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EFECTIVENESS OF MARINE PROTECTED AREA IN FISH RESOURCES REHABILITATION BASED ON MICROSATELLITE STUDY AND LARVAL DISPERSAL ANALYSIS

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ABSTRACT

The development of Marine Protected Areas (KKP) is one of the management strategies that is able to withstand changes in ecosystems due to the impacts of climate change and anthropogenic pressure, through the conservation of biodiversity. Complex ecosystem can offset the impact of climate change by the presence of more resilience organisms to support ecosystem function and role. One of MPA role is provide the recruit supply for surrounding waters through spill over mechanism. Protected broodsctock in MPA are expected to produce many and healthy eggs that disperse into surrounding area. The continuous supply of recruits from the MPA can maintain fish stocks and preserve the diversity. This study was carried out in TWP Pieh MPA, located in the west Sumatera region by collecting primary and secondary data. Primary data were collected through insitu sampling and laboratory analysis, secondary data was collected to figure out the condition of coral reef ecosystems inside MPA. Comparison of catches inside and outside the area, analysis of individual distribution and genetic mixing between inside and outside MPA and modeling of larval distribution with hydrodynamic models was carried out to compare the condition inside and outside MPA. The results study indicate that the TWP area. P. Pieh has been able to conserve the TWP Pieh area for fish resources and coral reef ecosystems within the protected area, however, the results of genetic analysis and larval distribution show that there is little possibility of genetic mixing between inside and outside the area, which is caused by factors of reproductive strategy and hydrodynamics. This shows that the fish population inside MPA is less support the recovery of fish stocks in the surrounding waters. To increase the role of the TWP Pieh MPA, some efforts that need to be done are to build conservation areas around TWP Pieh (satellite MPA). As well as expanding the core zone, particularly near the border area of MPA, to guarantee continues supply of larva from protected broodstock inside MPA to the surrounding waters.

1. Introduction

1.1 Research Background

Fish resources in West Sumatera region are under significant pressure from fishing effort that causing fish stock on fully exploited and over fishing condition (Ministerial decree No. 50/2017). Then, climate changes bringing additional pressure for fish resources through changes in ocean condition such as temperature and pH, that would directly impacted the biological condition of fishes (Cheung, 2018).

Developing marine protected area (MPA) is one of management strategy that withstands the changes in ecosystem due to the impact of climate changes, through conservation of biodiversity (Marzin et al., 2016). In a complex ecosystem, disturbance by climate change effect can be offset by the presence of other resources that still support the function of ecosystem it will increase the ecosystem resilience. Another role of MPA is supplier recruit for surrounding water through spill over mechanisms (Kough et al., 2019). Recruit spill over continuously from MPA are expected to maintain the fish stock and diversity sustainability.

Marine protected areas (MPAs) are an area-based conservation strategy commonly used to protect marine biodiversity and ecosystem services. Ecological connectivity governs the exchange of individuals among spatially fragmented habitats and is often highlighted as an important element in the design of MPAs (Balbar & Metaxas, 2019). The several forms of ecological spatial connectivity such as population, genetic, community are among the most important ecological processes in determining the distribution, persistence and productivity of coastal marine populations and ecosystems (Carr et al., 2017).

The role of MPA on fish rehabilitation can be shown through spillover effect. The protected population in the MPA, supposed to supply the surrounding waters with new

recruit. Polymorphic DNA microsatellite analysis is commonly used to investigate the spread or spill over using five DNA markers (Rivera et al., 2003).

Most marine animals have a planktonic life history period during which their eggs and larvae drift in the ocean for days, weeks, or even months until they settle back to benthic habitats. Settlement habitats range from being close to home (Jones et al., 2005) to being ten to hundreds of kilometers away from spawning locations (Jones, 2015). Larval dispersal by ocean currents is a critical component of systematic marine protected area (MPA) design. The complete process from spawning and dispersal to settlement is a key component of population connectivity. Modeling larva dispersal can show the population connectivity and optimize MPA role through systematically support the likely persistence and productivity of marine population.

The effectiveness of a conservation area can be seen by how much impact resulted on the restoration of ecosystem conditions in surrounding waters. Referring to Lester et al. (2009), the benefits and impacts of the existence of MPAs on fisheries can be measured using 4 indicators, namely (1) biomass, (2) density, (3) organism size and (4) species richness.

To increase the MPA area across the region is now became a target of government as one of fisheries management actions. There are also some initiatives from some countries to protect marine area on the national level, transboundary area or even in open sea. One of the biggest MPA in West Sumatera Region is TWP P. Pieh that has been implemented since 1998, it is covered about 39.000 hectares of marine area protected. The MPA existence ideally impacted on the stock recovery; nevertheless the stock status of grouper in west Sumatera Region is now is fully exploited and has not recover for several years, even after MPA was implemented. This research aims are to analysis the effectiveness of Pieh Island MPA on grouper stock status recovery by using the approach of individual genetic distribution and larva dispersal analysis.

1.2 Research Objectives

The objectives of the research are:

- To analyze individual distribution and connectivity between two population of target species of *Cephalopolis argus* and *Epinephelus areolatus*.
- To describe the model of larvae dispersal of two targeted species and to predict those settlement area.
- Develop MPA connectivity around TWP Pieh to maximize the MPA role on recruit supplier to surrounding waters.

1.3 Expected Outputs

This research is expected to result the information on the source population for recruitment process. Finding of the result can become a basis to develop MPA connectivity around TWP Pieh MPA to increase its role on fish stock recovery in surrounding waters.

2. Research benefits and the important of the research

Results of this study will inform the individual distributions of *Ephinephelus areolatus* and *Cephalopolis argus* which are including on high economic value and play an important role in coral reef ecosystems. Information on the larval distribution of these two types of fish will determine important locations that must be protected to maintain their sustainability. Distribution pattern can also show the effectiveness of the Pieh TWP MPA in support fish stock recovery in surrounding waters.

3. Methodology

3.1 Study sites

The research has conducted in West Sumatera waters particularly area that connect to TWP Pieh Island. Sampling was carried out in several landing places for reef fishes namely Air Manis and Purus in West Sumatera Province. Larva dispersal modeling was tagged several spot inside MPA as source location of larvae, based on physical characteritics.

3.2 Data collection

Data on development condition of coral reef ecosystem was collected from monitoring report of bio-physical condition monitoring conducted by TWP Pieh Island MPA. Primary data for fish resource condition was collected by fishing experiment was conducted twice on April 2020 and April 2021 by using hand lines and followed the local fisherman fishing operation for three days. To compare fish resource condition between protected and unprotected area, fishing experiment was carried out in two location at the same time, that are in core zone of Pandan Island as one of core zone in protected area and in outside border of MPA area around Bindalang Island, Sinyaru Island, Nyamuk Island, Pisang Islang and Sibonta Island.

The data needed for microsatellite analysis is genetic variation between two populations (inside and outside the MPA) to show parental linkage. DNA samples were extracted from fish tissues taken from *Cephalopolis argus* and *Epinephelus areolatus* that are captured inside and outside the MPA. Tissue sampling were carried out by taking a small part of the fish fin, then put it into microtube 2.0 ml containing 1,5 ml of 96% ethanol.

The fish samples were collected from two areas that represent the inside and outside of the MPA area. To make sure that fish samples are from the right location of the

MPA, samplings were carried out through some fishing experiments in the designated core zone.

The data needed for larva dispersal study are mostly secondary data collected from any resources. Hydrodynamic model were developed by using oceanographic data, such as the pattern of horizontal and vertical distribution of currents, temperature, salinity, pH, DO, and the existence of micro-Eddies as one mechanism in larva retention. The secondary biological data were collected to describe the condition of broodstock, eggs, and larvae are spawning methods and seasons, fecundity of broodstock, egg size, larva size, growth constant, swimming speed, and settlement time. Biological data collection were conducted monthly since April 2021 to November 2021 to collect length, weight and gonadal stage of *C. argus* and *E. areolatus* collected around Pieh MPA waters.

3.2 Data Analysis

Microsatellite analysis

There are five steps in microsatellite analysis, including laboratory and software analyses, comprise DNA extraction, amplification, electrophoresis, fragment analysis, and assignment test.

- DNA extraction was conducted referring to gSYNCTM DNA Extraction kit methodology to get the pure DNA material for the next steps.
- DNA amplification was carried out to increase the number of DNA targets in the samples using polymerase chain reaction (PCR). The primary targets are the core genes to describe the parental linkage. The amplification process used 4 specific microsatellite primers for grouper, which are CA (FAM), CA2 (FAM), CA3 (HEX), CA6 (FAM), and CA7 (HEX) (Rivera et al. 2003). The PCR process used the pre-optimized thermal points for pre-denaturation, denaturation, annealing, extension, and

final extension. The PCR optimization processes have been done for every primer used for optimum amplification.

- Electrophoresis was done to separate chemical compounds based on DNA material movement on the electricity (Maduppa et al., 2016). The electrophoresis used agarose 1,5% to run 2 μL of PCR product using 100 Volt electricity for 30 minutes.
- Fragment analysis was conducted in the First Base Laboratorium, Malaysia. The size of allele determined and corrected using PEAK SCANNER v1.0 software (Applied Biosystems) and GENEMARKER v 1.85 (SoftGenetics GeneMArker). MICRO CHECKER software used to detect the zero allele as the identification of the errors in data, including the errors in typing, typography, and valuation (Van-Oosterhout et al., 2004). CONVERT software (Glaubitz, 2004) was used to change the format of different softwares used.
- Assignment test was undertaken using GeneClass2 (Piry et al., 2004). Geneclass2 is a software that utilizes multilocus genotype to choose or exclude the population as a source individual (task and migrant detection). The probability value shows the individual that is included in the reference population (Cornuet et al., 1999).

Fish larval transport trajectory modeling

- General Setting

In general, the fish larval modelling was conducted in two parts, i.e., hydrodynamics modelling and fish larval transport trajectory (Pranowo, et al., 2004; Indrayanti et al., 2019). The hydrodynamics modelling concerned on tidal coupled with wind to govern momentum and continuity of ocean currents and sea surface dynamics (Mustikasari et al., 2015). Wind drag forces to the sea surface and manning roughness, which are created by the complexity of bathymetry and topography, also be considered

(Radjawane et al., 2006). The simulation was conducted to gain the influence of the monsoonal winds, such as the west monsoon (Dec-Feb), first transitional (March-May), east monsoon (June-August), and second transitional (September-October), as adopted from Siregar et al. (2017); in case the peak of each monsoonal periods can be referred for the simulation length, was adopted from Mustikasari et al. (2015). The hydrodynamics simulation results was further analyzed in both spatial and temporal of tidal time windowing, such as flood time, flood to ebb time, ebb time, and ebb to flood time (Pranowo et al., 2005).

- Dataset for Model Input

The tidal elevation dataset were derived from the global altimetric tidal constituent datasets (Brodjonegoro et al., 2005; Pranowo & Wirasantosa, 2011). Wind dataset will be derived from global dataset and/or assimilated to wind dataset from The National Agency of Meteorological, Climatology, and Geophysics (BMKG) (Muliati et al., 2018; 2019). The biology of fish eggs and larvae were identified during the in situ sampling survey. The secondary information of fish biological characteristics is completed using fishbase.org databases.

- Dataset for biological condition of broodstock

Biological sampling of two targeted species were undertaken monthly with the assistance of the field enumerator to take the data on fish size, sex, maturity, and egg size. The data of mature females will show the indication of source location and seasons.



Figure 1. Study site and tagged location for model simulation of grouper larvae inside TWP Pieh MPA

- Model Configuration for fish larvae distribution

Larvae are spread away by advection currents in space (Δx , y, z) and time (Δt) using Euler's scheme. The main current (V) used in the 2-dimensional simulation, at a certain depth ($\Delta z = 0$), has a current component that moves east-west (u) and a component of current movement in a north-south direction (v). The current calculation at each computational time step (t) is solved using the Runge-Kutta 2nd-order numerical method, see Equations 1, 2, 3 and 4.

Where x is longitude, y is latitude in radians, assuming 1 arc degree of latitude is 111,120 meters, and 1 arc minute latitude is equal to 1 nautical mile.

Larvae are not only spread by advection currents, they are also distributed by diffusion and randomly ($\partial L / \partial t$), so that the unit of diffusion distribution is centimeter per square

centimeter per time (cm2/s). In this case, the simulated diffusion is a representation of the horizontal eddy diffusivity in seawater ($D_{(x,y)}$). See Equations 5, 6.

$$D_x = \frac{1}{2} \frac{\sigma_x^2}{\Delta t} \dots (6)$$
$$D_y = \frac{1}{2} \frac{\sigma_y^2}{\Delta t} \dots (7)$$

Based on the calculations of equations (6) and (7), the coordinates of the latest position of the larvae (Δx , y) are randomly assigned with varying distances of longitude (dx) and latitude (dy), see Equation (8).

$$-\Delta x \le dx \le \Delta x$$

$$(\Delta x, \Delta y) \{ -\Delta y \le dy \le \Delta y \dots (8) \\ \Delta x = \Delta y \}$$

Based on Equation (8), the larvae have distribution variation values, both longitude (σ_x^2) and latitude (σ_y^2) , respectively, which can be presented in Equations (9) and (10).

$$\sigma_x^2 = \int_{-\Delta x}^{\Delta x} \frac{x_2}{2\Delta x} dx = \frac{\Delta x_2}{3}.....(9)$$

$$\sigma_x^2 = \int_{-\Delta x}^{\Delta x} \frac{x_2}{2\Delta x} dx = \frac{\Delta x_2}{3}....(10)$$

Based on Equation (9) then, the Larvae are propagated by advection to longitude by Equation (1) and by diffusion by Equation (9), then the position coordinates of Larvae are updated by Equation (11).

Similarly, the Larvae are propagated by advection to latitude by Equation (2) and by diffusion by Equation (10), so the position coordinates of Larvae are updated by Equation (12), as the simulation time goes on.

The main data used as input for the model simulation is the east-west and northsouth component flows extracted from Copernicus Marine Services, taking the time periods June 2020, August 2020, October 2020, December 2020, February 2021. June and August 2020 representing the east monsoon, October 2020 represents the transitional monsoon from the east monsoon to the west monsoon, while December 2020 and February 2021 are the west monsoon. The current data is the result of the generation of tidal and wind forces. Supporting data is sea temperature to analyze whether its temperature variability supports the life of grouper larvae and broodstock. Both data were extracted at a depth of 21 meters and 34 meters as the range of depth of grouper fish habitat.

Shoreline data were extracted from the Global Self-consistent, Hierarchical, Highresolution Geography Database belonging to the NOAA National Centers for Environmental Information (Wessel & Smith, 1996). Both types of datasets are adjusted to the model domain limits, namely 0.70 to -1.22 South Latitude and 99.816 to 100.4 East Longitude.

A total of 10,000 representative particles of grouper larvae were hypothetically released at each source over 6 hours. Larval distribution trajectory simulations were carried out 24 hours per month for the monsoon representatives mentioned above, with a computation time step of 1 hour. The simulation was carried out to determine whether the distribution reached small islands and/or coral reefs within the Pieh Island TWP area and its surroundings.

Visualization of model simulation results using Ocean Data View, which is equipped with bathymetry and topographic data from ETOPO 2 arcminute and GEBCO 30 arcsec (Schlitzer, 2020).

4. **Result and Discussion**

4.1 Observation on Gonad maturity

The collection of fish samples for microsatellite analysis and larval distribution was carried out in April 2021. A total of 25 fish samples were obtained with a composition of 17 samples of E. *areolatus* and 8 samples of *C. argus* (Table 1). Of the 25 fish samples collected, most of them were *E. areolatus*, but only a few of the *C. argus* species were caught in small sizes (Figure 1). *C. argus* is a fish that is closely associated with shallow coral reefs, and usually likes good coral reefs. At the time the sampling was carried out, namely in April 2021, not many fishermen were fishing at the edge of shallow coral reefs, due to high waves and strong winds, impacted on *C. argus* fish were difficult to find.

Fish originating from outside the conservation area were obtained from the catch of fishermen around Pulau Pisang, P. Sibunta and P. Sinyaru and landed around Air Manis beach and Purus Beach, Padang City. Meanwhile, fish obtained from within the area were obtained from experimental catching results around Banda Island, Pieh Island and Pandan Island.

No	Jenis	Panjang	Berat	Tanggal sampling	Daerah Penangkapan	Luar/dalam kawasan	Tingka Kematangan Gonad	Sex
1	Cepalopholis argus	15.7	63	5/4/2021	P. Pisang	Luar Kawasan	1	IU*
2	Ephinephelus areolatus	25	198	5/4/2021	P. Pisang	Luar Kawasan	1	IU
3	Ephinephelus areolatus	15.3	46	5/4/2021	P. Pisang	Luar Kawasan	1	IU
4	Ephinephelus areolatus	15.5	48	5/4/2021	P. Pisang	Luar Kawasan	1	IU
5	Ephinephelus areolatus	14	32	5/4/2021	P. Pisang	Luar Kawasan	1	IU
6	Ephinephelus areolatus	16.5	51	5/4/2021	P. Pisang	Luar Kawasan	1	IU
7	Ephinephelus areolatus	10.3	13	5/4/2021	P. Pisang	Luar Kawasan	1	IU
8	Ephinephelus areolatus	24.5	158	7/4/2021	P. Sinyaru	Luar Kawasan	1	IU
9	Ephinephelus areolatus	22.8	110	7/4/2021	P. Sinyaru	Luar Kawasan	1	IU
10	Ephinephelus areolatus	23.8	141	7/4/2021	P. Sinyaru	Luar Kawasan	1	IU
11	Ephinephelus areolatus	21.5	90	7/4/2021	P. Sinyaru	Luar Kawasan	1	IU
12	Ephinephelus areolatus	21.5	104	7/4/2021	P. Sinyaru	Luar Kawasan	1	IU
13	Ephinephelus areolatus	20	93	7/4/2021	P. Sinyaru	Luar Kawasan	1	IU
14	Cepalopholis argus	15.5	61	7/4/2021	P. Pisang	Luar Kawasan	1	IU
15	Cepalopholis argus	14	31	7/4/2021	P. Pisang	Luar Kawasan	1	IU
16	Cepalopholis argus	15.8	73	7/4/2021	P. Pisang	Luar Kawasan	1	IU
17	Cepalopholis argus	14.5	52	7/4/2021	P. Pisang	Luar Kawasan	1	IU
18	Cepalopholis argus	14.5	50	7/4/2021	P. Pisang	Luar Kawasan	1	IU
19	Ephinephelus areolatus	30	327	7/4/2021	P. Sibunta	Luar Kawasan	1	IU
20	Ephinephelus areolatus	24	195	8/4/2021	Gosong antara P. bando dan P. P	Dalam Kawasan	1	IU
21	Ephinephelus areolatus	29	317	8/4/2021	Gosong antara P. bando dan P. P	Dalam Kawasan	1	IU
22	Ephinephelus areolatus	25	197	8/4/2021	Gosong antara P. bando dan P. P	Dalam Kawasan	1	IU
23	Ephinephelus areolatus	26	231	8/4/2021	Gosong antara P. bando dan P. P	Dalam Kawasan	1	IU
24	Ephinephelus areolatus	26	204	8/4/2021	Gosong antara P. bando dan P. P	Dalam Kawasan	2	Jantan
25	Cepalopholis argus	28.5	372	9/4/2021	P. Pandan	Dalam Kawasan	2	Betina
26	Cepalopholis argus	30	463	9/4/2021	P. Pieh	Dalam Kawasan	1	Jantan
*IU: ti	dak teridentifikasi				-			

Table 1. Data of fish samples



Figure 2. Samples of E. areolatus (left) and C.argus (right)

4.2 Individual distribution based on microsatellite analysis

Fragment analysis showed two peaks allels from 28 invidious analyzed, 14 samples of *C. argus* and 14 samples for *E. areolatus* (Figure 3). Genotyping result from microsatellite locus for each invidious presented in Table 3. DNA microsatellite provides information on how to differentiate the samples base on genetic information of each sample. The genetic information shows an information on the number of allel per locus, allel frequency, heterozygote condition and polymorphism information content (PIC) in every locus. The polymorphism condition in every locus are divided into (1) very informative (PIC > 0.5); (2) informative (0.5>PIC<0.25); and less informative (PIC < 0.25) (Botstein et al., 1980). Resume of DNA microsatellite statistics analysis is provided in the Table 4.



Figure 3. Peak allel for day label of green (HEX) and blue (FAM)

Na	Leastian	Smaalag	Sample	Locus							
INO	to Location Species		ID	CA2		CA6		CA7	CA7		
1	Outside MPA	E. Aerolatus	D2	255	255	300	300	194	232	301	307
2	Outside MPA	E. Aerolatus	D3	263	269	302	308	192	228	301	305
3	Outside MPA	E. Aerolatus	17L	243	257	320	326	192	212	297	307
4	Outside MPA	E. Aerolatus	16	245	255	306	306	192	216	305	305
5	Outside MPA	E. Aerolatus	EA20	265	273	308	326	184	192	311	315
6	Outside MPA	E. Aerolatus	EA23	253	253	300	300	186	216	299	309
7	Outside MPA	E. Aerolatus	EA24	253	281	0	0	182	210	295	305
8	Inside MPA	E. Aerolatus	O2	247	275	306	334	184	192	297	307
9	Inside MPA	E. Aerolatus	O5	255	263	308	334	184	192	295	305
10	Inside MPA	E. Aerolatus	11	246	267	306	314	186	192	309	317
11	Inside MPA	E. Aerolatus	12	247	253	306	312	178	186	303	313
12	Inside MPA	E. Aerolatus	17D	255	281	308	334	192	232	307	309
13	Inside MPA	E. Aerolatus	18	247	253	326	334	184	192	297	307
14	Inside MPA	E. Aerolatus	EA19	259	263	300	300	192	230	305	317
15	Outside MPA	C. Argus	D29	265	275	0	0	206	230	289	295
16	Outside MPA	C. Argus	A4	253	265	286	296	0	0	285	295
17	Outside MPA	C. Argus	A5	253	281	296	296	0	0	285	295
18	Outside MPA	C. Argus	A7	245	265	286	296	200	208	285	295
19	Outside MPA	C. Argus	D27	265	275	286	296	206	206	285	295

Table 2. Genotyping result for microsatellite locus for every sample collected from inside and outside MPA

20	Outside MPA	C. Argus	D28	245	253	292	296	200	208	285	295
21	Outside MPA	C. Argus	E2	257	257	280	284	202	208	301	301
22	Inside MPA	C. Argus	1	255	277	280	280	200	210	295	295
23	Inside MPA	C. Argus	2	257	277	286	286	202	208	295	295
24	Inside MPA	C. Argus	4	247	259	286	286	202	208	285	295
25	Inside MPA	C. Argus	CA14	253	273	0	0	204	212	283	295
26	Inside MPA	C. Argus	CA15	351	255	314	314	208	216	283	295
27	Inside MPA	C. Argus	CA17	251	255	314	314	202	208	283	295
28	Inside MPA	C. Argus	CA18	257	273	312	312	208	216	283	295

Table 3. Microsatelite analysis resume for E. areolatus and C. argus collected from inside and outside MPA.

Locus	Label dye	Allele (bp)	k	PIC	Но	He	Prob	FIS
E. areolati	<i>E. areolatus</i> outside MPA (n=7)							
CA2	FAM	245-281	8	0.806	0.714	0.890	0.266	0.216
CA6	FAM	300-334	6	0.746	0.500	0.848	0.017	0.434
CA7	HEX	182-232	9	0.831	1	0.912	1	-0.105
CA3	HEX	295-315	8	0.818	0.857	0.901	0.697	0.053
E. areolati	us inside MP	A (n=7)						
CA2	FAM	243-275	10	0.866	1	0.945	0.3986	-0.063
CA6	FAM	300-334	8	0.829	0.857	0.912	0.6333	0.065
CA7	HEX	178-230	6	0.701	1	0.791	0.4817	-0.292
CA3	HEX	295-317	8	0.829	1	0.912	0.0355	-0.105
C. argus	outside MPA	(n=7)						
CA2	FAM	245-281	6	0.779	0.857	0.868	0.477	0.014
CA6	FAM	280-296	5	0.622	0.833	0.727	0.365	-0.163
CA7	HEX	200-230	5	0.720	0.800	0.844	0.346	0.059
CA3	HEX	285-301	4	0.600	0.857	0.714	0.010	-0.220
C. argus	inside MPA (n=7)						
CA2	FAM	247-351	9	0.853	1	0.934	1	-0.077
CA6	FAM	280-314	4	0.671	0	0.788	0.001	1
CA7	HEX	200-216	7	0.759	1	0.846	0.073	-0.200
CA3	HEX	283-295	3	0.427	0.714	0.538	1	-0.364

K = number of allel

PIC = polymorphic information content

Ho = Observed heterozygosity

He = Expected heterozygocity

Prob. = \hat{P} value on probability test of Hardy Weinberg

FIS = coefficient of inbreeding

Based on the results of statistical property analysis of microsatellite DNA (Table 4), no significant relationship disequilibrium was found for each pair of loci, indicating that all loci could be considered independent. In general, the level of polymorphism at each

microsatellite locus was ranked as very informative (PIC>0.5) except for the CA3 locus in the C.argus population in the MPA which showed a moderately informative value of 0.427. This indicates that all markers used in the analysis are classified as highly informative markers (Table 4). The probability test shows the locus is in the Hardy-Weinberg equilibrium with a value above 0.01. However, only the CA6 locus in the *C. argus* grouper in the MPA showed a value of 0.001. Probability test shows value of 0.001 means that there is a 0.1% chance that the genotypic difference is due to chance and a 99.9% chance that it is not due to chance. This p-value is significant, the null hypothesis is rejected, and the data is interpreted to mean that the population is not in Hardy-Weinberg equilibrium. Based on these results, the loci used remained in the dataset for further analysis.

Assignment test was conducted at the multi locus genotype in each invidious, to calculate the probability of belonging to a particular sub-population (Rannala and Mountain 1997; Waser and Strobeck 1998). The probability is used to observe the genotype-specific multi locus given the allelic frequency at each locus in the subpopulation. A small probability indicates that the sample is most likely to be a new immigrant. Comparing the probability value can be used to detect new immigrants or to identify the original population and inform that the invidious belongs to different populations. Table 4 and 5 show an assignment test results for *E. areolatus* and *C. argus* respectively. Simulation for assignment test was carried out for 1000 invidious by using alpha value 0,01.

Reference Population	Assigned Population	Probability	Nb Loci	of	Used Loci	<i>Missing</i> Loci
Inside MPA	Outside MPA	0.000	4		CA2 CA6 CA7 CA3	
Outside MPA	Inside MPA	0.000	4		CA2 CA6 CA7 CA3	
Reference Population	Assigned Sample	Probability	Nb Loci	of	Used Loci	<i>Missing</i> Loci
Inside MPA	D2	0.036	4		CA2 CA6 CA7 CA3	
Inside MPA	D3	0.017	4		CA2 CA6 CA7 CA3	
Inside MPA	17D	0.164	4		CA2 CA6 CA7 CA3	

Table 4. Assignment test result for *E. areolatus* collected from inside and outside MPA

Inside MPA	16	0.194	4	CA2 CA6 CA7 CA3	
Inside MPA	EA20	0.016	4	CA2 CA6 CA7 CA3	
Inside MPA	EA23	0.115	4	CA2 CA6 CA7 CA3	
Inside MPA	EA24	0.008	3	CA2 CA7 CA3	CA6
Outside MPA	O2	0.023	4	CA2 CA6 CA7 CA3	
Outside MPA	05	0.745	4	CA2 CA6 CA7 CA3	
Outside MPA	11	0.011	4	CA2 CA6 CA7 CA3	
Outside MPA	12	0.001	4	CA2 CA6 CA7 CA3	
Outside MPA	17L	0.002	4	CA2 CA6 CA7 CA3	
Outside MPA	18	0.132	4	CA2 CA6 CA7 CA3	
Outside MPA	EA19	0.097	4	CA2 CA6 CA7 CA3	

Table 5. Assignment test result for C. argus collected from inside and outside MPA

Reference Population	Assigned Population	Probability	Nb Loci	of	Used Loci	<i>Missing</i> Loci
Inside MPA	Outside MPA	0.000	4		CA2 CA6 CA7 CA3	
Outside MPA	Inside MPA	0.000	4		CA2 CA6 CA7 CA3	
Reference Population	Assigned Sample	Probability	Nb Loci	of	Used Loci	<i>Missing</i> Loci
Inside MPA	D29	0.000	3		CA2 CA7 CA3	CA6
Inside MPA	A4	0.020	3		CA2 CA6 CA3	CA7
Inside MPA	A5	0.004	3		CA2 CA6 CA3	CA7
Inside MPA	A7	0.018	4		CA2 CA6 CA7 CA3	
Inside MPA	D27	0.001	4		CA2 CA6 CA7 CA3	
Inside MPA	D28	0.008	4		CA2 CA6 CA7 CA3	
Inside MPA	E2	0.041	4		CA2 CA6 CA7 CA3	
Outside MPA	1	0.016	4		CA2 CA6 CA7 CA3	
Outside MPA	2	0.296	4		CA2 CA6 CA7 CA3	
Outside MPA	4	0.094	4		CA2 CA6 CA7 CA3	
Outside MPA	CA14	0.000	3		CA2 CA7 CA3	CA6
Outside MPA	CA15	0.001	4		CA2 CA6 CA7 CA3	
Outside MPA	CA17	0.004	4		CA2 CA6 CA7 CA3	
Outside MPA	CA18	0.005	4		CA2 CA6 CA7 CA3	

Assignment test for population level for *E areolatus* and *C. argus*, shows probability value of 0,00 for inside and outside population, indicating that there is no mixing population between inside and outside MPA. However, there is an indication of small mixing at individual level, that shows by a probability value in every sample analyzed. Assignment test of *E. areolatus* at individual level shows only about 8% at the average of samples from inside MPA are come from outside MPA, there are only 3 samples that shows probability value more than 10%. The average probability value for samples from outside MPA which are come from inside MPA are 14.4%, there are only 2 samples that shows probability value > 0,1 (sample no O5 and 18), and only one sample that significantly shows come from inside MPA namely sample no O5 (p value: 0.745). The probability value shows that there is possibility of population of *E. areolatus* in outside MPA come from inside MPA are higher compare to vice versa, meaning that population inside MPA can support the population in an outside MPA.

The average probability of *C. argus* population inside MPA that come from outside MPA is 0.013, none of seven samples shows probability value more than 0,1, indicate that there was very small possibility that *C. argus* population inside MPA are come from outside MPA. The possibilities of *C. argus* in outside MPA that come from inside MPA are also small, the average probability value is 0.06, indicate that there is 6% possibility of invidious in outside MPA are come from inside MPA. Probability value at individual level shows that there is an indication of gen mixture between two populations although in a small frequencies. Increase in sample number for microsatellite analysis expected to increase the accuracy of analysis.

4.3 Potential hydrodynamic condition to support larva dispersal

The distribution of fish larvae is strongly influenced by hydrodynamic condition such as current pattern that determined by water temperature distribution and wind. The development of a hydrodynamic model has been carried out based on the distribution of water temperatures at a depth of 21 meters, as a potential depth for spawning area for *C*. *argus* and *E. areolatus*. The temperature distribution mapping is carried out by modeling the distribution of daily temperatures at certain times every month from June 2020 to March 2021. The modeling result shows average temperature for 10 months is 29,9°C with the range is about 29.1 – 30.8°C. The warmest water occurred at September 2020 and the coolest occurred at January 2021. In June to July water temperature was higher in the northern area, there was a cooler water mass coming from southern area. Warmer water mass was coming from mainland in August then continue to September generate warmed up of water temperature around TWP Pieh and reach the maximum temperature in a year with an average value was 30,55°C. From October to January, the water temperature was slowly decreased into the lowest temperature in a year. Water temperature was increased during February to March when warmer water mass came from southern area and mainland.

Water current circulation are strongly influenced by monsoon wind, there are east monsoon and west monsoon in a year. East monsoon occur in June to August, generate the wind direction from North West to South East, and West monsoon occur in December to January when wind direction move from South East to North West. However, the wind pattern in Mentawai basin where the TWP islands located is not follow the general pattern of wind direction. In Mentawai Basin, west monsoon generate the water circulation move to the North West, and the East monsoon generate the current circulation to South East direction. The average current conditions on June to February are presented in Figure 4.



Prediction on larva dispersal was based on spawning season for *C. argus* and *E. areolatus*. Due to limited local data, we refer to the information on spawning season in

other tropical area that has a similar condition with Indonesia, that are Hawaii Island for *C. argus* spawning season, that occur in May to October (Shemmel et al., 2016), and for *E. areolatus* we refer to Kadir et al. (2016) who collect the spawning season data in Terengganu Malaysia.

Based on secondary data we predict that *C. argus* larvae from inside TWP Pieh will distribute to South East area of TWP Pieh (around Bungus Bay and Mandeh Bay). When we consider the current speed showed by the length of arrow, larvae from TWP Pieh will farther spread on June. When spawning took place on October the larvae from inside MPA will spread away to the North West area, however the current speed is slow causing the larva distribution area is not too far from MPA area and probably concentrate inside MPA area

According to Kadir et al. (2016) *E. areolatus* spawn at January to May, hydrodynamic model showed that in February water current direction was South Easterly imply to spread direction of *E. areolatus* larva from inside TWP Pieh to coastal area of mainland around Bungus Bay and surrounding waters. Current speed showed by the size of arrow, indicate that speed inside MPA is not as fast as outside MPA which facing Indian Ocean, it affect to the distance of larvae distribution. Low speed of current water implies to limit distribution area of larva causing larva to concentrate inside MPA. If we consider to 'home base'' distribution characteristic of coral reef fishes, spawning season take place when water current speed is low, it might be one of reproduction strategy to limit their distribution area.

4.4 Model for larva distribution

Biological parameters for larva dispersal modelling

Secondary data has been collected for E. areolatus and C. argus, as shown in Tabel 6 and Tabel 7.

Variable	Pendekatan	Nilai					
	SET UP RELEASE PAR	RTIKEL					
Jumlah partikel	Fekunditas	801.487 telur/induk betina					
Karakteristik release	Metode spawning	Patchy: 801.487 telur/patch					
Kedalaman release	Kedalaman habitat	60 – 80 m					
Radius release	Teritori area						
Jadwal release	Musim pemijahan	Agustus					
	SET UP TRANSPO	DRT					
Kecepatan renang larva		konstant					
Laju disipasi	Hatching rate, survival rate	Hatching rate telur: 70% Survival rate: sampai setlement 6.4%					
Pengaruh angina	Telur dan larva	Ada pengaruh angina terhadap larva,					
terhadap transport	pelagic/planktonis	karena sebagian besar larva bersifat					
		planktonic, dan plankton feeder					
		dengan daerah sebaran dari					
		permukaan sampai lapisan fotik					
		dengan asumsi mengikuti sebaran klo-					
		a					
	SET UP BIOLOG						
Fase awal	Ukuran telur	836 + 10 sampai 1000 mikron					
	Ukuran pertama kali telur menetas	1,53 – 2,4 mm					
Lingkungan hidup larva	Suhu letal	23 – 24oC					
Pertumbuhan	Koefisien pertumbuhan						
	Kisaran suhu optimum						
	SETUP SETLEMEN						
Kriteria rekrutmen	Panjang flexion						
Aktivitas rekrutmen	Kecepatan renang	Aktif di sekitar nursery grond					
Luasan area rekrutmen		3.500 – 10.500 m2					
Duarasi rekrutmen	Waktu settlement	Lama fase flexion sampai juvenil					

Table 6.	Larva dist	ersal variable	for E.	areolatus
			101 21	

Table 7. Larva dispersal variable for C. argus

.

Variabel	Pendekatan	Nilai				
SET UP RELEASE PARTIKEL						
Jumlah partikel	Fekunditas		150.000 - 282.000 telur/induk betina			
Karakteristik release	Metode spawning		Patchy: 150.000 – 282.000			
		telur/patch				
Kedalaman release	Kedalaman hab	oitat	1 - 15 m			
Radius release	ius release Teritori area		2.000 m^2			
Jadwal release	Musim pemijahan		Mei - Oktober			
SET UP TRANSPORT						
Kecepatan renang			konstant			
larva						
Laju disipasi Diffusivity koefisien		Horizontal eddy : 60 m2/s				
			Vertical eddy: 10m2/detik			

		Horizontal viscosity = $1,25 (10^{10})$			
		m^4/s^2 .			
		Time step : 12 menit			
Pengaruh angina	Telur dan larva	Ada pengaruh angina terhadap larva,			
terhadap transport	pelagic/planktonis	karena sebagian besar larva bersifat			
		planktonic, dan plankton feeder			
		dengan daerah sebaran dari			
		permukaan sampai lapisan fotik			
		dengan asumsi mengikuti sebaran			
		klo-a			
SET UP BIOLOGI					
Fase awal	Ukuran telur	880 mikron			
	Ukuran pertama kali telur	1,53 – 2,4 mm			
	menetas				
Lingkungan hidup	Suhu letal	Suhu dingin 25°C			
larva		Suhu panas: 27°C			
Pertumbuhan	Koefisien pertumbuhan	0,3/th			
	Kisaran suhu optimum	24,9 – 29,3 °C			
SET UP SETLEMEN					
Kriteria rekrutmen	Panjang flexion				
Aktivitas rekrutmen	Kecepatan renang	Aktif di sekitar nursery grond			
Luasan area		3.500 – 10.500 m2			
rekrutmen					
Duarasi rekrutmen	Waktu settlement	Lama fase flexion sampai juvenil			

Hydrodynamic model

The development of a hydrodynamic model has been carried out based on the distribution of water temperatures at a depth of 21 meters. The temperature distribution mapping is carried out by modeling the distribution of daily temperatures at certain times every month from June 2020 to March 2021. The modeling results show a temperature range of 21 meters deep for 10 months of observation is 29.1 - 30.80C, with an average temperature of 29, 90C. The distribution of temperature values is shown in Table 8.

No.	Rentang Waktu	Min [°C]	Max [°C]	Average [°C]
1	2020-06-01_08-31	30.1	30.3	30.2
2	2020-07-01_09-30	29.6	30	29.8
3	2020-08-01_10-31	29.5	30.3	29.9
4	2020-09-01_11-30	30.3	30.8	30.55
5	2020-10-01_12-31	29.8	30.2	30
6	2020-11-01_2021-01-31	29.5	29.8	29.65
7	2020-12-01_2021-02-28	29.3	29.8	29.55
8	2021-01-01_03-31	29.1	29.8	29.45
9	2021-02-01_04-30	29.5	30	29.75
10	2021-03-01_05-31	30.1	30.4	30.25

Table 8. Temperature range in 21 meters depth

The average water temperature in TWP Pieh in June 2020 was 30.2°C. The maximum temperature measured is 30.3°C and the minimum temperature is 30.1°C. The northern area of TWP Pieh shows higher value than Southern part. In July 2020 water temperature was lower than June, average temperature was 29.8°C there was cooler water mass coming from South meanwhile the temperature in northern area was warmer. In August 2020 water temperature increased up to 30,3°C, the water tends to be warmer in mainland area. There is a significant difference between the temperature around the waters of P. Air and P. Bando, where P. Air is influenced by warm temperatures that are stronger than the mainland, while P. Bando is affected by cold temperatures from Indian Ocean. In September the water temperature warmed up, and reached the highest temperature value with an average temperature of 30.55°C and a maximum temperature of 30.8°C. Similar to August when water temperature was higher around the mainland particularly in the southern (around Bungus waters). In September the water temperature dropped by about 0.55°C, the water temperature tends to be warm evenly throughout the TWP Pieh area with an average of 30°C. In November 2020, the water temperature appears to be lower in the central part of the TWP Pieh area, while the waters around the mainland and from the ocean are slightly warmer. In the following month, warm waters come from coastal waters close to the mainland. The temperature gets colder as the distance from the mainland

increases. Water temperature in January 2021 was the lowest temperature during observations, with an average of 29.45°C. In February 2021 the warmer water period will come from the south and around the coastal waters, while in the northern part the water period still tends to be lower particularly around Bando Island. In March 2021 the water temperature was warmer than the previous month. The water mass around the mainland appears to be higher which affects several islands in the Pieh TWP area, namely around P. Air, while islands farther from the mainland such as P. Toran, P. Pandan, P. Pieh and P. Bando are affected by higher temperatures. cold from the Indian Ocean. The temperature distribution model during June 2020 to March 2021, is shown in Figure 5.



Figure 5. Water temperature distribution at 21 meter depth on June 2020 - Maret 2021, read from left to right.

Wind sirculation

The general condition of wind circulation in the east monsoon which generally occurs between June and August is dry and cold wind blowing from the top of the Australian continent moving towards the Asian continent, passing through the Indonesian Maritime Continent. The wind generally moves from the southeast to the northwest.

This can also be seen in June and July 2020, wind conditions over the East Indian Ocean and parts of Sumatra to parts of the Karimata Strait, see Figure 6. What is interesting is when the wind from the southeast moves to the northwest over the Indian Ocean. East west of Sumatra, turning on the island of Siberut, then turning to the southeast along the Mentawai basin. The wind passes through the Pieh Island area and its surrounding, see the yellow box area in Figure 3. The wind that blows over the TWP Pulau Pieh area and its surroundings varies in speed, but the maximum can reach 5 mph (miles per hour) or equivalent to 10 km/h or the equivalent of 2 m/s.



Figure 6. Wind circulation in June 2020, comparison between west coast of Sumatera with East coast of Sumatera (Karimata Strait).

Wind circulation in October 2020 are almost the same as June and July 2020see Figure 5. There was a strengthening in velocity and it extends over the Mentawai Basin, It was influence the in direction and speed above the Mentawai Basin. In November 2020, the wind shifts from the east to the west monsoon (Figure 7). It can be seen that the wind generally moves from The Indian Ocean is heading east towards Sumatra, the wind then weakened when approaching Mentawai Islands. The deflection of the wind is clearly visible when passing through the North and South Pagai Islands, where there are winds that turn to the northwest, and some turn to the southeast. The wind that turned to the northwest then crossed the sky from TWP Pieh and its surroundings.



Figure 7. Wind circulation in October 2020, comparison between west coast of Sumatera with East coast of Sumatera (Karimata Strait).

Conditions of wind circulation in December 2020 to February 2021, are strengthened compare to November 2020, see Figure 8 Below. This strengthening is clearly seen that the wind generally moves from the direction of the central Indian Ocean to the east towards Sumatra, there was no direction split when approaching the Mentawai archipelago. The entire wind circulation moves to the southeast as it approaches the west coast of Sumatra. The wind velocity that crosses TWP Pieh and its surroundings in December 2020 ranges from 10 to 15 mph (miles per hour), or equivalent to 20-30 km/h, or the equivalent of 6 - 4 m/s.



Figure 8. Wind circulation in December 2020, comparison between west coast of Sumatera with East coast of Sumatera (Karimata Strait).

Water circulation at the depth of 21 meters

Surface current conditions in the waters of the Pieh Island TWP and its surroundings are strongly influenced by monsoon winds, as described in the previous subchapter on 'Wind Circulation Conditions'. In general, the prevailing conditions in the internal waters of the Indonesian Maritime Continent and the waters south of Java to Nusa Tenggara, in the east monsoon, the current at sea level generally moves from the northwest to the southeast. On the other hand, in the westerly monsoon, the current on the surface of the sea moves from the southeast to the northwest. Then during the transition from the east monsoon to the west monsoon, the movement pattern and current velocity are generally unstable, and generally weaker than the sea surface currents during the east monsoon and west monsoon. However, this general condition does not apply to the waters of the Mentawai Basin. The circulation of sea surface currents that occur in the west monsoon period is the wind and the monsoon currents move to the northwest. On the other hand, in the east monsoon period, the wind and monsoon currents move to the southeast. The average surface current condition in the Mentawai Basin at the end of the east monsoon period (June to August 2020) moves to the southeast. However, the current conditions in June 2020 were lower in speed than the current conditions in August 2020. See Figure 9.



Figure 9. Surface current around TWP Pieh on June and July 2020.



Figure 10 Surface current around TWP Pieh on October and November 2020.

The average surface current condition in the Mentawai Basin at the end of the transition period from the east monsoon to the west monsoon should be weaker than the current in the east monsoon and west monsoon periods. This can be seen in Figure 9, the current condition in October 2020 is stronger than the current in November 2020. The currents in both months generally show the same direction of movement, namely heading east-northeast, but in November, after heading easterly, then there is a current that is deflected to the west and/or southwest. See Figure 10.



Figure 11. Surface current condition around TWP Pieh on December and February 2020.

The condition of the average surface current in the Mentawai Basin in the westerly monsoon winds generally moves to the northwest. However, as seen in Figure 11, the current conditions in December 2020 and February 2021 contained a small portion of the current that moved to the southeast, and the current in February 2021 seemed to be stronger in speed than the current in December 2020.

Conditions for Grouper Larvae Distribution at a depth of 21 meters

The distribution trajectory of Grouper larvae at a depth of 21 meters generally follows the movement of the current, but the scope or length of the path does not always correlate with the average current velocity. The distribution trajectory of the larvae is strongly influenced by the hourly variability of the current generated by a combination of tides and winds blowing at sea level.



Figure 12. Projection of larvae distribution on June and July 2020

The distribution trajectory of the larvae in June and July 2020 in general is the same towards the southeast, but when viewed in more detail, there is a slight difference in the spatial interval of the distribution of the larvae. Differences in the spatial interval of larval distribution may occur due to the hourly variability of the current generated by a combination of tides and winds blowing over the sea surface. See Figure 12.



Figure 13. Projection of larvae distribution on October and November 2020

The distribution trajectory of the larvae in October and November 2020 in general is the same towards the northwest, but when viewed in more detail, there is a significant difference in the spatial interval of the distribution of the larvae. The trajectory of the larvae in November 2020, the trajectory is more widespread than the trajectory in October 2020. The spatial interval difference in the distribution of the larvae may occur due to the variability of the hourly currents generated by a combination of tides and winds blowing over the sea surface. Currents in November, after heading to the northeast, then there are currents that are deflected to the west and/or southwest. see Figure 13.



Figure 14. Projection of larvae distribution on December 2020 and February 2021

In general, the distribution trajectory of the larvae in December 2020 and February 2021 is the same towards the southeast, but in the direction of distribution there are several differences in the degree of distribution, and the length of the path. The trajectory of the larvae in December 2020, the trajectory is longer than the trajectory that occurred in February 2021. The direction of distribution in December 2020, actually looks more towards the mainland west coast of Sumatra than the direction of the trajectory of the distribution of larvae in February 2021. Differences in the spatial interval of larval distribution can occur caused by the variability of its hourly currents generated by a combination of tides and winds blowing over sea level. Currents in December 2020 are likely to be more dominantly influenced by tidal conditions. See Figure 14.

Conditions for Grouper Larvae Distribution at a depth of 21 meters

In general, the average current circulation pattern at a depth of 34 meters is not much different from the circulation conditions at a depth of 21 meters, but in more detail the hourly variability is slightly different. The strength of the current at a depth of 34 meters is relatively lower than the current velocity at a depth of 21 meters, but is more constant, so that when spreading grouper larvae, the distance between the larvae is quite close/not tenuous, and then the spatial range looks further. The larval distribution trajectory which is significantly different in direction and range only occurs in October 2020. This is understandable, because October and November 2020 are the transition period from the east monsoon to the west monsoon. See Figure 15.

The analysis of larvae connectivity among islands in TWP Pieh MPA based on simulation at the depth of 21 meters and 34 meters.

Based on the composite results from the simulation results of grouper larvae distribution trajectories at a depth of 21 meters and 34 meters in June 2020, July 2020, October 2020, November 2020, December 2020, and February 2021, it can be obtained an illustration that the connectivity of larval species within the TWP area can be obtained. Pieh and its environs have a very high probability. See Figure 15. The trajectory distribution of larvae in June-July 2020 and December-February 2021, both at 21 meters and 34 meters, are possible to reach the western coast of Sumatra such as: Bayur Bay, Bungus Bay, Karsik Bay, and the southern coast of West Sumatra.



Figure 15. Larvae distribution trajectories in June 2020, July 2020, October 2020, Novemebr 2020, December 2020 and February 2021 at the depth of 21 m (left) and 34 m (right)

5. Conclussion

Marine protected area of TWP Pieh has been able to support the protection of biodiversity inside MPA, as shown by several indicators was higher inside MPA compare to outside, such as:

- Total catch
- Fish size
- Fish diversity
- Economics value of species

However TWP Pieh MPA are need to be increased in their effort to support the fish resource recovery in its surrounding waters. Factors affecting those conditions probably are:

- Reef fishes distribution is limited only in reef area, microsatellite DNA showed that there is no mixing population between inside population with outside one.
- Spawning season of reef fishes occurred when hydrographic conditions support the survival and distribution of their larvae. They spawn at the time when ocean current are in low velocity.
- High rate of reef fishes exploitation that increases the pressure on fish.

6. Research team



Dr. Reny Puspasari, research coordinator, is a senior researcher in Center for Fisheries Research, the Agency of Marine and Fisheries Research and Human Resource Development, Ministry of Marine Affairs and Fisheries. Her focus study is on Marine Ecology and research focus on the environment impact on fish resources.



Dr. Aslan, member of research team, is a professional researcher in Marine sectors, focus on biodiversity, conservation biology, landscape ecology, spatial planning, philanthropy and humaniora. Now he is mostly work on the sustainability issues in marine sector.



Dr. Hawis Madduppa, M.Sc, member of research team, is a lecturer in Faculty of Fisheries and Marine Science, IPB University. He major is on biodiversity, management of fish natural resources. Now he is also a head of Marine Science Departement and active as the Executive Director of The Indonesia Assosiation of Swimming Crab <u>http://www.apri.or.id</u>)



Dr. Ing Widodo Setyo Pranowo, M.Sc., member of research team, is a research professor in MArine Research Center the Agency of Marine and Fisheries Research and Human Resource Development, Ministry of Marine Affairs and Fisheries. His research focused on applied oceanography. He is also active as a lecturer in Navy Tecnology University (STTAL).



Budi Nugraha, M.Si., member of research team. He is a senior researcher in Center for Fisheries Research, the Agency of Marine and Fisheries Research and Human Resource Development, Ministry of Marine Affairs and Fisheries. His focused study is on capture fisheries, particularly for tuna research.



Rita Rachmawati P.hD, **member of research team**. is a senior researcher in Center for Fisheries Research, the Agency of Marine and Fisheries Research and Human Resource Development, Ministry of Marine Affairs and Fisheries. Her research focus is marine ecology, majorly in coral reef and climate change. She is also active as guest lecturer in Faculty of Fisheries and Marine Science, IPB University.

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