Associative-mesofauna abundance and its correlation with sponges antibacterial activity in seagrass ecosystem

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Abstract. Sponge is one of the benthic organisms that could be found in seagrass ecosystem. Sponge is also could harbor various organisms within its tissue, as a biogenic habitat for those associative organisms. This interaction could benefit from enhancing marine biodiversity in the seagrass ecosystem. Aims of this research were study the abundance of associative mesofauna and its correlation with the sponges antibacterial activity. Sponges samples were preserved in 70% ethyl alcohol (0.5-1 cm³ thickness) and observed under stereomicroscope, to find the associative mesofauna. Meanwhile fresh tissue samples were tested against several pathogenic bacteria in antibacterial assay. Associative mesofauna that was found in 14 of 23 seagrass sponge species, belong to Ophiuridae, Mollusca, Gastropoda, Arthropoda, Polychaeta, and Oligochaeta groups. Mollusca and Polychaeta were highly correlate with most of the sponge species (8 of 14), based on statistical correspondence analysis (CA). Antibacterial assay on sponge tissue showed that only 6 of 14 sponge species has activity against several pathogenic bacteria. Statistical analysis (CA) showed that Mollusca and Polychaeta also have high correlation with the antibacterial activity. This suspected that sponges defense mechanism strategy against pathogenic bacterial infections, could influence the preference of associative mesofauna inhabiting seagrass sponges.

Keywords: associative invertebrate, ecological interaction, marine biodiversity

1. Introduction

Sponge is a benthic organism that could be found in various intertidal area, including in seagrass ecosystem (Archer et al 2015). Sponge also was known can harbor various associative organisms, both prokaryotic and eukaryotic (Thakur and Müller 2004, Radjasa et al 2011, and Huang et al 2008). Previous studies showed that those associative organisms could play roles in sponge adaptation, such as secondary metabolites production (Faulkner et al 1994, Kobayashi and Kitagawa 1994, Guyot 2002, Proksch et al 2003, Rahe 2004, Thakur and Müller 2004 and Zheng et al 2005).

Studies on associative mesofauna, both epi, and endofauna, of sponge, showed that there were ecological interaction between sponge and its fauna, that could be parasitic, commensalism and mutualism. Huang et al (2008) discovered that sponge endofauna could utilize sponge physical structure (spicules) and chemical composition (secondary metabolites) as a refuge from predatory activity in the environment.
Hence, sponge plays an important role as a habitat that provided the life and reproductivity of associative-mesofauna (Ribiero et al 2003), furthermore, plays an important role in maintaining biodiversity in the ecosystem.

Habitat environment provided by a benthic organism such as sponge, is known as biogenic habitat. Sponge, in this case, offer a shelter by its physical structure to the associative fauna, and protection from environmental stresses. This study was aimed to find the associative-mesofauna from seagrass sponge, and its ecological interaction, by observing the associative-mesofauna abundance in various sponge species and its relation to the sponge antibacterial activity.

2. Materials and methods

This research was conducted into field observation and sampling activity, as well as a laboratory procedure. Field observation and data sampling were carried out at Pramuka Island of Seribu Islands, Special Capital Region of Jakarta, Indonesia (figure 1).

Pramuka Island is located in the North Coast of Jakarta. As a part of Seribu Islands National Park area, in front of Jakarta Bay, this very small island is surrounded by moderate coral reefs cover. This island also has a mixed seagrass bed surrounding the island, comprised of Thallasia hemprichii, Cymodocea rotundata, Cymodocea serrulate, followed by small patches of Enhalus acoroides, Halophilla ovalis and Syringodium isoetifolium (Wisnubudi and Wahyuningsih 2014 and Iset et al 2016).

Field observation and sampling activity were undertaken at 4 different sites on each side of the island (figure 1). These sites were chosen for it have sponge community in the seagrass beds, with shallow and clear water characteristic. Before samples were collected, surveys were conducted in order to observe and estimate the sponge community in each site. Three replicates of 50×2 m belt transect were laid in each site, and each sponge species were collected, to be examined furthermore.

![Figure 1. Map of field observation and sampling location of the sponge community in seagrass beds of Pramuka Island, Seribu Islands, Jakarta (• = station 1, • = station 2, • = station 3 and • = station 4).](image-url)
2.1. Materials
The sponge specimens were rinsed in sterile seawater in an overflow vessel and preserved in 70% ethyl alcohol in jar bottle, to be examined under a stereomicroscope. Meanwhile, fresh sponge fragment (1 cm² and 0.5 cm thickness) from the same individual with associated mesofauna, were taken to study the antibacterial activity against several bacteria.

2.2. Methods
2.2.1. Taxonomic determination of associated mesofauna. Each sponge was cut into thin slices (0.5-1 cm) which were examined under the stereomicroscope. The associated mesofauna was separated with forceps and those retained on a < 0.5 mm (fine mesh) sieve were used for the taxonomic work (modified from Betancourt-Lozano et al 1998, Amsler et al 2009).

2.2.2. Antibacterial assay of sponge tissue. This assay was aimed to study the inhibition activity of sponge tissue against several bacteria and its correlation with the associated-mesofauna. Fresh sponge fragment (1 cm² and 0.5 cm thickness) from the same individual that has associated-mesofauna, were placed with the exopinacoderm intact with agar media after the media have been inoculated first for 24 h with targeting bacteria (Escherichia coli, Staphylococcus aureus and Pseudomonas aerophoba). Inhibition zones were observed after 24 h incubation in 35°C (Betancourt-Lozano et al 1998). This assay was conducted with three replications, on each sample against 3 targeting bacteria (E. coli, S. aureus, and P. aerophoba).

2.2.3. Statistical analysis. Associated-mesofauna abundance was determined by total n_i per total sponge volume, meanwhile, the relative abundance was total n_i phyla×100 per total n_i within samples. The correlation between sponges host with associated mesofauna was determined using Correspondence Analysis, as well as the correlation between sponges antibacterial activity with associated mesofauna abundance (XLStat 2014).

3. Results and discussion
3.1. Result
This research was conducted in midyear of 2016. The seagrass meadow in all sampling site was dominated by Thallasia hemprichii seagrass, followed by the Cymodocea rotundata seagrass (as well as found by Ismet et al 2016, and Ridzqiyyani et al 2018). Pramuka Island has around twenty-three species of Demospongia sponges, yet only 18 species were found and taken from the observation line (belt transect). Those 18 species were identified and examined under stereo microscope. The most dominant sponge species in all four observation sites were Agelas conifera, with relative abundance of 53.34%, followed by Tectitethya crypta (19.74%), Iotrochota arenosa (6.73%) and Plakinastrella onkodes (4.55%), relatively (figure 2).

3.1.1. Sponge associated-mesofauna. All eighteen (18) sponge species were examined, and the associated mesofauna was found from 14 of sponge species, as seen in table 1. There were five different groups of mesofauna that found from all the sponge species. Those groups were Polychaetes, Arthropods, Ophiuridae, Molluscs, and Gastropods, with the highest abundance was the Polychaetes group (figure 3). These invertebrates are defined as mesofauna for it have size less than (<0.5 mm), according to Amsler et al (2009) and Dervash et al (2018). Sponge with the highest associative mesofauna were C. pseudomolitba (Cp) with relative abundance of associative-mesofauna of 29.14%, followed by S. (Euspongia) officinalis tuba (Sot, 19.81%), A. conifera sponge (Ac, 19.81%), C. aruensis (Ca, 11.22%), T. crypta (Tc, 7.34%), and A. citrina (Aci, 6.39%), respectively (table 2).
Table 1. Associated- mesofauna groups of 14 seagrass- sponge species from observation sites (1, 2, 3, and 4) in Pramuka Island, DKI Jakarta.

| sponge species | Polychaetes | Arthropodes | Ophiuridae | Molluscs | Gastropods | Oligochaetes |
|---------------|-------------|-------------|------------|----------|------------|-------------|
| Ac            | √           | √           | 0          | 0        | 0          | 0           |
| Po            | 0           | 0           | 0          | 0        | 0          | 0           |
| Tc            | √           | √           | √          | 0        | 0          | 0           |
| Gd            | √           | 0           | 0          | 0        | 0          | 0           |
| Sv            | 0           | 0           | 0          | 0        | 0          | 0           |
| Ia            | √           | 0           | 0          | 0        | 0          | 0           |
| Spv           | 0           | 0           | 0          | 0        | 0          | 0           |
| Cp            | √           | √           | √          | 0        | 0          | 0           |
| Av            | 0           | √           | √          | 0        | 0          | 0           |
| Sot           | √           | √           | 0          | 0        | 0          | 0           |
| Ag            | 0           | 0           | 0          | 0        | 0          | 0           |
| Aci           | 0           | √           | 0          | 0        | 0          | 0           |
| Ca            | 0           | √           | 0          | 0        | 0          | 0           |
| Oc            | 0           | √           | 0          | 0        | 0          | 0           |

Ac. A. conifera; Po. P. onkodes; Tc. T. crypta; Gd. Geodia sp.; So. S. officinalis; Sv. S. virgultosa (Bowerbank 1866); Ha. Haliclona spp.; Ia. I. arenosa; Spv. Spheciospongia vesparium; Cp. Chalinula pseudomolitba; Av. Amphimedon viridis; Sot. S. (Euspongia) officinalis tuba; Ag. Agelasidae; Aci. A. citrina; Ca. Clathria aruensis; Hs. Halisarca sp.; Oc. Oceanapia sp.; Amc. A. compressa.

Figure 2. Sponge composition in seagrass bed of Pramuka Island. Relative abundance in percentage from all observation sites (Ac. A. conifera; Po. P. onkodes; Tc. T. crypta; Gd. Geodia sp.; So. S. officinalis; Sv. Suberites virgultosa (Bowerbank 1866); Ha. Haliclona spp.; Ia. I. arenosa; Spv. Spheciospongia vesparium; Cp. Chalinula pseudomolitba; Av. Amphimedon viridis; Sot. S. (Euspongia) officinalis tuba; Ag. Agelasidae; Aci. A. citrina; Ca. Clathria aruensis; Hs. Halisarca sp.; Oc. Oceanapia sp.; Amc. A. compressa.)
Figure 3. Relative abundance of sponge associated-mesofauna in seagrass beds
(■ = Polychaetes, □ = Arthropods, △ = Ophiuridae, ◼ = Mollusc and ● = Gastropods).

Table 2. Total number (individual), abundance (individual mm$^{-3}$) and relative abundance RA (%) of sponge associated-mesofauna.

| Phyla       | Ac | Po | Tc | Gd | Sv | Ia | Spv | Cp | Av | Sot | Ag | AcI | Ca | Oc | Total n phyla |
|-------------|----|----|----|----|----|----|-----|----|----|-----|----|-----|----|----|---------------|
| Polychaeta  | 8.0| 0.0| 14.0| 45.0| 1.0| 0.0| 2.0 | 4.0| 3.0| 8.0 | 0.0| 0.0 | 0.0| 1.0| 547.0        |
| Arthropoda  | 0.0| 1.0| 11.0| 0.0 | 1.0| 1.0| 2.0 | 4.0| 3.0| 8.0 | 0.0| 0.0 | 0.0| 1.0| 31.0         |
| Ophiuridae  | 1.0| 2.0| 44.0| 0.0 | 0.0| 0.0| 0.0 | 2.0| 0.0| 0.0 | 49.0| 5.0 | 9.0| 0.0| 112.0        |
| Mollusca    | 1.0| 0.0| 0.0 | 0.0 | 0.0| 0.0| 2.0 | 0.0| 0.0| 50.0| 1.0 | 0.0 | 0.0| 247.0        |
| Gastropoda  | 0.0| 0.0| 1.0 | 0.0 | 0.0| 0.0| 0.0 | 0.0| 0.0| 0.0 | 0.0 | 0.0 | 0.0| 0.0 | 8.0          |
| Oligochaeta | 5.0| 0.0| 0.0 | 0.0 | 2.0| 0.0| 0.0 | 7.0| 0.0| 0.0 | 0.0 | 0.0 | 0.0| 0.0 | 9.0          |
| Total n     | 56.0| 38.0| 70.0| 45.0| 26.0| 1.0| 2.0 | 278.0| 30.0| 189.0| 49.0| 61.0| 107.0| 2.0 | 954.0        |
| Abundance   | 5.3| 3.6| 6.7 | 4.3 | 2.5| 0.1| 0.2 | 26.5| 2.9| 18.0 | 4.7 | 5.8 | 10.2 | 0.2 | 90.9         |
| RA (%)      | 5.87| 3.98| 7.34| 4.72| 2.73| 0.1| 0.21| 29.14| 3.14| 19.81| 5.14| 6.39| 11.22| 0.21| 100.00      |

3.1.2. Associated-mesofauna abundance and its correlation with sponge host. Diversity values of associated-mesofauna were considerably varied within and between sponge species (host), as can be seen in table 2. In general, Polychaetes was found in 11 of 14 sponge species, followed by Arthropoda (in 11 sponge species), Ophiuridae (in 7 sponge species), Mollusca (in 6 sponge species), Gastropoda and Oligochaetes (each in 2 sponge species), respectively. The highest abundance of associated-mesofauna was found in *C. pseudomolitba* (Cp, 26.5 ind.mm$^{-3}$), with Polychaetes as the most dominant individual number (173 individual), as can be seen in figure 4. *C. pseudomolitba* sponge also had the most diverse mesofauna groups, with 5 of 6 mesofauna that found associated with seagrass sponge. Other sponges that have high mesofauna groups number were *T. tethya* (Tc) and *S. virgultosa* (Sv), with each having 4 different groups of associated-mesofauna. However, the abundance of associated-mesofauna in both sponges, Tc and Sv, was quite low, with 6.7 ind.mm$^{-3}$ (RA 7.34%) for Tc and 2.5 ind.mm$^{-3}$ (RA 2.73%), respectively.

Associated-mesofauna in *S. (Eupsongia) officinalis tuba* (Sot) sponge was the second-highest abundance, with 18 ind.mm$^{-3}$ (RA 19.81%), though it only has two groups of mesofauna association, Polychaetes (181 individuals) and Arthropodes (8 individuals). Hence, it can be said it comprised dominantly by the Polychaetes group. This probably due to sponge body structure, which is soft with spongin fiber and lack of spicules, that allowed a soft structure of mesofauna (Polychaetes) borer in the sponge tissues. Other sponges with high Polychaetes individual number was *C. aruensis* (Ca), with small number of Ophiuridae and Mollusca.
Figure 4. Sponge associative-mesofauna abundance, in an average of three slices tissue samples from each line transect (as replicates) from 4 observation sites ( = Oligochaeta, = Polychaetes, = Arthropods, = Ophiuridae, = Mollusc and = Gastropods).

Data analysis on associative mesofauna and its host were using correspondence analysis. The result showed that the correlation between sponge host and the associative mesofauna were about 78.15%, as can be seen in figure 5. This implies that the associative mesofauna abundance and diversity only correlate as much as 78.15% with sponge as habitat. Overall, there were 4 clusters of correlation based on the analysis. Most of sponge host was correlate with Polychaetes and Molluscs groups. Those sponge hosts were A. conifera (Ac), P. onkodes (Po), A. citrina (Aci), S. (Euspongia) officinalis tuba (Sot), C. aruensis (Ca), Geodia sp. (Gd), S. vesparium (Sv), and I. arenosa. Meanwhile, only three sponge host (Tc, Ag and Cp) correlate with Ophiuridae, and two sponge host with Arthropoda (Spv and Oc). This varied distribution and abundance of associated-mesofauna within sponge species, were due to the sponge species body structure and skeleton, including the canal system of sponge structure (Beepat et al 2014).

Figure 5. Correlation between Sponge host and its associated-mesofauna using correspondence analysis (CA). Blue circles were indicated clustering between sponge host (+) with associated mesofauna (*)
3.1.3. **Sponges antibacterial activity and its correlation to the associative-mesofauna.** All sponge hosts were tested against several bacteria, to study their inhibition (antibacterial) activity and its correlation to the associative mesofauna. The assay was conducted using sponge tissue, both the epidermis and endodermis part. The antibacterial assay showed that only six (6) of 14 sponge host that having antibacterial activity against *E.coli*, *S. aureus*, and *P. aeruginosa*. Those sponge species were *T. crypta* (Tc), *Geodia* sp. (Gd), *C. pseudomolitba* (Cp), *S.(Euspongia) officinalis tuba* (Sot), *A. citrina* (Aci), *C. aruensis* (Ca). Amongst all sponge host, *C. aruensis* (Ca) sponge was shown the highest activity against all targeting bacteria, though it still categorized as low to medium inhibition activity, which is between 3-9 mm inhibition zone (Radjasa et al 2007). However, the antibacterial activity of Ca epidermis and endodermis were varied between targeting bacteria, as can be seen in figure 6. Meanwhile, the antibacterial activity of other five sponge tissue were categorized as low inhibition activity (less than 3 mm in diameter of inhibition zone).

![Figure 6. Antibacterial activities of sponge tissue (epidermis and endodermis), showed as inhibition zone (mm), against several bacteria (*E.coli, S. aureus, and P. aeruginosa*).

The antibacterial activity of the sponge host’s tissue was assumed correlated to the inquilism level of the associative mesofauna. The inquilism term is using to define organism that is lodging (living) within other organisms, in this case is sponge, either accidental or intentional. Inquilism usually define as a commensal or mutualistic interaction between organisms and its host (A Dictionary of Biology 2019). In order to correlate the inhibition activity of sponge’s tissue with the inquilism level, a correspondence analysis was conducted. The result showed that the antibacterial activity of sponges and its association with the mesofauna were clustered three groups (figure 7). This association was explained as much as 70.12%, whereas Polychaetes appeared to stimulate the antibacterial activity of *C. aruensis* (Ca) and *S. (Euspongia) officinalis tuba* (Sot) sponges against all targeting bacteria. Meanwhile, even though mesofauna groups of Ophiuridae, Arthropodes, and Gastropodes related to *T. crypta* (Tc) and *C. pseudomolitba* (Cp), it has no correlation with the antibacterial activity of those sponges. As well as relationship between Molluscs mesofauna and *Geodia* spp. (Gd). This result suggests that the highest inquilism level was correlated with Polychaetes as the principal group, that has the highest abundance among other associative-mesofauna (Betancourt-Lozano et al 1998). At the same time, the Polychaetes inquilism of sponges, in general triggered the antibacterial activity of sponges. The association between Polychaetes inquilism and antibacterial activity possibility because Polychaetes could play roles as parasites within sponge.
3.2. Discussion
Seagrass ecosystem is known for its high productivity. Aside from the primary productivity from the seagrass vegetation, benthic assemblages also play an important role in the ecosystem. Studies showed that benthic fauna community in the seagrass ecosystem was influenced by the amount of plant available. Ansari et al (1991) and Barnes and Hamylton (2016) also stated that macrobenthic assemblages, including sponge will have a more diverse and dense community in vegetated area rather than in unvegetated area of ecosystem. Sponge community in Pramuka Island comprised of 23 sponge species, with only 18 species found only in the observation site. This founding has much more diverse sponge species than Demers et al (2015), which found 20 sponge species in Posidonia australis seagrass meadow in Jervis Bay (South-Eastern Coast, Australia). Demers et al (2016) recorded 1110 sponge individual from their observation site, with Tedania (Tedania) sp., Phoriospongia sp.1, and Haliclona spp. as the most widespread sponge species. They also found that the sponges were patchy in distribution with 58% occurrence of the transect sampled. Contrary to that, we found that in multispecific and patchy seagrass vegetation like in Pramuka Island, the most dominant sponge species were A. conifera (Ac) and T. crypta (Tc), which have lobate and massive structure, with more than 60% occurrence in distribution (53.34% of A. conifera and 19.74% of T. crypta). The dominant individual number of these both species possibly related to their ability to utilize sand sediment, which is the highest sediment fraction in the location, as substratum and also incorporated the sand fraction as body inclusion in their structural organization (Cerrano et al 2004). The high number of both sponge species also improved the sponge total individual number (2439 individual) compared to finding of Demers et al (2016).

Figure 7. Correlation between sponge host (•) and its antibacterial activity with inquilism level of associative-mesofauna (•), using correspondence analysis.
The high individual number of *A. conifera* (Ac) and *T. crypta* (Tc), thus, will amplify the associative-mesofauna community that inhabiting those sponge species. On average, both sponge species (AC and Tc) contributed 19.81% and 7.34%, respectively, of associative-mesofauna in relative abundance. The highest abundance of associative mesofauna was found in *C. pseudomolitibea* (Cp) sponge, which has a soft texture, with large internal canal. Faunal abundance is directly related to the sponge mean canal diameter. Thus, the larger internal canals of sponges will improve the associative-mesofauna abundance and richness. This also supported by Ribiero et al (2003) and Beepat et al (2014) that found number of macrofaunal species and individuals and their species richness were moderately significant related with sponge volume and water depth. *S. (Euspongia) officinalis tuba* (Sot) was the second-highest inhabited sponge by associative-mesofauna. This sponge also has a soft texture and large oscula at the lobe summits. Its lifeform and skeletons favoring the Polychaetes mesofauna to live within its body. On the contrary, *C. aruensis* (Ca) have tough, elastic body structure, yet it has high abundance of associative-mesofauna (RA 11.22%), with dominant individual number of Polychaetes (97 ind) and few individuals of Ophiuridae (9 ind). It probably related to the large oscula and numerous ostia on the body surface, that allowed the Polychaetes and Ophiuridae to move along the sponge body tissue. This result suggests that variation of sponge body structure could play roles in the associative-mesofauna species composition and abundance, as mentioned before by Voultiadou-Koukoura et al (1987) and de Britto-Costa et al (2015). In addition to that, seagrass ecosystem as detritus rich environment could stimulate the higher abundance of detritivore and suspension feeder, such as Polychaetes and Molluscs groups (Ansari et al 1991). Hence, it is not surprising, that those two groups of invertebrate also found as dominant associative-mesofauna.

As shown by the Correspondence analysis on sponge host and associated-mesofauna correlation, that there was variation on associated-mesofauna distribution and abundance within sponge species, that related to sponge body structure. Associated-mesofauna from Molluscan group tends to relate with sponge host with firm and brittle consistency with spong in network in the skeleton and many small to moderate opening (Ac, Po, Aci, and Sv). This probably due to its filter-feeding activity that utilizes the water flow in the sponge as feeding aid, as suggested by Beepat et al (2014). Meanwhile, Polychaetes group was correlated with more dense and elastic body structure of sponge, with many large opening (Sot, Ca, Gd and Ia). Polychaetes appeared to favor the internal canals for refugia and feeding on accumulated detritus within the base of sponge (Beepat et al 2014). The Ophiuridae associated with elastic, firm and brittle structure of sponge, with many large openings and internal spong in fiber. This assumed that could serve more spacious room for Ophiuridae movement, and more water passage through the sponge tissue. Hendler (1984) mentioned that there is a brittlestar-sponge association, whereas Ophiuridae could serve cleansing activity within sponge body, whilst sponge provides food and habitat. At the same time, there could be a predatory activity of Ophiuridae organism on inhabitant polychaetes, as explained by Beepat et al (2014). This could explain the lower number of Polychaetes in sponge host, which also inhabited by Ophiuridae. Yet, Sivadas et al (2014) suggest that most sponge species tend to dominated by single taxa of associated fauna. However, this finding could be explored further by doing mesofauna species identification and its relationship with sponge volume, substrate, and morphology.

Interestingly, amongst all sponge host that tested against several targeting bacteria (*E. coli, S. aureus, and P. aeruginosa*), only six sponge species showed an antibacterial activity (Tc, Gd, Cp, Sot, Aci and Ca). These sponge hosts have a close relationship with Polychaetes and Ophiuridae mesofauna groups. Sponge is known could produce various secondary metabolite compounds, that act as antibacterial, antifungal, antiparasitic, antitoxic and antbiofilm. Thoms and Schupp (2007) said that the secondary metabolites production of sponge suggested triggered by sponge externally and internally factor, such as environmental condition, predation level, associative organism and sponge health issue (disease). The associative-mesofauna occurrence is assumed could trigger secondary metabolites activity of sponges, according to Betancourt-Lozano et al (1998). This related to the sponge strategy of protection against
pathogenic bacterial infection that could occur during associative-mesofauna abundancy (Kelly et al 2003, Betancourt-Lozano et al 1998, and Ribiero et al 2003). Parasitic mesofauna could be found in sponge feeding on sponge soft tissue, as well as predation on other associative-mesofauna Huang et al (2008). As for Ophiuridae, previous studies showed that this mesofauna group could utilize sponge as habitat, as well as breeding ground. However the abundance may change seasonally due to the organism growth development. Hence, to confirm the ecological role of Ophiuridae group, further observation should be conducted according to time series on several sponges that harbor high number of Ophiuridae.

Our study suggests that sponge assemblage in the seagrass ecosystem of Pramuka Island contain numerous associative-mesofauna, that varied in individual number and diversity. This variation could be seen within sponge species and intrasponge. This could imply that sponge plays an important ecological role on the organism biodiversity in the seagrass ecosystem.

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