

Cynogloassus

by Sapto Andriyono

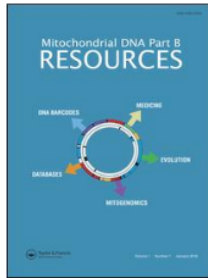
Submission date: 10-Jan-2023 01:23PM (UTC+0800)

Submission ID: 1990589932

File name: of_Cynoglossus_Senegalensis_Pleuronectiformes_Cynoglossidae.pdf (959.75K)

Word count: 1510

Character count: 8869



Mitochondrial DNA Part B Resources



ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

Characterization of the mitogenome of *Cynoglossus Senegalensis* (Pleuronectiformes: Cynoglossidae)

Fantong Zealous Gietbong, Nack-Keun Kim, Sapto Andriyono & Hyun-Woo Kim

To cite this article: Fantong Zealous Gietbong, Nack-Keun Kim, Sapto Andriyono & Hyun-Woo Kim (2018) Characterization of the mitogenome of *Cynoglossus Senegalensis* (Pleuronectiformes: Cynoglossidae), *Mitochondrial DNA Part B*, 3:2, 1191-1192, DOI: [10.1080/23802359.2018.1524728](https://doi.org/10.1080/23802359.2018.1524728)

To link to this article: <https://doi.org/10.1080/23802359.2018.1524728>



© 2018 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 26 Oct 2018.



[Submit your article to this journal](#)



Article views: 578



[View related articles](#)



[View Crossmark data](#)





Citing articles: 1 [View citing articles](#)

Full Terms & Conditions of access and use can be found at
<https://www.tandfonline.com/action/journalInformation?journalCode=tmdn20>

MITOGENOME ANNOUNCEMENT



Characterization of the mitogenome of *Cynoglossus Senegalensis* (Pleuronectiformes: Cynoglossidae)

Fantong Zealous Gietbong^{a,d}, Nack-Keun Kim^b, Sapto Andriyono^{b,c}  and Hyun-Woo Kim^{a,b,d} 

^aDepartment of Marine Biology, Pukyong National University, Busan, Republic of Korea; ^bInterdisciplinary Program of Biomedical, Mechanical and Electrical Engineering, Pukyong National University, Busan, Republic of Korea; ^cDepartment of Marine, Fisheries and Marine Faculty, Universitas Airlangga C Campus Jl. Mulyorejo Surabaya East Java, Indonesia; ^dKOICA-PKNU International Graduate Program of Fisheries Science, Graduate School of Global Fisheries, Pukyong National University, Busan, Republic of Korea

ABSTRACT

The complete mitogenome of the Senegalese tonguesole, *Cynoglossus senegalensis* was determined by Illumina MiSeq platform. The complete mitochondrial genome of *C. senegalensis* was 16,519 bp in length. The mitochondrial genome of *C. senegalensis* showed a cynoglossidae-characteristic gene organization, in which translocation of control region to the position between ND1 and tRNA-Gln gene, and also inversions in tRNA-Gln gene from L-strand position to H-strand position. Phylogenetic analysis showed that *C. senegalensis* is most closely related to *C. sinicus* and *S.bilineatus*, which supports the previous result that genus Cynoglossidae is evolutionary paraphyletic.

ARTICLE HISTORY

Received 13 August 2018
Accepted 31 August 2018

KEYWORDS

Mitochondrial genome;
Cynoglossus senegalensis;
sole; Cameroon; Africa

The Senegalese tonguesole, *Cynoglossus senegalensis*, is commercially important species in western Africa, which is mainly distributed along the coastal waters from Mauritania to Congo (Obiekezie and Lick 1994). Unfortunately, *Cynoglossus* fishery including *C. senegalensis* was overexploited in many African countries and this species is currently listed as 'Near Threatened' by the International Union for Conservation of Nature and Natural Resources Red List of Threatened Species since 2015 (Adeofe et al. 2015). Cynoglossidae is also interesting both from evolutionary and taxonomic perspective, as the family is fast-evolving (Pardo et al. 2005) and paraphyletic (Xu et al. 2008), genetic information of *C. senegalensis* is strongly required for the management of its resources in western Africa.

We determined the complete mitogenome of *C. senegalensis* collected from the coastal water in Bamusso (4° 00' 09" N 09° 14' 40" E), Cameroon, Africa. Species identification and frozen storage were conducted by Fisheries and Oceanographic Research Station (IRAD Batoke), Cameroon. Molecular identification of COI region showed 99% sequence identity to *C. senegalensis* (GenBank Number: EU513631). Genomic DNA was isolated by Accuprep Genomic DNA Extraction Kit (Bioneer, Korea). Two large PCR products amplified by PCR with sequence-specific primers targeting COX1 and ITS regions were further processed into the small-sized fragments (~350 bp) by Covaris® M220 Focused-ultrasonicator (Covaris Inc., USA). Library was constructed by TruSeq® RNA library

preparation kit V2 (Illumina, USA) and its quality and quantity were confirmed by 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). DNA sequencing was conducted by MiSeq sequencer (2 x 300 bp pair ends). The phylogenetic tree was constructed by MEGA7 with minimum evolution (ME) method (Kumar et al. 2016).

The complete mitochondrial genome of *C. senegalensis* was 16,519 bp in length (GenBank accession; MH709122), which contains 13 protein-coding genes, 22 tRNA genes, and 2 rRNA (12S and 16S), as well as two noncoding regions; control region (D-Loop) and origin of light-strand replication (OL). Non-canonical start codons were identified in two genes (GTG in COX1 and ATT in ND3) and incomplete stop codons were found in ND2, COX2, ND2, ND3, ND4, and ND5. The mitochondrial genome of *C. senegalensis* showed a cynoglossidae-characteristic gene organization; the translocation of control region to the position between ND1 and inversion of tRNA-Gln genes from L-strand to H-strand (Mjelle et al. 2008; Kong et al. 2009; Mu et al. 2015; Shi et al. 2015; Wei et al. 2016; Shi et al., 2014a; 2014b). All 22 tRNA genes (69 bp to 77 bp) formed the typical clover secondary structures according to the prediction by the ARWEN (Laslett and Canbäck, 2008). The phylogenetic analysis of *C. senegalensis* showed *C. senegalensis* was most closely related to hat identified close to *C. sinicus* (82%) and *C. bilineatus* (82%) (Figure 1). This result corresponds to the previous result that genus Cynoglossidae is evolutionary paraphyletic (Xu et al., 2008).

CONTACT Hyun-Woo Kim  kimhw@pknu.ac.kr Department of Marine Biology, Pukyong National University, Busan 48513, Republic of Korea

© 2018 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

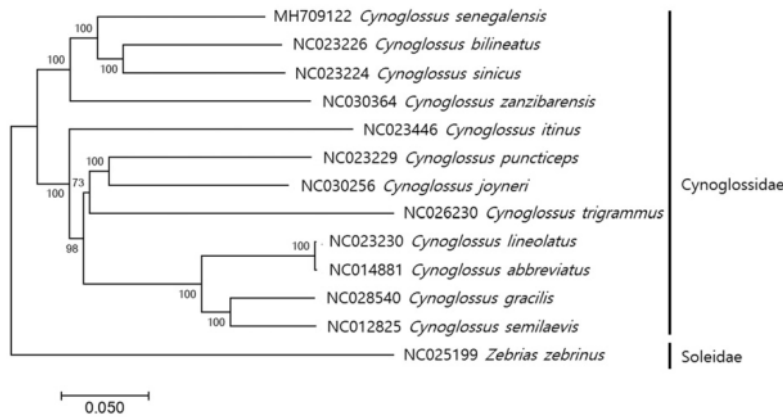


Figure 1. Phylogenetic tree of *Cynoglossus senegalensis*. Phylogenetic tree of complete genome was constructed by MEGA7 software with Minimum Evolution (ME) algorithm with 1000 bootstrap replications. GenBank Accession numbers were shown followed by each scientific name. The sequence data for phylogenetic analyses used in this study were as follows: *Cynoglossus senegalensis* (MH709122), *C. bilineatus* (NC023226), *C. sinicus* (NC023224), *C. zanzibarensis* (NC030364), *C. itinus* (NC023446), *C. puncticeps* (NC023229), *C. joyneri* (NC030256), *C. trigrammus* (NC026230), *C. lineolatus* (NC023230), *C. abbreviatus* (NC014881), *C. gracilis* (NC028540), *C. semilaevis* (NC012825), and *Zebrias zebrinus* (NC025199) as outgroup from Family Soleidae.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This research was a part of the project titled “Long-term change of structure and function in marine ecosystems of Korea”, funded by the Ministry of Oceans and Fisheries, Korea. This work was also supported by a grant from the KOICA-PKNU International Graduate Program of Fisheries Science, Graduate School of Global Fisheries, Pukyong National University

ORCID

Sapto Andriyono  <http://orcid.org/0000-0002-2566-1636>
Hyun-Woo Kim  <http://orcid.org/0000-0003-1357-5893>

Reference

- Adeofe TA, Camara K, Camara YH, Cissoko K, Mbye E, Munroe T, Sidibe A, Tous P, de Morais L, Sagna A, Sylla M. 2015. *Cynoglossus senegalensis*. The IUCN Red List of Threatened Species. 2015: e.T15602947A15604030.
- Kong X, Dong X, Zhang Y, Shi W, Wang Z, Yu Z. 2009. A novel rearrangement in the mitochondrial genome of tongue sole, *Cynoglossus semilaevis*: control region translocation and a tRNA gene inversion. *Genome*. 52:975–984.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol*. 33: 1870–1874.
- Laslett D, Canbäck B. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. *Bioinformatics*. 24: 172–175.

- Mjelle KA, Karlsen BO, Jørgensen TE, Moum T, Johansen SD. 2008. Halibut mitochondrial genomes contain extensive heteroplasmic tandem repeat arrays involved in DNA recombination. *BMC Genomics*. 9:10.
- Mu X, Wang X, Liu Y, Song H, Liu C, Gu D, Wei H, Luo J, Hu Y. 2015. An unusual mitochondrial genome structure of the tonguefish, *Cynoglossus trigrammus*: control region translocation and a long additional non-coding region inversion. *Gene*. 573:216–224.
- Obiekiezie A, Lick R. 1994. *Kudoa cynoglossi* n. sp., a New Species of *Kudoa* Meglitsch (Myxosporea: Multivalvulida) from the West African Tongue Sole, *Cynoglossus senegalensis* (Kaup) (Teleostei: Cynoglossidae). *Archiv Für Protistenkunde*. 144:201–205.
- Pardo BG, Machordom A, Foresti F, Porto-Foresti F, Azevedo MFC, Bañon R, Sánchez L, Martínez P. 2005. Phylogenetic analysis of flatfish (Order Pleuronectiformes) based on mitochondrial 16s rDNA sequences. *Scientia Marina*. 69:531–543.
- Shi W, Gong L, Kong X-Y. 2014a. The complete mitochondrial genome sequence of *Cynoglossus abbreviatus* (Pleuronectiformes: Cynoglossidae) with control region translocation and tRNA-Gln gene inversion. *Mitochondrial DNA Part A*. 27:1–2158.
- Shi W, Jiang J-X, Miao X-G, Kong X-Y. 2015. The complete mitochondrial genome sequence of *Cynoglossus sinicus* (Pleuronectiformes: Cynoglossidae). *Mitochondrial DNA*. 26:865–866.
- Shi W, Li D-H, Kong X-Y. 2014b. Gene rearrangements in the mitochondrial genome of *Cynoglossus bilineatus* (Pleuronectiformes: Cynoglossidae). *Mitochondrial DNA Part A*. 27:1–2162.
- Wei M, Liu Y, Guo H, Zhao F, Chen S. 2016. Characterization of the complete mitochondrial genome of *Cynoglossus gracilis* and a comparative analysis with other Cynoglossinae fishes. *Gene*. 591: 369–375.
- Xu H, Li J, Kong X, Xiao Z, Li Y, Zhang Y, Shi W, Wei Z, Yu Z. 2008. Phylogenetic relationship and length variation in the first ribosomal internal transcribed spacer of Cynoglossinae species. *Oceanologia et Limnologia Sinica*. 39:35.

Cynogloassus

ORIGINALITY REPORT

6%

SIMILARITY INDEX

4%

INTERNET SOURCES

2%

PUBLICATIONS

0%

STUDENT PAPERS

PRIMARY SOURCES

1

[1library.net](#)

Internet Source

1%

2

[dl.dropboxusercontent.com](#)

Internet Source

1%

3

[ppjpi.unair.ac.id](#)

Internet Source

1%

4

Catherine J. Gandy, Neil D. Gray, Obioma K. Mejeha, Angela Sherry, Adam P. Jarvis. "Use of propionic acid additions to enhance zinc removal from mine drainage in short residence time, flow-through sulfate-reducing bioreactors", *Journal of Environmental Management*, 2023

Publication

1%

5

Salvador Barahona, Yassef Yuivar, Gabriel Socias, Jennifer Alcaíno, Víctor Cifuentes, Marcelo Baeza. "Identification and characterization of yeasts isolated from sedimentary rocks of Union Glacier at the Antarctica", *Extremophiles*, 2016

Publication

1%

6

journal15.magtechjournal.com

Internet Source

1 %

7

onlinelibrary.wiley.com

Internet Source

1 %

Exclude quotes On

Exclude matches Off

Exclude bibliography On

Cynogloassus

GRADEMARK REPORT

FINAL GRADE

/100

GENERAL COMMENTS

Instructor

PAGE 1

PAGE 2

PAGE 3
