate dehydrogenase	LDH	Ldh-1	Eyes	MC 2
		Ldh-2	Eyes	MC 2
Malate dehydrogenase	MDH	Mdh-1	Eyes	MC 2
		Mdh-2	Eyes	MC 2
Mannose phosphate isomerase	MPI	Mpi	Liver	POULIK ½ TEB
Phosphoglucomutase	PGM	Pgm	Muscle	RW
6-Phosphogluconate dehydrogenase	6PGD	6Pgd	Liver	MC 2
Protein Total	PT	Prot-1	Muscle	MC 2
		Prot-2	Muscle	MC 2
Superoxide dismutase	SOD	Sod-1	Liver	POULIK 1/2
-		Sod-2	Liver	POULIK 1/2
		Sod-3	Liver	MC 2
		Sod-4	Liver	MC 2
Sorbitol dehydrogenase	SDH	Sdh	Liver	POULIK 1/2

**Table 2**: Enzymes systems, buffers, locus, tissue specificity and electrode buffer investigated in the study. MC 2, Morpholine citrate, pH 6.2; RW, Ridgeway, Lithium hydroxide-borate, pH 8.3; POULIK ½, boric acid-sodium hydroxide, pH 8.2; TEB, Tris-borate-EDTA, pH 8.6.



**Figure 2**: Phenogram produced by Phylip on 20 species of Pangasiidae. This tree was generated from distance matrix by Fitch Cluster Analysis. Bootstrap values were computed over 500 replications of resampled distance matrix.

significant. The cluster 1 is composed of P. hypophthalmus, P. gigas and P. pleurotaenia, the cluster 2 is defined by H. waandersii and H. typus, the cluster 3 by P. conchophilus, P. nasutus and P. larnaudii, the cluster 4 by Pangasius spl and P. Krempfi, the cluster 5 by P. diambal and P. bocourti, the cluster 6 by P. nieuwenhuisii and P. humeralis and finally the cluster comprises P. micronema 7 and P. lithostoma, P. polyuranodon and P. macronema. Pangasius sanitwongsei and Pangasius sp2 constitute a particular situation because they are characterised by the possession of many alleles shared with species belonging to clusters 3, 4 and 5. Pangasius sp1 and Pangasius sp2 mentioned above are probably new species because they were not identified with the specific keys proposed by Roberts & Vidthayanon (1991). Pangasius sp1 was caught both in Indonesia (Kalimantan at Samarinda on Mahakam River; Sumatra at Palembang on Musi River, Jambi on Batang Hari River and Rengat on Indragiri River) and in Vietnam (Binh Dai and Can Tho in Mekong delta). Pangasius spl is genetically related to P. krempfi, nevertheless they are reproductively isolated because no intermediate genotype where observed in sympatric condition as in the Mekong Delta. Pangasius sp2 was observed only in East Kalimantan at Tanjung Redeb on Berau River.

The multivariate analysis projections of individuals referring to their genotype multilocus relatedness is presented on Fig. 3. On the first projection (plan formed by axis 1 and 2) the axis 1 which is the most informative clearly show a huge genetic divergence between Schilbeidae and Pangasiidae families. Axis 1 also reveals a genetic differentiation between P. pleurotaenia and all other pangasiid species. On the second projection (plan formed by axis 2 and 3), the species belonging to genus Laides, P. hypophthalmus and P. gigas form three genetically independent entities, formally separated on axis 2 from the constituted pangasiids. group by other Helicophagus waandersii and H. typus are differentiated from the other species on axis 3.

#### DISCUSSION

#### Speciation and evolutionary processes

The tropical Asian catfish family Pangasiidae displays a strong genetic differentiation with 199

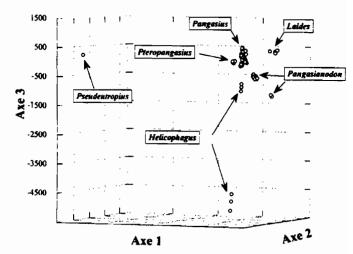


Figure 3: Multivariate analysis projections of individuals referring o their multilocus relatedness.

alleles evidenced on 23 loci. For comparison the phylogenetic relationships assessed by Pouyaud & Agnèse (1995) among species belonging to genera Oreochromis, Sarotherodon, Tilapia. Chilochromis, Pelmatochromis, Tylochromis, Hemichromis and Chromidotilapia (Cichlidae) revealed 95 alleles on 24 loci. Fossils record of the family Pangasiidae (Sanders, 1934 in Roberts & Vidthayanon, 1991) from Tertiary deposits (during period between 65 and 1 million years before present) in central Sumatra indicate that occurrence of this family in south-east Asia is ancient. Under these conditions, cumulative fluctuations of sea water levels during this period have undoubtedly fashioned the pangasiid group leading to the notable ecological and morphological diversity observed actually. Large river basins like Mekong, Tchao Phraya and Kapuas have probably played a major role in term of refuge zone during the past. These rivers possess P. nasutus (Malay peninsula, Indonesia); P. bocourti (Vietnam and Thailand) and P. djambal (Indonesia). The genetic distances between both couple of species (d = 0.109 between samples of P. nasutus from Muara Tewe in Kalimantan and P. conchophilus from Mekong in Vietnam; d = 0.158 between samples of P. bocourti from Thailand and P. djambal from Java in Indonesia) are comparable with average distances occurring within the species P. polyuranodon (d = 0.106 between population of Muara Tewe in Kalimantan and population caught in Tchao Phraya) or P. micronema (d = 0.145between population of Teluk Kuantan in Sumatra and population of Solo in Java).

#### Systematic implications

The multivariate analysis clearly indicate that *Laides hexanema* and *Laides sinensis* are genetically related with the pangasiid species. Nei's genetic distances (Table 3) confirm that *Laides* species are genetically closer to pangasiid species than to *Pseudeutropius* species. Therefore the genus *Laides* should be placed in Pangasiidae as firstly proposed by Roberts (1989).

	Pseudeutropius (Schilbeidae)	Laides
Laides	1.19	
Pangasiidae	1.05	0.52

Table 3: Nei's genetic distances betweenPangasiidae, Laides and Schilbeidae.

The phylogenetic tree obtained shows a clustering of species which validate the genus *Helicophagus* but cannot agree the actual composition of the genus *Pangasius* which is polyphyletic. *Neopangasius*, *Pangasianodon* and *Pteropangasius* are the three subgenus recognised by Roberts & Vidthayanon (1991).

Our study confirms the species relatedness described within these three groups except in the subgenus Neopangasius in which P. lithostoma could not be inserted. This species is genetically closer to P. micronema. Considering the genus Helicophagus as a reference, average genetic distances between each group (Table 4) suggest that Pangasianodon and Pteropangasius should be elevated to the genus level. The genus Pangasianodon would then be composed by P. hypophthalmus and P. gigas and the genus Pteropangasius by only one species P. pleurotaenia. Neopangasius may remain valid with P. nieuwenhuisii and P. humeralis as a subgenus of Pangasius. Pangasius lithostoma. P. micronema, P. macronema, P. polyuranodon, P. lithostoma. P. sanitwongsei, P. krempfi, P. larnaudii. P. nasutus. P. conchophilus, P. djambal, P. bocourti could be maintained in the genus Pangasius. Additional genetic analyses using other markers like ribosomal sequences may provide evidence of other subgenus in the *Pangasius* genus.

#### Possible finding of two new species

Pangasius sp1 was caught in Sumatra (Palembang, Musi River; Rengat, Indragiri River), in Kalimantan (Samarinda, Mahakam River) and in Vietnam (Mekong River). In these localities this species was misidentified as P. djambal. This species shares many characteristics with Pangasius pangasius like gill raker counts, its occurrence in saline waters (reported by fishermen both in Indonesia and Vietnam) and a relatively similar palatal dentition. As in P. pangasius, the palatal dentition is curved and constituted by related close-sets. Referring to the dentition picture available in Roberts & Vidthayanon (1991) for P. pangasius, the Pangasius sp1 dentition presents some differences. The two vomerine tooth plates are always linked like an horizontal number 8. On each side the palatine tooth plates are small, round and separated. As no samples of Pangasius pangasius could be obtained at this stage from India or Bangladesh for comparison, the status of Pangasius sp1 remains unclear. A detail morphological examination of the specimens collected during this study will be carried out in a near future. They may represent a new pangasiid species, but at the present state the possibility that these specimens belong to the species P. pangasius cannot be discarded. In this latter hypothesis, P. pangasius would become the pangasiid species with the largest geographic distribution, from India to Vietnam and Indonesian archipelago.

Pangasius sp2 was caught in East Kalimantan (Tanjung Redeb, Berau river). In this location the species was misidentified as *P. polyuranodon*. This species share genetic characteristics with species such as *P. djambal* and *P. bocouti*. The internal position of this fish in the phylogeny and its isolated biogeographic area (basin regarding to the Macassar strait along the Wallace line) may indicate that this species has colonised this area since a very ancient period. Further analysis will permit to precise if this species has conserved

	Pangasianodon	Pteropangasius	Helicophagus	Pangasius 1
Pteropangasius	0.656			
Helicophagus	0.701	0.675		
Pangasius 1	0.568	0.538	0.230	
Pangasius 2	0.607	0.530	0.180	0.080

Table 4 : Nei's genetic distances between each possible genus and subgenus in pangasiids.

primitive characters. The two vomerine form a single large median tooth plate like in *P. polyuranodon*, but the palatines tooth plates are very elongate and are parallel with the lateral sides of the vomerine plate. Up to now this shape of palatal dentition was never reported in the pangasiids.

#### Some new data on zoogeography

Helicophagus typus was considered as probably extinct in Sumatra because the last specimen was collected in Palembang in 1908 (Roberts & Vidthayanon, 1991). We can assume that *H. typus* still occurs in the Batang Hari River (Sumatra, Jambi) where 3 specimens (around 600 mm) were collected the 27 February 1997 and two supplementary specimens (621 and 342 mm SL) were found in the Kapuas River on the 27 June 1997 (Sanggau and Sintang, West Kalimantan).

Until now, *Pangasius djambal* was reported only from Java and Kalimantan, we can assume however that this species occurs in all major basins of Sumatra as Musi, Batang Hari and Indragiri Rivers. The species is abundant on the markets in these locations. Nevertheless, this species has a restricted distribution in Java where it seems to be present only in Solo and Brantas Rivers. Contrarily to the situation stated by Roberts and Vidthayanon (1991), *Pangasius djambal* was never utilised in aquaculture in Java until now, as anywhere else in Indonesia. The only pangasiid species cultured in Indonesia is *Pangasius hypophthalmus* which was introduced from Thailand in 1972.

Because of human activities located on river banks, organic and chemical pollution, dams construction, over-fishing, many endemic species are threatened with extinction as is the case of *Pangasius gigas* in the Mekong. In Indonesia, such a situation is observed in Java where *P. djambal* and *P. micronema* could be found only in the Brantas and Solo Rivers in central Java. Local information strongly suggests that these species have now disappeared from anywhere else on the island. By contrast, *Pangasius hypophthalmus* which has been found in the Citarum River (West Java) and Batang Hari River tributaries (Sumatra) could now be considered as part of the Indonesian ichthyofauna.

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## THE BIOLOGICAL DIVERSITY AND AQUACULTURE OF CLARIID AND PANGASIID CATFISHES IN SOUTH-EAST ASIA



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