Phylogeny analysis of complete mitochondrial DNA sequences for pelagic fishes from tuna fishery

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ABSTRACT

Pelagic fishes captured in the international tuna fisheries have attracted increasing attention in recent years because of declines in their populations. In this study, complete mitochondrial genomes of pelagic species from the classes Teleostean and Chondrichthyan were analyzed. The length of the 58 mtDNA sequences ranged from 15,598 to 18,880 bp, and all of which contained 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region. Our results suggested that mitochondrial genomes could be a powerful marker for resolving the phylogeny of pelagic fishes. Phylogenetic relationships based on the complete mitochondrial among 58 species indicated that Teleostean and Chondrichthyan were well separated. However, the control region length of Mobula japonica was much larger than the other species in this study. Additionally, the Prionace glauca was divided into the clade in the genus Caranx which provided a prospective taxonomic status of P.glauc.

Tuna fisheries have been prosecuted around the world since at least the pre-1950s (Miyake et al. 2004) and the fisheries brings important economic and social benefits to many nations and areas (Langley et al. 2009; Barclay 2010; Parris 2010). Tuna has a higher economic value compared to other species and the high market demands for tuna have led to significant overcapacity in tuna fishing fleets (Joseph 2003). Furthermore, most stocks of the principal marketable tuna species are nearly fully exploited (Majkowski 2007), as well as the production of bycatch from tuna fishery increases with the fishing fleets. Ecosystem-based fishery management (EBFM) is a new direction for fishery management, essentially reversing the order of management priorities to start with the ecosystem rather than the target species (Pikitch et al. 2004). Management practice proves the EBFM is a more effective management method in the pelagic fishes (Raakjaer et al. 2014; Skern-Mauritzen et al. 2016).

Molecular genetic data has widely been applied for marine fishery management (Waples et al. 2008). The mitochondrial (mt) genome has been widely used as a marker for molecular genetic studies because of its high rate of mutation and exclusively maternal mode of inheritance (Brown et al. 1979; Harrison 1989). Recent studies, however, demonstrated exceptions to these widely held concepts of mitochondrial biology (Ravago et al. 2002). In particular, the observation of mtDNA length variability within species (Rand 1993) challenges the view of evolution, which indicates that more ancient species have with larger genomes.

In this study, the molecular biology of samples from 58 pelagic fishes captured as bycatch in the tuna fishery was used to describe their phylogeny. All the 58 species were accessed from GenBank (Table 1). The mitochondrial DNA length of the 58 species ranged from 15,598 to 18,880 bp. However, the control region of Mobula japonica was observed to be as long as 3165 bp, while that of the other species in this study were smaller than 1500 bp. The patterns of mitochondrial DNA variation were investigated in pelagic species to examine their evolution.

A phylogenetic tree was constructed based on the complete mitochondrial DNA of 58 pelagic species from tuna fishery (Figure 1) to understand the evolutionary relationship and the position of pelagic species. Maximum-likelihood fits of 24 different nucleotide substitution models (Table 2) were tested before constructing the phylogenetic tree; the results showed that TN93 + G + I model fits these data the best for the neighbour-joining tree (NJ Tree). The NJ Tree was conducted in MEGA 5 (MEGA Inc., Englewood, NJ; Tamura et al. 2011) with bootstrap values of 1000 replicates. The NJ Tree successfully divided the Teleostean and Chondrichthyan into two separate groups, and all the genus species were well determined except for the Caranx and Prionace. The results of phylogenetic tree indicated that M. japonica is a more ancient species, since it stands at the root of the tree. The length of mitochondrial DNA of M. japonica was much larger (Table 1) than that of the other species in this study which

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provided further evidence that *M. japonica* is a more ancient species in the pelagic species.

*Prionace glauca* with different morphologic characters from *Carcharhinus*, such as long pectoral fins greater than internarial, a first dorsal fin origin well behind the rear angle of the pectoral fin, dermal gill rakers, bigger upper tooth with jaws, and much fewer rows of teeth than that of *Carcharhinus* (Compagno 1988). Moreover, a prolonged and gradual process of clasper of *P. glauca* making it rather difficult to be used for determining the maturation of males in *Prioncae* (Compagno 1984). Furthermore, the colour at the top of *P. glauca* is dark indigo blue, while generally brown, blue bronze, and olive in the species of *Carcharhinus*. But, Naylor’s allozyme electrophoretic analyses (Naylor 1989) indicated that *P. glauca* was included in the gene of *Carcharhinus*. And Dosay-Akbulut (2008) used the ribosomal IT1-2 regions sequences to present the phylogenetic relationship with the genus *Carcharhinus*, the bootstrap tree of the NJ (Kimura) indicated that *P. glauca* is a member of genus *Carcharhinus*. A bootstrap tree of NJ was constructed with the whole mtDNA sequences from tuna fisheries species in this study, which point out that *P. glauca* was cladded into

### Table 1. Fifty-eight complete mitochondrial DNA pelagic species from tuna fishery.

| Species                      | Accession number | Length  |
|------------------------------|------------------|---------|
| Xiphias gladius              | NC_012677        | 16,520  |
| Tetraprurus audax             | NC_012678        | 16,526  |
| T. angustirostris             | NC_012679        | 16,509  |
| Makaira mazara               | NC_012680        | 16,534  |
| M. indica                     | NC_012675        | 16,526  |
| Istiophorus platypterus       | NC_012676        | 16,524  |
| I. albicans                   | NC_022478        | 16,514  |
| Thunnus tonggol               | NC_020673        | 16,528  |
| T. thynnus                    | NC_014052        | 16,527  |
| T. obsesus                    | NC_014059        | 16,528  |
| T. maccouyi                   | NC_014101        | 16,527  |
| T. atlanticus                 | NC_025519        | 16,528  |
| T. albacares                  | NC_014061        | 16,527  |
| T. alalunga                   | NC_005317        | 16,527  |
| Scomberomorus semifasciatus   | NC_021391        | 16,548  |
| S. niphonius                  | NC_016420        | 16,646  |
| S. munnii                     | NC_021390        | 16,548  |
| S. cavalla                    | NC_008109        | 16,548  |
| Scomber scombrus              | NC_006398        | 16,560  |
| S. japonicas                  | NC_013723        | 16,568  |
| S. australasicus              | NC_013725        | 16,570  |
| Rastrelliger kanagurta        | NC_019624        | 16,537  |
| R. brachysoma                 | NC_013485        | 16,539  |
| Katsuonus pelamis             | NC_005316        | 16,515  |
| Gymnosarda unicolor            | NC_022496        | 16,510  |
| Gasterocormis melampus        | HQ425781         | 16,506  |
| Euthynus alletteratus         | NC_004530        | 16,520  |
| E. affinis                    | NC_025934        | 16,513  |
| Auxis thazard                 | NC_005318        | 16,506  |
| A. rochei                     | NC_005313        | 16,501  |
| M. japonica                   | NC_018784        | 18,880  |
| Sphyra zygaena                | NC_025778        | 16,731  |
| S. lewini                     | NC_022679        | 16,726  |
| Triaenodon obesus             | NC_026287        | 16,700  |
| P. glauca                     | NC_022819        | 16,705  |
| Carcharhinus plumbeus         | NC_024596        | 16,706  |
| C. melanopterus               | NC_024284        | 16,706  |
| C. longimanus                 | NC_025520        | 16,706  |
| C. leucas                     | NC_023522        | 16,704  |
| Rhincodon typus               | NC_023455        | 16,875  |
| Megachasma pelagias            | NC_021442        | 16,694  |
| Isurus paucus                 | NC_024101        | 16,704  |
| I. oxyrinchus                 | NC_022691        | 16,701  |
| Carcharodon carcharias        | NC_022415        | 16,744  |
| Cetorhinus maximus            | NC_023266        | 16,670  |
| Alopias superciliosus         | NC_021443        | 16,719  |
| A. pelagicus                  | NC_022822        | 16,692  |
| Pseudocarcharias kamoharai    | NC_026216        | 16,694  |
| Ranzania laevis               | NC_007887        | 16,478  |
| Mola mola                     | NC_005836        | 16,488  |
| Masturus lanceolatus           | NC_005837        | 16,481  |
| Lagophthalmus lagocephalus    | NC_015343        | 16,442  |
| Assurger anzac                | NC_022494        | 16,510  |
| Ruvettus pretiosus            | NC_022493        | 16,202  |
| Rhexa solandri                | NC_023952        | 16,350  |
| Seriola lalandi               | NC_016869        | 16,532  |
| Grammistes sexlineatus        | NC_024108        | 16,502  |
| Lampris guttatus              | NC_003165        | 15,598  |
Figure 1. Neighbour-joining tree of 58 pelagic species from tuna fishery.
Table 2. Maximum-Likelihood fits of 24 different nucleotide substitution models.

| Parameters       | BIC    | AICc   | lnL   |
|------------------|--------|--------|-------|
| TN93 + G + I     | 120    | 310,916.5 | 309,579 | -154,669 |
| HKY + G - I      | 119    | 311,048.6 | 309,724.2 | -154,743 |
| TN93 + G - I     | 119    | 311,932.7 | 310,608.4 | -155,185 |
| HKY + G          | 118    | 312,093.4 | 310,780.1 | -155,272 |
| GTR + G - I      | 123    | 315,473.4 | 314,104.5 | -156,929 |
| T92 + G - I      | 117    | 316,506.8 | 315,204.7 | -157,485 |
| GTR + G          | 122    | 316,521.1 | 315,163.4 | -157,460 |
| T92 + G          | 116    | 317,512.9 | 316,222  | -157,995 |
| K2 + G - I       | 116    | 317,604.1 | 316,313.1 | -158,041 |
| K2 + G           | 115    | 318,626.4 | 317,346.5 | -158,558 |
| TN93 + I         | 119    | 326,781.9 | 325,457.6 | -162,610 |
| HKY + I          | 118    | 327,024.2 | 325,710.9 | -162,737 |
| GTR + I          | 122    | 328,570.8 | 327,213  | -163,484 |
| T92 + I          | 116    | 330,908.6 | 329,617.6 | -164,693 |
| K2 + G - I       | 115    | 331,949.2 | 330,669.3 | -165,220 |
| JC + G - I       | 115    | 341,733.1 | 340,453.3 | -170,112 |
| JC + G           | 114    | 342,696.7 | 341,427.9 | -170,600 |
| TN93             | 118    | 364,714.3 | 363,401  | -181,582 |
| GTR              | 121    | 365,086.2 | 363,739.6 | -181,749 |
| HKY              | 117    | 365,107.1 | 363,805  | -181,785 |
| T92              | 115    | 366,807.8 | 365,527.9 | -182,649 |
| JC               | 114    | 367,965.7 | 366,697  | -183,234 |
| JC               | 113    | 388,505.1 | 387,247.5 | -193,511 |

Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best (shown in bold font). For each model, AICc value (Akaike Information Criterion, corrected), Maximum Likelihood value (lnL), and the number of parameters (including branch lengths) are also presented (Nei & Kumar 2000). GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; TN93: Tamura-Nei; T92: Tamura 3-parameter; K2: Kimura 2-parameter; JC: Jukes-Cantor. Non-uniformity of evolutionary rates among sites may be modelled by using a discrete Gamma distribution (+G) with 5 rate categories and by assuming that a certain fraction of sites are invariant sites. Assumed or estimated values of instantaneous substitution rates (r) and rates of base substitutions (f) are shown for each model, as well. They are followed by nucleotide frequencies (f) and rates of base substitutions (r) for each nucleotide pair. Relative values of instantaneous r should be considered when evaluating them. For simplicity, sum of r values is made equal to 1 for each model.

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Disclosure statement

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