

INVESTIGATION ON BIODIVERSITY AND CONSERVATION OF FRESHWATER FISHES IN INDONESIA

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ABSTRACT

Indonesia is one of the richest regions in the world in terms of biodiversity. However, recent evidence has shown that tropical forests destruction has maintained at a high rate over the last few years in this country. At the same time, living resources in Indonesian freshwater ecosystems are important: this country ranks at number seven in terms of production of inland capture fisheries with 323,150 tonnes in 2008. Freshwater fishes represent 42% of the total estimated ichthyofauna, concentrated in 0.01% of the total water covered environment. This environment is closer to human activities, making it critically vulnerable to adverse impacts. Furthermore, there has been some recent debates on the general sustainability of fisheries and aquaculture production systems. This research was focused on initiating a multi-scale study of fish biodiversity in freshwater environments. Two specific actions have been started. A review based on the analyses of the existing scientific literature and of databases on fish taxonomy and distributions. In parallel to this work, a global analysis of the distribution of fish diversity in Indonesia was undertaken. This work aims at identifying the major features of this resource as well as its current and future threats.

KEYWORDS: biodiversity, freshwater fish, conservation

INTRODUCTION

Living resources in freshwater ecosystems are important in Indonesia: this country ranks at number seven in terms of production of inland capture fisheries with 323,150 tonnes in 2008 (FAO, 2010). This number shows a slight decrease compared to 2004 when it reached 330,880 tonnes. This relative stagnation is paralleled with a substantial decrease in the number of inland fishermen (Table 1). Table 1 below shows the figures for the whole country, Sumatra Island (one of the main producing area of freshwater capture fisheries in Indonesia), and the Province of South Sumatra.

At the same time, the number of inland fish-farmers has increased considerably in Sumatra. By contrast, it has decreased slightly on the much smaller island of Java which is traditionally a location of intensive production of aquaculture (Table 2).

The increase in aquaculture production in Sumatra is clearly seen in the production figures from South Sumatra which have been multiplied by five during this four-year interval (Table 3). Table 3 gives detailed figures for two groups of fishes: the tilapia, *Oreochromis niloticus*, and catfishes, mainly from the genera *Clarias* and *Pangasius*).

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Table 1. Number of inland fishermen (capture fisheries production)

Location	Years	
	2004	2008
Indonesia	588,507	496,499
Sumatra	192,602	148,315
South Sumatra	87,356	63,430

Table 2. Number of inland fish-farmers (aquaculture production)

Location	Years	
	2004	2008
Indonesia	459,356	2,759,471
Sumatra	395,519	636,167
South Sumatra	44,321	183,144
Java	1,621,755	1,455,511

Table 3. Aquaculture production in South Sumatra (metric tonnes)

	Years	
	2004	2008
Total	24,735	130,478
Tilapia	30	40,154
Catfishes	0	38,543

On the other hand, this dynamics is extremely heterogeneous even within the island of Sumatra. For instance, the nearby Province of Jambi has shown a much smaller increase (though doubled) in aquaculture production from 10,205 to 21,202 tonnes with a moderate increase in its number of fish-farmers from 25,729 to 31,796.

Therefore, in spite of the apparent stagnation of the fishing pressure on freshwater ecosystems, the overall pressure from human activities has increased over the last few years through the extension of aquaculture activities. Besides, the pollution of rivers, the deforestation leading to important soil erosion, and the use of water by human populations has increased the stress on freshwater natural

habitats. The above figures suggest that this stress is certainly highly heterogeneous in space and in time.

Furthermore, the recent climatic changes, which effects in this region through a disturbed seasonal rain regime, lead to a great uncertainty with respect to the prediction of changes in living resources in Indonesian rivers.

Indonesia has shown since a few years a remarkable economic and demographic development. The country, with more than 240 millions inhabitants in 2009, ranks as number four in terms of population number, and is now part of the G20. The current socio-economical development in Indonesia leads to expect a greater pressure on the living resources of the country, both in terms of quantity and quality. It is crucial for Indonesia to plan for a sustainable use of these resources in order to insure the increasing demand linked to its ongoing economic growth.

MATERIAL AND METHOD

The research were focused on initiating a multi-scale study of fish biodiversity in freshwater environments. Two specific actions have been started. An important part of the work already conducted is to establish the current state of freshwater fish diversity in Indonesia. This is especially crucial considering the vastness of the country and the fact that many human populations rely on fishes as a resource, especially peoples living along rivers who are numerous in the Indonesian archipelago. Giving the current pressures on these resources, it is critical to assess the sustainability of their exploitation as well as to propose strategies for their conservation. This is based on analyses of the existing scientific literature and of databases on fish taxonomy and distributions.

In parallel to this work, a global analysis of the distribution of fish diversity in Indonesia was undertaken. This study aimed at identifying the major features of this resource as well as its current and future threats. It was based on the compilation of published data on fish distributions over Indonesia. A fundamental approach in this work was to develop a database made of all species of Indonesian fishes. To this end, a new technology named virtual database (VDB) was used. The principle of this technology is to connect individual databases

over internet and build a new virtual composite database. Therefore, the database does not have an actual existence: individual files do not exist and are created "on the fly". The advantage of this technology is that the virtual database can be rebuilt and refreshed when the individual distributed databases are updated. From a computational point of view, VDB is based on various languages including XML (eXtended Mark-up Language) and the R language (R Development Core Team 2011). As a contribution to the present collaboration, the code used during this project is provided in this report (Appendix II).

RESULT AND DISCUSSION

This work has sufficiently progressed to draw some preliminary results. The Indonesian freshwater fishes amount to 1,165 species in 81 families and 23 orders. Appendix I lists all the families of Indonesian freshwater fishes with their number of species. The number of species for each order is shown on Figure 1. This shows an interesting result that the orders with the highest numbers of species are those which are most important from an economic point of view: Perciformes (which include the guramies), Cypriniformes (carps), and Siluriformes (catfishes including the economically important species "ikan patin" and "ikan

lele"). It appears then that the vast majority of species (889 species, 76.3%) belong to only three orders.

It is therefore interesting to look at the correlation between these patterns of species diversity and the number of endemic species. The 95 species of Indonesian endemic freshwater fishes belong to 6 orders (Table 4). The order with the largest number of endemic species is Atheriniformes with nearly half of the species of the order present in Indonesia being also endemics.

Another interesting result from the above figures is that several orders have a marine origin (e.g., Clupeiformes, Mugiliformes, Pleuronectiformes, Carcharhiniformes, Rajiformes). This further underlines the singularity of the freshwater Indonesian ichthyofauna and emphasizes the ancient origins of some of its members. In addition to this, some groups are represented only by one or two species that are not established, such as Characiformes with *Colossoma macropomum*, or Salmoniformes with the two species *Oncorhynchus mykiss* and *Salmo salar*. These species have been introduced recently in Indonesia and are not yet fully established. It will be particularly important to consider with care the future of these species since the re-

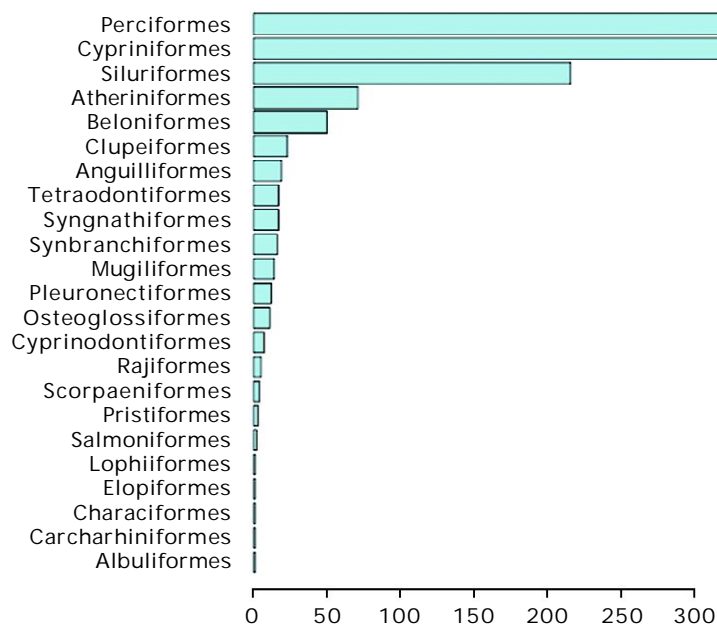


Figure 1. The number of species for each order

Table 4. The 95 Indonesian freshwater fish species endemic in Indonesia belong to 6 orders (in parentheses, the percentage of endemic in the order

	Order	Percentage (%)
Perciformes	24	-7.12
Cypriniformes	11	-3.27
Siluriformes	7	-3.24
Atheriniformes	34	-47.89
Beloniformes	17	-26.72
Syngnathiformes	2	-11.76

lease of these fish in natural habitats seems to be more and more frequent in Asian tropical countries as has been recently witnessed with the probable presence of other Amazonian species in Asia like the giant arapaima (*Arapaima gigas*). Though it is unlikely that the two salmon species (*O. mykiss* and *S. salar*) will become established in Indonesia, the case of *C. macropomum* is to be considered cautiously.

The status of the 1,165 Indonesian freshwater species of fish was assessed and classified into six categories: endemic, introduced, misidentification, native, not established, questionable. Table 5 gives the number of species in each of these categories.

Therefore, it appears that 8.2% of the freshwater species of fish are endemic to Indonesia, representing a high percentage of species that are restricted to this country. On the other hand, 2.3% of these 1,165 species are "aliens" that have been introduced or are not yet established. These represent a threat for local species that need to be assessed properly.

A further extension of the VDB technology as described above is to link it with geographical information systems (GIS) in order to screen the distributions of each species. One goal was to assess the potential sampling biases in the inferred distributions in order to point to some possible future effort to improve our knowledge. The two examples below show some applications of this approach.

The map below (Figure 2) shows the distribution of the "eel-like" walking catfish (*Clarias nieuhofii*) as can be derived from the geographical data in Fishbase. This graphical represen-

Table 5. Status of the 1,165 species of freshwater fishes present in Indonesia

Status	Number
Native	1,036
Endemic	95
Introduced	19
Not established	8
Questionable	4
Misidentification	3

tation allows one to assess the state of the knowledge available on the distribution of species as well as the physical and ecological factors regulating these distributions. In the case of the present species, it has been demonstrated that there is a high genetic divergence among their populations which strongly suggesting there are in effect three different species distributed respectively in North Sumatra, South and East Sumatra, and West Kalimantan, and East Kalimantan (Pouyaud *et al.*, 2009).

Figure 3 shows the distribution of the Frecklefin eel (*Macrogathus maculatus*). This species has a much more restricted range from the Malaysian Peninsula to the Kapuas Basin and up to the North of the Sarawak Province in Bornean Malaysia. Such results emphasize the patchy distribution of many fish species in Indonesia. Furthermore, giving the previous result regarding the high genetic divergence among populations of the walking catfish (Pouyaud *et al.*, 2009), this leads to the hypothesis that similar divergence also exists in other species. This clearly opens a wide range of perspectives on the genetic and biodiversity of Indonesian freshwater fishes.

Indonesia's territory is spread over more than 17,000 islands and over two continents: Asia on the west and Oceania on the east. These two parts are characterized by contrasted faunas and floras separated by the well-known Wallace Line. It was therefore interesting to investigate the distributions of the diversity of some groups on both sides of the Wallace Line.

Figure 4 shows the distribution of the diversity of an important group of ornamental fishes: the family Melanotaeniidae which includes notably the rainbow-fishes (*Melanotaenia* spp). First, it is necessary to comment that the

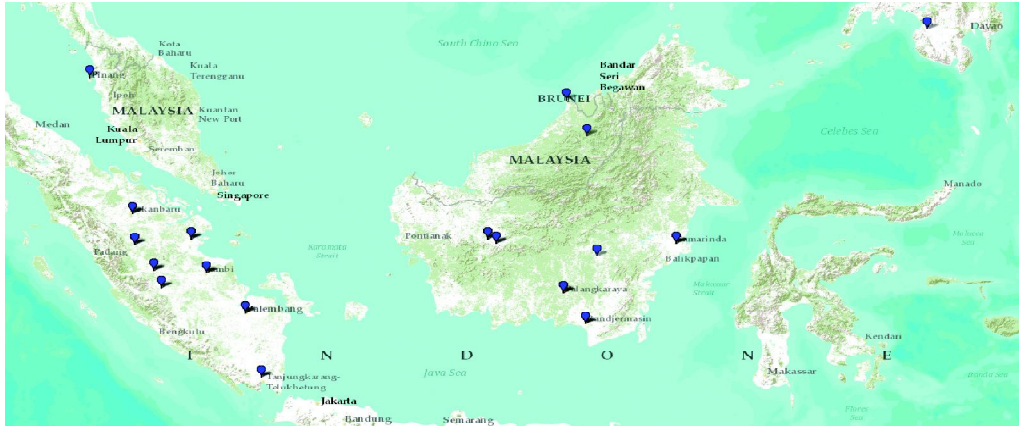


Figure 2. Map of the distribution of the "eel-like" walking catfish (*Clarias nieuhofii*)



Figure 3. Map of distribution of the Frecklefin eel (*Macrogathus maculatus*)

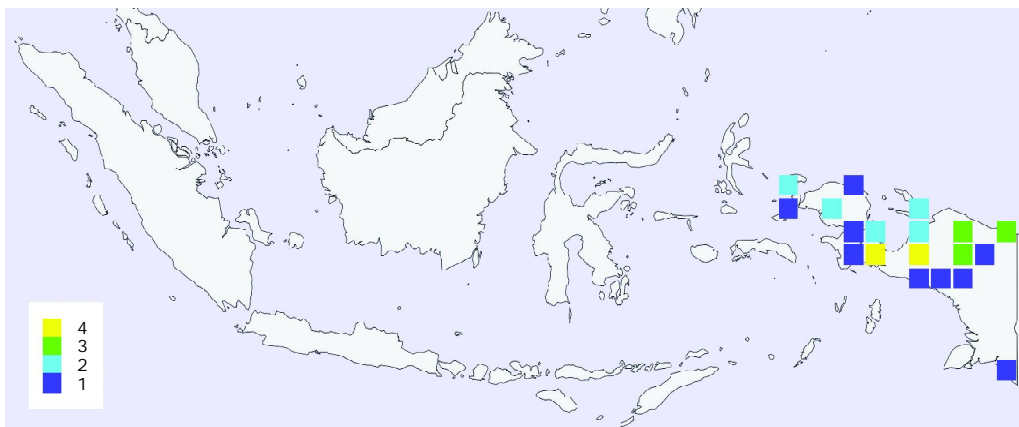


Figure 4. Map of distribution of the diversity of an important group of ornamental fishes: the family Melanotaeniidae

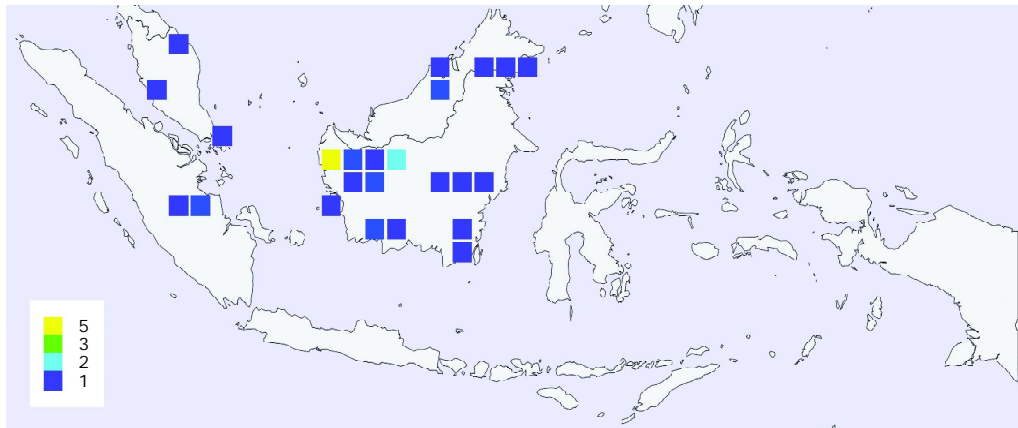


Figure 5. Map of distribution of species diversity for another genus of ornamental fishes: the betta (*Betta* spp.)

area where these fishes are found has been sampled regularly among the different sites where they are found, so it seems unlikely that the observed pattern is due to a sampling bias. It is thus important to note that the diversity of Melanotaeniidae is centered in the mountain range located in along the island of New Guinea (Kadariusman *et al.*, 2010). This result points to the importance of isolating mechanisms in creating new species in this area.

Figure 5 presents the distribution of species diversity for another genus of ornamental fishes: the betta (*Betta* spp). This shows a clear pattern of high diversity centre within the Kapuas Basin (Western Kalimantan). This emphasizes the importance of this river (one of the largest in Indonesia) for the conservation of Indonesian biodiversity.

CONCLUSION

Like for the previous analysis with Melanotaeniidae, it is critical to assess sampling biases in this inference. Sampling of species of freshwater fishes has been indeed very unequal through different geographical areas. The analyses with many species from the databases revealed that the most prospected areas of the islands of Borneo are in the Malay-

sian provinces of Sarawak and Sabah (results not shown here). Thus the fact that the biodiversity of *Betta* is higher in Kalimantan can be interpreted as not being particularly influenced by sampling biases and thus reveals a real pattern of center of biodiversity in the Kapuas river.

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Appendix 1

Family	Number of species
Adrianichthyidae	16
Akysidae	26
Albulidae	1
Ambassidae	18
Anabantidae	1
Anguillidae	9
Antennariidae	1
Aplocheilidae	1
Apogonidae	10
Ariidae	24
Atherinidae	4
Bagridae	60
Ballitoridae	70
Belonidae	4
Blenniidae	2
Carcharhinidae	1
Chacidae	2
Channidae	12
Characidae	1
Chaudhuriidae	4
Cichlidae	5
Clariidae	19
Clupeidae	11
Cobitidae	37
Cynoglossidae	5
Cyprinidae	228
Dasyatidae	5
Datnioididae	3
Eleotridae	42
Engraulidae	5
Gerreidae	1
Gobiidae	114
Gyrinocheilidae	1
Haemulidae	1
Helostomatidae	1
Hemiramphidae	30
Kuhliidae	2
Kurtidae	2
Latidae	1
Leiognathidae	1
Loricariidae	2

Continued Appendix 1

Family	Number of species
Lutjanidae	3
Mastacembelidae	10
Megalopidae	1
Melanotaeniidae	41
Monodactylidae	1
Mugilidae	14
Muraenidae	3
Nandidae	4
Notopteridae	6
Ophichthidae	7
Osphronemidae	77
Osteoglossidae	5
Pangasiidae	15
Phallostethidae	5
Plotosidae	10
Poeciliidae	6
Polynemidae	7
Pristidae	3
Pristigasteridae	2
Pseudomugilidae	5
Rhacichthyidae	1
Salmonidae	2
Scatophagidae	1
Schilbeidae	3
Sciaenidae	7
Serranidae	1
Sillaginidae	2
Siluridae	44
Sisoridae	11
Soleidae	7
Sparidae	1
Sundasalangidae	5
Synanceiidae	1
Synbranchidae	2
Syngnathidae	17
Telmatherinidae	16
Terapontidae	11
Tetraodontidae	17
Tetrarogidae	3
Toxotidae	5

Appendix 2

library(XML)

```
o <- readHTMLTable("CountryChecklist.php.html")
```

```
## the two next functions build URL addresses to connect  
## to remote databases
```

```
build.url <- function(genus, species)
```

```
{  
  if (missing(genus)) {  
    cat("Enter the genus name: ")  
    genus <- scan("", "")  
  }  
  if (missing(species)) {  
    cat("Enter the species name: ")  
    species <- scan("", "")  
  }  
}
```

```
paste("http://www.fishbase.tw/map/detail/CreateCSV.php?dsource=darwin_all&Spname=",  
      genus, "%02", species, "&pointmap=&SpecID=1753&user_session=", sep = "")  
}
```

```
buildURI <- function(i)
```

```
{  
  paste("http://www.fishbase.tw/map/detail/CreateCSV.php?dsource=darwin_all&Spname=",  
        gsub(" ", "%02", as.character(X$Species[i])), "&pointmap=&SpecID=1753&user_session=",  
        sep = "")  
}
```

```
xx <- "http://www.fishbase.tw/map/detail/CreateCSV.php?dsource=darwin_all&  
Spname=Clarias%20gariepinus&pointmap=&SpecID=1753&user_session="
```

```
y <- scan(xx, what = "")  
FILE <- gsub("href=", "", y[5])  
FILE <- gsub(">", "", FILE)
```

```
FILE <- paste("http://www.fishbase.tw/map/detail/", FILE, sep = "")  
n.data.point <- scan(FILE, skip = 6, nlines = 1, what = "", sep = "=")  
n.data.point <- as.numeric(n.data.point[1])
```

```
if (n.data.point > 0) {  
  col.nms <- scan(FILE, skip = 4, nlines = 1, what = "", sep = ",")  
  DF <- read.csv(FILE, skip = 5, header = FALSE)  
  names(DF) <- col.nms  
}
```

```
## ci-dessous OK mais ne lit que 100 données
```

```
u <- "http://www.fishbase.tw/map/OccurrenceMapList.php?genus=Clarias&species=  
gariepinus&dsource=darwin_all"  
a <- readHTMLTable(u)
```

```
#####
```

```
beta <- grep("Betta", X$Species)  
y <- OUT[[beta[1]][, 1:3]]  
for (i in beta[-1]) y <- rbind(y, OUT[[i]][, 1:3])
```


Continued Appendix 2

```

s <- y$Long < 150
plot(y$Long[s], y$Lat[s])

for (i in ii) {
  y <- OUT[[i]]
  if (!is.null(y)) {
    plot(y$Long, y$Lat)
    title(X$Species[i], sub = i)
    readLines(n=1)
  }
}

library(gstudio)
txt <- paste(rep("Locus(c(1))", nrow(y)), collapse = ", ")
txt <- paste("c(", txt, ")")
z <- Population(Longitude = y$Long, Latitude = y$Lat,
  stratum = factor(1:nrow(y)), txt)

fl <- paste(gsub(" ", "_", X$Species[i]), "kml", sep = ".")
pies.on.map(fl, z, "stratum", "loci")

#####

# Do the melanotaeniidae map

library(maps)

melano.fam <- which(X$Family == "Melanotaeniidae")
tmp <- OUT[[563]][1, ]
tmp[, 2] <- as.numeric(as.character(tmp[, 2]))
OUT[[563]] <- tmp
y <- OUT[[melano.fam[1]]], 1:3]
for (i in melano.fam[-1]) y <- rbind(y, OUT[[i]], 1:3])

xmin <- 95
xmax <- 141
ymin <- -11
ymax <- 7

xx <- seq(xmin, xmax)#, 0.5)
yy <- seq(ymin, ymax)#, 0.5)
ncell.x <- length(xx) - 1L
ncell.y <- length(yy) - 1L
XXX <- matrix(0L, ncell.x, ncell.y)

for (k in melano.fam) {
  y <- OUT[[k]]
  for (i in seq_len(ncell.x)) {
    for (j in seq_len(ncell.y)) {
      if (any(y$Long >= xx[i] & y$Long < xx[i + 1] &
        y$Lat >= yy[j] & y$Lat < yy[j + 1], na.rm = TRUE))
        XXX[i, j] <- XXX[i, j] + 1L
    }
  }
}
}

```

Continued Appendix 2

```
map("world", xlim = c(xmin, xmax), ylim = c(ymin, ymax),
    bg = "grey90", fill = TRUE, col = "white")
box()
COL <- c("darkblue", "lightblue", "red", "gold")
for (i in seq_len(ncell.x)) {
  for (j in seq_len(ncell.y)) {
    if (!XXX[i, j]) next
    points((xx[i] + xx[i + 1])/2, (yy[j] + yy[j + 1])/2,
           pch = 15, col = COL[XXX[i, j]], cex = 3)
  }
}
## text(xmin + 1, ymin + 1, "© Emmanuel Paradis", adj = 0)

abline(v=xmin:xmax)
abline(h=ymin:ymax)
abline(h=0, col = "yellow")

# do the Betta map;

betta <- grep("Betta", X$Species)
BETTA <- matrix(0L, ncell.x, ncell.y)
for (k in betta) {
  y <- OUT[[k]]
  for (i in seq_len(ncell.x)) {
    for (j in seq_len(ncell.y)) {
      if (any(y$Long >= xx[i] & y$Long < xx[i + 1] &
            y$Lat >= yy[j] & y$Lat < yy[j + 1], na.rm = TRUE))
        BETTA[i, j] <- BETTA[i, j] + 1L
    }
  }
}

map("world", xlim = c(xmin, xmax), ylim = c(ymin, ymax),
    bg = "grey90", fill = TRUE, col = "white")
box()
COL <- c("darkblue", "lightblue", "red", "gold", "yellow")
for (i in seq_len(ncell.x)) {
  for (j in seq_len(ncell.y)) {
    if (!BETTA[i, j]) next
    points((xx[i] + xx[i + 1])/2, (yy[j] + yy[j + 1])/2,
           pch = 15, col = COL[BETTA[i, j]], cex = 3)
  }
}
mtext("Betta", font = 3, line = 2)

map("world", xlim = c(xmin, xmax), ylim = c(ymin, ymax),
    bg = "grey90", fill = TRUE, col = "white")
box()
ncat <- 10
COL <- topo.colors(ncat)
TMP <- ceiling(ncat * SILURI / MAX.SILURI)
for (i in seq_len(ncell.x)) {
  for (j in seq_len(ncell.y)) {
    if (!SILURI[i, j]) next
```

Continued Appendix 2

```
      points((xx[i] + xx[i + 1])/2, (yy[j] + yy[j + 1])/2,
            pch = 15, col = COL[TMP[i, j]], cex = 3)
    }
}

PANGAS <- matrix(OL, ncell.x, ncell.y)
pangas <- grep("Pangasius", X$Species)
for (k in pangas) {
  y <- OUT[[k]]
  if (is.null(y)) next
  for (i in seq_len(ncell.x)) {
    for (j in seq_len(ncell.y)) {
      if (any(y$Long >= xx[i] & y$Long < xx[i + 1] &
            y$Lat >= yy[j] & y$Lat < yy[j + 1], na.rm = TRUE))
        PANGAS[i, j] <- PANGAS[i, j] + 1L
    }
  }
}

map("world", xlim = c(xmin, xmax), ylim = c(ymin, ymax),
    bg = "grey90", fill = TRUE, col = "white")
box()
COL <- c("darkblue", "red", "gold")
for (i in seq_len(ncell.x)) {
  for (j in seq_len(ncell.y)) {
    if (!PANGAS[i, j]) next
    points((xx[i] + xx[i + 1])/2, (yy[j] + yy[j + 1])/2,
          pch = 15, col = COL[PANGAS[i, j]], cex = 3)
  }
}
```