

Poster_ISGA

by Mochamad Syaifudin

Submission date: 22-Jan-2019 06:14AM (UTC+0700)

Submission ID: 1066756456

File name: ISGA-poster2015-M.Syaifudin.pptx (2.93M)

Word count: 958

Character count: 4681

DNA TYPING ACROSS TEN TILAPIA SPECIES USING CYTOCHROME C OXIDASE SUBUNIT I (COI)



Syaifuldin M.^{1,2*}, Bekae³, Taggart J.B.⁴, Hulata G.⁴, D'Cotta H.⁴, Baroiller J.F.⁴, Penman D.J.^{4,5}, McAndrew B.J.¹
¹Institute of Aquaculture, University of Stirling, Stirling FK9 4LA, Scotland, UK
²Program Study of Aquaculture, Agriculture Faculty, University of Sriwijaya, Indonesia
³Institute of Animal Science, Agricultural Research Organization, The Volcani Center, Israel
⁴Grad, Persyst, UMR ISEM, Campus International de Baillarguet, Montpellier, France
⁵m.s.yaifuldin@stir.ac.uk

INTRODUCTION

The tilapias are a group of African and Middle Eastern cichlid fish that are widely cultured in both developed and developing countries (major producers include China, Egypt, Indonesia, Philippines, Thailand and Brazil), with total world aquaculture production of 4.5 million t and total value of 7.6 billion USD in 2012 (FAO, 2014). Of this, 3.8 million t was *O. niloticus*, representing 84.13% of the total. With many different species and sub-species of tilapia, and extensive use of interspecies hybrids, identification of tilapia species is of importance in aquaculture and wild populations where introductions have occurred. Mitochondrial DNA cytochrome c oxidase subunit I (COI) sequence is widely used as a "barcode of life" for species identification. The conserved sequence of the 5' region of the mitochondrial gene cytochrome oxidase subunit I (COI or Cox1) has been widely used for distinguishing, for example Australian fish (Ward et al., 2005), marine fishes (McCusker et al., 2013) and tilapia species (Wu & Yang, 2012).

OBJECTIVES

- To confirm species authentication in tilapia using cytochrome c oxidase subunit I (COI).
- To construct a gene tree based on COI nucleotide sequences between tilapia species

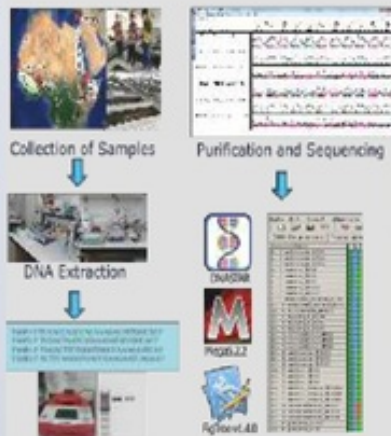
MATERIALS AND METHODS

This study involved ten species of tilapia from all three common genera, and included more than one population and/or subspecies from the major commercial species. It was undertaken in parallel to research to develop species-specific markers from nuclear DNA using double-digest restriction site associated DNA sequencing (ddRADseq).



Ten samples were collected from ten different tilapia species. The *O. niloticus* samples consisted of two sub-species (*O. n. niloticus* and *O. n. cancellatus*) from two populations in the former case; *O. aureus*, *O. mossambicus* and *Tilapia zillii* (Gervais) comprised samples from two populations each, while *O. karongwe* (Trewavas), *O. urolepis hornorum* (Norman; originally from Tanzania), *O. andersonii*, *O. macrochir*, *Sarotherodon galilaeus* (Linnaeus) and *S. melanotheron* consisted of one population each.

METHODOLOGY



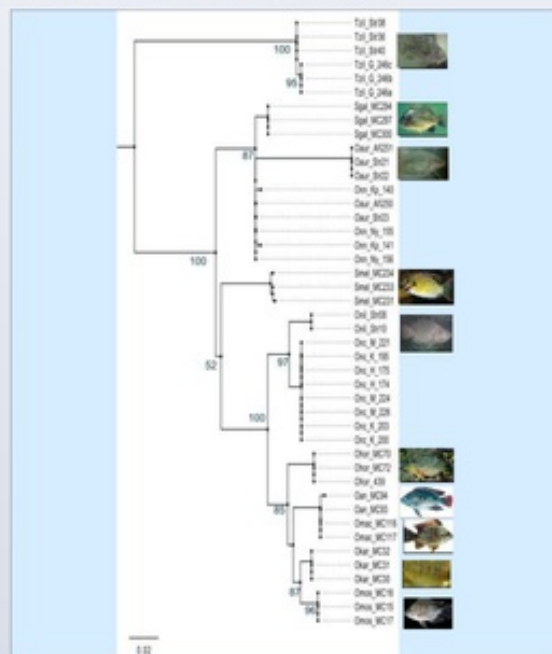
Polymerase Chain Reaction
 A 655 bp of the COI gene from mitochondrial DNA were amplified with primer pairs from Ward et al. 2005.

ACKNOWLEDGMENTS

We are grateful to Dr. Andrew M. Daines for the *O. andersonii* and *O. macrochir* samples. We thank Keith Ranson of the Tropical Aquaculture Facility at the Institute of Aquaculture, University of Stirling, for help in rearing fish. The authors acknowledge the support of the MASTS pooling initiative Marine Alliance for Science and Technology for Scotland and also thank to Director General of Higher Education, Ministry of Research, Technology and Higher Education (Kementerian Dikti), Indonesia for funding PhD scholarship of M5 at the University of Stirling.

RESULTS

The COI partial sequences of the tilapia species that were retrieved varied between 395-631 bp and agreed with those in the Barcode of Life Data System (BOLD) and the NCBI GenBank Database. The COI gene tree indicated a large discrimination between tilapia genera (*Tilapia*, *Sarotherodon* and *Oreochromis*). The largest group consisted of most of the *Oreochromis* species. West African *O. niloticus* (Onn_Kp and Onn_Ny) exhibited COI haplotypes typical of *O. aureus*, as previously reported in Rognon & Guyomard (2003), although nuclear markers clearly indicated the differences between these two species. While the last group consisted of the two populations of *T. zillii* being the most distant species from the *Oreochromis* genus.



DISCUSSION

The COI gene tree generally agrees with previous publications using allozymes (Sodsuk & McAndrew, 1991; Pouyaud & Agnès, 1995) and the mitochondrial control region (Nagl et al., 2001), in that *Sarotherodon* species were not clearly separated from *Oreochromis* (unlike our ddRADseq study using >600 SNP, in which all three genera were separated). We also could not separate *O. andersonii* and *O. macrochir* or West African *O. niloticus* from *O. aureus* using COI sequence. These issues seem from the COI being only a single, maternally inherited marker.

SUMMARY

The COI DNA barcode is able to resolve most, but not all, of the species involved in this study. As a single, maternally inherited marker it is of limited use in analysing cases of hybridization/introgression. However, it is still likely to be useful in combination with multiple nuclear DNA markers.

REFERENCES

- FAO., 2014. FAO year book 2012.
 Nagl, S. et al., 2001. Molecular Phylogenetics and Evolution, 20(3): 361-74.
 Pouyaud, L. & Agnès, J.-F., 1995. Journal of Fish Biology, 47(1): 26-38.
 Rognon, X., & Guyomard, R. (2003). Molecular Ecology, 12: 435-445.
 Sodsuk, P., & McAndrew, B. J. (1991). Journal of Fish Biology, 39 (Supplement 5A): 301-308
 Ward, R.D. et al., 2005. Series B, Biological sciences, 360(1462): 1847-57.
 McCusker, M.R. et al., 2013. Molecular Ecology Resources, 13(2): 177-88.
 Wu, L. & Yang, J., 2012. PloS One, 7 (12): p.e51731.

Poster_ISGA

ORIGINALITY REPORT

13%

SIMILARITY INDEX

9%

INTERNET SOURCES

8%

PUBLICATIONS

6%

STUDENT PAPERS

PRIMARY SOURCES

1	link.springer.com Internet Source	3%
2	eprints.unsri.ac.id Internet Source	2%
3	evols.library.manoa.hawaii.edu Internet Source	2%
4	Submitted to Mahidol University Student Paper	2%
5	Submitted to Coventry University Student Paper	2%
6	Xing Bingpeng, Lin Heshan, Zhang Zhilan, Wang Chunguang, Wang Yanguo, Wang Jianjun. "DNA barcoding for identification of fish species in the Taiwan Strait", PLOS ONE, 2018 Publication	2%

Exclude quotes Off

Exclude bibliography On

Exclude matches < 2%