REVIEW

Lobster Fishery Connectivity and Management In Indonesia Waters

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ABSTRACT

The distribution of lobsters in Indonesian waters is very wide, even lobster species in Indonesia are also scattered in the tropical waters of the western Pacific Ocean, the Indian Ocean, Africa to Japanese waters. Indonesian waters are divided into 11 (eleven) Fishery Management Zone (FMZ). Lobsters in Indonesia may come from various water areas, both national and regional water zones, and they're called the sink population. Its spread is influenced by the movement of the current. Lobster seed is nurtured by nature through ocean currents from Australia, East Indonesia, Japan, then back to Australia. Lobsters have a complex life cycle, where adult lobsters inhabit coral reefs as a place to lay eggs, then hatch into planktonic larvae, and grow up in open seas and carry out diurnal and ontogenetic vertical migrations before returning to nurseries in shallow coastal areas and reefs, coral, as well as habitat by the type of species. Literature research had used at least two methodologies to estimate the distribution and connection sensitivity matrices of marine organism larvae. The two most common approaches are using genetic markers and numerical biophysical modeling. Thus, this research uses molecular genetic techniques to explain the genetic structure of lobster populations using a biophysical model approach that can explain the genetic structure of lobsters, as well as the distribution based on regional oceanographic synthesis data and lobster biology known in Indonesian waters. This model has four components, namely: 1) a benthic module based on a Geographical Information System (GIS) which is a lobster habitat in the spawning and recruitment process, 2) a physical oceanography module containing daily velocity in the form of a three-dimensional hydrodynamic model, 3) a larva biology module that describes larval life history characteristics, and 4) a Lagrangian Stochastic module that tracks the individual trajectories of larvae.

1. Background

Lobster in English is known as *Crayfish* or *Spiny Lobster*, while in Indonesia it is known as the *Crayfish* or *Barong Shrimp*. A name scientifically well-known is Panulirus belonging to the *Palinuridae family* [1]. In Indonesia, six types of *Crayfish* are found, that are scattered from western waters to eastern Indonesian waters with conditions different habitats. They are Barong Shrimp (*Panulirus Versicolor*), Stone Shrimp (*Panulirus paniculate*), King Shrimp (*Panulirus longipes*), Ketangan Shrimp, Pine Shrimp or Pearl Lobster (*Panulirus ornatus*), Jatropha shrimp (*Panulirus polyphagus*), Green Sand Lobster

(*Panulirus hommarus*) [2,3,4,5].

The distribution of lobsters in Indonesian waters is very wide, even lobster species in Indonesia are also scattered in the tropical waters of the western Pacific Ocean, the Indian Ocean, Africa to Japanese waters [6]. Indonesian waters are divided into 11 (eleven) Fishery Management Zone (FMZ), namely FMZ 571 (Malacca Strait and Andaman Sea waters), FMZ 572 (Indian Ocean waters next door West Sumatera and the Sunda Strait), FMZ 573 (Southern Indian Ocean waters Java to the south of Nusa Tenggara, the Savu Sea, and parts of the West Timor Sea), FMZ 711 (Karimata Strait, Natuna Sea, and the South China Sea), FMZ 712 (Java Sea waters), FMZ 713 (Makassar Strait waters, Bone Bay, Flores Sea, and the Bali Sea), FMZ 714 covering the waters of Tolo Bay and the Banda Sea), FMZ 715 (waters of Tomini Bay, Maluku Sea, Halmahera Sea, Seram Sea, and Berau Bay), FMZ 716 covering waters of the Sulawesi Sea and north of Halmahera Island), FMZ 717 covering the waters of the Cendrawasih Bay and the Pacific Ocean), and FMZ 718 (Sea waters Aru, Arafuru Sea, and the East Timor Sea) [7]. Any FMZ existing in Indonesia has the different potential abundance and types of lobster resources. The potential for lobsters in each FMZ has estimated, of which 11 FMZ are classified into 3 (three) clusters of water areas, namely was Indian Ocean Cluster (FMZ 571, 572, 573), Sunda Shelf cluster (FMZ 711, 712, 713) and the Sahul Exposure cluster (FMZ 714, 715, 716, 717, 718). Estimation results show that the potential of lobster seeds in the Indian Ocean cluster reaches 3,128 tons. From this potential value, about 1,563 tons are female lobsters. If 10% of female lobster seeds to grow into broodstock lobsters, the potential for lobster broodstock females in the Indian Ocean cluster reached 15,630 tons or it can be estimated that they reached 11,265 female lobster broods. Thus, the total female lobster broodstock can produce as many as 7,815,000,000 eggs. However, like all the eggs that exist, about 1% can survive for each cycle, leaving only about 78,150,000 lobster eggs in the cluster Indian Ocean. Likewise with the potential for lobster seeds in the Sunda Shelf cluster reach around 3,337 tons with an estimated number of female seeds as much as 1,669 tons and an estimate of which become breeders of 16,685 tails, with a potential number of capable eggs gradually life reaches 83,425,000 eggs. While the potential number of broodstock lobsters in the Sahul Exposure cluster totaled 117,375,000, thus estimates the potential for lobster in all FMZ in Indonesia is around 278 billion eggs, 250 billion larvae and the estimated number of lobster seeds (Peurulus) reached 12.5 billion. The assumed data on the potential lobster seeds in each FMZ Indonesia are shown in Table 1 [8].

Lobsters in Indonesia may come from various water areas, both national and regional water zones, and they're called the sink population. Its spread is influenced by the movement of the current. Lobster seeds nurtured by nature through ocean currents from Australia, East Indonesia, Japan, then returned to Australia [9,10]. Lobsters have a complex life cycle, where adult lobsters inhabit coral reefs as a place to lay eggs, then hatch into planktonic larvae, and grow adults in the open ocean and perform diurnal and ontogenetic vertical migrations before return to the nursery area in shallow coastal areas and coral reefs, and habitats suitable for the species [11]. On when it becomes a planktonic larva, it has a sufficient duration of pelagic larvae length which could take around 5-9 months (depending on species), as planktonic larvae [12], where these larvae have the potential to spread among lobster populations in all waters [13]. For example, that stock of lobster seeds in each FMZ in Indonesia in terms of type, quantity, and source of seed origin different. This corresponds to the *sink population* in which the planktonic larvae will be spread to other areas along with the movement and circulation of currents in the region of Indonesian waters. When viewed geographically, Indonesian waters are located in tropical regions, it can be assumed that two water areas function as spawning (*spawning ground*) lobster, which is in the waters between Papua New Gini and Australia, as well as Philippine waters. Lobsters will spawn in the waters between them Papua New Gini and Australia, then the larvae will be scattered in the direction of and movement of currents to the north through the Solomon Sea, the Bismarck Sea north of Papua New Gini, and northern Papua, which crosses the western Pacific Ocean to the water Philippines. In the Philippine Sea, there is a *sink population* and it spreads back into two water areas, the first is to spread towards the Makassar Sea and the second is towards South China Sea (including Hong Kong, Vietnam, and Malaysia) and towards the Sea Java. The movement of lobsters across the Makassar Sea and the South China Sea both meets and gathers (*sink population*s) in the waters of West Nusa Tenggara, especially in Lombok Strait. The lobster population that met in the Lombok Strait then spread in two directions across the Indian Ocean, the first is to spread out and back again towards the waters between Papua New Gini and Australia, and the second is to the west across the Indian Ocean to the west of Sumatera. The dispersal and genetics of lobster in Indonesian waters is shown in Figure 1 [9,10].

Table 1. The assumed data on the potential lobster seeds in each FMZ Indonesia

FMZ	Potency (ton)	Concrete estimation (ton)	Female estimate will be parent 10% (ton)	The estimate number of broodstock (lobsters)	Estimated number of eggs	SR 1% (per per sycle all type of lobsters)	Species of pearl and sand lobsters (10% of all type of lobsters)	10%	20%	50%
HINDIA OCEAN CLUSTER										
571	673	336.5	3.365	3,365	1,682,500,000	16,825,000	1,682,500	168,250	336,500	84,250
572	1483	741.5	7.415	7,415	3,707,500,000	37,075,000	3,707,500	370,750	741,500	1,853,750
573	970	485	4.850	4.850	2,425,000,000	24,250,000	2,425,000	242,500	485,000	1,212,500
SAHUL SHELF CLUSTER										
711	1421	710.5	7.105	7,105	3,552,500,000	35,525,000	3,552,500	355,250	710,500	1,776,250
712	989	494.5	4.945	4,945	2,472,500,000	24,725,000	2,472,500	247,250	494,500	1,236,250
713	927	463.5	4.635	4,635	2,317,500,000	23,175,000	2,317,500	231,750	463,500	1,158,750
SAHUL SHELF CLUSTER										
714	724	362	3.62	3,620	1,810,000,000	18,100,000	1,810,000	181,000	362,000	905,000
715	846	423	4.23	4,230	2,115,000,000	21,150,000	2,115,000	211,500	423,000	1,057,500
716	894	447	4.47	4,470	2,235,000,000	22,350,000	2,235,000	223,500	447,000	1,117,500
717	1044	522	5.22	5,220	2,610,000,000	26,100,000	2,610,000	261,000	522,000	1,305,000
718	1187	593.5	5.935	5,935	2,967,500.000	29,675,000	2,967,500	296,750	593,500	1,483,750
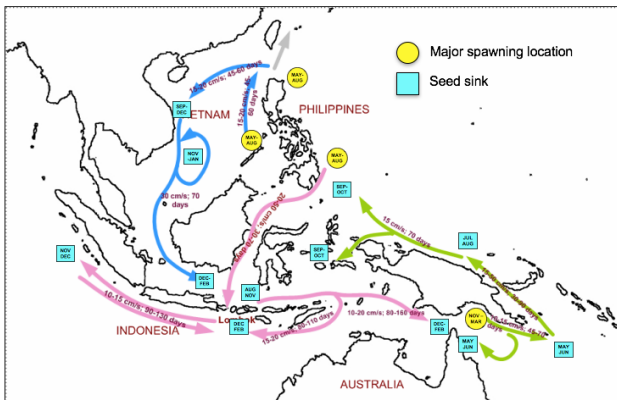
Figure 1. The dispersal and genetics of lobster in Indonesia waters [9,10]

Based on the distribution pattern of larvae originating from the northern region of Australia to the Philippine Sea crosses the western Pacific Ocean, South China Sea, Java Sea, and the Indian Ocean, there are two very important groups of events of distribution lobster larvae, namely spawning (*major spawning ground*) and foraging places (*seed sinking*) for the lobster. The time it takes to do trips starting from spawning ground in the territorial waters of Australia, Pacific Ocean western part, Philippines, South China Sea, Makassar Sea, Java Sea, and Ocean The Indies to return to Australia required a certain speed of spread as well as a very long duration. Broadly speaking, lobsters will spawn in Australian waters in November-March,

while spawning in waters Philippines occurs in May-August. Based on the spawning time, you can assume that general lobsters will spawn twice deep a year [10]. Based on the distribution of lobsters that cross and enter FMZ in Indonesia, four main areas become the *sink population*, namely Sumbawa Island (9 locations, with a total area of 249.93 km^2), Lombok (14 locations, with an area a total of 80.94 km^2), Bali (2 locations, with a total area of 68 km^2) and Java Island (58 locations, with a total area of 1,198.36 km^2). The total area of *sink population* on the Java and Bali Islands is shown in Table 2 and Figure 2 [14].

The life cycle of most marine animals including lobsters starts from the larval stage planktonic last for hours to months connecting populations one another between regions. Hence, knowledge about connectivity larvae is very important for understanding population dynamics and managing the ocean sustainable based on biogeographically dispersed taxa. Recent studies on larval connectivity using natural or artificial tagging [15,16,17], biophysical modeling [18,19,20], larvae tracking methods [21], and analysis genetic [22,23,24], suggests that the population recruitment rate depends on exogenous supply and larvae in the sea [25]. The ability to predict the spread of larvae that is in the waters starting from the spawning grounds to the nursery is level science which is quite rare and interesting. Therefore, it needs to be studied more deeply to explain how a biophysical model is based on oceanographic parameters and biology empirically to provide estimates of larvae

supply and can be used to determine the origin of larvae, destination, and distribution path of lobster larvae in Indonesia FMZ.

Table 2. The total area of *sink population* on the Java and Bali Islands

No	Location	Number of *sink population*	Percentage of number location (%)	Area (km²)	Percentage of area (%)
1	Sumbawa	9	11	249.93	16
2	Lombok	14	17	80.94	5
3	Bali	2	2	68.00	4
4	Java	58	70	1,198.36	75
Total		83	100	1,597.23	100
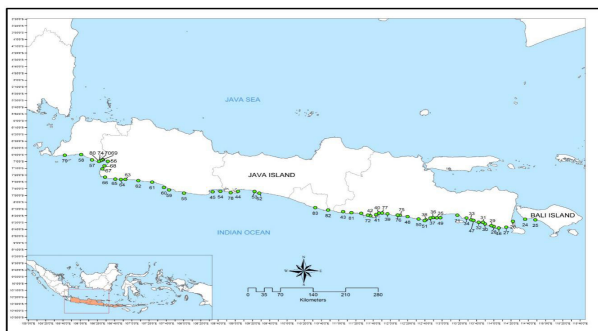
Figure 2. The total area of *sink population* on the Java and Bali Islands

Demographic connectivity studies have mostly focused on taxa with planktonic larvae (e.g. bivalves and reef fish) have contributed substantially scientifically, although there is a considerable bias over the broader spatial scale [26]. Demographic population connectivity between populations at scale spatial area (> 1000 km) is based on tagging and genetic methods undetectable [27,28]. Several approaches have also been taken to evaluate connectivity between populations of marine organisms, including genetic markers (e.g. mitochondrial DNA or microsatellites), geochemical markers (e.g. deep microchemical signatures shells), and/or the use of high-resolution biophysical models, but not one Neither of these approaches can be convincing in isolation and in knowing connectivity between populations [29,30,31]. Currently, the studies that have been conducted are limited to the dispersion model hydrodynamic species *Panulirus ornatus* in a limited area of species distribution. Previous studies in eastern Australian waters and in the Philippines focus on short-term larval dispersal within one generation *Panulirus ornatus* (e.g. from spawning grounds to nursery sites) [32,33]. According to in this model most of the larvae are released from the spawning grounds in the Coral Sea, such as The Gulf of Papua, will be brought back to the northeast Queensland coastline, in the interim some of them can move north to the Vitiaz Strait of eastern Papua New Gini within three months [32]. From different spawning places on the west and east coast of the Philippines, the larvae will be scattered towards the north of Taiwan, then spread towards the South China Sea, or spread into the interior of the Sulawesi Sea. Will but based on this study has not been able to answer the problem of connectivity *Panulirus ornatus* in the wider Southeast Asian archipelago [33].

The bathymetry and oceanography of the Southeast Asian archipelago are complex, with numerous shoals, straits, islands, coral reefs, and semi-enclosed seas, and mass flows water is carried by currents between the Pacific and the Indian Ocean. There is currently no scale model Oceanography covers the entire archipelago to aid in understanding that in-depth related factors that affect the genetic structure of *Panulirus ornatus*, or even the connectivity of other types of marine organisms. Existing oceanographic models includes several small-scale models that are the focus of conservation areas in the region the archipelago [34], and a medium-scale model of the entire domain [35] which has a grid size that is too coarse to complete the mass flux of water that goes through the Philippine Strait, so that produces an analysis that ignores connectivity between the Philippine Sea and the China Sea South and western Pacific Ocean [36]. For example, adult *Panulirus ornatus* was found in waters with depths of 1-50 m and occupy a variety of habitats such as sandy and muddy substrates, coral reefs, rocky bottoms, and even murky coastal waters [37]. *Panulirus ornatus* is known to migrate by walking along the seafloor as far hundreds of kilometers from fairly extensive spawning aggregations, for example, *Panulirus* adult *ornatus* from Torres Strait, Australia, migrate up to 500 km to the place spawning near Yule Island in the Gulf of Papua [38,39,40]. Furthermore, P. ornatus larvae have phases planktonic length that lasts 135-210 days [38,39,40,41]. Before completion, the larvae metamorphose to the puerulus stage, which is the end of the larval stage with strong swimming abilities, this phase lasts between 9-25 days [38,42]. The larval development period is this length, puerulus swimming ability, and the potential for phyllosoma admixture (planktonic larvae) in the Southeast Asian Archipelago region will produce levels low population genetic structure [43]. However, the hypothesis until recently has not been tested. Therefore, some methods are both quick and affordable and not limited by phyllosoma (planktonic larvae), namely the biophysical modeling method [44,45]. Thus, this study uses techniques of molecular genetics to explain the genetic structure of lobster populations by approaching biophysical models that can explain the genetic structure of lobsters, as well

as pathways distribution based on regional oceanographic synthesis data and lobster biology known in the Indonesian FMZ. This model has four components, namely: 1) benthic module based on Geographical Information System (GIS) which is the habitat for deep lobsters spawning and recruitment process, 2) physical oceanography module contains velocity daily in the form of three-dimensional hydrodynamic models, 3) larvae biology module describe the life history characteristics of larvae, and 4) the Lagrangian Stochastic module which tracks the individual trajectories of the larvae.

In making a model of connectivity between populations, a parameter model is made based on spatial-temporal spawning and planktonic larvae behavior patterns, then verify the model by comparing the simulation results with the data empirical on the spatial-temporal pattern of larval supply in several FMZs in Indonesia. Oceanographic circulation models in three-dimensional form as well as larvae behavior models, where both affect the trajectory of the dispersal process [46].

2. Formulation of the Problem

Most of the marine macroinvertebrates, one of which is lobsters, in general, has a two-phase life cycle, consisting of the adult benthic phase and the pelagic larvae has the potential to spread from one region to another due to its existence movement of currents so that the benthic population has the potential to have a level of relationship genetically between populations and regions. To find out the level of population relations between regions genetically, a fundamental understanding of the flow is needed genes and adaptations of marine organisms. The basic thing that must be considered is the biological parameters of organisms that interact with physical and oceanographic parameters chemistry as a driver in the transfer of larvae between regions.

Indonesia's territorial waters are classified into eleven territories Fisheries Management Area (FMZ) with quite complex physical oceanographic characteristics, it is very likely that these oceanographic conditions will assist the process spread of larvae of marine organisms such as lobsters from one FMZ area to the FMZ others, so that the stock of lobster seeds in each FMZ in Indonesia, in terms of type, quantity and the source of origin of the seeds is different. This is related to the *sink population* where the larvae are planktonic will spread to other areas along with the movement and circulation of currents in Indonesian territorial waters. When viewed geographically, Indonesian waters located in the tropics, it can be assumed that two water areas serve as a *spawning ground* (*spawning ground*) lobsters, namely in the waters between Papua

New Gini and Australia, as well as Philippine waters. The lobsters will do spawning in the waters between Papua New Gini and Australia, then the larvae will be scattered following the direction and movement of currents towards the north through the Solomon Sea, Bismarck Sea north of Papua New Gini and north of Papua which crosses the western Pacific Ocean up to Philippine waters. In the Philippine Sea, there is a *sink population* and it is spreading back into two water areas, the first is to spread out to the sea Makassar and the second to the South China Sea (including Hong Kong, Vietnam, and Malaysia) and towards the Java Sea. Movement of lobsters across the Makassar Sea and The two South China Sea meet and gather (*sink population*s) in the waters of Nusa West Southeast especially in the Lombok Strait. Lobster populations that meet in the Strait Lombok then spread in two directions across the Indian Ocean, the first is spreading and returning to the waters between Papua New Gini and Australia, and the second is westward across the Indian Ocean to the West Sumatera [9,10] (Dao *et al*., 2015; Priyambodo, 2020). Based on the distribution of the lobster crossing and entering FMZ in Indonesia, four main areas become *sink population* namely Sumbawa Island (9 locations), Lombok (14 locations), Bali (2 locations), and south coast of Java Island (58 locations) [14].

Several research results have been carried out to determine inter-connectivity population based on genetic and oceanographic factors, although still on a spatial scale narrower, and focus on a single species, so several approaches have not been able to convince in knowing the connectivity between population [29,30,31]. Several methods have been developed including visual tracking marine larvae, artificial tagging, and natural tagging, and biophysical modeling numeric. Visual tracking of individual larvae is the only method applied directly, but can only be applied to large larvae with larval duration pelagic short, so its application is limited. There are also many other methods used, but the level of confidence is still small because there are still many factors in biology that have not been considered such as certain life-history traits, physiology, or anatomy of the study target. All methods have an intrinsic uncertainty depending on the type of marker, the analysis procedure, and the statistical methodology used.

Literature research has been conducted which collected a total of 507 research articles published since 1990 demonstrated that 41 studies have used at least two methodologies for estimating dispersion and connection sensitivity matrices of marine organism larvae. Two the most common approach is to use genetic markers and modeling numerical biophysics. Thus, this research uses molecular genetic techniques to explain the genet-

ic structure of lobster populations using a biophysical model approach which can explain the genetic structure of lobsters, as well as the distribution pathways based on regional oceanographic synthesis data and known lobster biology in FMZ Indonesia. This model has four components, namely: 1) benthic based module Geographical Information System (GIS) which is the lobster habitat in the spawning process and recruitment, 2) physical oceanography module contains daily speed in the form of three hydrodynamic model dimensions, 3) larvae biology module that describes the characteristics life history of larvae, and 4) Lagrangian Stochastic modules that track individual trajectories larva [47].

3. The Urgency of Future Research

The urgency of future research is determined: 1) lobsters distribution in Indonesian FMZ based on genetic analysis, 2) lobster connectivity in Indonesia FMZ based on oceanographic data and lobster biology.

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