



## GENETIC AND PHYLOGENETIC VARIATIONS OF YELLOWFIN TUNA (THUNNUS ALBACARES) AS A BASIS FOR SUSTAINABLE FISHERY RESOURCES MANAGEMENT IN NORTH MOLUCCAS

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### ABSTRACT

Yellowfin tuna, a big pelagic fish, is highly abundant in the waters of North Molucca. Increases fishing activities result in a decrease in population stock. The sustainability and resources status can be understood through genetically approaches. The objective of this research is to understand phylogenetic and genetic variations of yellowfin tuna in the North Molucca waters. Sample collection was done in Mei-July 2016 in the islands of Morotai, Obi, and Sanana, while the secondary data were from the islands of Ternate, Bacan, and Ambon. In total, there were 72 samples collected and analyzed. The results showed that the genetic variations of yellowfin tuna were 0.97 in Morotai, 1.00 in Sanana, 0.97 in Obi, 0.98 in Bacan, and 1.00 in Ternate and Ambon. Nucleotide variations analysis resulted 0.022 in Morotai, 0.026 in Sanana, 0.018 in Obi, 0.029 in Bacan, 0.027 in Ternate, and 0.025 in Ambon. The genetic variations value found suggests that yellowfin tuna is still in good condition based on criteria. The high variety of genetic diversity and specific haplotypes provides an illustration that there has been no genetic change in yellowfin tuna populations. Haplotype distribution analysis found 44 haplotype-specific, 11 haplotype mixed among locations, and 4 similar haplotype. Phylogenetic reconstruction showed that yellow fin tuna is panmixia population indicating all samples do not have significant genetic differences. The strategy for sustainable fishery management has to be done based on several proposed recommendations; first knowledge of genetic information on an ongoing basis covering the deployment area. Second is a population measurement based on morphological size information temporally. Third is the increase of tuna fish stock through restocking activities. The recommendations are important to be implemented in order to keep the stability and sustainability of yellow fin tuna population in the area.

**KEYWORDS:** *genetic variations, phylogenetic, yellowfin tuna, North Moluccas.*



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## INTRODUCTION

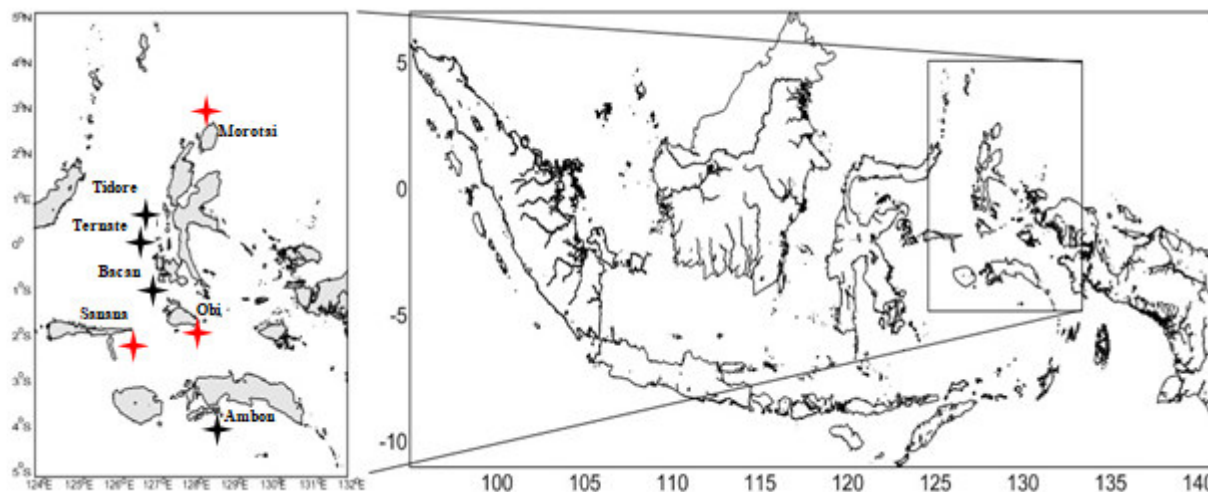
<sup>1</sup>Yellowfin tuna is a big pelagic fish and has high economic values. <sup>2</sup>This species is found in almost entire world's sea waters as it has high migratory ability. <sup>3</sup>Tuna fishing has been done for more than five decades and the fishing rates are steadily increased by 5.45% per year. Reported that the fishing production of yellowfin tuna in the Pacific Ocean in 2010 was 2,296,000 tonnes which decreased by 3% from the previous year, in the Indian Ocean the production in 2010 was 843,000 tonnes which decreased by 4% from 2009, and in the Atlantic Ocean the production was 419,600 tonnes which increased by 2% from the previous year. The potency of large pelagic fishes, especially tuna, is found in the waters of North Molucca. In 2014, fishing production in the area was 216,000 tonnes. The export of tuna in 2010-2015 was 142.00 tonnes, increased by 15. This total potency indicates that the North Molucca waters are part of the migration routes of large pelagic fishes. The abundance of tuna resources is affected by the geographical location that directly connected to the Pacific Ocean, Seram Sea, Molucca Sea, Halmahera Sea and Banda Sea which are the path of the Indonesian throughflow.<sup>4</sup> The North Molucca waters are also the spot of biodiversity as it is in the world coral triangle area. <sup>5</sup>High fishing rate leads to a decrease of yellowfin stock size in terms of weight-length, individual size and population size.<sup>2</sup> Stated that the status of yellowfin tuna in the coral triangle area is fully exploited and that of big eye tuna is overfishing.<sup>6</sup> If fishing of these species is done continuously, it could decrease the population as their life cycle may be. <sup>2</sup>Therefore, the program of tuna management and conservation through genetic conservation is needed that can be used to establish the policy of management and genetic conservation of yellow fin tuna. Research reported<sup>7</sup> on yellow fin tuna variations in the Pacific Ocean,<sup>8, 1</sup> in the Pacific and Indian Oceans,<sup>9</sup> in the Indian Ocean, and at along the coast of India.<sup>10</sup> Population structure can be determined through a morphology study and population sustainability can be determined through a genetic analysis.<sup>11</sup> Genetic variations relate to sustainable resources utilization and conservation aspects, and also affect the development of paired organs in animals.<sup>12, 13, 14, 15, 16</sup> The information of tuna genetic variations is useful for population structure identification optimization, breeding programs, stock development and management for sustainable resources.<sup>1</sup> The high

commercial and economic values of yellowfin tuna become the reason of the importance of genetic variation understanding for an effective sustainable fishery resources management.<sup>17</sup> The knowledge about the structure can be used in fishery management and conservation efforts for commercial valuable pelagic fishes in Indonesia. The objective of this research is to understand the genetic and phylogenetic variations of yellowfin tuna in North Molucca waters. <sup>18</sup>PCR-sequencing method was used to find the information of genetic variations of a population. This method can be used to obtain the alkali sequence of nucleotides in DNA molecule.<sup>19</sup> Had been research on the genetic variations and structures of yellowfin tuna in North Molucca, Indonesia. These researches, however, do not provide yet complete information about tuna genetic variations, therefore additional information from some other areas in the North Molucca waters is needed. The information of genetic variations of yellowfin tuna in the waters of North Molucca is scarce, but the information is needed to know the population status and to formulate a management policy. This study correlates the results of field data and secondary data from.

### *Research methodology*

#### *Samples and Methods*

Samples of tuna were collected in May-June 2016 in three locations in the North Molucca Province, i.e. Morotai Island (10 samples), Obi Island (10 samples), dan Sanana Island (10 samples). The tuna fishing area is located in the waters of Morotai Island in the north and west, on the island of Obi the fishing operation is in the south and east while for Sanana Island itself the fishing area is in the south, east and west. The location of the fishing is based on the migration of the tuna waters of each island. Samples were fish caught in the waters around the research locations that landed at Fish Landing Centers (Pangkalan Pendaratan Ikan, PPI) and Archipelagic Fishing Port (Pelabuhan Perikanan Nusantara, PPN) (Figure 1). The Secondary data in the form of tuna sequences are taken from<sup>19</sup> research results located in Ternate, Bacan and Ambon. All secondary data were from the previous research. Each sampled fish was pictured and measured its length. A piece of about 3 cm in length was taken from pectoral fins and placed inside a tube contained 96% ethanol for preservation. Samples analysis were carried out in the Indonesian Biodiversity Research Center (IBRC) Bali.



**Figure 1**  
**Sampling locations of yellow fin tuna (*Thunnus albacores*) in the waters of North Molucca**  
 (red stars = primary data, black stars = secondary data)

<sup>20</sup>The DNA samples were isolated using Chelex 10% solution. Extraction was started with putting a sample in a tube and then vortexed and centrifuged for  $\pm 20$  seconds. Next, it was heated using a heat block at  $95^{\circ}\text{C}$  for  $\pm 45$  minutes. After that, the tube was re-vortexed and centrifuged for 20 seconds. <sup>21</sup>The Polymerase Chain Reaction amplification process was focused on the locus of mtDNA control region with forward primer CRK 5'-AGCTC AGCGC CAGAG CGCCG GTCTT GTAAA-3' and reverse primer CRE 5'-CCTGA AGTAG GAACC AGATG-3'. The procedure in PCR was started with a pre-denaturation at  $94^{\circ}\text{C}$  for 15 seconds, 38 cycles including denaturation at  $94^{\circ}\text{C}$  for 30 seconds, annealing at  $50^{\circ}\text{C}$  for 30 seconds, and extension at  $72^{\circ}\text{C}$  for 45 seconds and then further extension at  $72^{\circ}\text{C}$  for 5 minutes. The quality of DNA produced by PCR was examined using an electrophoresis. In this stage a 1 gr agarose gel was made and put in an erlenmeyer, added TAE 1x 75mL and heated in a microwave and then added EtBr 4  $\mu\text{L}$ . After that, the agarosa gel was poured into a tray that had a wells maker comb and left for 30 minutes.<sup>18</sup> The PCT products were sent to Berkeley Sequencing Facility using Sanger method.

#### Data Analysis

The analysis of mtDNA control region sequence used MEGA5 software consisting of genetic distances, phylogenetic using neighbour joining method, Kimura's 2-parameter evolution model and 1000 bootstraps replications. Species identification used Blast (Basic Local Alignment Tools) application. Variation analysis of haplotype ( $H_d$ ) and nucleotide ( $\pi$ ) in the mtDNA sequences was based on<sup>26</sup> using DnaSP 4.0 application<sup>23</sup>.

## RESULTS and DISCUSSION

#### Molecular Characteristics

The fragment of mtDNA control region was obtained 512

bp (base pairs) in length of 72 yellow fin tuna (*T. albacares*) samples including 42 secondary data from Ternate (12 samples), Bacan (23 samples), and Ambon (8 samples). The obtained DNA fragment was similar to the findings of<sup>7, 19</sup> i.e. 517 bp and of i.e. 500 bp. Other tuna research found short DNA fragments, for example<sup>21</sup> found 400 bp, <sup>1</sup>366 bp, and <sup>7</sup>304 bp. These fragment length variations are due to the quality of DNA samples and the number of samples collected. <sup>24</sup>These variations, however, do not indicate any effects on the results of sequence analysis. In fact, some research done, for example, by<sup>25,26</sup> found 600–700 bp in shark samples, while<sup>23</sup> found 860 bp in big eye tuna, and<sup>24</sup> found 526 bp in grouper *Epinephelus* spp.

#### Genetic variations

Genetic variations were found to be very high with varied of haplotype total and nucleotide variations (Tabel 1). Haplotype ( $H_d$ ) variations in each location samples showed that Sanana (nucleotide 0.026), Ternate (nucleotide 0.027), and Ambon (nucleotide 0.025) had the highest genetic variations of 1.00. In Bacan (nucleotide 0.029), the variation value was 0.98, while in Morotai (nucleotide 0.022) and Obi (nucleotide 0.018) had 0.97 variation value. High genetic variation value of yellow fin tuna had been reported, for examples <sup>7</sup>0.840 in the Pacific Ocean, <sup>8</sup>0.878, 0.992 in the western Pacific Ocean and <sup>10</sup>0.999 in the western Indian Ocean, and <sup>9</sup>0.998.<sup>27, 28, 29, 30, 31, 32, 15, 16, 17</sup> High genetic variations also had been reported for other migratory species like big eye tuna (*Thunnus obesus*), albacore (*Thunnus alalunga*), skipjack (*Katsuwonus pelamis*), frigate mackerel (*Auxis thazard*), bonito (*Euthynnus affinis*), Spanish mackerel (*Scomberomorus commerson*), stripped mackerel (*Rastrelliger kanagurta*).<sup>33</sup> Migration ability allowing inter-population encounters, and high genetic variations in tunas are characteristics of *Scrombridae* family.

Table 1

**The number of haplotype ( $H_n$ ), haplotype variation ( $H_d$ ), nucleotide variation ( $\pi$ ) and the number of samples ( $n$ ) of yellow fin tuna (*Thunnus albacares*).**

Location	$n$	$H_n$	$H_d$	$\pi$	Base Pairs
Morotai	10	9	0,97	0,022	512
Sanana	10	10	1,00	0,026	
Obi	10	9	0,97	0,018	
Bacan	23	20	0,98	0,029	
Ternate	11	11	1,00	0,027	
Ambon	8	8	1,00	0,025	

<sup>22</sup>Based on the criteria of genetic variations, the findings indicated that the yellow fin tuna is still in good condition. Even though this species is the target catch in all areas, but with their migration ability and fast reproduction, this tuna population could continue to exist. <sup>34</sup>Stated that tuna migration rate is higher than other saltwater fishes, so the probability to meet and inter-breed with other populations is even greater. <sup>35</sup>  
<sup>36</sup>Genetic variations provide the ability to adapt to climate and environmental change and diseases, and indicate that the species has large population size. The

results of genetic variation analysis revealed 58 haplotype from 72 samples (Table 2). Overall, the haplotype variations indicated that there were 44 haplotype-specific, 11 haplotype mixed among locations, and 4 similar haplotype which occurred in two species from the same location. The tuna fish are migration and have migration routes at each research site. The overall research sites are feeding areas and tuna migration paths. This provides evidence that the waters around North Maluku are where live habitats tuna fish.

Table 2

**The number of haplotype ( $H_d$ ) variation in yellow fin tuna (*Thunnus albacares*)**

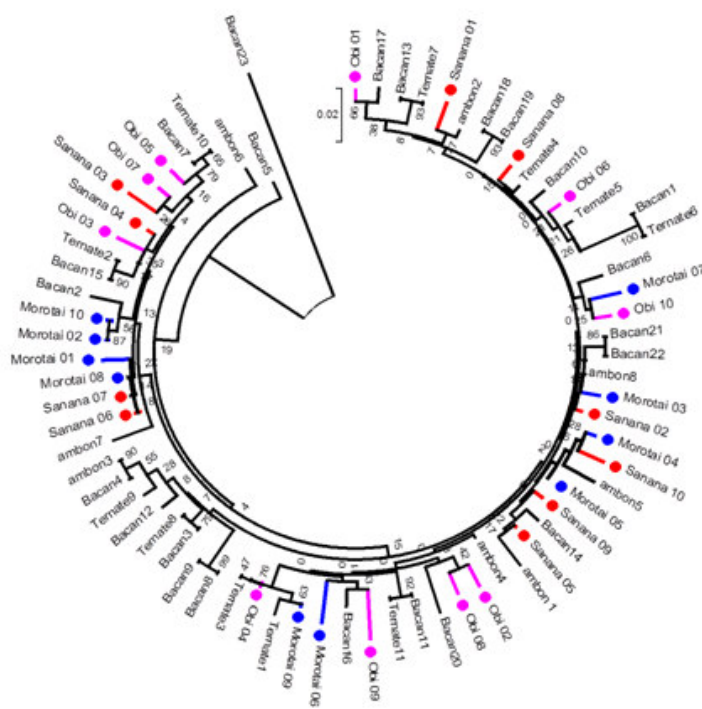
No	Haplotype ( $H_d$ )	No	Haplotype ( $H_d$ )
1	Hap_1: 1 [Morotai]	30	Hap_30: 2 [Bacan3 Ternate8]
2	Hap_2: 2 [Morotai Morotai]	31	Hap_31: 2 [Bacan4 ambon3]
3	Hap_3: 1 [Morotai]	32	Hap_32: 1 [Bacan5]
4	Hap_4: 1 [Morotai]	33	Hap_33: 1 [Bacan6]
5	Hap_5: 1 [Morotai]	34	Hap_34: 2 [Bacan7 Ternate10]
6	Hap_6: 1 [Morotai]	35	Hap_35: 2 [Bacan8 Bacan9]
7	Hap_7: 1 [Morotai]	36	Hap_36: 1 [Bacan10]
8	Hap_8: 3 [Morotai Sanana Sanana]	37	Hap_37: 2 [Bacan11 Ternate11]
9	Hap_9: 1 [Morotai]	38	Hap_38: 1 [Bacan12]
10	Hap_10: 1 [Sanana]	39	Hap_39: 2 [Bacan13 Ternate7]
11	Hap_11: 1 [Sanana]	40	Hap_40: 1 [Bacan14]
12	Hap_12: 1 [Sanana]	41	Hap_41: 2 [Bacan15 Ternate2]
13	Hap_13: 1 [Sanana]	42	Hap_42: 1 [Bacan16]
14	Hap_14: 1 [Sanana]	43	Hap_43: 1 [Bacan17]
15	Hap_15: 1 [Sanana]	44	Hap_44: 2 [Bacan18 Bacan19]
16	Hap_16: 1 [Sanana]	45	Hap_45: 1 [ambon]
17	Hap_17: 1 [Sanana]	46	Hap_46: 1 [ambon2]
18	Hap_18: 1 [Obi]	47	Hap_47: 1 [ambon4]
19	Hap_19: 1 [Obi]	48	Hap_48: 1 [ambon5]
20	Hap_20: 1 [Obi]	49	Hap_49: 1 [ambon6]
21	Hap_21: 2 [Obi Ternate3]	50	Hap_50: 1 [ambon7]
22	Hap_22: 1 [Obi]	51	Hap_51: 1 [ambon8]
23	Hap_23: 1 [Obi]	52	Hap_52: 1 [Bacan20]
24	Hap_24: 1 [Obi]	53	Hap_53: 2 [Bacan21 Bacan22]
25	Hap_25: 1 [Obi]	54	Hap_54: 1 [Bacan23]
26	Hap_26: 1 [Obi]	55	Hap_55: 1 [Ternate1]
27	Hap_27: 1 [Obi]	56	Hap_56: 1 [Ternate4]
28	Hap_28: 2 [Bacan1 Ternate6]	57	Hap_57: 1 [Ternate5]
29	Hap_29: 1 [Bacan2]	58	Hap_58: 1 [Ternate9]

High genetic variations and varied haplotype-specific indicate that there are no genetic structure changes yet in yellow fin tuna population because it still has various gene variations. Haplotype variations had been reported by<sup>1</sup>, where there were 111 different haplotype of 124 total samples. Moreover,<sup>37</sup> from 28 samples found 18 haplotype -specific in each individual fish, 8 haplotype distributed in two individuals and 1 haplotype distributed in 4 individuals.<sup>17</sup> Reported 172 haplotype from 177 analyzed samples.<sup>15</sup> found 98 haplotype from 118 total samples observed in big eye tuna. Yellow fin tuna that widely distributed in the world oceans has big population with high haplotype variations. This indicates that the population has high survival against environmental disturbances.<sup>38</sup> Various haplotype composite types are also contributed highly to increase the genetic variations of a population.<sup>22</sup> Several reports on haplotype variations in populations including in a big population, the environmental variations and the history of threatened population life were steadily going up.

### Phylogenetic *Thunnus albacares*

The reconstruction of family relationship among yellow fin tuna population in each location found that there occur an individual mixture (Figure 1). Reported similar finding that an individual mixture occurred among populations. Moreover,<sup>9</sup> also found no genetically difference in the Indian Ocean based on phylogenetic

reconstruction.<sup>39</sup> Reported that a mixture had been occurred between yellow fin tuna from the Philippines and from Spain.<sup>40</sup> Various researches had also reported the close family relationship based on phylogenetic tree in the Pacific Ocean,<sup>31, 32</sup> in the Atlantic Ocean,<sup>15</sup> China Sea, the Philippines and the western Pacific Ocean, and<sup>16</sup> in the Indian Ocean for big eye tuna (*T. obesus*). This indicates that the population has a genetic closeness and shows a strong relationship among populations.<sup>41</sup> Explained that in order to reveal low population difference, migration involving several individuals per generation could be a key to produce far genetic homogeneity. Geographically, the North Molucca has many islands. The distance between research locations, i.e. Morotai, Obi and Sanana are quite far, this however, did not limit the movement and mobility of tuna.<sup>39</sup> Stated that tuna generally can migrate for long distance as they are able to adapt to ocean environment changes, and then in winter they migrate to tropical waters. Besides, the North Molucca waters are the route of the Indonesian throughflow that helps to distribute fish partially in each location.<sup>42</sup> Stated that ocean flow could affect population distribution and fish genetic structures.<sup>43</sup> Revealed that gene exchange processes occurred among populations in the tropical Indo-Pacific resulted in a genetic closeness among populations, and therefore giving a chance for tuna to meet in the area with a big population and from different locations.



Gambar 1

**Phylogenetic tree of yellow fin tuna (*Thunnus albacares*) analyzed using a neighbor-joining method with Kimura 2-parameter, (Primary Data: Pink Dot = Obi, Blue Dot = Morotai, and Red Dot = Sanana).**

The constructed phylogenetic tree supported by quite high bootstrap values at each branches. This indicates that reconstructed family tree has a good accuracy. The bootstrap values ranged from 55 to 99%. The analysis result concludes that the yellow fin tuna is panmixia population, which explains that there are no genetic differences among populations. Other tuna species had been reported by<sup>15</sup> that big eye population is panmixia

mixed among populations of the South China Sea, Philippines waters, western Pacific Ocean. In addition,<sup>31</sup> reported that there is genetic closeness in big eye tuna of the Indo-Pacific and the Atlantic Ocean. Furthermore,<sup>16</sup> provided evidence of individual mixing of big eye tuna in the Indian Ocean.<sup>44</sup> This big eye tuna similarity occur as there are gene flows from the western Pacific Ocean to the Indian Ocean and then to the Atlantic Ocean.<sup>45, 46.</sup>

<sup>47</sup> Pelagic fishes are found to have small genetic differences even though they are far separated geographically as they have big populations and high dispersal distances.

### **Tuna fishery management concept**

The potency of fish resources in Indonesian waters is high. Globally, the annual catch tends to increase. <sup>48</sup>The catch data indicated that tuna fishing production in Indonesian waters reached 1.2 million tonnes in 2013. Economic incentives generated by fishing activities were 3.3 million work forces and US\$ 68 millions due to export of skipjack, tuna and others. Reported that there was an increase of 10.96% in 2015 comparing in 2013 with the production value of 236 billion, while the total of fish capture production reached 6.4 million tonnes. Showed that the global fishing of skipjack and yellow fin tuna tended to increase reached 2,2 and 1,4 million tones, respectively, in 2003, and the catch of big eye tuna was 493,000 tonnes in 2000 which was lower than the previous year. Surely, the high potency of big eye tuna resource needs a special attention. This is useful in conserving and guaranties the sustainability of tuna resources in Indonesia. <sup>49,50,51</sup>Fishing activities have potential impacts on maturity processes and the reduction of population density and body size. Therefore, in the future the knowledge of catch and stock status becomes crucial managerial information for fishery resources management. <sup>52</sup>Besides, the use of technology in fishing raises a big problem, i.e. predominantly young fish in pole and line fleets catches. <sup>53, 54</sup>Consequently, a nonstop fishing can threaten the sustainability of the existed fish resources. The high genetic variations found in the North Molucca waters indicate that the tuna populations are still able to adapt to the occurred environmental changes. However, it is needed an action to avoid biological lost including genetic aspect. Activities to be carried out to safeguard tuna resource populations; First knowledge of genetic information on an ongoing basis covering the extent of the dispersal area, it is important to serve as the basis for determining population status. <sup>55, 56</sup>This is important primary data in determining population status. Genetic

### **REFERENCES**

1. Wua GCC, Chianga HC, Choua YW, Wong ZR, Husc CC, Chend CY, Yanga HY. Phylogeography of yellowfin tuna (*Thunnus albacares*) in the Western Pacific and the Western Indian Oceans inferred from mitochondrial DNA. *Fish Res.* 2010;105(3): 248-253.
2. Bailey M, Flores J, Pokajam S, Sumaila UR. Towards better management of coral triangle tuna. *Ocean Coast Manage.* 2012 Apr;63:30-42.
3. Witomo CM, Wardono B. Potret perikanan tangkap tuna, cakalang, dan layang di Kota Bitung. *Bul Ris Sosek Kel dan Perik.* 2012;7(1):7-13.
4. Allen GR. Indo-Pacific coral-reef fishes as indicators of conservation hotspots. *Proc 9th Inter Coral Reef Symp, Bali, Indonesia 23-27 October 2000* [Cited 2016 August 6]. Available form [http://www.coremap.or.id/downloads/ICRS9th\\_Allen.pdf](http://www.coremap.or.id/downloads/ICRS9th_Allen.pdf).

observations are unlimited efforts in potency management of commercial species. <sup>57</sup>Besides, genetic information can become a reason to conserve a species. The second is population measurement based on temporal information of morphological measurements. <sup>58</sup>An approach to know the population status can be done through measurement based on morphology. <sup>59</sup>This analysis is as the first step to observe the existence of a big size population based on phenotypic features. <sup>52</sup>Biological data set like this can be made as scientific evidences in developing a sustainable fishery management. The third is to increase tuna stock through restocking action. This process is started with collecting tuna juveniles through fishing and then cultured. This action aims to create stock development and stability in a sea. The restocking can, however, be done regularly using juveniles from hatcheries. We suggest this action to be made as a basis in tuna fishery management in the future.

### **CONCLUSION**

All the results show that genetic variations and haplotype composites are still high and inter-population relation are very strong. This information indicates that yellow fin tuna population in the waters of North Molucca is not vulnerable to the prevailing environmental change. A strong fishery resources management has to be implemented as a form of protection and conservation of tuna for the future.

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### **CONFLICT OF INTEREST**

Conflict of interest declared none.

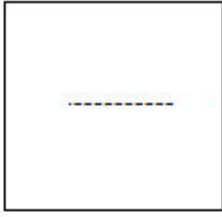
5. Kantun W, Yahya A. Hubungan bobot panjang ikan tuna madidihang *thunnus albacares* dari perairan majene selat Makassar Sulawesi barat. *J Balik Diwa.* 2013;4(2):39-43.
6. Kawimbang E, Paransa IJ, dan Kayadoe ME. Pendugaan stok dan musim penangkapan ikan julung-julung dengan soma roa di perairan Tagulandang, Kabupaten Kepulauan Siau Tagulandang Biaro. *J Ilmu dan Tek Perik Tangkap.* 2012 Juni;1(1):10-17.
7. Scoles DR, Graves JE. Genetic analysis of the population structure of yellowfin tuna, *Thunnus albacares*, from the Pacific Ocean. *Fish B-NOA.* 1993;91(4):690-698.
8. Moria SB, Permana GN, dan Hutapea. Karakteristik tiga lokus mikrosatelit pada telur larva tuna sirip kuning, *thunnus albacares*. *J Fish Sci.* 2009;XI(2):144-149.
9. Kunal SP, Kumar G. Cytochrome oxidase I (COI) sequence conservation and variation patterns in

- the yellowfin and longtail tunas. *Int J Bioinform Res Appl.* 2013;9(3):301-309.
10. Taniguchi N, Sugama K. Genetic variation and population structure of red sea bream in the coastal waters of Japan and the east China sea. *Nippon Suisan Gakkaishi.* 1990;56(7):1069-1077.
  11. Abulias MN, Bhagawati D. Bilateral symmetry fish character: The study of morphological diversity as a basis for aquaculture development. *Depik.* 2012 August;1(2):103-106.
  12. Dinesh KR, Lim TM, Chua KL, Chan WK, Phang VP. RAPD analysis: an efficient method of DNA fingerprinting in fishes. *Zoolog Sci.* 1993 Oct;10(5):849-54.
  13. Garcia DK, Benzie JAH. RAPD markers of potential use in penaeid prawn (*Penaeus monodon*) breeding programs. *Aquaculture.* 1995 Feb;130:137-144.
  14. Tassanakajom A, Pongsomboon S, Rimphanitchayakit V, Jarayabhand P, Boosaeng V. Random amplified polymorphic DNA (RAPD) markers for determination of genetic variation in wild population of the black tiger prawn (*Penaeus monodon*) in Thailand. *Mol Mar Bio and Biotech.* 1997;6(2):110-115.
  15. Chiang HC, Hsu CC, Lin HD, Ma GC, Chiang TY, Yang HY. Population structure of bigeye tuna (*Thunnus obesus*) in the South China Sea, Philippine Sea and western Pacific Ocean inferred from mitochondrial DNA. *Fish Res.* 2006;79:219-225.
  16. Chiang HC, Hsu CC, Wu GCC, Chang SK, Yang HY. Population structure of bigeye tuna (*Thunnus obesus*) in the Indian Ocean inferred from mitochondrial DNA. *Fish Res.* 2008; 90:305-312.
  17. Jackson AM, Ambariyanto, Erdmann MV, Toha AH, Stevens LA, Barber PH. Phylogeography of commercial tuna and mackerel in the Indonesian Archipelago. *Bull Mar Sci.* 2014;90(1):471-492.
  18. Sanger F, Nicklen S, Coulson AR. DNA sequencing with chain-terminating inhibitors. *Proc. Natl Acad Sci USA.* 1977 Dec;74(12):5463-5467.
  19. Akbar N, Zamani NP, Madduppa HH. Keragaman genetik ikan tuna sirip kuning (*Thunnus albacares*) dari dua populasi di Laut Maluku, Indonesia. *Depik.* 2014 Apr;3(1):65-73.
  20. Walsh PS, Metzger DA, Higushi R. Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *Bio Techniques.* 1991 Apr;10(4):506-513.
  21. Lee WJ, Conroy J, Howell WH, Kocher TD. Structure and evolution of teleost mitochondrial control regions. *J of Mol Evol.* 1995 Jul;41(1):54-66.
  22. Nei M. *Molecular evolutionary genetics.* at 61 West 62 Street. New York, 10023: Columbia University Press. 1989. 512 pp.
  23. Rozas J, Sanchez-DelBarrio JC, Messeguer, Roza R. DnaSP, DNA polymorphism analyses by the coalescent and other methods. *Bioinformatics.* 2003 Jul;19(18):2496-2497.
  24. Jefri E, Zamani NP, Subhan B, Madduppa HH. Molecular phylogeny inferred from mitochondrial DNA of the grouper *Epinephelus* spp. in Indonesia collected from local fish market. *Biodiversitas.* 2015 Oct;16(2):254-263.
  25. Prihadi, Sembiring A, Kurniasih EM, Rahmad, Arafat D, Subhan B, Madduppa HH. DNA barcoding and phylogenetic reconstruction of shark species landed in Muncar fisheries landing site in comparison with Southern Java fishing port. *Biodiversitas.* 2015 Apr;16(1):55-61.
  26. Sembiring A, Pertiwi NPD, Mahardini A, Wulandari R Kurniasih EM, Kuncoro AW, Cahyani NKD, Anggoro AW, Ulfa M, Madduppa H, Carpenter KE, Barber PH, Mahardika GN. DNA barcoding reveals targeted fisheries for endangered sharks in Indonesia. *Fish Res.* 2014 Nov;3993:1-5.
  27. Bremer JRA, Naseri I, Ely. Orthodox and unorthodox phylogenetic relationships among tunas revealed by the nucleotide sequence analysis of the mitochondrial DNA control region. *J of Fish Bio.* 1997 March;50(30):540-554.
  28. Grant WS, Bowen BW. Shallow population histories in deep evolutionary lineages of marine fishes: insights from sardines and anchovies and lessons for conservation. *The J of Heredity.* 1998;89(5):415-426.
  29. Carlsson J, McDowell JR, Diaz Jaimes P, Carlsson JE, Boles SB, Gold, JR, Graves JE. Microsatellite and mitochondrial DNA analyses of Atlantic bluefin tuna (*Thunnus thynnus thynnus*) population structure in the Mediterranean Sea. *Mol Eco.* 2004 Aug;13:3345-3356.
  30. Ely B, Vinas J, Alvarado Bremer JR, Black D, Lucas L, Covello K, Labrie AV, Thelen E. Consequences of the historical demography on the global population structure of two highly migratory cosmopolitan marine fishes: the yellowfin tuna (*Thunnus albacares*) and the skipjack tuna (*Katsuwonus pelamis*). *BMC Evol Bio.* 2005 Feb 22;5(19):1-9.
  31. Martínez P, Zardoya R. "Genetic structure of bigeye tuna (*Thunnus obesus*) in the Atlantic Ocean. *Sci Pap ICCAT.* 2005;57(1):195-205.
  32. Martinez P, Gonzales GE, Castilho R, Zardoya R. Genetic diversity and historical demography of Atlantic bigeye tuna (*Thunnus obesus*). *Mol phylo and evol.* 2006 Sep 26;39:404-416.
  33. Zardoya R, Castilho R, Grande C, Favre Krey L, Caetano S, Marcato S, Krey G, Patarnello T. Differential population structuring of two closely related fish species, the mackerel (*Scomber scombrus*) and the chub mackerel (*Scomber japonicus*), in the Mediterranean Sea. *Mol Eco.* 2004 March;13:1785-1798.
  34. Wild A. A review of the biology and fisheries for yellowfin tuna, *thunnus albacares*, in the eastern Pacific ocean. *Proceedings of the First FAO Expert Consultation on interactions of Pacific Tuna Fisheries 3-11 December 1991 Noumea, New Caledonia.* 1991 [Cited 2016 August 12];2:252-107. Available form: <http://www.fao.org/docrep/014/t1817e/t1817e.pdf>.
  35. Lande R. *Genetics and demography in biological conservation.* Science. 1988 Sep 16;241(4872):1455-1460.

36. Nuryanto A, Kochzius M. Highly restricted gene flow and deep evolutionary lineages in the giant clam *Tridacna maxima*. *Coral Reefs*. 2009 March 12;28:607–619.
37. Niwa Y, Nakazawa A, Margulies D, Scholey VP, Wexler JB, Chow S. Genetic monitoring for spawning ecology of captive yellowfin tuna (*Thunnus albacares*) using mitochondrial DNA variation. *Aquaculture*. 2003 Jan;218:387-395.
38. Smith MH and RK Chesser. Rationale for conserving genetic variation of fish gene pools. *Ecol Bull*. 1981;34:13-20.
39. Wijana IMD, Mahardika IGN. Struktur genetik dan filogeni yellowfin tuna (*Thunnus albacares*) berdasarkan sekuens dna mitokondria control region sitokrom oksidase I pada diversitas zone biogeografi. *J Bumi Lestari*. 2010 Aug;10(2):270-274.
40. Grewe P, Hampton J. An assessment of bigeye (*Thunnus obesus*) population structure in the Pacific Ocean, based on mitochondrial DNA and DNA microsatellites analysis. Working Paper WPYRG7/15, 7th Meeting of the Western Pacific Yellowfin Tuna Research Group, 18–20 June 1997, Nadi, Fiji [Internet]. 1997 Jun [Cited 2016 August 9]. Available from: <https://scholar.google.co.id/scholar?hl=id&q=40.%09Grewe+P%2C+Hampton+J.+An+assessm+ent+of+bigeye+%28Thunnus+obesus%29+popul+ation+structure+in+the+Pacific+Ocean%2C+base+d+on+mitochondrial+DNA+and+DNA+microsatelli+tes+analysis&btnG=>
41. Ward RD. Population genetics of tunas. *J of Fish Bio*. 1995;47(sA):259-280.
42. Gaylord B, Gaines SD. Temperature or transport? Range limits in marine species mediated solely by flow. *The American Naturalist*. 2000 June;155(6):769-789.
43. Gordon AL, Fine R. Pathways of water between the Pacific and Indian oceans in the Indonesian seas. *Nature*. 1996 Jan 11;379:146-149.
44. Durand JD, Collet A, Chow, Guinand B, Borsa P. Nuclear and mitochondrial DNA markers indicate unidirectional gene flow of Indo-Pacific to Atlantic bigeye tuna (*Thunnus obesus*) populations, and their admixture off southern Africa. *Marine Bio*. 2005 March 5;147:313-322.
45. Ward R D, Woodwark M, Skibinski DOF. A comparison of genetic diversity levels in marine, freshwater, and anadromous fishes. *J of Fish Bio*. 1994 March;44:213-232.
46. McQuinn IH. Metapopulations and the Atlantic herring. *Rev in Fish Bio and Fish*. 1997;7:297-329.
47. Nesbo CL, Rueness EK, Iversen SA, Skagen DW, Jakobsen KS. Phylogeography and population history of Atlantic mackerel (*Scomber scombrus* L.): a genealogical approach reveals genetic structuring among the eastern Atlantic stocks. *Proc R Soc Lond B*. 2000;267:281-292.
48. Claussen J. Indonesia Fisheries: Review, A report on trends in coastal marine resources and fisheries management in Indonesia. Program Officer, Western Pacific The David and Lucile Packard Foundation [Internet]. 2015 [Cited 2016 August 11]. 1-90. Available from <https://www.packard.org/wp-content/uploads/2016/09/Indonesia-Fisheries-2015-Review.pdf>.
49. Jennings S, Greenstreet SPR, Reynolds JD. Structural change in an exploited fish community: a consequence of differential fishing effects on species with contrasting life histories. *J of Animal Ecol*. 1999 May; 68(3):617-627.
50. Bianchi G, Gislason H, Graham K, Hill L, Jin X, Korateng K, Manickchand Heileman S, Paya I, Sainsbury K, Sanchez F, Zwanenburg K. Impact of fishing on size composition and diversity of demersal fish communities. *ICES J of Marine Sci*. 2000;5:558-571.
51. Tissot BN, Hallacher LE. Effects of aquarium collectors on coral reef fishes in Kona, Hawaii. *Conservation Bio*. 2003 Dec;17(6):1759-1768.
52. Karman A, Martasuganda S, Sondita MFA, Baskoro MS. Basis biologi cakalang sebagai landasan pengelolaan perikanan berkelanjutan di Provinsi Maluku Utara. *J Ilmu dan Tek Kel Tropis*. 2016 June;8(1):159-173.
53. Murawski SA. Definitions of overfishing from an ecosystem perspective. *ICES J of Marine Sci*. 2000;57:649-658.
54. Myers RA, Worm B. Rapid worldwide depletion of predatory fish communities. *Nature* 2003 May 15; 423:280-283.
55. Utter FM. Biochemical genetics and fishery management: an historical perspective. *J of Fish Bio*. 1991 Dec;39(sA):1-20.
56. Carvalho GR, Hauser L. Molecular genetics and the stock concept in fisheries. *Rev in Fish Bio and Fis*. 1994; 4:326-350.
57. Shaffer ML. Minimum population sizes for species conservation. *Bio Sci*. 1981 Feb;31(2):131-134.
58. Ihssen PE, Booke HE, Cas Selman JM, Mcglade JM, Payne NR, Utter FM. Stock identification: materials and methods. *Can. J Fish Aquat Sci*. 1981 Dec;38:1838-1855.
59. Daud SK, Mohammadi M, Siraj SS, Zakaria MP. Morphometric analysis of Malaysian oxudercine goby, *Boleophthalmus boddarti* (Pallas, 1770). *Pertanika J Trop Agric Sci*. 2005;28(2):121-134.



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