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CORAL REEF RESISTANCE AND RESILIENCE: A CONSERVATION GENETIC PERSPECTIVE IN SUPPORTING CORAL REEF CONSERVATION PROJECT

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Abstract

A coral reef ecosystem is home to thousands of marine species and is utilised for feeding, reproduction and as a nursery ground. Coral reefs are areas of high biodiversity, and typically fish diversity and density are positively correlated with a living coral cover. Hence any threat to the coral ecosystem is also likely to have an impact on a high number of other species and may alter an environmental landscape. For instance, the decline of the coral population may reduce fish's abundance and increase shoreline erosion. Contributions to the decline of coral reefs ecosystem from physical, chemical and biological sources such as increasing water temperatures (due to climate change), pollution, human disturbance and coral diseases. Therefore, it is important to understand factors which are related to the resistance and resilience of coral reef ecosystem.

This review aims to broaden our understanding of coral reef resistance and resilience in the Indo-Pacific region by taking a genetic perspective. There are four primary aspects that are essential for coral resistance and resilience which will be reviewed here; the ability to respond to disturbance, the ability to adapt to the changing climate, the connectivity between coral populations (linked to larval dispersal), and the application of genetics to support coral reef conservation and management project.

This paper is important to support our understanding of coral's adaptability and resistance in facing disturbances such as climate change. Furthermore, it may benefit future conservation projects, as it explains genetic attributes that need to be considered for conservation and management projects such as local genetic diversity.

Keywords: *coral reef, conservation, genetic and population*

I. Introduction

Coral reef ecosystems support thousands of marine organisms. It is estimated that 4,000 fish species depend on coral reef ecosystems, which is almost a quarter of the total marine fish species worldwide (Spalding *et al.*, 2001). The ecosystem mainly formed by a large number of reef-building coral colonies, which belong to the phylum of Cnidarian, and lives symbiotically with microalgae (zooxanthellae) in their body tissue. This tremendously diverse ecosystem, often called by 'the tropical rain forest of the ocean', can be found in the water below 91 m between 18^{o}C to 33^{o}C (Salm, 2006).

However, this ecosystem is threatened by various disturbances from human activities, natural disasters and global climate change. The report of the Status of Coral Reef (Wilkinson, 2008) investigated that 19% of coral reefs worldwide had been destroyed and had never recovered, 15% are under threat, and 20% may be disappeared in the future. Furthermore, NOAA Coral Reef Watch recently reported that coral bleaching events have increased due to the effects of the 2015 El Nino. The coral bleaching continues to be the most widespread and longest events that ever been recorded. It contributes to the 50% and up to 90% of coral mortality from the Port Douglas to the Torrest Strait in the Great Barrier Reefs[1].

Damaged ecosystems do not only have reduced biodiversity, but there are also wider impacts of the ecosystems degradation. The livelihoods of over 500 million people depend on goods and services derived from coral reefs, such as building materials, food, coastal protection and tourism. This includes 30 million people who live on coral atolls: land directly produced by coral reef ecosystems, who will lose their home if the degradation of this ecosystem continues (Wilkinson, 2008).

In the respond to this issue, many conservation programs have been established worldwide. In the Indo-Pacific, the Coral Triangle Initiative was established in 2006. This partnership between six countries aims to reduce the threats to coral reefs and strengthen their resistance and resilience to significant chronic disturbance such as climate change (Wilkinson, 2008). In Indonesia, COREMAP (Coral Reef

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[1] *http://www.coralwatch.org/c/document_library/get_file?uuid=6d71a098-db00-4e21-8066-7be0e6bef438&groupId=10136*

Rehabilitation and Management Program; 1998-2019) uses local community participation to help manage and protect a pristine coral reef ecosystem. However, half of the marine conservation projects worldwide are considered to have failed based on management goal criteria such as monitoring activities, the design of artificial reef, regulation, user conflict and environmental assessment (a review of 30 projects by Baine (2001)). Therefore, it is important to support coral conservation project using all the scientific disciplines, including genetics.

Genetics is a store of information which may describe character, ability and traits of particular species. At a population level, it can represent the diversity of an individual within a population, identify reductions in population size and distinguish differences between populations, including identifying populations that may have importance for conservation. Furthermore, genetic information is crucial for management systems because it explains population connectedness and evolutionary history, which helps to analyse behaviour traits, dispersal and resistance ability (Beger *et al.*, 2014).

The two biggest issues in conservation and management of coral reefs are the resistance and the resilience of the particular ecosystem. Resistance is the ability of the coral reef to resist disturbance or the changing climate by keeping their function and structure (Odum, 1989). Whereas resilience is the capacity of the coral reef to recover from disturbance within a certain period of time (Carpenter *et al.*, 2001). This review focuses on addressing coral reefs resistance factors such as adaptive bleaching and coral symbiont (zooxanthellae); and the resilience factors such as population diversity, spatial connectivity and geographic range. It aims to (1) understand the mechanism of bleaching events following periods of increased water temperatures; (2) describe the genetic diversity of coral; (3) present the spatial connectivity between regions within the coral reef community in the Indo-Pacific; (4) explore the genetic attributes beneficial in supporting coral reef conservation and management project.

A. Understanding the mechanism of bleaching events following the phenomena of climate change

A thirty-year long study of coral reef abundance and the environment demonstrated the type of disturbance affecting the abundance and recovery of the coral reef. The disturbance may not only kill or damage the coral population but may also change their biological and physical environment. In the very worst case, the chronic disturbance caused a great decline in coral cover, and the ecosystem has shown no sign of recovery (Connell *et al.*, 1997).

Furthermore, many studies show that the mass decline of coral reefs is caused by changing seawater temperatures due to El-Nino events and the warmer climate (Hoegh-Guldberg *et al.*, 2007; Winter *et al.*, 1998; Hoegh-Guldberg and Salvat, 1995; Glynn and D'croz, 1990). However, it is also argued that the main causes of the mass decline of coral reef are natural disasters (e.g. storms), human disturbance, predators, chronic diseases and pollution (Bodmer *et al.*, 2015; Edinger *et al.*, 1998; Connell *et al.*, 1997). Human disturbance may be mostly responsible for the severe damage to coral reef ecosystems in the South-east Asian region. The damage caused by irresponsible fishing (using explosives and poisons such as cyanide), water pollution, high sediment flow from coastal development, land reclamation and mangrove deforestation. However, it is estimated that of the 16% of the worlds coral that was damaged by the bleaching events of 1998, 40% have either fully or partially recovered (Côté and Reynolds, 2006). Below is a picture representing coral reef bleaching events in the Indo-Pacific region. It shows that almost all of the ecosystem has been affected by coral bleaching over the last ten years.

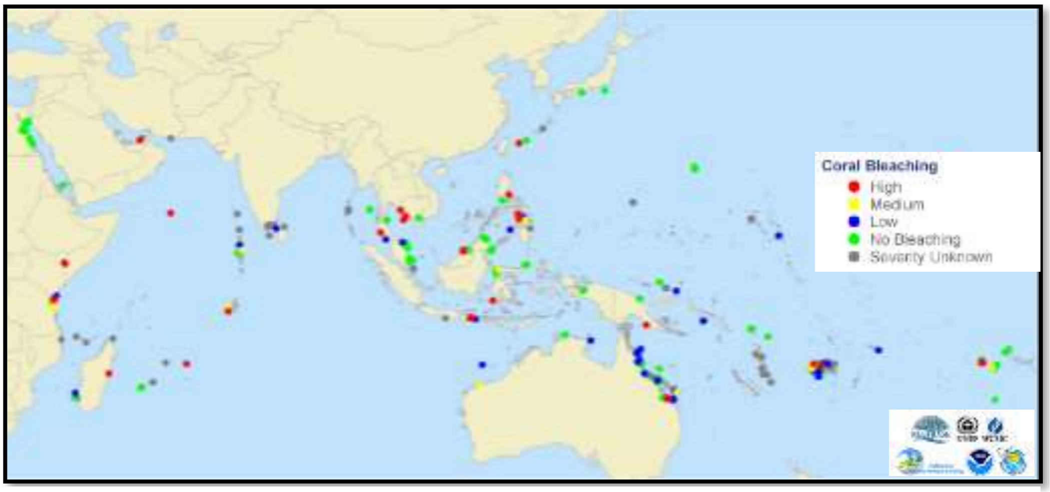

Figure 1: Coral reef bleaching events in the Indo-Pacific region. Data from January 2005 to January 2015.
Source: data and map provided by ReefBase (*http://reefbase.org*)

Bleaching mechanism

It is widely known that coral lives in symbiosis with algae and microorganisms such as bacteria inside their tissue cells. However, the symbiosis between coral and algae (known as zooxanthellae) is believed to be the most significant relationship, as corals are dependent on zooxanthellae as a primary producer. Furthermore, the majority of coral decline caused by bleaching events involves this symbiosis mechanism with zooxanthella, which belongs to the genus of Symbiodinium.

Bleaching occurred when zooxanthellae detached themselves from the coral's tissue. Zooxanthellae phycycally appears in yellow-brown colour because they own various carotenoids, chlorophyll a and c2 (Douglas, 2003). This is in contrast to the coral's tissue which is transparent. Hence it is obvious when bleaching events occur, due to the loss of pigmentation (Douglas, 2003). Firstly, it is important to know the cause of coral bleaching before addressing any mechanism involved. The rise of temperature may be the trigger causing stress which leads to the coral bleaching. However, stress in the organism is not only caused by the increase of temperature but by various abiotic aspects such as salinity, and the change of light exposure. This stress will lead to the production of reactive oxygen species (ROS). However, the toxicity of ROS is removed by the antioxidant system (e.g. carotenoids), causing further damage to the cell. In several cases when the antioxidant system reached its maximum effort of protection, the toxicity is spread massively and destroys the cell leading to metabolic dysfunction (Baird *et al.*, 2009). Furthermore, a review of the mechanisms behind coral bleaching revealed there are several pathways that can in taken (Baird *et al.*, 2009), including (1) a decline in the "D1 protein of photosystem II reaction" within Symbiodium cells (Warner *et al.*, 1999); (2) a change of epidermis and apoptosis of gastrodermis cells (Ainsworth *et al.*, 2008); (3) photosynthesis inhibition caused by *Vibrio shiloi* (Banin *et al.*, 2001).

Adaptive bleaching and coral symbiont (Zooxanthella)

Although it is not clear whether the adaptability of coral is due to their species adaptability or that of their symbiotic (zooxanthellae), it is believed that one of the reasons coral can increase their resilience to withstand environmental stresses such as climate change is because their symbiont can adapt to warmer water temperatures

(Baker *et al.,* 2004). Furthermore, the coral symbiont is critical to support the adaptability of coral, with recent findings showing that certain coral species containing an additional symbiont species (genus Symbiodinium) might have a greater adaptability to the bleaching (Rowan *et al.,* 1997) than those with a single species. Additionally, the survival of the coral in the warmest waters is associated with the newly discovered symbiont *Symbiodium thermophilium* (Hume *et al.,* 2016).

To understand how this recent finding of *S. thermophilium* is connected to the resilience of coral reef, several studies were investigating locations that have suffered from bleaching events due to the El-Nino. The mechanism of bleaching involves the detachment of zooxanthellae. Therefore after bleaching occurred, a particular taxa of zooxanthellae which has a high adaptability of warmer temperature are likely to dominate within the recovered coral population (Starger *et al.,* 2010, Baker *et al.* 2004; Glynn, 1991). In support of this finding, a study in molecular genetics shows that Symbiodinium clade D is more abundant in reef ecosystems after severe bleaching and mortality (43% of colonies containing clade D survived bleaching events) (Baker *et al.*, 2004). The mechanism of symbiont selection in association with increased temperatures may depend on (1) the ability of coral to associate with the new species/clade of zooxanthellae;(2) the resistance of the particular type of zooxanthellae;(3) their ability to adapt to the increased temperature without support from their symbiont (Baums, 2008).

However, the coral species may also contribute to the high adaptability to the changing climate. A particular coral species such as *Porites* sp. can survive bleaching events even though they do not have Symbiodinium clade D as their symbiont (Baker *et al.,* 2004). In the Great Barrier Reef, corals belong to the genus Acropora, and Porites were moderately affected by bleaching events. Whereas bleaching profoundly influenced both these species on Kenyan reefs (McClanahan *et al.,* 2004). It is then summarised that the complex adaptability to bleaching events depends on phylogenetically constrained traits such as the physiology and morphology of coral (McClanahan *et al.*, 2004) and their particular symbiont (Rowan *et al.*, 1997).

B. Genetic diversity of coral

Measures of genetic diversity are important to support the effectiveness of coral reef conservation and management projects, as they may help to explain the variability of coral reef ecosystem resistance and resilience to the changing climate. Genetic diversity in coral reef ecosystems is dependent on variation at the individual level and describes the allelic richness or level of heterozygosity within a population (Baums, 2008). Furthermore, genetic diversity may be related to the ability of a population to respond to environmental disturbance, because the decrease in genetic diversity may reduce coral resistance to withstand climate change (Willi and Hoffmann, 2009).

There are two common ways to measure genetic diversity in coral reefs population. Firstly, by looking at the expected heterozygosity within a population (Nei, 1973). Secondly, by looking to the allelic richness (number of alleles per locus; Beger *et al.*, 2014). Thus, the decrease of allelic diversity will be related to the increase of inbreeding within a population (Baums *et al*., 2012).

Coral reef communities are widely distributed in the Atlantic, Pacific and Asian regions. However, the diversity of coral is far lower in the Atlantic than in the Indo-Pacific. The highest genetic diversity was discovered around Southeast Asia (Spalding *et al*., 2001). Furthermore, using a projected matrix of genetic diversity, a previous study conducted by Kool *et al*., (2011), suggested that reefs in East Indonesia, the Philippines, the Sulu Archipelago and the Papua New Guinea, are expected to have high genetic diversity with the mean diversity in Indonesia being about Hz = 0.48.

There has been no further explanation as to why a particular area has a high genetic diversity. If we look into the biodiversity of coral in the Coral Triangle, it is reported that this area has the highest coral biodiversity worldwide. But it is important to remember that genetic diversity and biodiversity may increase gradually on different time-scales (Rotondo *et al.*, 1981). Thus, the highest regions of biodiversity may not correlate with the highest regions of genetic diversity.

Table 1 Genetic diversity of coral among places

No.	Location	Coral species	AMOVA analysis (F-statistic)		Genetic marker
1	Papua (Raja Ampat, Teluk Cendrawasi, Fakfak/Kaimana)	*Pocillopora damicornis*	among localities	-0.028	Microsatellite
			among localities within regions	0.158	
			within localities	0.132	
		Seriatopora hystrix	among localities	-0.068	
			among localities within regions	0.324	
			within localities	0.370	
2	Great Barrier Reef (Lizard Island, Davies Reef and Heron Island)	*Acropora cuneata*	within locations	0.067	Allozyme
			among locations Great Barrier Reef (GBR)	0.089	
			Within GBR vs. One location (700 km apart)	0.287	
		P. damicornis	within locations	0.045	
			among locations Great Barrier Reef (GBR)	0.024	
			within GBR vs. One location (700 km apart)	0.153	
3	Southwest Australia	*P. damicornis*	among High-latitude coral reef (HLRs)	0.320	Allozymes
			HLRs vs GBR	0.240	
			HLRs vs GBR	0.000	
4	Lord Howe Island	*P. damicornis*	within population	0.102	Allozymes
5	GBR	*P. damicornis*	among sites (one tree island)	0.062	Allozymes
6	Along the coast of Kenya and Tanzania	*P. damicornis*	Among populations	0.023	Microsatellite
7	Indonesia	*P. damicornis*	among populations from Aceh to Manokwari	0.063	Microsatellite
		S. hystrix	among populations from Aceh to Manokwari	0.171	

References: (1) Starger *et al*., 2013; (2) Ayre and Hughes, 2004; (3) Miller and Ayre, 2008; (4) Miller and Ayre, 2004; (5) Sherman *et al*. 2006; (6) Souter *et al.* 2009; (7) Starger *et al.* 2010.

However, a review of coral population genetics in the Indo-Pacific region (see Table 1 above) drew several conclusions regarding genetic diversity within or among particular areas. *Firstly*, the genetic diversity of coral may depend on the coral species and their geographic area. It was discovered that genetic diversity declined with an increase in latitude (see case study number 3 in Table 1). The study demonstrated that Pocillopora morphology and genetic diversity is lower than other species such as Acropora and Montipora (Pinzón *et al.*, 2013). Furthermore, the genetic diversity of *Porites lobata* in Central Pacific is lower than in Eastern Pacific (Baums *et al*., 2012).

Secondly, the management system within the area may also contribute to the level of genetic diversity. In the Great Barrier Reef, Marine Protective Areas (MPA) showed higher genetic diversity compared to non-protected areas (Miller and Ayre, 2008).

Thirdly, genetic diversity has a strong connection with larval dispersal that will be discussed in the subsequent section. For example, genetic diversity among Lord Howe showed high levels of subdivision (see case number 4). It describes low larval connectivity with even small distances (sites separated by a kilometre). The significant genetic subdivision (F_{st} 0.102) was considered to be a result of inbreeding population from sexual reproduction (Miller and Ayre, 2004).

Overall, most of the studies revealed that significant genetic differentiation was found at large spatial scales. However, a study of coral reef populations in Africa (see case study 6) showed that less than 10 km separation showed significant genetic differentiation (Souter *et al.*, 2009).

Although it is not clear what factors are contributing to the variance in genetic diversity between sites, or to the genetic structure of populations, it has been suggest that the use of different molecular markers between studies is one of the factors contributing to the differences (Kool *et al.*, 2011; Underwood *et al.*, 2007). For example, a most common marker used in the genetic analysis for coral diversity are allozymes and microsatellites. Using microsatellite allow us to analyse both nDNA and organelle DNA polymorphism. Furthermore, analysing mutation rates also possible for intrapopulation studies. Whereas allozymes may detect the low levels of polymorphism in a very limited range of nuclear-encoded enzymes (Lowe, et al., 2009). Moreover, it may give less accurate gene variation analyses due to codon redundancy and substitution of nucleotide (Nei, 1987).

However, knowing the genetic diversity may improve our understanding of the characteristics of sites, and may help determine conservation priorities. For example, in Indonesia areas of high genetic diversity are located around Sulawesi and Flores

Island (within the Coral Triangle region, see Figure 2). Both of these locations may be considered as a larval sink or the population that could not survive without receiving larval supply from another region (Pulliam, 1988). Whereas, the outer area of the Coral Triangle may be a larval source or the population that could survive without external larval supply, as they possess a lower genetic diversity. Thus, it is believed that the outer area of the Coral Triangle, which has a low genetic diversity, may need to be protected as it is more prone to the effects of the climate change than the inside area (Kool *et al.*, 2011).

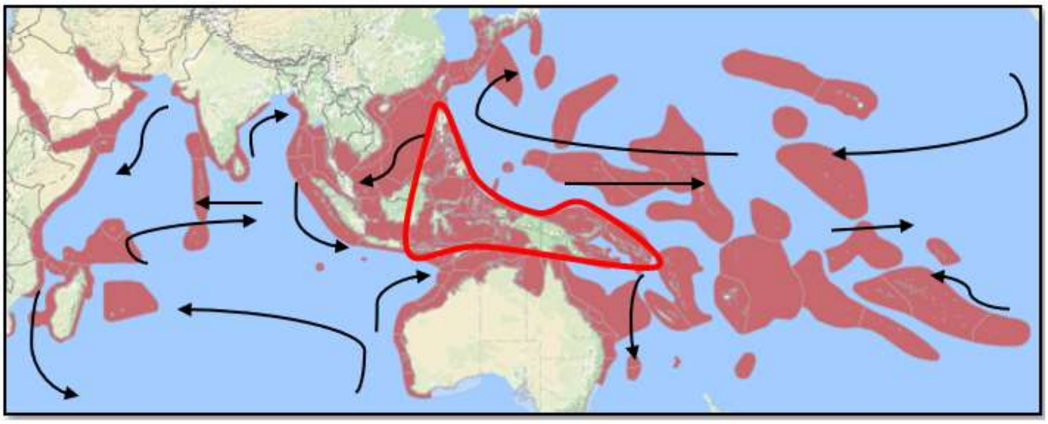

Figure 2 The geographic distribution of Pocillopora in Indo-Pacific region. The red-triangle represents the area of the Coral Triangle Region, and black arrows represent the sea-surface current (Briggs, 1974).
Source: data and map provided by Coral of the World, *http://www.coralsoftheworld.org*

Looking closely at the Pocillopora species, Figure 2 above shows a geographic distribution of Pocillopora in Indo-Pacific regions. The sea-surface current pattern clearly affects the dispersal of coral larvae. Moreover, the long distances of larval dispersal are also influenced by the strong sea-surface currents (Gaines, *et al.*, 2003). Overall, genus Pocillopora in Indo-Pacific is dispersed locally, and their dispersal was influenced by sea-surface currents. Supporting this finding, a study of genetic diversity analysis of P.*damicornis* between (1) Aceh Island and Krakatau; (2) Bali and Lombok; and (3) Krakatau and Biak in Indonesia region showed there is no significant genetic diversity different between the two populations (Starger *et al*. 2010).

C. Spatial connectivity between regions within coral reef community in Indo-Pacific

Understanding genetic connectivity is essential for determining the demographic relatedness between regions, and understanding which sites are likely to be larval sinks or sources and explaining the character of population scale (Cowen *et al.*, 2002). It is closely related to both the larval dispersal and its patterns between regions which are responsible for shaping population genetic structure. Furthermore, the physical attributes such as ocean currents may play a greater role in larval dispersal pattern (this will be discussed in a subsequent section). However, based on the exploration of larval dispersal patterns in many studies, it may show a different result because the analysis mainly depends on the historical factors, life-history traits and type of genetic marker used (Kool *et al.* 2011).

The larval dispersal refers to the ability of larvae to transform into a new individual coral. The ability will depend on the species and period of larval survival (Starger *et al*. 2010), the distance of larvae to attach into a new habitat (e.g. the ability of larvae to travel more than 60 km) (Underwood *et al.* 2007), and the availability of suitable habitat (Kool *et al*. 2011). For instance, increased larval survival time will contribute to an increased dispersal distance; for example, the larvae of *Seriotopora hystrix* dispersing from Scoot Reef can survive between 24 to 48 hours, hence their dispersal is considered to be locally limited, with no dispersal further than 60 km identified (Underwood *et al.* 2007). In contrast, *Pocillopora damicornis,* tend to have a greater dispersal distances than *Seriotopora hystrix* (Starger *et al*. 2010), because of its longer planktonic larval residence time (Pinzon *et al*., 2013). Furthermore, larvae from Indonesia which enter to the Pacific region but do not pass the suitable habitat for coral to grow will lose and die (Kool *et al*. 2011).

The larval dispersal pattern refers to the physical attributes that contributed to the larvae flow such as oceanic current. For instance, the low genetic interconnectivity between Asia and Pacific regions is suggested to be a result of the Halmahera eddy which pushes larvae back into the Pacific (Arruda and Nof, 2003). Furthermore, the spatial connectivity between Mid-Pacific regions seems to be weak because of a high level of mortality due to the geographic isolation (Kool *et al*. 2011).

Low genetic connectivity is also identified in the Indo-Pacific region due to geographic isolation where reefs of the eastern area of the Coral Triangle and the Pacific are genetically distinct to reefs in Southeast Asia, although the high genetic connectivity is present within the South-east Asian region (Kool *et al*. 2011).

D. The recovery of coral reef population

The ability of coral reefs to recover quickly from disturbances is necessary to maintain its function and services. However, a destroyed population depends entirely on the supply of larvae from other sites to rebuilt and regenerate their population. If the population does not receive larvae donors, then the recovery may be slower or non-existant, and it will increase the probability of non-random mating (Underwood *et al.* 2007). Thus, the recovery of a coral reef is correlated to the degree of larval dispersal and genetic connectivity between locations. Unfortunately, many coral species such as *Seriatophora hystrix* and *Pocillopora damicornis* have local larvae dispersal of less than 60 km (Underwood *et al.* 2007). Hence when large areas are affected by bleaching events, natural recolonization is reduced or unlikely.

In contrast to this, a study of the new population of coral in Krakatau that was naturally restored after the volcanic eruption in 1883, showed that the new population has a higher genetic diversity than other sites in Indonesia (Starger *et al*. 2010). It is suggested that the increase in environmental heterogeneity may increase the genetic diversity within the population (Underwood *et al*. 2007).

E. Reef Conservation and Management Project

The success of coral reef conservation management needs genetic information to understand various issues, such as adaptability, diversity, mating strategies and prioritising locations for protection. There are several genetic attributes possible to support conservation issues such as genetic diversity of the site, genetic distinctness of sites, historical rates of gene flow among sites, self-recruitment rates of sites and hybrid zones (Beger *et al*. 2014). All of the genetic information above could be used for a particular objective of conservation that is needed to achieve. Several genetic studies for coral reef conservation project can be found in Table 2 below:

Tabel 2 Genetic studies to support conservation efforts in several areas

No.	Genetic study	Method	Coral species	Application
1.	Understanding genetic connectivity and dispersal pattern to increase the resilience of coral reef ecosystem in Marine Protected Area (MPA) network	DNA sequencing and population genetic analysis (pairwise Fst value)	*Acropora hyacinthus*	This study aims to examine the effectivity of MPA network in Palau's Island. The result of the study suggests that MPA should be expanded around the island as they found a low genetic connectivity, low larval exchange and self-recruitment problem.
2.	Measuring the expression of candidate heat response genes in three genetically distinct colonies of coral.	Using vivo assay for mitochondrial activity to understand the metabolism response.	*Acropora millepora*	This study helps to understand the coral genetic determinants of thermal tolerance. Furthermore, a future study which involves coral symbiont may enable scientist to identify loci that control the temperature response expression in both coral and coral symbiont's gene.
3.	Analysing changes in coral gene expression related to the change of water temperature, salinity and UV light.	Using cDNA array of coral genes for genetic analysis.	*Montastraea faveolata*	Identify specific gene expression in respond to the change of environment.
4.	An experimental study which provides a new genetic analysis method to understand coral's stress response and evolutionary adaptation to the climate change.	Sequencing and transcriptome using 454 GSFIx	*Acropora millepora*	Understanding potential ability for coral to adapt to the climate change (the increase of water temperature) of coral reef ecosystem from Magnetic Island, Australia

References: (1) Cros, *et al.*, 2017; (2) Meyer, *et al.*, 2009b; (3) Edge *et al.*, 2005; (4) Meyer, *et al.*, 2009a.

The design of marine conservation sites will involve genetic measurement of coral reef connectivity within and among regions (see case number 1 in Table 2). The information may describe genetic linkages and the possibility of larval exchange between regions to ensure the ecosystem is self-sustaining and able to maintain the high level of biological diversity (Briggs, 2003). Furthermore, this information should also be used to decide the size of conservation area (Palumbi, 2003; Cowen *et al*. 2002). In this case, a study on genetic connectivity of coral reefs in the Indo-Pacific demonstrated that genetic connectivity is mostly limited to regions. It showed that self-recruitment was that greatest source of larvae throughout the year. Thus, conservation efforts aimed at maintaining coral reef ecosystems in Indo-Pacific should focus locally (Kool *et al*. 2011).

Moreover, there are several ways to restore the destroyed reef population, such as coral transplantation; *in-situ* and *ex-situ* coral nurseries; and the provision of artificial reefs. Therefore, based on genetic perspective, a restoration project that uses very limited coral donors from another site (for coral transplantation) can reduce the gene flow through hybridization (Young *et al*. 1996). Furthermore, the understanding of genetic population may be beneficial to reduce factors causing the loss of fitness in restored populations. It may include founder effects, genetic swamping, inbreeding and outbreeding (Baums, 2008).

Other genetic studies (see case number 2 to 4 in Table 2) may support our understanding of coral resistance to the rise of temperature due to the climate change. In the future, these studies may develop to the population genetic level which describes allele frequency and adaptation in supporting our understanding to the future of coral population threaten by climate change (Meyer *et al*., 2009b).

Furthermore, if the aim of conservation or restoration project is to increase fauna in surrounding areas (e.g., fish, crustacean, etc.), genetic diversity of the coral reef should also be considered. A study in plant ecosystem (the relationship between plant *Solidago altissima* and arthropoda *Rhopalomyia solidaginis*) showed that the genetic composition of the plants influenced the diversity and distribution of the *R. solidaginis* in the ecosystem (Crawford *et al*., 2007). Additionally, genetic information can be used to decide appropriate coral donors, the spatial arrangement of transplanted coral and monitoring the performance of F2 (transplants) (Baums, 2008).

Conclusion

The threats of coral reef ecosystem are associated with several disturbances such as human activities, natural disaster and climate change. It is likely possible to reduce the threats from human by increasing social awareness of people to protect the reefs. However, an unprecedented threat such as natural disaster and climate change are harder to control. Therefore, it is important to understand how coral responds to the changing environment by studying their resistance and resilience. A genetic analysis of coral reef is important to support our understanding of resilience factors such as adaptive bleaching and coral symbiont, and resilience factors such as population diversity, spatial connectivity and geographic range.

The application of genetic study in coral reef conservation and management is also vital to support the ecosystem sustainability in the future. Overall, Indo-Pacific coral reefs population is dispersed locally with genetic connectivity is no further than 60 km (vary among species and regions). Therefore, conservation project should be managed locally with the network design between marine reserves should be built closely one to another. Furthermore, in designing Marine Reserve Areas, one should consider choosing places which are a larvae source (has a lower genetic diversity) and taking coral donors from a place which is a larval sink (has a higher genetic diversity). Looking at the resistance factors, it is believed that a particular coral species such as *Porite*s sp. and *S.symbiodinium*, as the coral symbiont, are highly resistance to the warmer temperature. Thus, considering these species for coral donors to rebuild the destroyed reefs is suggested.

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