

Mitochondrial genomes and phylogenetic relationships of *Lates japonicus*, *Lates niloticus*, and *Psammoperca waigiensis* (Perciformes: Latidae)

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ABSTRACT

The complete mitochondrial genomes of four fish species of the commercially important family Latidae were sequenced using the Illumina MiSeq, thereby significantly increasing the mitogenomic resources for the family. Whole mitogenome-based phylogenetic analysis supports the monophyly of the genus *Lates* and more generally the family Latidae. The mitogenome sequences from this study will be useful for future assessments of the diversity within and between *Lates* species and studies of phylogenetic relationships within the diverse and taxonomically challenging perciform fishes.

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The family Latidae currently contains 13 extant perch-like fishes from three genera, *Hypopterus* Gill, 1861, *Lates* Cuvier, 1828 and *Psammoperca* Richardson, 1848, which are found in a range of freshwater, brackish, and marine environments across Asia, Africa, and the Western Pacific and Indian oceans (Eschmeyer et al. 2016; Nelson et al. 2016). Despite low diversity, the family contains a number of commercially important species including the Asian sea bass or barramundi, *Lates calcarifer* and the Nile Perch, *L. niloticus*.

Psammoperca waigiensis or the Waigieu sea perch is the only member of the genus *Psammoperca* (Froese & Pauly 2016) and ranges widely across the Indo-West Pacific, from the Bay of Bengal to Japan to the northern and western coasts of Australia (Randall et al. 1990). In contrast, *L. japonicus* or akame or the Japanese lates has a relatively restricted range in the north western Pacific around Japan (Masuda et al. 1984). It is morphologically similar to both *P. waigiensis* and *L. calcarifer*, and was only declared a distinct species in 1984 (Katayama & Yasuhiko 1984). Unlike most of the other members of the family above, *L. niloticus* or the Nile perch is a purely freshwater species from north Africa that is of both economic importance and conservation concern as it has been introduced to several African lakes including the biological diverse Lake Victoria (Pringle 2005).

With the exception of *L. calcarifer* (Lin et al. 2006; Vij et al. 2014), genomic resources for the family Latidae are still fairly limited. In addition, from an evolutionary and taxonomic perspective, the status and relationships of the family to other Perciform groups is uncertain or unresolved (Vij et al. 2014; Harrington et al. 2016).

The sample of *L. japonicus* (Shi04) used for this study was collected from Shiomi River, Miyazaki Prefecture, Japan as described elsewhere (Takahashi et al. 2015). The sample of *P. waigiensis* was collected from Vestey's Beach, Darwin, in the Northern Territory, Australia (12.436° S, 130.829° E) with tissue and matched voucher specimen held at the Museum and Art Gallery of the Northern Territory (catalogue number: S.16708-010). The samples of the commercially important *L. calcarifer* and *L. niloticus* were obtained as muscle (fillets) from fish markets in Darwin, Australia sourced from the Northern Territory and Lake Victoria (imported), respectively.

Genomic DNA (gDNA) was extracted from approximately 50 mg fin clip or muscle tissue using the EZDNA Tissue extraction kit (OmegaBioTek, Norcross, GA). Approximately 100–200 ng of gDNA was sheared to 500 bp using a M220 focused-ultrasonicator (Covaris, Woburn, MA), prepped using NEBNext Ultra DNA library prep kit and subsequently sequenced on the MiSeq desktop sequencer (Illumina, San Diego, CA) located at the Monash University Malaysia Genomics Facility. Mitogenome assembly was performed using MITObim (Hahn et al. 2013). For *L. niloticus*, *L. japonicus*, and *P. waigiensis*, the *COX1* gene fragment for each species was used as the bait for iterative mapping assembly while for the *L. calcarifer* sample, the complete mitogenome already available for the species (GenBank: DQ010541) (Lin et al. 2006) was used instead. Each mitogenome was recircularized based on the presence of flanking repeat sequence as previously described (Gan et al. 2014) and annotated using MitoAnnotator (Iwasaki et al. 2013). For the construction of maximum-likelihood tree, 13 protein-coding genes and 2

stated origin from near Darwin, Australia. Within the genus *Lates* our sample of *L. calcarifer* exhibits a similar pair-wise nucleotide identity (whole mitogenome alignment) to *L. japonicus* and *L. niloticus* (86.7% and 86.2%, respectively).

ModelFinder identified four partitions as the best-fit partitioning scheme for the 13 PCG and 2 rRNA genes utilized for phylogenetics inference as follows: Partition1 = 12S and 16S; Partition2 = *ATP6*, *CYTB*, *COX3*, *ND3*, *COX1*, *COX2*; Partition3 = *ATP8*, *ND3*, *ND3*, *ND4L*, *ND2*; Partition4 = *ND6*. Phylogenetic analysis using maximum likelihood, based on the final partitioned nucleotide alignment consisting of 14,270 DNA characters, supports the monophyly of the genus *Lates* and to a certain extent the monophyly of the families Latidae, Carangidae, and Xiphiidae (Figure 1). However, within the Latidae a sister grouping between *L. japonicus* and *L. calcarifer* was only weakly supported (ultrafast bootstrap support = 56%) and the relationships among all three species of *Lates* should be considered pending further taxon and gene sampling. In general, the evolutionary relationships among the different families included in the study are poorly supported and may similarly benefit from a more extensive taxon and gene sampling, which is beyond the scope of this study.

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Disclosure statement

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