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Molecular identification of sharks and rays species from Aceh waters, Indonesia

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ABSTRACT

Shark is a cartilaginous fish that is widely hunted because it has high economic value. The waters of Aceh are directly adjacent to the Indian Ocean and the Malacca Strait making it a preferred habitat for pelagic fish, especially sharks. Information on shark species landed in the waters west and east of Aceh is very limited due to difficulties in identification and commonly used local names. This study aimed to determine the types of sharks landed in Banda Aceh, Meulaboh, Langsa, Southwest Aceh and Simeulu and to find out specifically what species of sharks are most often landed in Aceh waters. Primary data gathering consisted of four stages, namely sample collection, identification using identification books, molecular identification cytochrome oxidase subunit I (COI) and phylogenetic analysis. The results of the molecular analysis of 46 tissue samples from five locations identified 13 species of sharks, namely *Carcharhinhus sorrah, Carcharhinhus amboinensis, Triaenodon obesus, Isurus oxyrinchus, Sphyrna zygaena, Sphyrna lewini, Loxodon macrorhinus, Hemipristis elongaria, Stagostoma fasciatum, Nebrius ferrugineus, Chilloscyllium punctatum, Isurus oxyrinchus, Alopias pelagicus, Alopias supercillosus* and 1 species of rays, namely *Rhynchobatus australiae.* Phylogenetic tree reconstruction using the Neighbor Joining method of 610 basepairs consisting of two large clades separates the species *Alopias pelagicus* and *Isurus oxyrichus* with *Carcharhinus sorrah*, *Sphyrna lewini*, *Loxodon macrorhinus* and *Rhyncobatus australiae* with boostrap values of 87% and 64%. The haplotype diversity shown ranged from 0.667-0.889 while the nucleotide diversity ranged from 0.001-0.097. These values indicates high diversity because of the variance in the number of species found.

Introduction

Sharks and rays are commercially important fish species found around the world. The growth rate, life span, late maturity, and long gestation period of sharks and rays (Stevens *et al.*, 2000) make them extremely vulnerable to anthropogenic pressures including high exploitation, environmental changes, and pollution (Dulvy *et al.*, 2014). As apex predators, sharks have no natural predators other than humans (Hoq *et al.*, 2011).

Aceh waters are bordered on the west by the Indian Ocean and on the east by the Malacca Strait (Ramadhaniaty *et al.*, 2018). This strategic area classifies the waters of Aceh as calm waters that serve as a nursery ground for pelagic species, particularly sharks and rays. Sharks and rays that are caught as by-catch are considered to have high economic value, often even having a market value that is higher than the main target species. The high market value of sharks is due to the presence of their fins, a consumable item that is regarded as prestigious. The catch of sharks and rays surged in 2008 and has continued to rise since then. Awanis *et al.* (2019) mentioned that as many as 747 sharks of 32 species from the Malacca Strait and the Indian

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Ocean were landed at the Fishing Port of Lampulo in Aceh. The high demand for the fins of sharks and rays has resulted in a dramatic drop in shark populations (Domingues *et al.*, 2018). Among pelagic fish species, sharks and rays have the highest risk of extinction (Dulvy *et al.*, 2014; Bräutigam *et al.*, 2015).

After the finning process of separating the fins and body sections of fish, sharks and rays are typically found at fish landing locations in the form of cut-up body parts, which poses a significant challenge to the species identification procedure. This identification is very important because the high demand for products for sharks and rays causes high levels of illegal fishing (Simpfendorfer *et al.*, 2017). The proper identification process can help the effort to track shark and ray products so as to increase the capacity for species management and conservation. This tracking activity can prevent illegal fishing, especially species that are listed on CITES (Pavitts *et al.*, 2021). Yusof *et al.* (2021) identified several factors related to the supply chain traceability of shark and ray products, one of which is resources derived from sharks and rays. These must be cleared by regulations and laws for their use. These regulations must be determined based on the certainty of species types that can be answered by DNA Barcoding.

Morphological identification is possible, but requires additional precision and can lead to errors. To date, molecular DNA has become a crucial tool for identifying and determining the population structure of marine biota (Boudry *et al.*, 2003). DNA barcoding is a great technique for species-specific identification. Genetic tools are a scientific advancement that can assist in identifying species, inter-population connectedness, and dangers linked with demographic disparities and inbreeding (Allendorf, 2017). DNA barcoding is an effective way of identifying species, and it also contributes to taxonomy and population structure (Hajibabaei *et al.*, 2007).

Sembiring *et al.* (2015) conducted extensive research on the molecular identification of sharks and rays in order to identify the most commonly landed shark species, namely *Carcharinus falciformis* and *Sphyrna lewini*. Similar research was conducted by Mopay *et al.* (2017), who identified *Carcharhinus amblyrhynchos* as the most commonly captured species. Ichsan (2015) conducted research linked to molecular identification and discovered seven species of sharks and rays in the Fishing Port of Lampulo, including *Carcharinus sorrah, Carcharinus albimarginatus, Carcharinus amblyrinchos, Carcharinus falciformis, Triaenodon obesus, Sphyrna lewini*, and *Centrophorus granulosus*. Accurate species identification is vital for the development of conservation and management programs in fisheries. This study attempts to determine the shark species with the highest demand for fins and the highest catch rates in Aceh waters. The results of this investigation will also help confirm the high diversity of sharks and rays in the waters of Aceh. This information is meant to help the development of sustainable sharks fisheries management and conservation plans, and to serve as a reference.

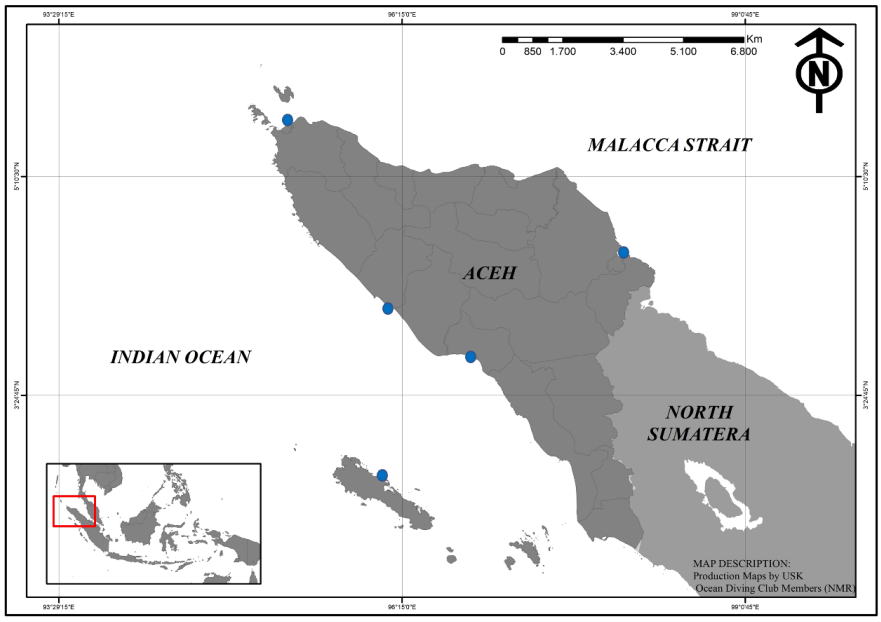

Figure 1. Map of research sites at fish landing sites in Aceh.

Materials and Methods

Location and time of research

The method used in this study consisted of four stages, namely sample collection, physical identification using an identification book, molecular identification (COI) and creating a phylogenetic tree. A total of 46 samples of sharks and rays fin tissues were taken from 5 fish landing sites and fin collectors representing the western and eastern waters of Aceh, namely Susoh Fishing Port (Southwest Aceh), Simeulue Fishing Port, Ujong Baroh Fishing Port (Meulaboh), Kuala Langsa Fishing Port (Langsa) and Lampulo Fishing Port (Banda Aceh) (Figure 1). The fin collection was conducted based on the species with the highest catch intensity. The collected tissue was then preserved by storing it in a tube containing 96% alcohol.

DNA extraction from the shark and ray fins was done using the Chelex 10% protocol (Walsh *et al.*, 1991). The results obtained were then used for the DNA amplification process. Amplification of the extracted samples was performed using the in-vitro Polymerase Chain Reaction (PCR) technique with mitochondrial cytochrome oxidase subunit-1 (COI). The composition of each PCR reaction consisted of AmplyTaq RedTM (Applied Biosystems, DDH2O and Primer Fish-BCl (5' TCAACYAATCAYAAAGATATYGGCAC) and Fish-BCH (5'TAAACTTCAGGGTGACCAAAAAATCA) (Baldwin *et al.*, 2009). PCR reactions were carried out at the denaturation temperature of 94^{0}C for 15 minutes, with 38 cycles of 94^{0}C for 30 second, 50^{0}C for 30 second, and 72^{0}C for 45 second, followed by a final extension period at 72^{0}C for 5 minutes Electrophoresis. The results of the PCR were then analyzed using 1.0% 0.5 grams agarose gel and the addition of ethidium bromide (EtBr). Translation process was then carried out on the PCR results that have been successfully amplified to obtain the sequence base pairs. Sequencing was done by sending the PCR product to the University of California Berkeley Sequencing Facility using the Sanger *et al.* (1977) method to obtain the sequence base pairs of nucleotide sequences. The results were aligned using MEGA 6 (Tamura *et al.*, 2012). Then, to identify species by matching nucleotide bases to GenBank and BOLD Systems to obtain the percentage of species similarity.

Data analysis

Identification and Reconstruction of phylogenetic trees.

Molecular identification was carried out after obtaining the sequencing results by matching the sequences with Genbank (NCBI) and Boldsystem. Furthermore, the reconstruction of the phylogenetic tree using the Neighbor-Joining method, 2-parameter Kimura evolution model, and 1000x bootstraps replication from MEGA 6 software (Tamura *et al.*, 2013).

Analysis of genetic diversity and haplotype diversity

Genetic diversity analysis was carried out using DNAsp which was used to calculate the haplotype composition, and haplotype diversity (Hd), nucleotide diversity (π). The level of variation of the MtDNA COI gene in the population was analyzed by counting nucleotides while the haplotype diversity index was analyzed using the DNAsp program (Rozas *et al.*, 2003).

Results

Samples collected from five fish landing locations in Aceh, including PPS Lampulo, yielded a total of 46 shark and ray fins. The discovered species composition included 13 species of sharks, namely *Carcharhinhus sorrah, Carcharhinhus amboinensis, Triaenodon obesus, Isurus oxyrinchus, Sphyrna zygaena, Sphyrna lewini, Loxodon macrorhinus, Hemipristis elongaria, Stagostoma fasciatum, Nebrius ferrugineus, Chilloscyllium punctatum, Isurus oxyrinchus, Alopias pelagicus*, and *Alopias supercillosus* and one species of ray, namely *Rhynchobatus australiae.*

Phylogenetic tree

Reconstruction of the phylogenetic tree from the 610 base pairs was done using the Neighbor Joining method. The phylogenetic tree displays the divide of two clades that distinguish the species *Alopias pelagicus* and *Isurus oxyrichus* with *Carcharhinus sorrhah, Sphyrna lewini, Loxodon macrorhinus*, and *Rhynchobatus australiae* by means of 87 and 64 percent boostraps, respectively (Figure 2).

Carcharhinus sorrah, *Carcharhinus amboinensis* and *Triaenodon obesus* form one clade together with a bootstrap amount of 96-100%. The second clade consists of the same genus, namely *Sphyrna zigaena* and *Sphyrna lewini* with bootstrap values of 62 and 100%. Clade 3 only consists of one species, namely *Loxodon macrorhinus* with a bootstrap value of 100%. The next clade consisted of *Nebrius ferruginus, Stegostoma fasciatum* and *Chiloscylium punctatum* with

60% and 99% bootstrap values. Furthermore, *Rhynchobatus australiae* which is representative of the ray species has a separate clade with a bootstrap value of 100. The last clade consists of sharks of the same genus, namely *Alopias superciliosus* and *Alopias pelagicus* with a bootstrap value of 88%.

According to the IUCN, ten species of sharks found off the coast of Aceh are classified as Vulnerable, three species as Near Threatened, and one species as Data Deficient (Figure 3). The species with the closest genetic distance are *Carcharhinus amboinensis* and *Triaenodon obesus*, which is 0.044, according to the table (Table 1). The species with the greatest genetic distance are *Isurus oxyrinchus* and *Rhynchobatus australiae*, with a genetic distance of 0.301 (Table 2). *Isurus oxyrinchus* demonstrates the greatest genetic distance between populations of the same species, with a value of 0.007.

From the five populations based on the fish landing sites, a total of 24 haplotypes were derived, with Banda Aceh exhibiting the highest level of variety, followed by Meulaboh. *Alopias pelagicus* showed the greatest number of haplotypes with 6 haplotypes from 2 populations, followed by *Carcharhinus sorrah* with 5 haplotypes from 3 populations. Haplotype diversity ranged between 0.667 and 0.889, while nucleotide diversity varied between 0.001 and 0.097.

The nucleotide base compositions obtained from the 14 sharks and rays samples showed an AT composition of 56.885-62.131% and GC 37.869-47.978% (Table 3). Haplotype diversity ranged from 0-0.889 indicating low to high diversity categories. Nucleotide diversity values ranged from 0-0.097 with the highest value recorded for *Isurus oxyrinchus* and the lowest value recorded for *Alopias pelagicus*.

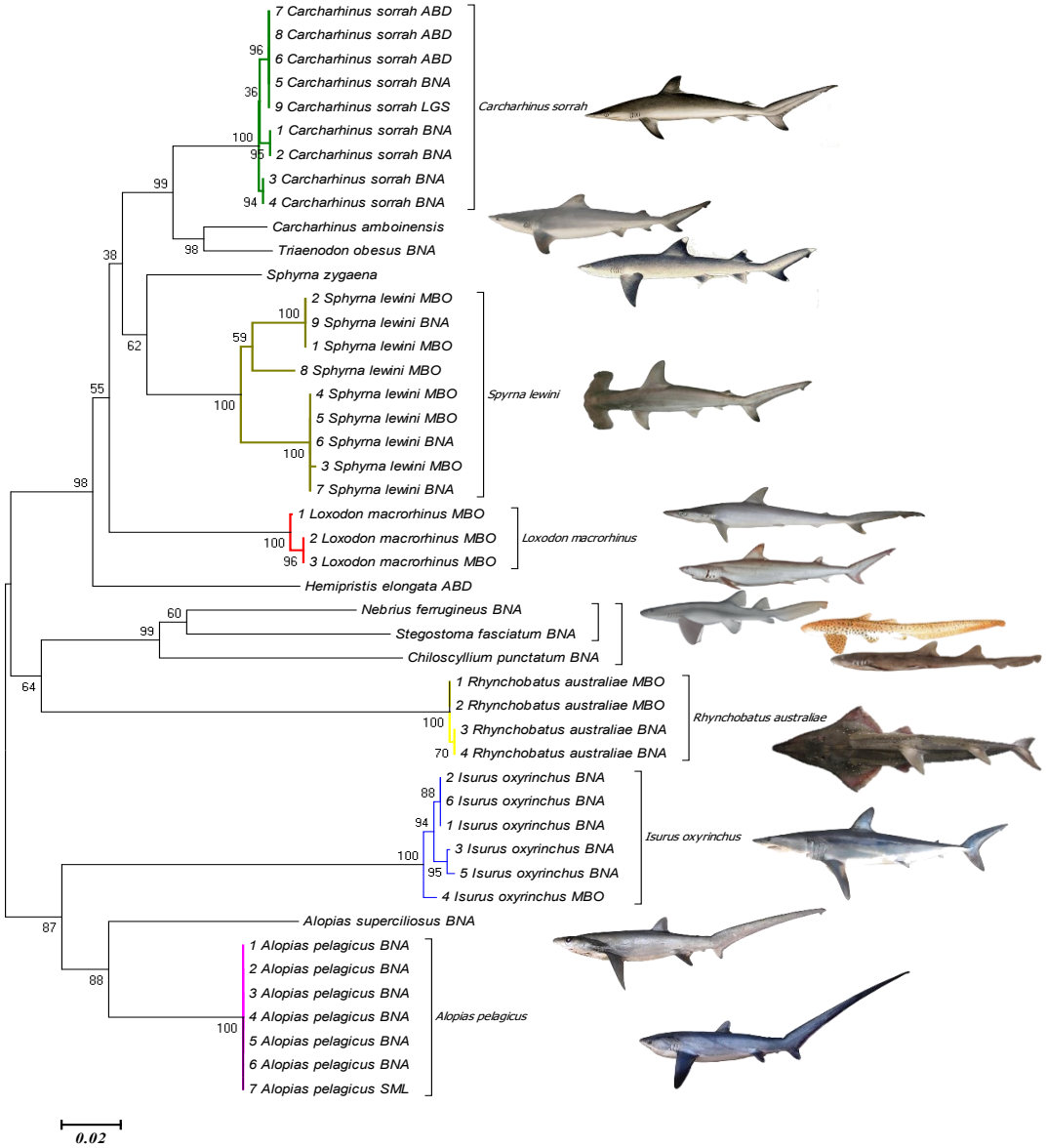

Figure 2. Sharks and rays phylogenetic tree using the neighbor-joining method with 2-parameter Kimura from Aceh Waters.

Table 1. Conservation status of sharks and rays found in Aceh waters.

Species	Common Name	Local Name	IUCN Red List Status	n
Carcharhinhus sorrah	Spot-tail shark	Yee Kilip	Near Threatened	9
Carcharhinhus amboinensis	Java/Pigeye shark	Yee Beuton	Data Deficient	1
Triaenodon obesus	Whitetip reef shark	Yee Kareng	Near Threatened	1
Isurus oxyrinchus	Shortfin mako shark	Yee	Vulnerable	6
Sphyrna zygaena	Smooth hammerhead	Yee Rimba	Vulnerable	1
Sphyrna lewini	Scalloped hammerhead	Yee Rimba	Vulnerable	9
Loxodon macrorhinus	Sliteye Shark	Yee	Vulnerable	3
Hemipristis elongata	Snaggletooth shark	Yee Munjom	Vulnerable	1
Stagostoma fasciatum	Zebra shark	Yee Limeng	Vulnerable	1
Nebrius ferrugineus	Tawny nurse shark	Yee	Vulnerable	1
Chilloscyllium punctatum	Brown banded bamboo shark	Yee Plok	Near Threatened	1
Rhynchobatus australiae	White-spotted guitarfish	Yee	Vulnerable	4
Alopias pelagicus	Pelagic thresher shark	Yee Tikoh, Yee Pesawat	Vulnerable	7
Alopias supercilliosus	Bigeye thresher shark	Yee Tikoh, Yee Pesawat	Vulnerable	1

Table 2. Genetic distance between and within species

Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14
A. pelagicus	**0.000**													
A. superciliosus	0.110	**N/A**												
C. amboinensis	0.168	0.181	**N/A**											
C. sorrah	0.164	0.180	0.064	**0.004**										
C. punctata	0.210	0.226	0.226	0.223	**N/A**									
H. elongata	0.174	0.203	0.135	0.126	0.215	**N/A**								
I. oxyrinchus	0.202	0.200	0.246	0.233	0.239	0.259	**0.007**							
L. macrorhinus	0.181	0.206	0.119	0.119	0.225	0.150	0.221	**0.003**						
N. ferrungineus	0.196	0.222	0.204	0.207	0.162	0.203	0.273	0.223	**N/A**					
R. australiae	0.247	0.272	0.215	0.246	0.255	0.248	**0.301**	0.232	0.256	**0.001**				
S. zygaena	0.151	0.194	0.094	0.095	0.231	0.126	0.253	0.120	0.204	0.223	**N/A**			
S. lewini	0.187	0.206	0.106	0.112	0.232	0.158	0.251	0.117	0.212	0.244	0.094	**N/A**		
T. obesus	0.166	0.181	**0.044**	0.065	0.228	0.131	0.247	0.119	0.199	0.224	0.102	0.114	**N/A**	
S. fasciatum	0.228	0.246	0.221	0.224	0.146	0.213	0.256	0.197	0.126	0.256	0.217	0.219	0.219	**N/A**

Table 3. Nucleotide Composition and Population Structure of Sharks and Rays

Species	N	Hn	T (%)	C (%)	A (%)	G (%)	AT (%)	GC (%)	Hd	π
Alopias pelagicus	7	1	32.295	23.934	28.197	15.574	60.492	39.508	0	0
Alopias superciliosus	1	1	30.328	26.066	26.557	17.049	56.885	43.115	-	-
Carcarhinus amboinensis	1	1	34.754	23.607	26.885	14.754	61.639	38.361	-	-
Carcarhinus sorrah	9	3	34.900	23.060	26.958	15.082	61.858	38.142	0.667	0.003
Chiloscylium punctatum	1	1	33.443	22.623	28.689	15.246	62.131	37.869	-	-
Hemipristis elongata	1	1	35.082	23.934	24.918	16.066	60.000	40.000	-	-
Isurus oxyrinchus	9	6	28.497	29.781	23.525	18.197	52.022	47.978	0.889	0.097
Loxodon macrorhinus	3	2	32.077	26.284	25.847	15.792	57.923	42.077	0.667	0.003
Nebrius ferrugineus	1	1	33.115	21.803	28.852	16.230	61.967	38.033	-	-

Rhyncobatus australiae	4	2	31.475	24.754	27.131	16.639	58.607	41.393	0.667	0.001
Sphyrna zigaena	1	1	34.098	23.607	26.721	15.574	60.820	39.180	-	-
Sphyrna lewini	9	4	33.279	24.554	26.412	15.756	59.690	40.310	0.75	0.025
Stegostoma fasciatum	1	1	31.148	23.115	29.344	16.393	60.492	39.508	-	-
Trianodon obesus	1	1	34.590	23.770	26.393	15.246	60.984	39.016	-	-

Description: N = Number of sample; Hn = Haplotype amount; T and C = Pyrimidine base; A and G = Purin base; Hd = Haplotype diversity; π = Nucleotide diversity.

Table 4. Composition of haplotypes spread over five landing sites

Species	Haplotype	Location					Total
		Banda Aceh	Simeulue	Langsa	Meulaboh	Southwest Aceh	
A. pelagicus	1	6	1				7
A. superciliosus	2	1					1
C. amboinensis	3	1					1
	4	2					2
C. sorrah	5	2					2
	6	1		1		3	5
C. punctatum	7	1					1
H. elonata	8					1	1
	9	3					3
I. oxyrinchus	10	1					1
	11				1		1
	12				1		1
L. macrorhinus	13				1		1
	14	2					2
N. ferrugineus	15	1					1
R. australiae	16				2		2
	17	2					2
S. zigaena	18	1					1
	19				3		3
S. lewini	20				1		1
	21	2			2		4
	22				1		1
S. fasciatum	23	1					1
T. obesus	24	1					1

Discussion

In recent years, molecular identification has significantly advanced our understanding of species and population structure (Liu *et al.*, 2011). Several fish landing sites were sampled for fin samples, including 27 individuals from the Fishing Port of Lampulo representing 12 species, two individuals from PPI Simeulu representing two species, one individual from Langsa representing *Carcarhinus sorrah*, 12 individuals from PPI Ujong Baroh representing 4 species, and 4 individuals from TPI Susoh representing 2 species. The diversity of the sampled shark species revealed that *Loxodon macrorhinus* and *Sphyrna lewini* was only found at PPI Ujong Baroh. This is in line with the prevalence of these two shark species in the Western Indian Ocean, inhabiting coastal to semi-oceanic areas (Warmenbol and Smith, 2018).

Alopias pelagicus is a shark that was only found in PPS Lampulo. Fish landed at PPS Lampulo are caught from a very large fishing area, so that these sharks are often caught together with tuna. According to Dharmadi *et al.,* (2013), *Alopias pelagicus* is often caught by tuna gill nets operating in the Indian Ocean. Sampling of fins indicates the arrangement of the most common shark and ray catches. *Carcharhinus sorrah* and *Sphyrna lewini* are the two shark species with the highest number of all samples, and the IUCN Red List status of these two sharks are Near Threatened and Vulnerable respectively (Table 1).

Molecular identification was carried out using the COI gene and blast-sequenced results using NCBI and Boldsystem. The identity value shows 98-100% in 46 samples. Molecular identification is an efficient method used for species-level identification, as it plays a role in taxonomy and population structure (*Hajibabaei et al., 2007*). The reconstruction of the phylogenetic tree was intended to illustrate the genetic distance between 15 species of sharks and rays by visualizing the separation between these species clearly (Wang *et al.*, 2004). Reconstruction of trees from these three observation stations using the Neighbor-joining method (Garrick *et al.*, 2010; Hey *et al.*, 2018) which was evaluated by the 1000x bootstrap method. The distance calculation is based on the 2-parameter Kimura method (Tamura *et al.*, 2013).

The resulting phylogenetic tree (Figure 2) shows the separation of 2 large clades between *Sphyrna lewini* and *Alopias pelagicus*. The largest clade is divided into 4 large clusters including the *Carcharhinhus sorrah, Sphyrna lewini, Rhynchobatus australiae* and *Loxodon macrorhinus* groups with a boostrap value of 64%. While the small clade includes the group *Alopias pelagicus* and *Isurus oxyrinchus* with a boostrap value of 87%. The phylogenetic results can be confirmed by the results of genetic distance where the distance between these clades is the highest value of 0.301 from the species *Rynchobathus australiae*. This species belongs to the ray group, so it has a high genetic distance from all other shark species, however, *Isurus oxyrhinchus* has the farthest kinship. The lowest genetic distance was shown by *Triaenodon obesus* and *Carcarhinus amboinensis* and also connected to the clade *Carcarhinus sorrah*. These three species come from the same family, namely Carcharhinidae, although in terms of their genus name (*Triaenodon*), they are different because they are not classified as Carcarhinus.

The similarity of morphological characteristics that group these species into one family is that *T. obesus* has white tips on its fins, while *C. amboinensis* has black tips that are more faintly visible compared to other Cacarhinus genera. The existence of this tip style indicates that they come from the same family (Bott, 2014; Mundy-Taylor and Crook, 2013).

This tree illustrates the genetic variance and genetic diversity present within the class of elasmobranchs, all of which have a common ancestor. This phylogenetic study can reveal how their genes have been passed down throughout evolution. The evolutionary link between sequences is represented as a tree, with the sequences as its branches. The branching structure of the tree indicates the degree to which distinct sequences are interrelated. Phylogenetic trees provide classification information based on the evolutionary relationships between populations.

In phylogenetic tree reconstruction, molecular data is employed more frequently than morphological data since it is regarded as more stable in the evolutionary process (Dharmayanti, 2011). Each clade shares comparable morphological characteristics and is derived from the same genus. However, *Nebrius ferrugineus*, *Chiloscylium punctatum* and *Stegostoma fasciatum* belong to the same lineage with boostrap values of 99 and 66%, as evidenced by the flatness of their bodies and how their tail fins attach to their body. These three species of sharks all belong to the Orectolobiformes order. The order Orectolobiformes, according to Gujranwala (2013), has a mouth located under the eyes and a barbell/tentacle near the nose.

The highest average nucleotide composition was *Chiloscylium punctatum* species, namely AT (62.131%) GC (37.869%) (Table 3). Meanwhile, the low base pair value is the *Isurus oxyrinchus* species with AT (52.022%) and GC (47.978%) values. The average value for all species is AT (56.679%) and GC (40.321%). These values indicate a high composition of AT compared to GC, where AT shows a very fast base substitution value. If two different species have more base composition A+T then the species will have many similarities due to independent parallel substitutions and consequently they will group because of similarity in the base composition (Lam and Morton, 2006). This high value is due to the behavior of sharks, which are migratory animals with highly active movements across oceans (Portnoy *et al.*, 2015).

Gene flow is the cause of high genetic diversity which can be a solution to limit evolutionary processes and maintain shark biodiversity in all waters (Rougemont *et al.*, 2022; Moller *et al.*, 2011). Adaptation to significantly different water conditions results in high levels of genetic variation among shark species (Ferreira *et al.*, 2016), this can be seen from the high value of genetic diversity which ranged from 0.667-0.889 (Table 3). This value shows a high diversity at 0.6–1.00 (Excoffier *et al.*, 1992), as can be seen from the number of shark species found (14 species) indicating very high genetic variation. In this study, *C. sorrah* was a shark with three population compositions belonging to one haplotype, namely Banda Aceh, Langsa, and Southwest Aceh (Table 4). Haplotype is the mixing of genetic material between individuals that occurs

during the mating process. The long-term survival of a species is highly dependent on the degree of haplotype diversity within and between populations.

The mixing of these haplotypes indicates that there is no inbreeding which can reduce the genetic diversity of a species (Domingues *et al.*, 2018). The results of high nucleotide diversity were also shown by Domingues *et al.* (2018). They collected research related to the genetic diversity of sharks and rays for the last 20 years, the results obtained were in the range of 0.06-0.08, this value is the same as the range of the results of this study which ranged from 0.01 to 0.09. The value of haplotype diversity and nucleotide diversity are indicators of population diversity and the conservation status of a particular shark. High levels of genetic diversity can increase the ability of living organisms to adapt to pressure from the environment (Rougemout *et al.*, 2022).

Mutations or gene variation within each species reveal the relationship between genetic adaptation to climate fluctuation and the contribution of that species to environmental changes (Ellegren and Galtier, 2016). Because sharks are widely distributed and have a breeding season that permits them to travel to calmer waters, sharks and rays have life cycles with extensive distribution ranges (Bineesh *et al.*, 2017). Due to the process of adaptation to different environmental settings, this cycle causes shark species to exhibit great levels of variety.

The ongoing exploitation of sharks and rays is another factor that can contribute to genetic diversity. Exploitation is one of the factors that determine whether a population's haplotype and nucleotide diversity levels are high or low (Kochzius and Nuryanto, 2008). Heterozygosity is typically regarded as the most important indicator of the genetic diversity of a population (Zhong *et al.*, 2016). The presence of sharks and rays at fish landing sites in Aceh indicates that numerous sharks with a vulnerable classification are still being caught (Table 1). Overfishing can cause rapid population losses due to the shark's long life cycle, moderate growth rate, extended gonadal maturity time, and poor fertility (Blaber *et al.*, 2009); Graham *et al.*, 2011). The high intensity of shark fishing can result in overfishing, leading to the extinction of these Chondrchithyans in the wild. Chondrchithyans are a fragile group of cartilaginous fish (Akhilesh *et al.*, 2014; Dulvy *et al.*, 2014). Several shark species are listed as threatened on the International Union for Conservation of Nature and Natural Resources (IUCN) Red List of Threatened Species. On the other hand, shark fisheries have given economic value and have long served as the primary source of income for fishermen, traders, collectors, and exporters in numerous regions of Indonesia. In light of these conditions, shark resources must be managed correctly to meet both the economic interests of fishing communities and their protection.

Conclusion

Molecular identification of 46 samples found 14 species of sharks and rays, namely *Carcharhinhus sorrah, Carcharhinhus amboinensis, Triaenodon obesus, Isurus oxyrinchus, Sphyrna zygaena, Sphyrna lewini, Loxodon macrorhinus, Hemipristis elongaria, Stagostoma fasciatum, Nebrius ferrugineus, Chilloscyllium punctatum, Rhynchobatus australiae, Isurus oxyrinchus, Alopias pelagicus*, and *Alopias supercillosus*. Genetic diversity showed a high value, which ranged from 0.667-0.889. The status of sharks based on the IUCN list shows that as many as 10 species are included in the Vulnerable status, three species are Near Threatened and one species is included in the Data Deficient status.

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