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High genetic connectivity in a scleractinian coral (*Lobophyllia corymbosa*) around Sulawesi, Indonesia

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Abstract. *Umar W, Tassakka ACMAR, Jompa J. 2019. High genetic connectivity in a scleractinian coral (*Lobophyllia corymbosa*) around Sulawesi, Indonesia. Biodiversitas 20: 3484-3492.* The life cycle of scleractinian corals begins with a pelagic larval phase subject to the influence of currents, with the potential to disperse propagules over vast geographical distances. We investigated the mitochondrial COI genome to investigate genetic population structure and potential biophysical barriers (in particular water mass movements) that could affect connectivity between populations in the seas around Sulawesi, in the Indonesian Coral Triangle. *Lobophyllia corymbosa* was selected as representative of corals with a broadcast spawning reproductive strategy and relatively long Pelagic Larval Dispersal (PLD) period. Analysis of mtDNA sequences from 103 colonies collected at depths of 3 to 10 meters in 4 locations (Manado, Toli-Toli, Spermonde, and Wakatobi) resulted in F_{ST} = 0.00632, indicating no genetic isolation or significant differentiation. The tendency towards genetic homogeneity across the entire population indicates that gene flow has been maintained, most likely through widespread dispersal of propagules within the study area. The dominant surface flow directions recorded during the reproductive period of this species provide support for this gene flow model, as the currents could enable dispersal and recruitment patterns maintaining connectivity between *L. corymbosa* populations around Sulawesi.

Keywords: COI, Sulawesi, current patterns, larval dispersal, Scleractinian coral

INTRODUCTION

Genetic connectivity, biological factors, and oceanography condition are critical information partitions in the design of the management of marine conservation area networks (Palumbi 2003). Genetic approaches are currently used as tools to provide information which is useful or even necessary to support efforts to conserve aquatic organisms; for example, a study by Lundgren (2011) found that different genotypes of a coral (*Acropora millepora)* showed different responses to stresses experienced over a range of periods. Such information on the association between genetic variation found in individual corals and their ability to tolerate specific disturbances could be used to manage and predict the health of coral reefs in the future.

The principles of genetic connectivity in water differ from those which obtain on land. Changing water conditions, the length of organism life cycles, and the influence of several other natural factors can greatly influence the aquatic communities that are formed, and the nature of the networks of aquatic ecosystem (Cowen and Sponaugle 2009; Helberg 2009). Physical water movements, e.g. water flow or currents, become the prime mover in the process of distribution and migration of species possessing a planktonic phase (Nathan and Muller-Landau 2000; Strathmann et al. 2002; Mayorga-Adame et al. 2017). In particular, for the many species with planktonic larvae, the duration of the PLD phase is a critical factor, while the effects of anthropogenic activity, habitat, and pollution are also essential things to consider (Connolly and Baird 2010).

Geographically, Indonesia is flanked by both the Pacific Ocean and the Indian Ocean, resulting in extremely complicated flow patterns within the Indonesian archipelago. In addition to the dynamics of the Indonesian Through Flow (ITF) that moves under the thermocline layer and carries biological material from the Pacific Ocean to the Indian Ocean (Timm et al. 2017), complex surface flows also become a transportation medium for marine organisms whose dispersal and/or settlement phases take place in shallow waters.

Sulawesi is located in central Indonesia, within the geographic bioregion referred to as the Coral Triangle (Briggs 2009). The waters around Sulawesi and its satellite archipelagos are considered as rich in biodiversity (Veron et al. 2009), but also as being among the most threatened (Burke et al. 2006). The small islands and island groups around the main island of Sulawesi are generally close together and could be used as transit areas or stepping stones for the attachment of migrating coral larvae as they near the end of their planktonic dispersal phase. The larvae of these sessile animals can move following the flow from the location where they were spawned to areas that will become a place to settle, live and grow, and eventually spawn in their turn. This displacement can take place over a distance of several thousands of kilometers, depending on the duration of the coral larvae PLD phase and

oceanographic conditions in the area (Vollmer 2007; Lequeux et al. 2018).

The bipartite life cycle of coral organisms, adhering to the reef substrate during the sessile growth and adult phases and floating in the water column during the pelagic larval phase, allows these organisms to disperse and colonize other reef areas (Mayorga-Adame et al. 2017). The natural distribution of corals in the oceans is supported by the flow of water masses and other geographical movements within a given area. The effectiveness of this natural coral distribution strategy is reflected in the diversity and the percentage of coral cover in particular waters (Hutabarat 2001). In Indonesia, the most extensive coral reefs are found in the eastern part of the country, including the waters around Sulawesi, covering an area of approximately 862,267 hectares (Giyanto et al. 2017).

Scleractinian corals, in general, adopted one of two main reproductive strategies (Shlesinger et al. 1998) These are so-called "brooders" where fertilization is internal, and the fertilized eggs are brooded during their early larval development before being released into the water column, and broadcast spawners, where eggs and sperm are released into the water column where fertilization occurs. Typically, brooding corals have a shorter PLD phase than broadcast spawners (Atoda 1947; Baird 1998). Research on the brooding coral *Acropora cervicornis* (Hemond and Vollmer 2010) in the Caribbean Sea and the waters around Florida, found a strongly differentiated genetic structure indicating minimal gene flow between these two regions. The question arises as to whether such a marked genetic structure might be found for broadcast spawners, or whether their prolonged PLD phase could maintain connectivity and genetic diversity across similarly large distances and potential geophysical barriers. A lifestyle with external fertilization, and therefore a more prolonged PLD phase to "drift" in the water column, could have a distinct advantage because it should increase the opportunity for larvae to be dispersed far from their place of origin, and to maintain relatively even and high levels of genetic diversity across wide regions.

This study focused on the genetic connectivity of a broadcast spawning coral *L. corymbosa* in the seas and archipelagos around the island of Sulawesi. Unlike *A cervicornis*, this scleractinian coral is rarely exposed in the media and has not been extensively used in research; however, *L. corymbosa* has commercial value as an ornamental coral (Yusuf et al. 2019) and is ubiquitous on reefs around Sulawesi (Umar et al. 2019). The study aimed to combine the analysis of genetic characters (mitochondrial DNA COI sequences) of *L. corymbosa* populations at strategic sites around Sulawesi with hydrodynamic information in order to determine the genetic structure and evaluate the processes underlying the observed distribution of genetic diversity and inferred connectivity patterns. The study should thus provide crucial data to inform marine conservation management in the seas around Sulawesi.

MATERIALS AND METHODS

Sample collection

The *L. corymbosa* fragments used in this study were collected during March 2018 from four sites around Sulawesi (Table 1). These sites (Manado, Toli-Toli Spermonde and Wakatobi) represent the four corners of the Sulawesi region which is bisected by the equator. Each sample (coral fragment) was taken from a different colony, with a distance of 2-10 meters between colonies. This distance was determined in order to minimize the likelihood of collecting samples from genetically identical clones due to asexual reproduction (fragmentation) (Hemond and Vollmer 2010). The samples were collected at depths of 3-10 meters by cutting 3-5 cm fragments of each colony using a hammer and chisel. Each collected sample was preserved in ethanol (95-97%) in a labeled jar and stored at room temperature.

Molecular analysis procedures

The DNA extraction was carried out using standard DNeasy Blood and Tissue kits from Qiagen and following the manufacturer's protocol. Extraction product that was not used immediately was stored at 4ºC (short term) or -20 ºC (longer-term). The PCR (Polymerase Chain Reaction) amplification was carried out in 0.2 ml tubes with a total reaction volume of 26 µl using a previously tested MyTaq RedMix (Bioline) reagent master mix (Umar et al. 2019) and mt COI CAGG CGCT ATGT TAGG AGATG as forward primer and mt COI CCCG CTAA TACA GGCA AAG ATA as a reverse.

The PCR protocol was initiated by pre-denaturation at 95ºC for 15 min, followed by 38 cycles (denaturation at 94ºC for 1 min, annealing at 53ºC for 1 min, and extending at 72ºC for 105 s), with a final extension stage at 72ºC for 10 min. PCR product obtained from each of the 103 samples was sent for Sanger sequencing (Kortschak et al. 2003) to the Berkeley Sequencing Center. The sequencing results were edited and aligned using MEGA 6 software (Tamura et al. 2013). The sequence data have been uploaded to the Genbank library with accession numbers MK905084-MK905186 (provided in Table S1-supplementary material).

Table 1. List of sampling sites and number of samples collected at each site in Sulawesi, Indonesia

Region	Study site	Number of samples
Northeast	Manado	23
Northwest	Toli Toli	26
Southwest	Spermonde (Barrang Lompo and Badi Island)	28
Southeast	Wakatobi (Hoga and Kaledupa Island)	26
Total		103

Data analyses

Genetic population statistics

The edited sequence data (Table 1, n = 103) were analyzed by using DNAsp. 5.10 (Rozas et al. 2003; Librado and Rozas 2009). The output included haplotype data and grouping information, both of which were used for further analysis. Using the haplotype data, we tested the deviations from standard values of Tajima's D (Tajima 1989), Fu and Li's D, and Fu and Li's F (Fu and Li 1993).

Genetic population structure and network

The genetic population structure was produced using the Analysis of Molecular Variance (AMOVA) routine (Excoffier et al. 1992) in Arlequin 3.5.2 (Schneider et al. 2000). To evaluate the level of differentiation between populations in the structure produced, *p*-values were used at the 95% level of confidence ($\alpha = 0.05$). To evaluate the genetic distance between populations, the pairwise difference-distance method was used to produce overall and paired F_{ST} values. Within population, F_{ST} values should be zero, and significant genetic differentiation would be indicated by F_{ST} values greater than 0.05.

RESULTS AND DISCUSSION

Gene flow and diversity

The total length of the edited sequences obtained was 449 base pairs and 103 sequences from four locations (Table 1) comprised eleven unique haplotypes (Table 2). Of the four sites, the Spermonde Archipelago had the lowest diversity in terms of nucleotides ($\pi = 0.00650$) and haplotypes (h = 0.53175). The Manado population had the highest nucleotide and haplotype diversity ($\pi = 0.00919$ and h = 0.72727). The theta values (h_{seq} and h_{site}) and neutrality tests (Tajima D, Fu & Li D, Fu & Li F) did not show any significant deviations from neutrality. mtDNA haplotypes

The proportion of the most common haplotypes was relatively similar between regions and did not appear to be significantly influenced by large scale spatial conditions. However, the distribution of certain haplotypes appeared to be unique to one or two populations. Haplotypes 1, 2, 3, and 6 (h1, h2, h3, and h6) were found in at least two populations. However, the remaining haplotypes were only found in one population and did not appear to have dispersed to other populations or regions (Table 3). Only the Spermonde site did not have any unique haplotypes among the specimens collected in this study.

Genetic structure

Our results show little genetic differentiation formed between the populations of *L. corymbosa* in the four study locations around Sulawesi, as reflected in the AMOVA results (Table 4). The genetic structure among the four populations was quite low, with an all-site F_{ST} value of 0.00632 (<0.05), indicating high levels of gene flow in the waters around Sulawesi. The distance between study sites was approximately 450 km to 1000 km. Thus, the dispersal of genetic material from this coral species appears to occur on a regional scale (450 km or more).

Table 2. Observed haplotype diversity of *Lobophyllia corymbosa* (437 basepair Control Region I mtDNA sequences)

Population	Nt	S	#hap	h	π	h_{seq}	h_{site}	Tajima D	Fu & Li D	Fu & Li F
Manado	23	10	6	0.72727	0.00919	2.70943	0.00672	1.76351	0.41388	0.94365
Toli- Toli	26	12	5	0.56333	0.00820	2.64833	0.00657	0.99579	-0.12310	0.24605
Spermonde (Badi and Barrang Lompo Island)	28	8	3	0.53175	0.00650	2.05579	0.00510	1.29898	1.32679	1.53731
Wakatobi (Hoga and Kaledupa Island)	26	9	5	0.59544	0.00792	2.33498	0.00579	1.66469	0.80510	1.24053

Notes: Total number of sequences analyzed per population (Nt), number of polymorphic sites/segregating sites (S), Number of haplotypes (#hap), Haplotype diversity (h), Nucleotide diversity (π), Theta per sequence (hseq) and Theta per site (hsite).

Table 3. Observed haplotypes in four *Lobophyllia corymbosa* populations around Sulawesi

Haplotype (h)	Manado	Toli-Toli	Spermonde (Badi and Barrang Lompo Island)	Wakatobi (Hoga and Kaledupa Island)	Total
h1	10	5	7	7	29
h2	7	16	18	16	57
h3	1		3		4
h4	1				1
h5	1				1
h6	3			1	4
h7		2			2
h8		1			1
h9		1			1
h10				2	2
h11				1	1
Total	23	25	28	27	103

Table 4. Genetic structure of four *Lobophyllia corymbosa* populations around Sulawesi based on AMOVA.

Source of variation	d.f	Sum of squares	Variation components	Variation (%)
Between populations	3	6.177	0.01125 Va	0.63
Within population	99	175.202	1.76972 Vb	99.37
Total	102	181.379	1.78097	
F_{ST}	0.00632			

Table 5. Distance analysis of the pairwise difference based on F_{ST} values between four *Lobophyllia corymbosa* populations around Sulawesi

	Manado	Toli- Toli	Spermonde (Badi and Barrang Lompo Island)	Wakatobi (Hoga and Kaledupa Island)
Manado	0.00000			
Toli- Toli	**0.01413**	0.00000		
Spermonde (Badi and Barrang Lompo Island)	0.07628	**-0.01283**	0.00000	
Wakatobi (Hoga and Kaledupa Island)	**0.00347**	**-0.02818**	**-0.01661**	0.00000

Note: Significance level: < 0.05

The paired F_{ST} values (Table 5) ranged from 0 to 0.07628, indicating different levels of genetic population connectivity between individual sites within the study area around Sulawesi. The pairwise F_{ST} was lowest between the Spermonde and Toli-Toli populations (F_{ST} = -0.01283), and highest between the Spermonde and Manado populations (F_{ST} = 0.07628).

Discussion

*Genetic diversity and connectivity within Sulawesi Scleractinian Corals (*Lobophyllia corymbosa *as a representative species)*

The high gene flow with Sulawesi waters indicates substantial distribution of genetic material in the region. Genetic diversity and recruitment of larvae should be good for restoring the condition of coral populations that are vulnerable to environmental changes. High genetic variation in a location has been significantly associated with high population size in an area (Hemond and Vollmer 2010). However, several researchers have also stated the opinion that if genetic changes occurred because efforts for self-defense against current environmental changes were not lethal and were passed down to the next generation, it would increase variation in the population. However, if the changes were lethal, they would reduce the size and diversity of the population.

The level of genetic variation observed in *L. corymbosa* in Sulawesi waters was reasonably good based on the genetic diversity index developed by Nei (1987). Several factors could contribute to high genetic diversity in a population, including gene mutation, reproduction, migration/distribution, and differential natural selection (Chiu et al. 2013; Scitable 2014). The Manado population had the highest genetic variation in the molecular marker used (mtDNA COI fragment), followed by the Wakatobi, Toli-Toli, and finally the Spermonde in the waters of southwest Sulawesi. The genetic variation was closely related to the number of haplotypes in a population, as seen in Table 2. Overall, the frequency and proportion of the emerged haplotypes in each population indicate a reasonably even distribution. The geographical position of Manado, on the northern coast of Sulawesi, may be an important factor as it should enable this area to receive genetic material from the Sulawesi Sea to the west as well as from the Pacific Ocean to the east. It was suspected that barriers to gene flow might exist between these locations, based on the location and geographical complexity of Sulawesi and the waters around this island. The lack of significant genetic structure in the *L. corymbosa* population in the sampling area was unexpected; not only because the sampling distance between locations was 450 km or more, but also because the four sites have different environmental conditions, for example, different seas (e.g. Makassar Strait and Banda Sea) as well as straddling the north and south hemispheres. The absence of significant genetic differentiation indicates that, at least for this broadcast spawning coral, gene flow within the region is quite high at regional levels or even more widely. However, it is possible that one reason for this apparent lack of structure and low differentiation is the limitation of the sampling design used in this study. The results of a study on clownfishes and sea squirts in the Spermonde Islands by Timm et al. (2017) found fine-scale gene flow patterns which were limited to this small scale region.

The high gene flow that crossed the waters of Sulawesi in tandem with the rate of the current surface could be a trigger for high productivity for corals that was quite good between populations. Genetic diversity and high recruitment of larvae in each population could help to restore coral populations that were at risk or even damaged (Hemond and Volmer 2010; Lundgren 2011). If we look at the dominant of the current pattern in Figure 1, the possibility for the disperse of biological material for organisms with a low degree of flexibility was quite significant. The distribution of material regionally or on a large scale in Sulawesi waters had a high chance, but it did not rule out the possibility that similar things would happen on a small scale.

Considering that target coral larvae reproduced throughout the year, making genetic material from spawning results could be effectively distributed in various connected areas (Chiu et al. 2013). The low fixation value predicted the existence of gene flow that belongs to the entire population, which was likely to be influenced by the transport media from the genetic material itself. The long-life cycle of the organism's target starting from the larval phase made the phase of drifting and transported by water flow would cause the displacement of these larvae quite fast. Oceanographic processes could not fully explain low genetic differentiation at the study site. The possibility of a better and correct explanation for the low genetic structure in the population was that the structure was blurred by the *non-equilibrium* process that was geographically from Sulawesi waters. The same thing happened in Philippine waters, a study conducted by Casilagan on *Tripneustes gratilla* was found no evidence for significant differences of population structure data obtained although spatially, the sampling points they did were quite far, ranging from 116-1060 km (Casilagan et al. 2013).

The high gene flow in each sampling population illustrated that the connectivity between populations in Sulawesi waters was quite functional. The linkages formed an ecological network, especially in the Scleractinian coral, where *L. corymbosa* was the representative of the spawner type. This relationship provided goals for the preservation of coral reefs in Sulawesi waters, which was also said to be the center of *Indonesian Coral Triangle.*

The role of current patterns

The role of physical oceanographical factors on the dispersal of coral larvae appears to be very influential in this case, It should be borne in mind that, as reported by Johannesson et al. (2018) in the North Sea, such currents could carry biological organisms for hundreds of kilometers. Observations by teams from Hasanuddin University indicate that most large-polyped corals, including *L. corymbosa*, tend to reproduce (spawn) during the west monsoon period, typically November to March (Syafyuddin Yusuf, personal communication 2019), in South Sulawesi, including the Spermonde Archipelago. The illustration of the dominant current directions in the waters around Sulawesi (Figure 1) is based on data for surface currents (down to a depth of 15 meters) during the west monsoon of 2017 to 2018 from a global current website provided by ESA GlobCurrent, and compiled by the authors.

Figure 1 shows the complexity and divergences in currents around Sulawesi. Although the dominant current flow in terms of mass transport is from north to south, both east and west of Sulawesi (e.g. the flow from Manado southwards towards the Banggai Archipelago), there are other factors which complicate the patterns. A clockwise rotation occurring in the waters north of the northern arm of Sulawesi represents refraction flows from the meeting of the Sulawesi Sea and Pacific Ocean. The westward flow to the south of this rotation branched south with a trajectory entering the Makassar Strait (thus from Manado towards Toli-Toli, and potentially down towards the Spermonde Archipelago), while the eastward rotation to the north flowed towards the Maluku Sea, with a proportion returning towards Manado. Off the western coast of Sulawesi, in the Mamuju area of the Makassar Strait channel, there was a tendency for currents to diverge, with north and south-flowing branches. However, variations in weather, longshore currents and tidal effects could enable a proportion of the surface waters entering the Makassar Strait from the North to join the south-flowing branch, and thus reach the Spermonde Islands, and/or join the eastwards flow around the south of Sulawesi towards the Flores Sea and the Wakatobi Archipelago in the southern reaches of the Banda Sea. Refraction was also seen to occur in the waters to the east of Sulawesi, driven by the upwelling in the Banda Sea, bringing cold and warm water masses into contact. The resulting rotational pattern shows currents moving north towards Tolo Bay, including Luwuk and the Banggai Archipelago, as well as southerly currents that could transport surface water from the north (e.g. Manado area), potentially reaching the Wakatobi Islands under certain conditions.

The complexity of current vectors and the geographical distances between the selected sites in the study area no doubt greatly influenced the formation of the observed genetic connectivity. It could be seen from the genetic distance values that the populations were not significantly differentiated. The geographical conditions of Sulawesi have enabled the eastern and western populations to remain connected to each other, with the presence of longitudinal current transport media primarily (but not exclusively) from east to west in the north and west to the east in the south. High gene flow due to oceanographic factors can create and maintain opportunities for the adaptation and recovery of marine organisms, especially corals, when impacted by increasingly varied stress factors (Kawecki and Ebert 2004).

The prediction of larval distribution based on genetic distances and dominant current patterns in Sulawesi waters during the spawning period originally assumed that the propagules of broadcast spawners with a wide distribution could reach far distant settlement sites. Gaonkar et al. (2012) stated that monsoons (west and east) play an essential role in the distribution of organisms in the tropical Indo-Pacific region. The current patterns can have a major effect on the direction and distance of larval travel from released until settlement on an appropriate substrate (Gleason and Hofmann 2011). It has been noted that flows play an essential role in maintaining connectivity between coral reef populations (Botsford et al. 2009; Underwood et al. 2013). The distribution of larvae is also influenced by the time of release and the duration of the pelagic phase (Cowen and Sponaugle 2009), as well as the characteristics of the sink or the settlement area (Tay et al. 2012). In the case of *L. corymbosa*, while the long PLD and complex current patterns could enable direct connectivity around much of Sulawesi, it is perhaps more likely that stepping stone models are more common, with gene flow between the studied populations mediated through populations spread along the Sulawesi coasts and the many small islands in the waters surrounding Sulawesi.

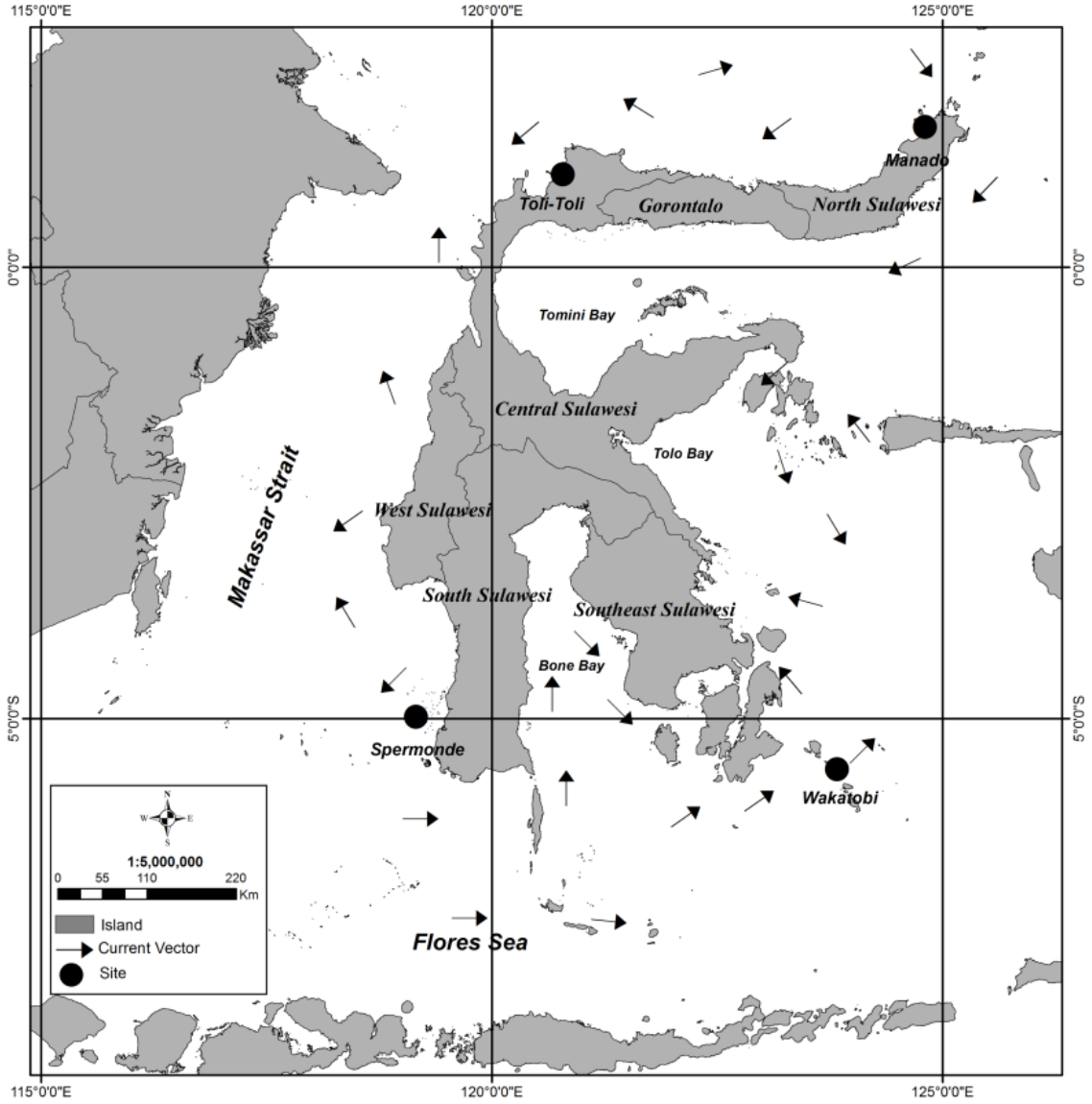

Figure 1. Dominant current vectors around Sulawesi during the west monsoon (November 2017-March 2018) based on data retrieved from Global Current (http: //www.globcurrent.org/)

The extent to which populations are connected can have several potentially significant consequences for understanding how species respond to selection and adapt to environmental changes (Frankham et al. 2010). Even rare genetic exchanges between populations separated by large spatial scales could reduce the likelihood of adaptive changes to the local environment and the possibility of eventual speciation by genetically homogenizing the population. Conversely, without significant connectivity among populations, specific populations could be at higher risk local extinction (extirpation), especially in the case of heavily exploited organisms, as the number of scattered individuals arriving through dispersal from other sites (populations) might not be enough to enable depleted populations to recover.

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Table S1. *L. corymbosa* sample origin and Genbank accession numbers of mtDNA CO1 sequences produced under this study.

Bankit_Reference	Site	Species	Accession Number
BankIt2222158 Seq1	Spermonde (Badi island)	*L. corymbosa*	MK905084
BankIt2222158 Seq2	Spermonde (Badi island)	*L. corymbosa*	MK905085
BankIt2222158 Seq3	Spermonde (Badi island)	*L. corymbosa*	MK905086
BankIt2222158 Seq4	Spermonde (Badi island)	*L. corymbosa*	MK905087
BankIt2222158 Seq5	Spermonde (Badi island)	*L. corymbosa*	MK905088
BankIt2222158 Seq6	Spermonde (Badi island)	*L. corymbosa*	MK905089
BankIt2222158 Seq7	Spermonde (Badi island)	*L. corymbosa*	MK905090
BankIt2222158 Seq8	Spermonde (Badi island)	*L. corymbosa*	MK905091
BankIt2222158 Seq9	Spermonde (Badi island)	*L. corymbosa*	MK905092
BankIt2222158 Seq10	Spermonde (Badi island)	*L. corymbosa*	MK905093
BankIt2222158 Seq11	Spermonde (Badi island)	*L. corymbosa*	MK905094
BankIt2222158 Seq12	Spermonde (Badi island)	*L. corymbosa*	MK905095
BankIt2222158 Seq13	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905096
BankIt2222158 Seq14	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905097
BankIt2222158 Seq15	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905098
BankIt2222158 Seq16	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905099
BankIt2222158 Seq17	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905100
BankIt2222158 Seq18	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905101
BankIt2222158 Seq19	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905102
BankIt2222158 Seq20	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905103
BankIt2222158 Seq21	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905104
BankIt2222158 Seq22	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905105
BankIt2222158 Seq23	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905106
BankIt2222158 Seq24	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905107
BankIt2222158 Seq25	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905108
BankIt2222158 Seq26	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905109
BankIt2222158 Seq27	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905110
BankIt2222158 Seq28	Spermonde (Barrang Lompo Island)	*L. corymbosa*	MK905111
BankIt2222158 Seq29	Manado	*L. corymbosa*	MK905112
BankIt2222158 Seq30	Manado	*L. corymbosa*	MK905113
BankIt2222158 Seq31	Manado	*L. corymbosa*	MK905114
BankIt2222158 Seq32	Manado	*L. corymbosa*	MK905115
BankIt2222158 Seq33	Manado	*L. corymbosa*	MK905116
BankIt2222158 Seq34	Manado	*L. corymbosa*	MK905117
BankIt2222158 Seq35	Manado	*L. corymbosa*	MK905118
BankIt2222158 Seq36	Manado	*L. corymbosa*	MK905119
BankIt2222158 Seq37	Manado	*L. corymbosa*	MK905120
BankIt2222158 Seq38	Manado	*L. corymbosa*	MK905121
BankIt2222158 Seq39	Manado	*L. corymbosa*	MK905122
BankIt2222158 Seq40	Manado	*L. corymbosa*	MK905123
BankIt2222158 Seq41	Manado	*L. corymbosa*	MK905124
BankIt2222158 Seq42	Manado	*L. corymbosa*	MK905125
BankIt2222158 Seq43	Manado	*L. corymbosa*	MK905126
BankIt2222158 Seq44	Manado	*L. corymbosa*	MK905127
BankIt2222158 Seq45	Manado	*L. corymbosa*	MK905128
BankIt2222158 Seq46	Manado	*L. corymbosa*	MK905129
BankIt2222158 Seq47	Manado	*L. corymbosa*	MK905130
BankIt2222158 Seq48	Manado	*L. corymbosa*	MK905131
BankIt2222158 Seq49	Manado	*L. corymbosa*	MK905132
BankIt2222158 Seq50	Manado	*L. corymbosa*	MK905133
BankIt2222158 Seq51	Manado	*L. corymbosa*	MK905134
BankIt2222158 Seq52	Toli-Toli	*L. corymbosa*	MK905135
BankIt2222158 Seq53	Toli-Toli	*L. corymbosa*	MK905136
BankIt2222158 Seq54	Toli-Toli	*L. corymbosa*	MK905137
BankIt2222158 Seq55	Toli-Toli	*L. corymbosa*	MK905138
BankIt2222158 Seq56	Toli-Toli	*L. corymbosa*	MK905139
BankIt2222158 Seq57	Toli-Toli	*L. corymbosa*	MK905140
BankIt2222158 Seq58	Toli-Toli	*L. corymbosa*	MK905141
BankIt2222158 Seq59	Toli-Toli	*L. corymbosa*	MK905142
BankIt2222158 Seq60	Toli-Toli	*L. corymbosa*	MK905143
BankIt2222158 Seq61	Toli-Toli	*L. corymbosa*	MK905144
BankIt2222158 Seq62	Toli-Toli	*L. corymbosa*	MK905145
BankIt2222158 Seq63	Toli-Toli	*L. corymbosa*	MK905146

BankIt2222158 Seq64	Toli-Toli	*L. corymbosa*	MK905147
BankIt2222158 Seq65	Toli-Toli	*L. corymbosa*	MK905148
BankIt2222158 Seq66	Toli-Toli	*L. corymbosa*	MK905149
BankIt2222158 Seq67	Toli-Toli	*L. corymbosa*	MK905150
BankIt2222158 Seq68	Toli-Toli	*L. corymbosa*	MK905151
BankIt2222158 Seq69	Toli-Toli	*L. corymbosa*	MK905152
BankIt2222158 Seq70	Toli-Toli	*L. corymbosa*	MK905153
BankIt2222158 Seq71	Toli-Toli	*L. corymbosa*	MK905154
BankIt2222158 Seq72	Toli-Toli	*L. corymbosa*	MK905155
BankIt2222158 Seq73	Toli-Toli	*L. corymbosa*	MK905156
BankIt2222158 Seq74	Toli-Toli	*L. corymbosa*	MK905157
BankIt2222158 Seq75	Toli-Toli	*L. corymbosa*	MK905158
BankIt2222158 Seq76	Toli-Toli	*L. corymbosa*	MK905159
BankIt2222158 Seq77	Wakatobi (Hoga Island)	*L. corymbosa*	MK905160
BankIt2222158 Seq78	Wakatobi (Hoga Island)	*L. corymbosa*	MK905161
BankIt2222158 Seq79	Wakatobi (Hoga Island)	*L. corymbosa*	MK905162
BankIt2222158 Seq80	Wakatobi (Hoga Island)	*L. corymbosa*	MK905163
BankIt2222158 Seq81	Wakatobi (Hoga Island)	*L. corymbosa*	MK905164
BankIt2222158 Seq82	Wakatobi (Hoga Island)	*L. corymbosa*	MK905165
BankIt2222158 Seq83	Wakatobi (Hoga Island)	*L. corymbosa*	MK905166
BankIt2222158 Seq84	Wakatobi (Hoga Island)	*L. corymbosa*	MK905167
BankIt2222158 Seq85	Wakatobi (Hoga Island)	*L. corymbosa*	MK905168
BankIt2222158 Seq86	Wakatobi (Hoga Island)	*L. corymbosa*	MK905169
BankIt2222158 Seq87	Wakatobi (Hoga Island)	*L. corymbosa*	MK905170
BankIt2222158 Seq88	Wakatobi (Hoga Island)	*L. corymbosa*	MK905171
BankIt2222158 Seq89	Wakatobi (Hoga Island)	*L. corymbosa*	MK905172
BankIt2222158 Seq90	Wakatobi (Hoga Island)	*L. corymbosa*	MK905173
BankIt2222158 Seq91	Wakatobi (Hoga Island)	*L. corymbosa*	MK905174
BankIt2222158 Seq92	Wakatobi (Hoga Island)	*L. corymbosa*	MK905175
BankIt2222158 Seq93	Wakatobi (Hoga Island)	*L. corymbosa*	MK905176
BankIt2222158 Seq94	Wakatobi (Hoga Island)	*L. corymbosa*	MK905177
BankIt2222158 Seq95	Wakatobi (Hoga Island)	*L. corymbosa*	MK905178
BankIt2222158 Seq96	Wakatobi (Hoga Island)	*L. corymbosa*	MK905179
BankIt2222158 Seq97	Wakatobi (Hoga Island)	*L. corymbosa*	MK905180
BankIt2222158 Seq98	Wakatobi (Kaledupa Island)	*L. corymbosa*	MK905181
BankIt2222158 Seq99	Wakatobi (Kaledupa Island)	*L. corymbosa*	MK905182
BankIt2222158 Seq100	Wakatobi (Kaledupa Island)	*L. corymbosa*	MK905183
BankIt2222158 Seq101	Wakatobi (Kaledupa Island)	*L. corymbosa*	MK905184
BankIt2222158 Seq102	Wakatobi (Kaledupa Island)	*L. corymbosa*	MK905185
BankIt2222158 Seq103	Wakatobi (Kaledupa Island)	*L. corymbosa*	MK905186