Chiang Mai J. Sci. 2011; 38(3) : 485-502
http://it.science.cmu.ac.th/ejournal/
Contributed Paper

Fish Distribution in a River Basin in the Lower Northern of Thailand and a Strategy for Conservation Following River Damming

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Recieved : 2 September 2010
Accepted : 15 March 2011

ABSTRACT

Distribution patterns of 157 fish species, including 7 IUCN- and 2 exotic- species, in the river basin of Phisanulok Province, Central of Thailand were analyzed by an adaptive learning algorithm called a "self organizing map" (SOM) using a presence/absence data of the fish species in 26 sampling sites, conducted between 2003 to 2008. Sampling sites were classified according to the hydrographic system and covered the area of the recently completed, Khwae Noi Reservoir. The results from SOM were partitioned the sampling sites into three main clusters with two sub-clusters, due to the similarity of fish compositions. The lowest species richness was observed in the high altitude hill stream area (i.e. cluster I) and gradually increased along the longitudinal river gradient (i.e. from cluster II to IIIb). The predicted occurrence probability (OP) showed the potential of individual species to establish in each area. Each species had its own range of distribution and could be classified into 8 groups according to their visualization gray scale on SOMs. Distribution pattern, of each group, was related to the biological functions and ecological trait of the species. Implication for fish conservation, especially due to damming the Khwae Noi Reservoir, by declaration of reserves is proposed.

Keywords: damming, self organizing map, IUCN fish species, reserves, Phitsanulok Province.

1. INTRODUCTION

Thailand is similar to many other countries in Southeast Asia, where agriculture is the main commodity of the country's gross domestic product. Therefore, demanding on freshwater for agricultures is increasing continuously, as supplementary irrigation, and is now required every year. Dam-building for impoundment of rivers, as a consequence, to provide irrigation water has been widely planned and constructed. The inevitable impact of this infrastructure development is the changing of the aquatic ecosystem from flowing-water to stagnant-water ecosystems after a river is damming. This change eventually affects to the livings in the river ecosystem species by species from the micro-components (e.g. phytoplankton and diatoms [1]) to macro-components (e.g. macroinvertebrates and fish [2, 3]).

Changes in fish communities, due to an anthropogenic stress, are very crucial, as for the baseline information to achieve effective conservation strategies. However, this information is difficult to obtain, if there is a gap in knowledge about the composition and abundance of fish species prior to the perturbations into the system [4]. A solution to this problem that is often advocated by selecting a large set of 'reference sites', distributed across a broader region, and develop a numerical model associating spatial variation in biological assemblages among these sites with environmental variables [5, 6]. Then, by estimating the total number of extant species and the abundance of individual species, an understanding of the structure and composition in communities can be provided [7]. This approach could be achieved by combining the theories of complex systems and by using computers, which eventually allow us a new approach to the understanding and/or predicting of nature [8].

Human activities expose freshwater ecosystems to a wide range of stressors thereby threatening biodiversity and ecosystem processes [9], the objective of this study is to make an insight analysis of fish distributions in the recent regulated river basin in Thailand, the Khwae Noi. The basin was divided into 'reference site' classified by a hydrographic system. The self organizing map (SOM) [10, 11] was employed to characterize the distribution pattern of fish species living in the basin and assess the vulnerability of each of them in the impounded area, and then to develop a strategy to minimize the impact of environmental changes by identifying potential reserves in the basin [12].

2. MATERIALS AND METHODS

2.1 Study Area

The Khwae Noi River Basin (Figure 1) is among one of the most important river basins in the country due to its biological diversity, especially fishes, in which 169 fish species were recorded [13, 14]. The basin locates in east of Phitsanulok Province, Central of Thailand. It is a sub-basin of the Nan River Basin in the northeast of the Chao Phraya Basin, with a catchment area of 4,841 km^2. There are mountains ranging from 1,400 to 2,100 m in height in the northern area and mountains ranging from 1,500 to 1,750 m in the east part of the basin [15].

The basin was recently regulated by the Khwae Noi Reservoir, which was built in 2003 and started to impound water in 2009. The Khwae Noi Reservoir (latt. 17^o 11′ N and long. 100^o 25′ N) is an irrigation and flood control reservoir. The dam *per se* was built by blocking the Khwae Noi River in Watbot District, Phitsanulok Province. The reservoir storage volume is 769 m^3 at 132 m above sea level and covers an area of 6,139 ha [16].

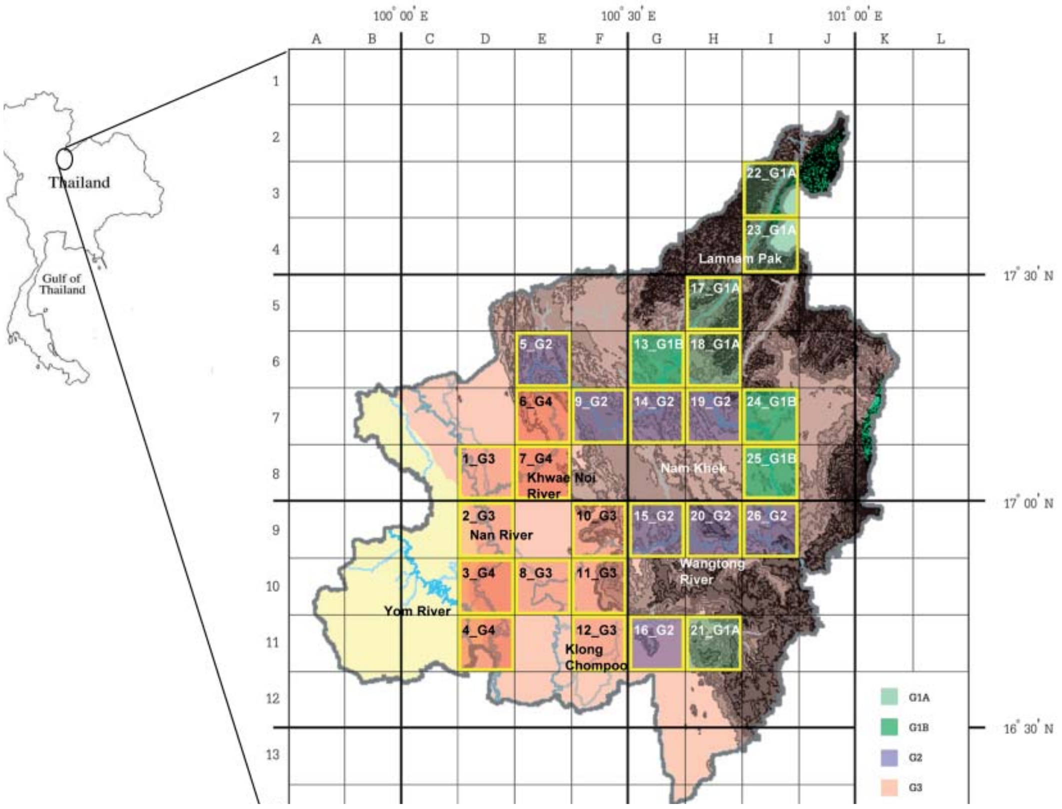


Figure 1. Map of the Khwae Noi River Basin and sampling. Each grid size is 100 km^2 (10 ^{x} 10 km^2).

2.2 Fish Collections

Data on fish assemblages were collected from 26 stations in the Nan River Basin Phitsanulok Province, covered by the Khwae Noi and nearby river-systems, which were likely to be impacted by the damming [13, 14]. Sampling stations were classified by the hydrographic system (i.e. longitudinal sections in a river basin) and divided into 5 zones (Figure 1) [17]. Stations were all in the rural area to avoid any pollution sources and chosen on the basis of accessibility, similarity in habitat types, and to maximize the diversity of habitat types (e.g. pool, cascade and riffle) at each zone as followed

1. **G1A:** the hill streams at high altitude (i.e. above 1,700 m) comprised 5 stations in the Lamnam Pak Tributary and the headwater of the Klong Chompoo Tributary (Stations 17-18 and 21-23)
2. **G1B:** the mountain creeks, lying between 1,500 and 1,700 m, represented the headwater area and incorporate the small tributaries. There were 3 stations in this group located in the headwater of the Khwae Noi River and the confluence of the Lamnam Pak Tributary connected to the Khwae Noi River (Stations 13 and 24-25).

3. **G2:** the main canals in the Nam Khek Tributary and eupotamons (i.e. main river channel) of the Khwae Noi River and the Klong Chompoo Tributary, which run through the high altitude rain-fed area. These stations are the junctions of the mountain creeks and comprised of 8 stations (Stations 5, 9, 14-16, 19-20 and 26).
4. **G3:** the eupotamons of the lower reaches of the Wangtong River and the Klong Chompoo Tributary as well as the confluence of the Khwae Noi River connected to the Nan River (Stations 1-2, 8 and 10-12).
5. **G4:** the lowland rivers with marshes, which run through the floodplain areas, the lower reaches of the Khwae Noi and the Nan Rivers (Stations 3-4 and 6-7).

A total of 11 survey-trips were conducted [13] *viz.*, 2 trips in 2003 (April and October), one trip in 2004 (July) and 4 trips in both 2005 and 2008 (January, April, July and October). All 26 stations were not sampled in every trip due to financial constraints but at least twice in dry (January and April) and wet (July and October) seasons and recorded as presentation of species in each sampling site. All stations were approximately 35 or 40 mean stream widths in length. Therefore, the wider the stream was, the longer the station [18]. Fishes were sampled by using beach-seine net, gill nets (mesh size: 20, 30, 40, 55, 70 and 90 mm) and electro-fishing by an AC shocker (Honda EM 650, DC 220V). Samples were anaesthetized in Tricaine-Methane-Sulfonate (i.e. MS222) at approximately 150 mg $\cdot l^{-1}$. Each individual species was then counted and weighed, and after recovery the samples were released. Unidentified samples were sacrificed in 10% formalin and further taxonomically classified in laboratory.

2.3 Data Analysis

A self-organizing map (SOM) with a Kohonen unsupervised learning algorithm was used in the study for ordering samples [10, 11, 19]. The SOM is a kind of artificial neural networks (ANN) method, which is widely applied in the last decade for solving problems in aquatic ecology, because it is capability of clustering, classification, estimation, prediction and data mining [20]. SOM is an efficient method for analyzing systems ruled by complex non-linear relationships and provides an alternative to traditional statistical methods for classifying complex data (i.e. contained a lot of surveys and variables) [20, 21]. It has been recognized as a powerful tool for describing species distribution and assemblages [19-21]. In this study, The SOM was simulated and the cluster analysis was performed by MATLAB (Ver. 6.1.0) by using SOM-toolbox, which developed by the Laboratory of Computer and Information Science (CIS), Helsinki University [20],

The SOM consists of two layers *viz.* the input and output layers, which connected with the weight vectors. The input layer receives input values from the data matrix, whereas the output layer consists of output neurons, which displayed as a hexagonal lattice for better visualization. During the learning process, the SOM weights are modified to minimize the distance between weight and input vectors. The map (i.e. SOM, output layer) obtained after the learning process contains all the samples assigned to neurons. Generally, samples assigned to the same neurons, or to nearby neurons, are similar and samples assigned to distant neurons differ. Additionally, samples assigned to nearby neurons differ considerably if those neurons belonged to different clusters, which were identified with use of a hierarchical cluster analysis (Ward linkage, Euclidean distance). The detailed algorithm of the SOM can be found in [10, 11, 19, 20]. The occurrence probability of each species in each cluster can be approximately estimated during the learning process and seen in SOM, in which the gray scale gradient account for probabilities of occurrence [21], with dark corresponding to high probability and light *vice versa* [19, 21].

The presence/absence data of the 157 taxa (see Table 1) from the 26 sampling sites were presented as a data matrix into the input layer. The number of neurons for the SOM was firstly defined according to the formula $C = 5\sqrt{n}$ proposed by (CIS) [20], where c is the number of cells and n is the number of samples. The number of neurons was started at 30 neurons and then varied. Finally the output layer of 16 neurons, was organized into an array with 4 rows and 4 columns of cells (i.e. 4 x 4 hexagonal lattice). This SOM map size was chosen because of its minimum the topographic and quantization errors as well as clear classification (i.e. no many empty cells left) [20, 21].

The analysis of similarity (ANOSIM) was used to test of significant difference among clusters by using occurrence probability, which approximately estimated from the connection intensity of the SOM during the learning process [21]. ANOSIM was employed by using library "vegan" [22] in Program R. The statistical differences of species richness among clusters were analyzed using Kruskal–Wallis (H) and Dunn's post-hoc tests. All statistical analyses were carried out with Program R software [23].

3. RESULTS

Fish samples were classified taxonomically into 157 species (37 Families: Table 1). Fishes in the family Cyprinidae were the most dominant group (37.9%), in terms of number of species, followed by the Bagridae (6.8%). In all samples, there was only one species of elasmobranch fish, *Himantura signifier,* which is also an endangered species in the IUCN list. Other species in the list were 5 vulnerable species *viz.*, *Oxygaster pointoni*, *Crossocheilus reticulates*, *Hemibagrus bocourti*, *Rhinogobius chiengmaiensis* and *Monotretus cambodgiensis* and one near threatened species i.e. *Syncrossus beauforti*. Except for tilapia *Oreochromis niloticus*, an Indian major carp *Labeo rohita*, was another introduced exotic species found.

The output layer of the SOM was partitioned into three main clusters with two sub-clusters, due to the similarity of fish species composition in each sampling stations. The SOM map was clearly classified and obviously seen similar pattern in fish assemblage within each zone (i.e. sampling stations in each zone were grouped together) (Figure 2). The similarity within cluster were much more than among clusters (ANOSIM, R = 0.790, $P < 0.001$, Based on 1,000 permutations). In cluster I, it is characterized by the sampling stations in G1A and G1B zone. Cluster II includes the sampling stations in the river channel that were located in the higher altitude, i.e. G2. Meanwhile the lowland sampling stations were contained in cluster III, which was further divided into 2 sub-clusters (i.e. IIIa and IIIb).

Species richness significantly increased (Kruskal-Wallis Test, $P < 0.001$) from clusters I to cluster IIIb (Figure 3), indicating a strong gradient distribution. To refine the common species (i.e. species which usually be found) in each cluster, the connection intensity between input and output layers calculated during the learning process were considered as the occurrence probability (OP) for each species in each cluster (Table 1). In cluster I, *Gyrinocheilus aymonieri* (OP = 0.934) dominated, followed by *Channa gachua* (OP = 0.922), *S. beauforti*, *Schistura nicholsi* and *Nemacheilus binotatus* (each OP = 0.920). In cluster II, the dominant group was comparatively

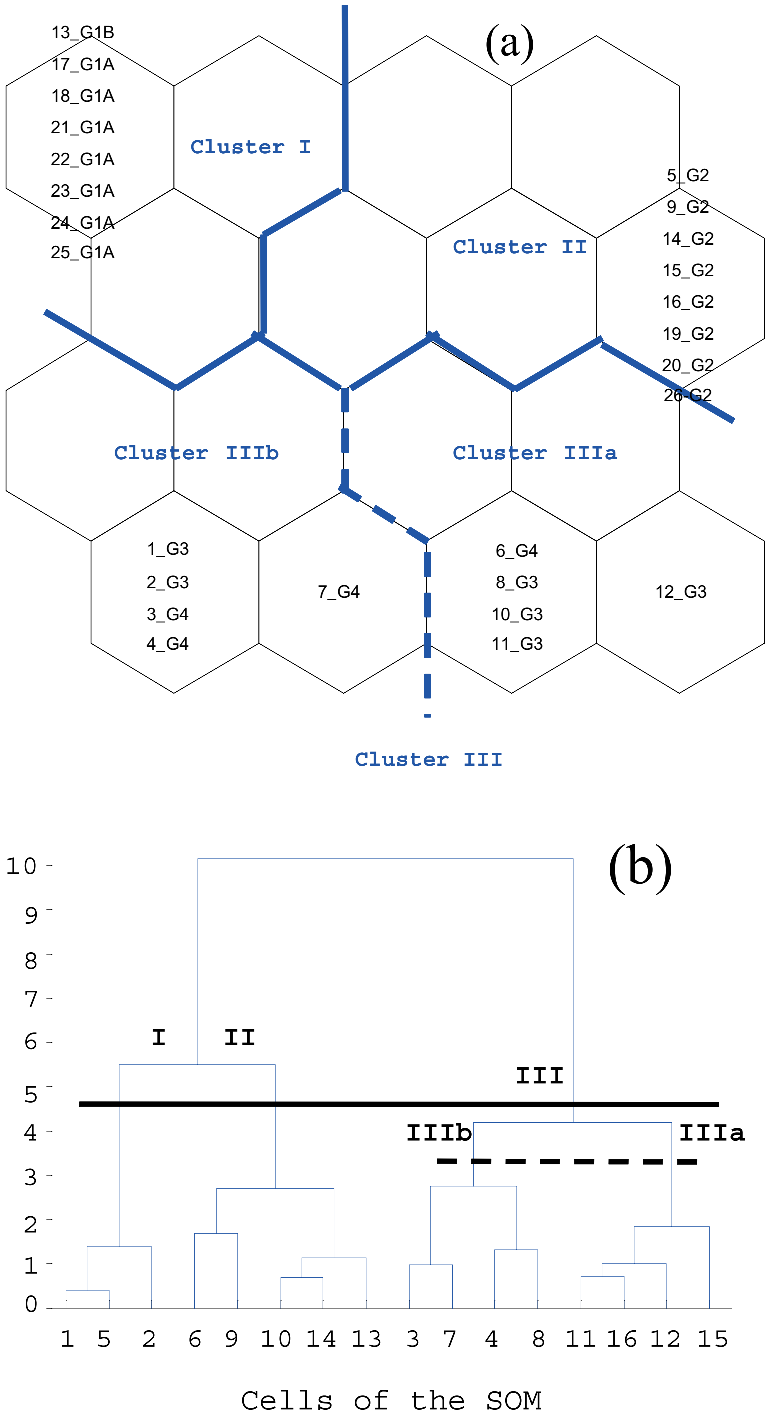


Figure 2. (a) Results of the SOM model. Classification of sites on SOM using presence/absence data of fish species. (b) Dendrogram of the SOM output matrix shows groups of the similarity of cells on SOM. Two levels cut-off allowed the identification of 3 main clusters (bold lines) and cluster III divided into 2 sub-clusters (dotted lines).

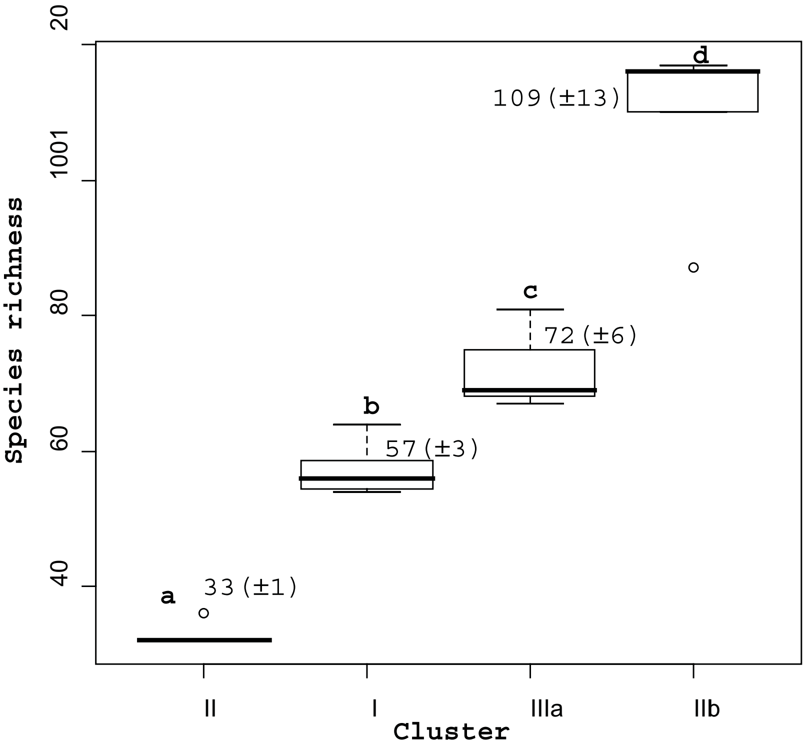


Figure 3. Box plots of specific richness in each cluster. Number at each box indicates mean (± SD) Bold line within each box plot indicates the median and circle is outlier. The letters over the box plots shows pairwise significant differences between clusters (Kruskall–Wallis test and Dunn's post test; p < 0.05).

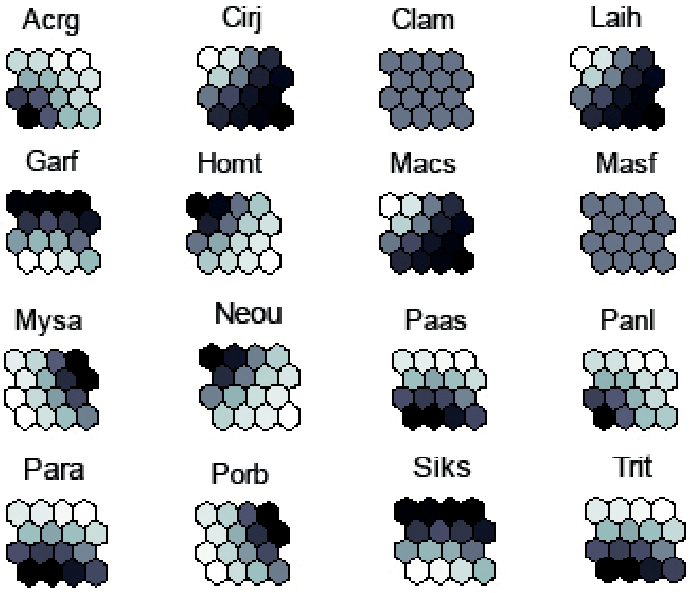


Figure 4. Visualization of relative abundance of fish species calculated in the trained SOM in gray scale.

similar to those in cluster I, but there were differences in occurrence probability as *C. gachua* (OP = 0.904), *S. beauforti*, *S. nicholsi*, *N. binotatus* and *Garra fuliginosa* (each OP = 0.891). In cluster IIIa, there were 26 species that showed occurrence probability at 1.00, which implied that these fish could be found in every station contained in this cluster. Cluster IIIb showed low OP among the high OP species, in which *Pristolepis fasciatus* was the species that had highest value (OP = 0.814), followed by *Macrognathus taeniagaster*, *Mystus mysticetus*, *Mystus singaringan* and *Mystus multiradiatus*, all with OP values around 0.78. It is generally accepted that species that show an OP value higher than 0.6 has been successfully established in that area. The results showed that the numbers of established species was getting higher from cluster I to IIIb, i.e. higher altitude to lower reach in which there were 21, 43, 51 and 64 species, respectively (Table 1).

The distribution patterns of each fish species, in the unit of SOM, were displayed in gray scale, which were also, implied the probability of each species being observed at sampling sites (i.e. relative abundance). Figure 4 showed the examples of the SOM maps of sixteen fish species, in which the dark represent a high occurrence probability of occurrence in each neuron, whereas light is low. The distribution of 157 species can be grouped together, based on their similarity of SOM maps, and further divided into 8 groups from the mountainous area (group **A**) to the low land area (group **H**) (Figure 5). Each group indicated that each fish species has its own range of distribution in the river basin, although some species were more commonly distributed in the basin such as *Oxyeleotris marmorata*, *Mastacembelus* spp. and *Clarias* spp. The distribution of the IUCN-list species can be also seen by the SOM maps (Figure 5). Four species in group **H** (i.e.*, H. signifier*, *O. pointoni*, *C. reticulates* and *M. cambodgiensis*) extensively occupied the lower reaches of the floodplain of the basin (i.e. dark gray in cluster IIIb area, the bottom left corner). The dark gray shade in cluster IIIa area (i.e. the bottom right corner) in the SOM map of *H. bocourti* implies that this fish usually occupies the mainstream of the lower reach (i.e. group **E**). Meanwhile the dark gray shade in the SOM map of *R. chiengmaiensis* located in cluster II area (i.e. top right corner) means that this fish preferred the condition of the mainstream at higher altitude areas with high river flow rate (i.e. group **C**). For the near threatened species, *S. beauforti*, dark gray shade in the upper part of the map (clusters I and II) shows that this species preferred to live in the mountainous area (group **A**) similar to the result obtained for the exotic *L. rohita*.

4. DISCUSSION

The algorithm of SOM is useful for analyzing nonlinear relationships between variables and those with strongly skewed distributions [20]. Another advantage of using the SOM method on a qualitative dichotomous (presence/absence) data of fish species is that it can be possible to predict the probability of each species being present where it was not actually collected [12, 20]. The absence of a species in certain samples is expressed by zeros, which makes the distribution of rare species counts strongly skewed and thus difficult to be normalized by any transformation [20]. Thus, the distribution of individual species in the basin can be estimated and understood. Moreover, the presence/absence data is an advantage to identify patterns in fish assemblage structures, since it prevents trivial clustering due to the decline in fish abundance over time [24].

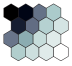
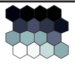
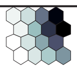
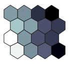
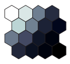
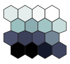
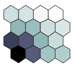
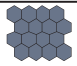
Group		Cluster (s)	Species
A		I	Glyl, Glym, Glyt, Glyf, Homi, Homl, Homs, Homt, Schd, Neou (10 species)
B		I & II	Chag, Cals, Gyra, Garf, Neob, Schn, Synb, Croo, Cros, Epaf, Garc, Labr, Siks, Danr (14 species)
C		II	Rhic, Schs, Porb, Sysb, Mysa, Neos (6 species)
D		II & IIIa	Chas, Chal, Helt (3 species)
E		II, IIIa & IIIb	Cham, Prif, Mact, Macs, Laih, Panm, Panp, Hemb, Hemw, Hemy, Synh, Acac, Bagm, Osth, Ostl, Ostm, Cirj, Cirm, Danl, Morc, Bars, Hamm, Punb, Cyca, Cycm, Cyce, Cycr, Myam, Opsk, Clua (30 species)
F		IIIa & IIIb	Monc, Monf, Trim, Trip, Trit, Triu. Ospg, Anat, Dorb, Ichc, Mona, Paas, Para, Parw, Xenc, Ders, Bagb, Beld, Kryb, Mica, Micb, Ompb, Omph, Wala, Cror, Mysa, Mysl, Mysm, Mysy, Myss, Hens, Lobr, Barg, Cycl, Bara, Thrt, Ambt, Hims, Oxyp, Notn (40 species)
G		IIIb	Eurh, Cynf, Cynm, Bets, Triw, Polm, Toxc, Toxm, Oren, Braa, Hems, Pecf, Aplp, Helw, Panh, Pand, Panl, Acrg, Kryc, Kryr, Wall, Yasm, Yaso, Leph, Lepm, Pana, Pano, Osti, Ostw, Cirp, Labs, Lobd, Sysp, Barn, Cosh, Punp, Raig, Ambc, Leph, Lucb, Chio, Parh, Pars, Parr, Part, Parm (46 species)
H		All	Oxym, Masa, Masf, Clab, Clam, Hemf, Pses, Syso (8 species)

Figure 5. Distribution patterns of fish species in the SOM. Gray-scale gradients account for occurrence probability, with dark corresponding to high probability and light to low probability.

Table 1. List of species found during the surveys and their occurrence probabilities in each cluster estimated by SOM.

Species	Abbreviation	code	Cluster			
			I	**II**	**IIIa**	**IIIb**
Family Dasyatidae						
Himantura signifer	Hims	1	0.00	0.01	0.03	0.05
Family Notopteridae						
Chitala ornata	Chio	2	0.06	0.02	0.17	0.56
Notopterus notopterus	Notn	3	0.09	0.40	0.82	0.78
Family Clupeidae						
Clupeichthys aesarnensis	Clua	4	0.05	0.21	0.24	0.37
Family Cyprinidae						
Paralaubuca harmandi	Parh	5	0.06	0.00	0.09	0.48
Paralaubuca siamensis	Pars	6	0.06	0.00	0.09	0.48
Paralaubuca riveroi	Parr	7	0.06	0.00	0.09	0.48
Paralaubuca typus	Part	8	0.06	0.00	0.09	0.48

Table 1 (cont.) List of species found during the surveys and their occurrence probabilities in each cluster estimated by SOM.

Species	Abbreviation	code	Cluster			
			I	II	IIIa	IIIb
Oxygaster pointoni	Oxyp	9	0.07	0.06	0.46	0.70
Parachela maculicauda	Parm	10	0.02	0.01	0.08	0.16
Raiamas guttatus	Raig	11	0.03	0.00	0.05	0.29
Opsarius koratensis	Opsk	12	0.11	0.76	1.00	0.79
Amblypharyngodon chulabhornae	Ambc	13	0.01	0.00	0.02	0.11
Danio regina	Danr	14	0.92	0.89	0.35	0.22
Leptobarbus hoevenii	Leph	15	0.07	0.03	0.25	0.60
Luciosoma bleekeri	Lucb	16	0.06	0.00	0.09	0.48
Thryssocypris tonlesapensis	Thrt	17	0.03	0.03	0.17	0.26
Neolissochilus stracheyi	Neos	18	0.01	0.09	0.05	0.00
Neolissochilus subterraneus	Neou	19	0.13	0.03	0.00	0.03
Amblyrhynchichthys truncatus	Ambt	20	0.08	0.10	0.60	0.77
Cosmochilus harmandi	Cosh	21	0.03	0.00	0.05	0.29
Cyclocheilichthys apogon	Cyca	22	0.11	0.76	1.00	0.79
Cyclocheilichthys armatus	Cycm	23	0.11	0.76	1.00	0.79
Cyclocheilichthys enoplos	Cyce	24	0.11	0.76	1.00	0.79
Cyclocheilichthys lagleri	Cycl	25	0.07	0.08	0.51	0.71
Cyclocheilichthys repasson	Cycr	26	0.11	0.76	1.00	0.79
Mystacoleucus argenteus	Mysa	27	0.08	0.39	0.69	0.79
Mystacoleucus marginatus	Myam	28	0.11	0.76	1.00	0.79
Puntioplites proctozysron	Punp	29	0.06	0.00	0.09	0.48
Barbonymus altus	Bara	30	0.07	0.08	0.51	0.71
Barbonymus gonionotus	Barg	31	0.07	0.08	0.51	0.71
Barbonymus schwanenfeldii	Bars	32	0.11	0.76	1.00	0.79
Poropuntius bantamensis	Porb	33	0.03	0.65	0.37	0.00
Hampala macrolepidota	Hamm	34	0.11	0.76	1.00	0.79
Puntius brevis	Punb	35	0.11	0.76	1.00	0.79
Sikukia stejnegeri	Siks	36	0.92	0.89	0.35	0.22
Systomus binotatus	Sysb	37	0.03	0.65	0.37	0.00
Systomus orphoides	Syso	38	0.01	0.01	0.01	0.01
Systomus partipentazona	Sysp	39	0.03	0.00	0.05	0.29
Barbichthys nitidus	Barn	40	0.06	0.00	0.09	0.48
Cirrhinus jullieni	Cirj	41	0.11	0.76	1.00	0.79
Cirrhinus molitorella	Cirrm	42	0.11	0.76	1.00	0.79
Cirrhinus prosemion	Cirrp	43	0.06	0.00	0.09	0.48
Dangila lineata	Danl	44	0.11	0.76	1.00	0.79
Henicorhynchus siamensis	Hens	45	0.08	0.09	0.59	0.76
Labeo rohita	Labr	46	0.13	0.12	0.05	0.02

Table 1 (cont.) List of species found during the surveys and their occurrence probabilities in each cluster estimated by SOM.

Species	Abbreviation	code	Cluster			
			I	II	IIIa	IIIb
Labiobarbus siamensis	Labs	47	0.06	0.00	0.09	0.48
Lobocheilos davisi	Lobd	48	0.06	0.00	0.09	0.48
Lobocheilos rhabdoura	Lobr	49	0.08	0.09	0.59	0.76
Morulius chrysophekadion	Morc	50	0.11	0.76	1.00	0.71
Osteochilus hasseltii	Osth	51	0.11	0.76	1.00	0.79
Osteochilus lini	Ostl	52	0.06	0.76	1.00	0.79
Osteochilus melanopleurus	Ostm	53	0.11	0.76	1.00	0.79
Osteochilus microcephalus	Osti	54	0.11	0.00	0.09	0.48
Osteochilus waandersi	Ostw	55	0.06	0.00	0.09	0.48
Crossocheilus oblongus	Croo	56	0.92	0.89	0.35	0.22
Crossocheilus reticulatus	Cror	57	0.07	0.08	0.51	0.71
Crossocheilus siamensis	Cros	58	0.92	0.89	0.35	0.22
Epalzeorhynchos frenatus	Epaf	59	0.92	0.89	0.35	0.22
Garra cambodgiensis	Garc	60	0.92	0.89	0.35	0.22
Garra fuliginosa	Garf	61	0.92	0.89	0.35	0.22
Family Balitoridae						
Homaloptera indochinensis	Homi	62	0.89	0.24	0.00	0.21
Homaloptera leonardi	Homl	63	0.89	0.24	0.00	0.21
Homaloptera smithi	Homs	64	0.89	0.24	0.00	0.21
Homaloptera tweediei	Homt	65	0.89	0.24	0.00	0.21
Nemacheilus binotatus	Neob	66	0.92	0.89	0.35	0.22
Schistura deansmarti	Schd	67	0.13	0.03	0.00	0.03
Schistura nicholsi	Schn	68	0.92	0.89	0.35	0.22
Schistura spiesi	Schs	69	0.00	0.03	0.02	0.00
Family Cobitidae						
Syncrossus beauforti	Synb	70	0.92	0.89	0.35	0.22
Syncrossus helodes	Synh	71	0.11	0.76	1.00	0.79
Yasuhikotakia modesta	Yasm	72	0.06	0.00	0.09	0.48
Yasuhikotakia morleti	Yaso	73	0.06	0.00	0.09	0.48
Acanthopsis choirorhynchos	Acac	74	0.10	0.63	0.95	0.78
Lepidocephalichthys hasselti	Leph	75	0.06	0.02	0.17	0.56
Lepidocephalichthys cf. macrochir	Lepm	76	0.01	0.00	0.02	0.11
Pangio anguillaris	Pana	77	0.07	0.03	0.25	0.60
Pangio oblonga	Pano	78	0.11	0.03	0.25	0.60
Family Gyrinocheilidae						
Gyrinocheilus aymonieri	Gyra	79	0.93	0.89	0.37	0.32
Family Bagridae						
Bagriichthy macracanthus	Bagm	80	0.11	0.76	1.00	0.79

Table 1 (cont.) List of species found during the surveys and their occurrence probabilities in each cluster estimated by SOM.

Species	Abbreviation	code	Cluster			
			I	II	IIIa	IIIb
Hemibagrus bocourti	Hemb	81	0.11	0.76	1.00	0.79
Hemibagrus filamentus	Hemf	82	0.01	0.01	0.01	0.01
Hemibagrus wyckii	Hemw	83	0.11	0.76	1.00	0.79
Hemibagrus wyckioides	Hemy	84	0.11	0.76	1.00	0.79
Mystus atrifasciatus	Mysa	85	0.02	0.17	0.22	0.00
Mystus albolineatus	Mysl	86	0.08	0.17	0.69	0.79
Pseudumystus siamensis	Pses	87	0.01	0.01	0.01	0.01
Mystus multiradiatus	Mysm	88	0.08	0.17	0.69	0.79
Mystus mysticetus	Mysy	89	0.08	0.17	0.69	0.79
Mystus singaringan	Myss	90	0.08	0.17	0.69	0.79
Family Siluridae						
Belodontichthys dinema	Beld	91	0.08	0.17	0.69	0.79
Kryptopterus bicirrhis	Kryb	92	0.00	0.01	0.03	0.05
Kryptopterus cheveyi	Kryc	93	0.06	0.00	0.09	0.48
Kryptopterus cryptopterus	Kryr	94	0.06	0.00	0.09	0.48
Micronema apogon	Mica	95	0.08	0.10	0.60	0.77
Moicronema bleekeri	Micb	96	0.08	0.10	0.60	0.77
Ompok bimaculatus	Ompb	97	0.08	0.10	0.60	0.77
Ompok hypophthalmus	Omph	98	0.08	0.10	0.60	0.77
Wallago attu	Wala	99	0.08	0.10	0.60	0.77
Wallago leeri	Wall	100	0.03	0.00	0.05	0.29
Family Schilbeidae						
Laides hexanema	Laih	101	0.11	0.76	1.00	0.79
Family Pangasiidae						
Helicophagus waandersi	Helw	102	0.06	0.00	0.09	0.48
Pangasianodon hypophthalmus	Panh	103	0.06	0.00	0.09	0.48
Pangasius djambal	Pand	104	0.06	0.00	0.09	0.48
Pangasius larnaudii	Panl	105	0.06	0.00	0.09	0.48
Pangasius macronema	Panm	106	0.11	0.76	1.00	0.79
Pangasius pleurotaenia	Panp	107	0.07	0.76	1.00	0.79
Family Skysidae						
Acrochordonichthys gyrinus	Acrg	108	0.01	0.00	0.02	0.11
Bagarius bagarius	Bagb	109	0.08	0.10	0.60	0.77
Glyptpthorax fuscus	Glyf	110	0.89	0.24	0.00	0.21
Clyptothorax lampris	Glyl	111	0.89	0.24	0.00	0.21
Glyptothorax major	Glym	112	0.89	0.24	0.00	0.21
Acrochordonichthys gyrinus	Glyt	113	0.89	0.24	0.00	0.21

Table 1 (cont.) List of species found during the surveys and their occurrence probabilities in each cluster estimated by SOM.

Species	Abbreviation	code	Cluster			
			I	II	IIIa	IIIb
Family Claridae						
Clarias batrachus	Clab	114	0.01	0.01	0.01	0.01
Clarias macrocephalus	Clam	115	0.01	0.01	0.01	0.01
Family Ariidae						
Hemipimelodus siamensis	Hems	116	0.06	0.00	0.09	0.48
Family Loricariidae						
Peckoltia cf. filicaudatus	Pecf	117	0.01	0.00	0.02	0.11
Family Belonidae						
Xenentodon cancila	Xenc	118	0.08	0.10	0.60	0.77
Family Hemiramphidae						
Dermogenys siamensis	Ders	119	0.08	0.10	0.60	0.77
Family Aplocheilidae						
Aplocheilus panchax	Aplp	120	0.03	0.00	0.05	0.29
Family Syngnathidae						
Doryichthys boaja	Dorb	121	0.08	0.10	0.60	0.77
Ichthyocampus carce	Ichc	122	0.08	0.11	0.65	0.78
Family Synbranchidae						
Monopterus albus	Mona	123	0.08	0.11	0.65	0.78
Family Mastacembelidae						
Macrognathus taeniagaster	Mact	124	0.11	0.72	1.00	0.79
Macrognathus siamensis	Macs	125	0.11	0.76	1.00	0.79
Mastacembelus armatus	Masa	126	0.01	0.01	0.01	0.01
Mastacembelus favus	Masf	127	0.01	0.01	0.01	0.01
Family Chandidae						
Parambassis siamensis	Paas	128	0.08	0.10	0.60	0.77
Parambassis apogonoides	Para	129	0.08	0.10	0.60	0.77
Parambassis wolffi	Parw	130	0.08	0.10	0.60	0.77
Family Polynemidae						
Polynemus multifilis	Polm	131	0.07	0.14	0.24	0.56
Family Toxotidae						
Toxotes chatareus	Toxc	132	0.07	0.03	0.25	0.60
Toxotes microlepis	Toxm	133	0.03	0.00	0.05	0.29
Family Nandidae						
Pristolepis fasciata	Prif	134	0.24	0.79	1.00	0.81
Family Cichlidae						
Oreochromis niloticus	Oren	135	0.06	0.00	0.09	0.48
Family Eleotridae						
Oxyeleotris marmorata	Oxym	136	0.01	0.01	0.01	0.01

Table 1 (cont.) List of species found during the surveys and their occurrence probabilities in each cluster estimated by SOM.

Species	Abbreviation	code	Cluster			
			I	II	IIIa	IIIb
Family Gobiidae						
Brachygobius aggregatus	Braa	137	0.01	0.00	0.02	0.11
Calamiana siamensis	Cals	138	0.92	0.89	0.35	0.22
Rhinogobius chiengmaiensis	Rhic	139	0.01	0.13	0.07	0.00
Family Anabantidae						
Anabas testudineus	Anat	140	0.08	0.11	0.65	0.78
Family Helostomatidae						
Helostoma temmincki	Helt	141	0.00	0.01	0.05	0.02
Family Osphronemidae						
Betta splendens	Bets	142	0.06	0.00	0.09	0.48
Trichogaster microlepis	Trim	143	0.08	0.09	0.59	0.76
Trichogaster pectoralis	Trip	144	0.08	0.09	0.59	0.76
Trichogaster trichopterus	Trit	145	0.08	0.09	0.59	0.76
Trichopsis pumila	Triu	146	0.08	0.09	0.59	0.76
Trichopsis vittatus	Triw	147	0.07	0.02	0.21	0.58
Osphronemus gouramy	Ospg	148	0.08	0.09	0.59	0.76
Family Channidae						
Channa gachua	Chag	149	0.92	0.90	0.40	0.23
Channa lucius	Chal	150	0.00	0.01	0.05	0.02
Channa micropeltes	Cham	151	0.00	0.45	0.68	0.59
Channa striata	Chas	152	0.00	0.01	0.05	0.02
Family Soleidae						
Euryglossa harmandi	Eurh	153	0.06	0.00	0.09	0.48
Family Cynoglossidae						
Cynoglossus feldmanni	Cynf	154	0.06	0.00	0.09	0.48
Cynoglossus microlepis	Cynm	155	0.06	0.00	0.09	0.48
Family Tetraodontidae						
Monotretus cambodgiensis	Monc	156	0.07	0.08	0.51	0.79
Monotretus fangi	Monf	157	0.00	0.01	0.03	0.05

It can be seen from the SOM maps and occurrence probability (OP), which were calculated from connection intensities of SOM, that each species has its own associated habitat. Distribution of individual species is likely to be driven by the biological functions and ecological traits of the species [25]. Group **A** fish are species that live in fast flowing freshwater streams with swift currents and stony to rocky substrate [26]. Species such as *Glyptothorax* spp., and *Homaloptera* spp. have flatten forms and are equipped with suckers or spines so they can fix onto substrates in strong currents [26, 27]. A cave inhabitant *Neolissochilus subterraneus* is also member of this group since the specific location of caves are in mountainous area [28]. Group **B** fish included pool-riffle inhabitants [26, 29] such as *R. chiengmaiensis*, *Schistura spiesi* and *Neolissochilus stracheyi*, which are specifically distribution only in the **G2** area. The morphology of the fish in this group are similar to group **A** species, indicating that they live mainly at the bottom of swift flowing water, where they can eat small invertebrates, algae and detritus from the bottom [29]. Group **C** fish are more diverse and can migrate between the fast flowing freshwater streams to slack regions of river flow near the junction to main channels. The members of this group are the species that have sucking mouths to stick onto boulder in a swift river as *Gyrinocheilus aymonieri*, and small-sized fish, which prefer pool-riffle structures and include such species as *Crossocheilus oblongus* and *Garra cambodgiensis* [29].

In groups **A** to **C**, some other species such as *Channa gachua*, *Sikukia stejnegeri* and *Labeo rohita* deal with the current mostly through behavioral strategies, i.e. feeding. As to be expected, their generalized feeding apparatus allows them to have a very generalized and opportunistic diet, feeding on aquatic insect larvae, algae, terrestrial insects and plants, obtained through a variety of feeding tactics, such as collecting items carried by the current and at the water surface [30]. Similar to group-**C** fish, fishes in groups **D** and **E** showed the movement between areas, i.e. upper and lower sections of the river system. This is likely due to their opportunistic feeding habit and the reproductive behavior with the parental stock moving to the upper parts, where environmental conditions are suitable for spawning and nursing the new hatches [27], especially for the cyprinids such as *Osteochilus* spp. and *Cyclocheilichthys* spp. [31]. In lower reaches of the streams, high level of fish species in groups **F** and **G** is very common. Various fish species, with different biological traits, occupy the lower reaches of the river because it is a nutrient rich area and comprises of various aquatic habitats ranging from running-water to stagnant-water habitats that would suitable for different habitats requirement to complete their life cycles [27, 31, 32]. Higher species richness in group **F** than group **G** could be also caused by the presence of productive floodplain in the **G4** zone [13, 14], which greatly influences the population dynamics of many fish spec.

5. IMPLICATION FOR CONSERVATION

Numbers of scientific papers have evaluated changes of fish assemblages due to damming the rivers and have shown consistent results in declining in species richness both upstream and downstream after damming. It is not only because of the change from running-water to stagnant-water ecosystems but also the changes with the timing, duration, amplitude and other characteristics of flow and flood regimes of the river [12, 27, 32]. In this study, the Khwae Noi Reservoir *per se* located in **G2** zone, which is an exclusive area for the pool-riffle inhabitants (i.e. group **C** fish), implying that they are likely to be the most vulnerable from Khwae Noi damming. They are sensitive to catastrophic and habitat flows and can be damaged by disturbances to pool-riffle structure, such as seasonal desiccation or increases in sediment load that chokes the interstitial spaces [27]. Species in this group included the IUCN-vulnerable *R. chiengmaiensis*, as well as *S. beauforti* and *H. bocourti* that showed their temporal movement to the **G2** zone. Impact on the group **A** fish should also be paid attention to, as they share the habitats in high altitude area (i.e. **G1** zone) and junction to **G2** zone. Decreasing flow rate due to the high water volume in **G2** zone would alter their riffle habitats and affect their living condition [27, 30]. Meanwhile other fish groups (i.e. groups **D** to **H**) that prefer the low land condition seem to have suffered less impact from the damming. Therefore, according to these likely impacts, a strategy to declare reserves for fish, which have limited distribution in high altitude area (i.e. group **A** to **C)**, particularly the IUCN-vulnerable species, should be developed. It is meant that the **G1** (both **G1A** and **G1B**) and **G2** areas in Phitsanulok Province other than the reservoir *per se*, should be declared fish sanctuaries, where anthropogenic pressures could be banned.

Exotic species, *L. rohita* and *O. nilocus*, showed different distributions in the respective high altitude and low land areas. Although exotic in the basin, impacts of them on biodiversity conservation should be of less concern than impacts from changes in the ecosystem. These species showed no significant impacts on native fish species [33, 34]. The primary reason that most exotic species do not tend to influence the biodiversity inland waterbodies, in Southeast Asia, is that they are generally unable to reproduce in substantial numbers and thereby form large populations that would compete for common resources [34]. Nevertheless, scrutinized studies on the impact of these exotic fishes should be applied. A fish monitoring program in the reserves should be also implemented to observe successful biodiversity conservation of both adult- and young- fishes, which can be a lesson learnt for other impoundment projects in the high latitude areas in the country.

ACKNOWLEDGEMENT

Analyses were conducted under the Franco-Thai program, PHC 16598RJ "Conservation of Freshwater Ecosystems to Sustain Fish Biodiversity, a Food Resource for the Near Future" led by Prof. Sovan Lek, University Paul Sabatiér (Toulouse III), France. The authors are grateful to Department of Fisheries, for allowing us to collaborate and access the survey data. We also thank Prof. Michael D. Hare, Ubon Ratchathani University, for editing the English language of the manuscript.

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