



# Reduced Genetic Diversity in the Clown Anemonefish *Amphiprion ocellaris* in Exploited Reefs of Spermonde Archipelago, Indonesia

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Populations of the clown anemonefish in Spermonde Archipelago, one of the main collection sites for ornamental fish in Indonesia, are potentially overfished, which might lead to a reduction in population size and genetic diversity. Loss of genetic diversity can reduce the adaptability, population persistence and productivity of the targeted species. Therefore, a study investigating the genetic diversity and its potential correlation to population densities of *A. ocellaris* was conducted. Two islands were chosen as study sites that differed in the degree of exploitation. Barrang Lompo has a high fishing pressure, whereas Samalona has less. Underwater visual censuses showed that population densities in Samalona were threefold higher than in Barrang Lompo ( $p = 0.005$ ). Analysis of eight microsatellite loci in 364 tissue samples of *A. ocellaris* revealed that genetic diversity (numbers of alleles, private alleles, and allelic richness) was significantly reduced at the island with high fishing pressure. Allelic richness was also positively correlated with fish density ( $p < 0.05$ ). These results indicate that ornamental fishery might be a factor contributing to the loss of genetic diversity in *A. ocellaris*. Therefore, the marine ornamental trade in Spermonde Archipelago needs to be managed (e.g., management of the fishing strategy, implementation of marine protected areas, regular monitoring, and quota determination). Otherwise the populations of *A. ocellaris* might collapse.

**Keywords:** exploited species, allelic diversity, genetic variation, fishery management, coral triangle

## INTRODUCTION

Many marine fish populations are currently impacted due to fishing activities and environmental changes. The most obvious impacts of excessive fishing are observable changes in size and age structure in the fish populations (e.g., Trippel, 1995; Cardinale and Modin, 1999; Ottersen et al., 2006), and a reduction in population density (Gaggiotti and Vetter, 1999). Due to exploitation, many stocks are depleted and some species are even endangered (e.g., Musick et al., 2000; Hutchings and Reynolds, 2004; Dankel et al., 2008). Excessive fishing and environmental changes are not only affecting the spatial distribution and structure of populations, but also causing changes in

their genetic diversity (e.g., O'Brien, 1994; Heino and Godø, 2002; Reusch et al., 2005; Pinsky and Palumbi, 2014). Reduced population size enhances genetic drift, which in turn causes a higher loss of genetic variability per generation. Increased genetic drift augments the loss of variability and the ability of adaptation (Hauser et al., 2002; Spielman et al., 2004). A number of studies revealed a loss of genetic diversity in marine fish due to exploitation, for example, *Hoplostethus atlanticus* (Smith et al., 1991) and *Pagrus auratus* in New Zealand (Hauser et al., 2002).

More than 1,000 marine ornamental fish species were traded globally in the period from 1997 to 2002, of which damselfish (Pomacentridae) comprised about 47% (Wabnitz et al., 2003). The clown anemonefish *Amphiprion ocellaris* is the number one fish species in ornamental trade and Indonesia is one of the world's leading exporters (Wabnitz et al., 2003). In Spermonde Archipelago, The fishermen are unselectively exploiting *A. ocellaris* and their hosts, without considering the sizes (Madduppa et al., 2014a). Intensive fishing on *A. ocellaris* caused a decrease in density and reduction in body size (Madduppa et al., 2014a), indicating overfishing. This situation may lead to a loss of genetic diversity in *A. ocellaris*.

Due to its biological and behavioral characteristics, *A. ocellaris* is vulnerable to intensive fishing. The species forms an obligate symbiosis with only three different host anemones (*Heteractis magnifica*, *Stichodactyla gigantea*, and *S. mertensii*), which are collected and traded as well in Spermonde Archipelago (Madduppa et al., 2014a), reducing the available habitat. Each anemone is usually inhabited by two to six individuals of *A. ocellaris*. The two largest individuals in the colony are the breeding pair and others remain non-breeders (Fricke and Fricke, 1977). The fish is characterized by protandrous monogamy (i.e., only one breeding pair lives in a host anemone, and males change sex to become females). The life cycle of *A. ocellaris* consists of two phases, dispersing larvae (8–10 days in captivity, Gopakumar et al., 2009) and sedentary adults. *Amphiprion ocellaris* prefers to settle in smaller groups in order to avoid long breeding queues, maximizing their likelihood of attaining social dominance (Mitchell, 2005). All individuals will follow the social-rank rule within one anemone by adjusting their size and growth rate (Buston, 2003), and the social structure only changes when one individual dies or is removed, after which some time is required for the male reproductive anemonefish to change sex to become the reproductive female (Fricke and Fricke, 1977; Madhu et al., 2010). The present study was conducted to investigate the impact of marine ornamental fishing on the genetic diversity of *A. ocellaris* by using eight microsatellite loci.

## MATERIALS AND METHODS

### Study Sites

Spermonde Archipelago consists of about 150 islands and is located in the Makassar Strait southwest of Sulawesi (Tomascik et al., 1997). The region is part of the Coral Triangle (Briggs, 2009) and is considered to be the world's center of marine biodiversity (Allen and Werner, 2002; Allen, 2008; Veron et al., 2009), but is also the most threatened coral reef system in the world (Bryant et al., 1998; Burke et al., 2006). Habitat degradation

occurs in the area due to destructive fishing activities (Pet-Soede and Erdmann, 1998). Artisanal fishing and harvesting for the marine ornamental trade adds additional pressure (Erdmann, 1995; Pet-Soede et al., 1999, 2001; Madduppa et al., 2014a).

This study was conducted in Barrang Lompo (5°02'52.07''S, 119°19'45.25''E) and Samalona (5°07'30.48''S, 119°20'36.48''E). These two islands are located in the mid-shelf of the Spermonde Archipelago, close to the city of Makassar. Samples were collected at five sites in Barrang Lompo and four sites in Samalona (Figure 1, Table 1). About 5,000 people are living on Barrang Lompo and only about 100 on Samalona. Coral reefs in Barrang Lompo have been impacted by high fishing pressure, while Samalona has been less impacted by fishing (Madduppa et al., 2014a).

### Fish Survey

*Amphiprion ocellaris* was counted using the underwater visual census technique during free-swim surveys in an approximately 5 m-wide area for about 1.5–2 h for each survey at a depth of 1–11 m by scuba diving. The surveys were carried out in May and June 2009. GPS positions of the start and endpoints were noted at each survey in order to estimate the length of each transect. This technique has been successfully used to census the population of anemone fish in larger areas in previous studies (Shuman et al., 2005; Jones et al., 2008; Madduppa et al., 2014a).

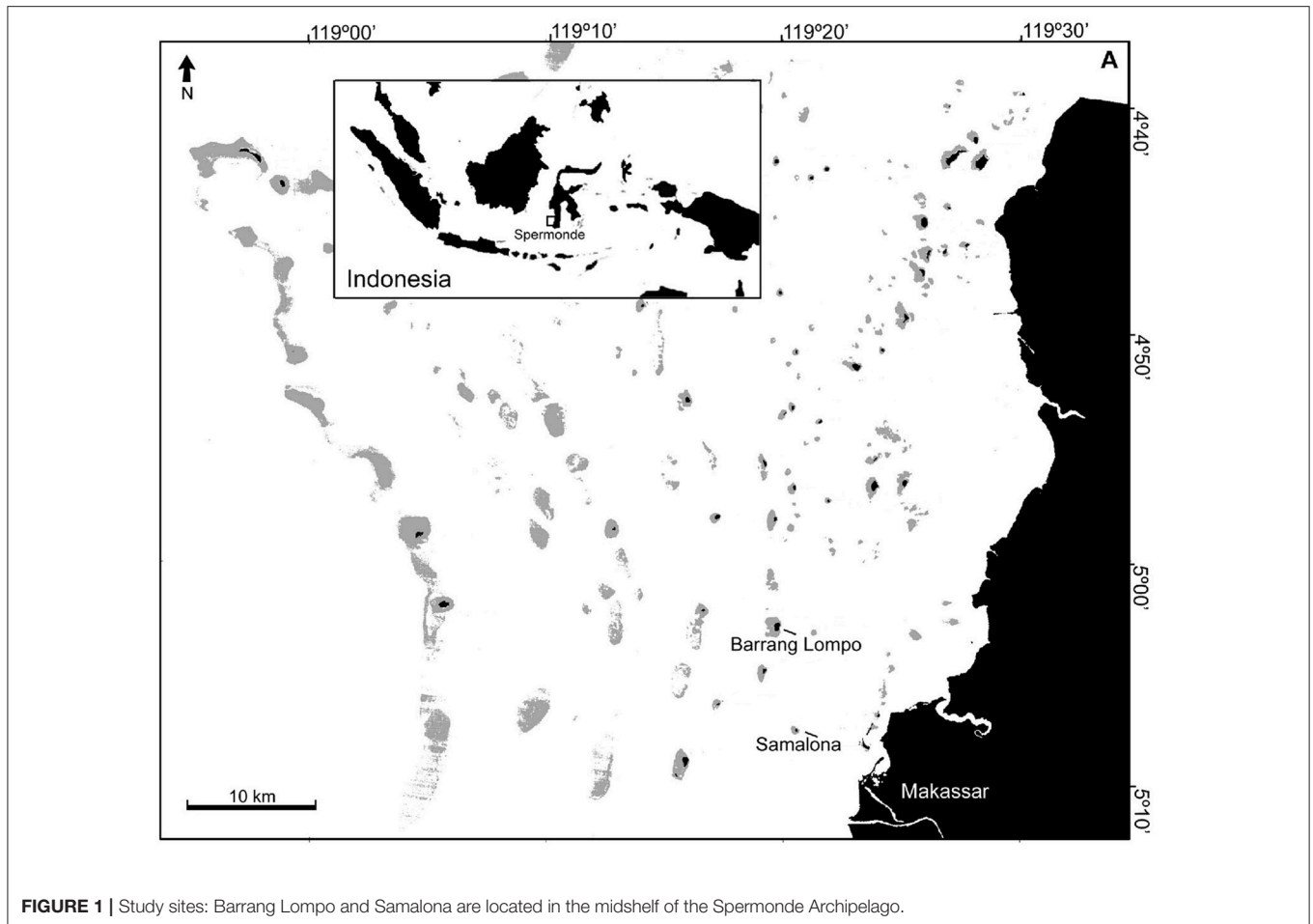
### Ethics Statement

Fin-clipping is a non-destructive, minimally invasive and the most commonly used method to obtain tissue from living fishes in the wild (e.g., Almany et al., 2007; Planes et al., 2009; Saenz-Agudelo et al., 2011) and in aquaculture (e.g., Wang et al., 2012). We took great care to minimize harm, and ensured survival by safely releasing the fishes back into their host anemones. An ethics approval was not required for this research as per our university (Bogor Agricultural University) regulations and as per Indonesian laws and guidelines. Tissue sampling of these anemonefishes was permitted within the framework of the German-Indonesian SPICE project (Science for the Protection of Indonesian Coastal Ecosystems), in cooperation with the Hasanuddin University, Makassar, Indonesia.

### Tissue Sampling and Microsatellite Analysis

A total of 364 tissue samples of *A. ocellaris* were collected in Barrang Lompo and Samalona from October to November 2008 and May to June 2009 (Table 1). All individuals (adults, juveniles, and recruits) in a colony were caught with two aquarium nets and the caudal fin was clipped to obtain a tissue sample. Subsequently they were released into their host anemones. The samples were preserved in 96% ethanol and finally stored at 4°C.

Genomic DNA was extracted with the NucleoSpin Tissue Extraction kit (Macherey-Nagel, Germany), following the manufacturer's guidelines. All DNA extracts were analyzed by gel electrophoresis to monitor DNA quality prior to PCR (polymerase chain reaction) amplification of microsatellite loci. GeneRuler™ 1 kb DNA Ladder Plus (Applied Biosystems) was used as a reference. PCRs were carried out in a total volume



**TABLE 1 |** Study sites: geographical coordinates, length of free swims (m), survey area (m<sup>2</sup>), number of individuals, *Amphiprion ocellaris* density (fish/100 m<sup>2</sup>), and the survey period.

Sites, sub-sites	Geographical coordinates	Length of free swims (m)	Survey area (m <sup>2</sup> )	Number of individuals	<i>A. ocellaris</i> density (ind/100 m <sup>2</sup> )	Time of survey
<b>BARRANG LOMPO:</b>						
West	S 05° 02.541' E 119° 19.355'	763	3,815	18	1.363	May 2009
Southwest	S 05° 03.324' E 119° 19.276'	293	1,465	10	1.775	May 2009
North	S 05° 02.507' E 119° 19.571'	677	3,385	29	0.679	May 2009
South	S 05° 03.317' E 119° 19.490'	395	1,975	22	2.633	May 2009
East	S 05° 03.280' E 119° 19.836'	383	1,915	9	1.567	May 2009
Mean		502	2,511	17.6	1.603	
±SD		205	1,025	8.4	0.707	
<b>SAMALONA:</b>						
West	S 05° 07.010' E 119° 20.006'	220	1,100	52	4.818	June 2009
North	S 05° 07.009' E 119° 20.007'	560	2,800	72	2.643	June 2009
East	S 05° 07.005' E 119° 20.009'	470	2,350	111	4.809	June 2009
South	S 05° 07.011' E 119° 20.009'	230	1,150	41	3.565	June 2009
Mean		370	1,850	69.0	3.959	
±SD		171	857	30.8	1.056	

of 25  $\mu$ l, containing 2.5  $\mu$ l of 10x PCR buffer, 3  $\mu$ l of 25 mM  $MgCl_2$ , 1  $\mu$ l 2 mM of each dNTP, 1  $\mu$ l of 10 mM each forward and reverse primer, 0.1  $\mu$ l (5 unit/ $\mu$ l) of Taq polymerase (F100L Taq DNA), and 1  $\mu$ l (1–10 ng) genomic DNA. PCRs were performed in a Tprofessional Thermocycler (Biometra) and a MasterCycler EP (Eppendorf) with the following thermo-profile: 94°C for 2 min, followed by 35 cycles of 94°C for 30 s as denaturing step, 50–65°C for 30 s as annealing step (see **Table 2** for annealing temperature at each locus), 72°C for 1 min for polymerization, and finally 72°C for 2 min. Eight polymorphic microsatellite loci were utilized: two isolated from *A. clarkii* (AC137 and AC1578, Liu et al., 2007), four from *A. percula* (Cf39, Cf29, Cf42, and Cf9, Buston et al., 2007), and two from *A. polymnus* (45 and 120, Quenouille et al., 2004). The PCR products were diluted in pure water prior to fragment analysis. Dilution factors were determined empirically for each locus, and ranged from 1:5 to 1:30. For fragment analysis, 1  $\mu$ l of diluted PCR product was combined with 8.85  $\mu$ l HiDiTM formamide and the 0.15  $\mu$ l GENESCAN LIZ-500 size standard (Applied Biosystems). Microsatellite fragments were size fractionated using an Applied Biosystems Inc. (ABI) 3730 48 capillary sequencer with 50 cm capillary length. Allele sizes were determined and corrected with PEAK SCANNER v1.0 (Applied Biosystems) and GENEMARKER v1.85 (SoftGenetics GeneMarker).

## Data Analysis

Hardy-Weinberg equilibrium (HWE) exact tests and loci combinations for linkage disequilibrium with the Markov chain methods were conducted using GENEPOP on the web (Raymond and Rousset, 1995; Rousset, 2008). Possible presence of null alleles was tested using the software MICROCHECKER (Van-Oosterhout et al., 2004). Several indices of genetic diversity were used and analyzed per sub-site at each island. The number of alleles per locus, allele frequencies and observed and expected heterozygosities (Nei, 1973) were calculated with the program CERVUS 3.0 (Marshall et al., 1998). The value of the heterozygosity may range from zero (no heterozygosity) to

nearly 1.0 (for a system with a large number of equally frequent alleles). Private alleles are defined as alleles observed in only one population. Allelic richness (mean number of alleles per locus) and gene diversity (the proportion of polymorphic loci across the genome) were calculated with the program FSTAT 2.9.3 (Goudet, 1995). F-statistics were calculated using FSTAT in order to detect non-random mating within populations ( $F_{IS}$ ) and genetic differentiation between the two island populations ( $F_{ST}$ ) (Weir and Cockerham, 1984). The software CONVERT 1.3.1 (Glaubitz, 2004) was used to anticipate different types of input file formats for the various programs used for the analysis.

Density data for fish were standardized as the number of specimens per 100 m<sup>2</sup>, and were compared between the two islands using a *t*-test. For molecular data, allelic richness, number of private alleles, observed heterozygosity,  $F_{IS}$ , and gene diversity, were compared between the two islands using all individual genotypes from all loci, and tested for significance using the *t*-test. For unequal variances, the Welch's *t*-test was used. Linear regression analysis was used to identify a possible correlation between allelic richness and fish density. Here, the nine sites at the two islands were treated as replicates. The statistical analysis was conducted in STATISTICA 7 (StatSoft, 2004).

## RESULTS

### Microsatellite Properties, Genetic Diversity, and Differentiation

One of the eight loci (Cf39) departed from HWE, showing a heterozygote deficit (**Table 2**). At the same locus, null alleles were detected with the programme MICROCHECKER, possibly causing the departure from HWE. However, the test for linkage disequilibrium found no linkage in the pairwise combinations of the eight microsatellite loci. Therefore, all loci were used in the further analysis. The inbreeding coefficient ( $F_{IS}$ ) values in Barrang Lompo ranged between  $-0.065$  for locus CF29 and  $0.285$  for CF39 ( $0.067 \pm 0.125$ , mean  $\pm$  SD), which was slightly higher

**TABLE 2** | Indices for genetic diversity based on eight microsatellite loci for populations from Barrang Lompo and Samalona.

Locus	Barrang Lompo (N = 88)								Samalona (N = 276)							
	He	Ho	Na	Nap	A	D	HD	$F_{IS}$	He	Ho	Na	Nap	A	D	HD	$F_{IS}$
CF9	0.80	0.81	10	0	10	0.797	0.01	-0.010	0.80	0.82	11	1	11	0.800	0.02	-0.019
CF29	0.92	0.98	18	1	18	0.917	0.07	-0.070	0.90	0.97	21	4	21	0.900	0.07	-0.075
CF39	0.95*	0.68	32	2	32	0.949	-0.28	0.285	0.95*	0.63	37	7	37	0.947	-0.33	0.331
CF42	0.93	0.96	25	1	25	0.930	0.03	-0.030	0.93	0.94	30	7	30	0.931	0.00	-0.004
45	0.67	0.52	12	0	12	0.675	-0.22	0.225	0.58	0.57	14	1	14	0.580	-0.01	0.013
120	0.54	0.50	5	0	5	0.539	-0.07	0.073	0.59	0.59	9	4	9	0.592	0.00	-0.004
AC137	0.92	0.92	20	1	20	0.923	0.00	0.003	0.93	0.91	30	12	30	0.926	-0.01	0.015
AC1578	0.79	0.73	8	0	8	0.792	-0.08	0.082	0.81	0.78	9	1	9	0.810	-0.03	0.033
Mean	0.82	0.76	16	1	16.20	0.815	-0.07	0.067	0.81	0.78	20	5	20.13	0.811	-0.04	0.042
$\pm$ SD	0.15	0.19	9	0.74	9.17	0.146	0.12	0.125	0.15	0.16	11	3.89	11.01	0.149	0.12	0.123

N, sample size; He, expected heterozygosity; Ho, observed heterozygosity; Na, number of alleles; Nap, number of private alleles; A, allelic richness; D, gene diversity; HD, Heterozygote deficit;  $F_{IS}$ , non-random mating within populations. Asterisk indicates locus departure from HWE after sequential Bonferroni correction ( $P < 0.01$ ).



than the values observed in Samalona, ranging from  $-0.075$  for locus CF29 to  $0.331$  for CF39 ( $0.042 \pm 0.123$ , mean  $\pm$  SD).

Significantly lower values were found in Barrang Lompo for the number of alleles, the number of private alleles, and allelic richness (Table 3). There was no significant difference between the two populations for observed heterozygosity, expected heterozygosity, coefficient of inbreeding and gene diversity (Table 3). A significant genetic differentiation ( $F_{ST}$ ) between the two populations was found ( $0.065 \pm 0.048$ ,  $p = 0.01$ ).

## Population Size and Its Relation to Allelic Richness

The ecological survey conducted in 2009 revealed that the density of *A. ocellaris* was significantly lower in Barrang Lompo than in Samalona ( $t$ -test,  $t = 4.02$ , d.f. = 7,  $p = 0.005$ ; Table 3). The mean density of *A. ocellaris* at Barrang Lompo was  $1.60 \pm 0.71$  ind/100 m<sup>2</sup> (mean  $\pm$  SD), while it was more than twice as high in Samalona (mean  $\pm$  SD,  $3.96 \pm 1.06$  ind/100 m<sup>2</sup>; Table 1). Linear regression analysis showed a positive correlation between fish density and allelic richness ( $p = 0.03$ ,  $r^2 = 0.43$ , Figure 2).

## DISCUSSION

### Genetic Variability and Differentiation Between Two Island Populations

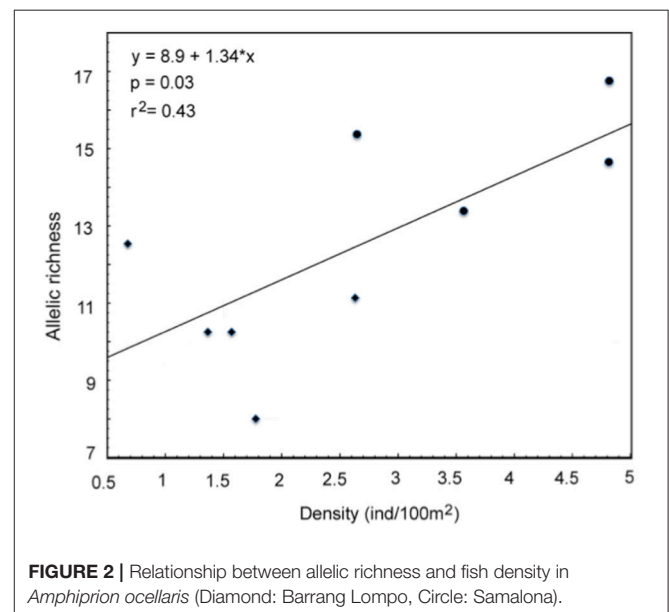
The amount of genetic variability in a population can be estimated by measuring the number of alleles, number of private alleles, and allelic richness. Studies revealed that allelic richness may be more sensitive to a population bottleneck and environmental stress than heterozygosity (Allendorf, 1986; Petit et al., 1998; Leberg, 2002; Pini et al., 2011). Accordingly, lower allelic richness in overharvested populations was recorded in many cases, which suggests that overharvest drives the decay of genetic diversity across a wide range of marine fishes (Pinsky and Palumbi, 2014). A significant decrease in both allelic richness and heterozygosity over 50 years since the onset of exploitation was revealed in the silver seabream *Pagrus auratus* by using seven microsatellite loci (Hauser et al., 2002). In addition, a loss of allelic richness was found in the damselfish *Dascyllus aruanus* due to a high mortality during the recruitment stage, which was induced by environmental stress (Pini et al., 2011).

Our study is in agreement with these previous findings, by showing significantly lower values in allelic number and allelic richness in Barrang Lompo than in Samalona. Gene diversity and expected heterozygosity between Samalona and Barrang Lompo were not found to be significantly different ( $p > 0.05$ ). Both island populations showed high gene diversity and heterozygosity values (mean HE and  $D > 0.8$ ). The expected heterozygosity in *A. ocellaris* for both populations (0.54–0.95) was in a similar range to the previous study on this species (0.54–0.92; Timm et al., 2012). The observed heterozygosity in Barrang Lompo was slightly lower than in Samalona and the heterozygote deficiency at Barrang Lompo was higher than at Samalona, but these differences were not significant ( $p > 0.05$ ). For both populations, no inbreeding effects were revealed, which was indicated by low inbreeding coefficients. However, the value of the inbreeding coefficient in Barrang Lompo was higher than in Samalona, which could be an indication of the effect of overharvesting. Inbreeding in a population could cause a reduction in the heterozygosity and an increase in the homozygosity, as shown in overharvested populations (Pinsky and Palumbi, 2014).

Despite dispersing larvae, *A. ocellaris* showed a significant genetic differentiation between the two island populations ( $F_{ST}$  536 =  $0.065 \pm 0.048$ ,  $p = 0.01$ ), which was also shown in a previous study (Timm et al., 2017). In a study on the anemonefish species *A. clarkii* significant  $F_{ST}$ -values (=0.028) were found between sites on a similarly small scale in the Philippines (Pinsky and Palumbi, 2014). A strong genetic population structure was also found at a larger scale in the same species as well as in other coral reef organisms in this region (Kochzius and Nuryanto, 2008; Timm and Kochzius, 2008; Knittweis et al., 2009; Nuryanto and Kochzius, 2009; Timm et al., 2012; Dohna et al., 2015; Hui et al., 2016, 2017). In addition, the previous study on these two island populations revealed high self-recruitment in *A. ocellaris* of about 40–60% (Madduppa et al., 2014b), which explains the genetic differentiation.

**TABLE 3** | Summary of  $t$ -test for density and genetic variation metrics of *Amphiprion ocellaris* between Barrang Lompo and Samalona (\*  $<0.05$ , n.s., not significant).

Variation metrics	$t$	d.f.	$P$
Density	4.017	7	*
Number of alleles	3.716	7	*
Number of private alleles	3.306	7	*
Allelic richness	3.717	7	*
Observed heterozygosity	0.580	7	n.s.
Expected heterozygosity	0.263	7	n.s.
Coefficient of inbreeding	1.620	7	n.s.
Gene diversity	-1.140	7	n.s.



**FIGURE 2** | Relationship between allelic richness and fish density in *Amphiprion ocellaris* (Diamond: Barrang Lompo, Circle: Samalona).

## Relationship Between Population Size and Genetic Diversity

The relative population size in Barrang Lompo was threefold lower than in Samalona ( $p = 0.005$ ). The coral reef around Barrang Lompo, as well as many other reefs within Spermonde Archipelago, has been overexploited for a long time (Erdmann, 1995; Pet-Soede et al., 1999, 2001). Reefs within the archipelago suffer from destructive fishing, anchor damage, and pollution from the city of Makassar. The number of coral genera at both islands decreased by about 25% from 1985 to 1995 (Edinger et al., 1998). A decline in abundance is considered to be the first and most obvious response of a fish population to exploitation (Shuman et al., 2005). Reduced population sizes drive the alteration of genetic and phenotypic variability (Gaggiotti and Vetter, 1999; Marteinsdóttir and Pardoe, 2008) and might cause a loss of genetic diversity and, therefore, potentially reduce the adaptability, population persistence, and productivity of the targeted species (Hauser et al., 2002). In a study across 140 species of highly abundant marine fish, it was also observed that reduced genetic diversity is a general consequence of overharvesting (Pinsky and Palumbi, 2014).

The current study revealed that allelic richness from eight microsatellite loci and fish density in *A. ocellaris* were positively correlated ( $p < 0.05$ ). Thus a decrease in fish density because of exploitation can lead to a reduction of genetic diversity. Since many individuals were removed from the population in Barang Lompo by the marine ornamental fishery, it is likely that some alleles were also removed. Fishing activities, which usually remove the older and bigger individuals, are potentially removing the most heterozygous individuals (Smith et al., 1991). In addition, due to a reduced population size, genetic drift might increase, and alleles will eventually be lost (Garza and Williamson, 2001). This should therefore be taken into account when managing marine ornamental fisheries in the region, as described below.

## Implications for Management and Conservation

Several forms of action to prevent the loss of genetic diversity in marine species are proposed, which include: (1) maintaining a large number of individuals of each population and (2) minimizing fisheries-induced selection (Kenchington et al., 2003). The clown anemonefish *A. ocellaris* has been heavily exploited in Southeast Asian countries to meet the global demand for the aquarium trade (Wabnitz et al., 2003). It has recently been revealed that the marine ornamental fishery in the Spermonde Archipelago has reduced the density and average size of *A. ocellaris* (Madduppa et al., 2014a). In addition, the current study indicates that the population of *A. ocellaris*, in Barrang Lompo has a lower density and genetic diversity than the population at Samalona, which is likely due to the higher fishing pressure in Barrang Lompo.

Based on the results of this and previous studies (Madduppa et al., 2014a,b), the marine ornamental trade in Spermonde Archipelago needs to be managed. Otherwise, the populations of *A. ocellaris* might collapse. The present study supports the

previously proposed management strategies for conservation of *A. ocellaris* in this region (Madduppa et al., 2014a). First, management of the fishing strategy is required, such as leaving the breeding pair in a colony or placing a restriction on the maximum catch size of 50 mm. This strategy prevents the loss of rare alleles from older and bigger individuals. Second, the implementation of marine protected areas (MPAs), which take into account high self-recruitment in *A. ocellaris* (Madduppa et al., 2014b) and the limited connectivity of populations (Timm and Kochzius, 2008; Timm et al., 2012, 2017). High self-recruitment implies that the populations are more vulnerable to fishing activity (Thorrold et al., 2001). MPAs are an important tool to prevent overexploitation and to ensure the sustainable use of living marine resources (Tundi Agardy, 1994). Therefore, MPAs have been proposed for managing marine fisheries in Indonesia (Mous et al., 2005). They could also be an effective tool for protecting the genetic diversity (Pérez-Ruzafa et al., 2006). Third, regular monitoring and quota determination of the *A. ocellaris* populations are necessary to control their status. This regular monitoring could also assess other factors (e.g., anthropogenic, environmental parameters) which may influence the status of *A. ocellaris*.

## CONCLUSIONS

In conclusion, even though only two populations of *A. ocellaris* were assessed in this study, we could demonstrate that allelic richness and the number of alleles and private alleles in Barang Lompo, the site exposed to a higher fishing pressure, were reduced. A positive correlation between allelic richness and fish density was revealed. This study suggests that allelic richness might serve as indicator for detecting loss of genetic diversity at an early stage. Therefore, management actions are needed in Spermonde Archipelago, especially in Barrang Lompo and other similar islands within the region, to prevent locally extinct of this valuable marine organisms.

## AUTHOR CONTRIBUTIONS

HM and MK: conceived and designed the experiments; HM: performed the experiments; HM, JT, and MK: analyzed the data; MK: contributed reagents, materials, analysis tools; HM, MK, and JT: wrote the paper.

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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