

Length-weight relationship and population genetic of two marine gastropods species (Turbinidae: *Turbo sparverius* and *Turbo bruneus*) in the Bird Seascape Papua, Indonesia

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Abstract. Saleky D, Setyobudiandi I, Toha HA, Takdir M, Madduppa HH. 2016. Length-weight relationship and population genetic of two marine gastropods species (Turbinidae: *Turbo sparverius* and *Turbo bruneus*) in the Bird Seascape Papua, Indonesia. *Biodiversitas* 17: 208-217. *Turbo sparverius* and *Turbo bruneus* are herbivorous grazers gastropod that lived on the rocky intertidal area, which have a role in maintaining algae on the intertidal ecosystem. Local people in Papua have exploited them for food and souvenirs. Even though this exploitation might affect their genetic diversity and population, a study of the genetic structure of these species has not been previously reported. This study aimed to analyze the morphometric, genetic diversity, population structure and connectivity of *T. sparverius* and *T. bruneus* in coastal water of West Papua, Indonesia. The results showed that the growth pattern of *T. sparverius* and *T. bruneus* in all populations were negative allometric, which means that weight gain was slower than length. Haplotype diversity value of all population *T. sparverius* and *T. bruneus* were 0.657-0.705 and 0.739-0.816, respectively. In addition, the haplotype diversity of each population showed a high level of diversity. The genetic structure was found in all population of *T. sparverius* and *T. bruneus* with F_{ST} value-0.037-0.201 and 0.031, respectively. Population structure and phylogenetic tree showed the closeness of genetic due to gene flow between both *T. sparverius* and *T. bruneus*. Genetic distance value between populations *T. sparverius* and *T. bruneus* are very low were 0.002 and 0.003-0.004, respectively. High genetic similarity might occur due to condition and direction of current flow mediating of gene transport among population, and the similarity of habitats in each population.

Keywords: Coral triangle, genetic diversity, morphometric, phylogenetic, *Turbo*

INTRODUCTION

The bird seascape of West Papua, including Cendrawasih Bay and Raja Ampat Archipelago, are located in the Coral Triangle region, which has the most diverse mollusks (Veron et al. 2009). *Turbo sparverius*, common name the corded turban, is a species of sea snail, gastropod marine mollusk in the family Turbinidae. The gastropods *Turbo* sp. or locally named “bia mata bulan”, including *T. sparverius* and *T. bruneus* are herbivorous gastropods whose feed on algae living in the intertidal rocky area, often found in crevices of rocks or reef flat (Lee and Chao 2004; Quinones and Michel-Morvin 2006). *T. sparverius* and *T. bruneus* have a thick operculum with various coloration such as black, dark green, white or brownish (Dharma 2005). The operculum has a plate shape that necessary to protect the animals when they withdraws their self into the shell (Quinones and Michel-Morvin 2006). Despite their functional role in the ecosystem, some of *Turbo* species such as *T. marmoratus*, *T. setosus* and *T. argyrostomus* became a target species at South Pacific (Kikutani et al. 2002). Also, *T. bruneus* have been exploited for their meats and shells in the Socorro

Archipelago, Mexico (Yamaguchi 1993; Quinones and Michel-Morvin 2006).

Shell's morphology has various shapes that contribute to species identification, classification and taxonomic information (Chiu et al. 2002; Moneva et al. 2012; Caill-Milly et al. 2012). The analysis of morphological characters such as the length-weight relationship of species is useful in marine organism management and also important to determine population condition (Turan 1999; Udo 2013). The difference of gastropod shell morphology are influenced by several factors such as substrate composition (Tan 2009), adaptation to waves exposure (Boulding et al. 1999), pollution (Chiu et al. 2002; Urra et al. 2007), self-protection from of predator, and depth variation (Olabarria and Thurston 2003; Marquez et al. 2011). The length-weight relationship and condition factor have been broadly investigated in gastropod to obtain the index of the physical condition of populations and evaluate habitat quality (Albuquerque et al. 2009). Species identification based on shell's morphometric is quite difficult because morphology and color patterns of the shell are affected by the changes in environment factor (Mauro et al. 2003). Therefore, some gastropods identification

based on genetic analysis are conducted to clarify the former founding (Marquez et al. 2011), and also other marine organisms (Madduppa et al. 2014; Prehadi et al. 2015; Sembiring et al. 2015; Jefri et al. 2015).

Genetic diversity becomes an important part of population (Hoffman et al. 2009) because genetic diversity gave information about the changes in nature and also in the monitoring of biodiversity and conservation (Schwartz et al. 2006). Genetic diversity defines the ability of the population to adapt to environment condition (Booy et al. 2000). More adapted species produced more genetic and morphological variation in response to environmental changes (Taylor and Aarssen 1988). Population with a high level of genetic diversity has more chance to survive (Bonde et al. 2012). Basic knowledge about genetic diversity is useful for conservation because low level of genetic diversity would increase the extinction risks (Jena et al. 2011).

Analysis of population structure aims to examine the dynamic of the natural populations (Hoffman et al. 2009). Life history traits and gene flow are strongly affected population structure (Storfer 1999; Hoffman et al. 2010) but tracking gene flow and larval dispersal in the marine environment are quite difficult (Weersing and Toonen 2009). Each organism has different dispersal pattern in response to various environmental and oceanographic conditions (Crandall et al. 2008). Habitat type, geography, and natural selection are also an important factor in shaping population structure and differentiation (Colson and Hughes 2004).

Genetic connectivity plays a central role in conservation because it helps maintain population and restoration from damages (Neel 2008), connectivity is also an important concern in almost all conservation plan (Luque et al. 2012). Benthic organism often shows a complex life cycle, and the connectivity among the population is maintained by individual transfer during pelagic larval phase (Cowen and Sponaugle 2009). Knowledge about the complexity of larval dispersal was critical in conservation of marine ecosystem because pelagic larval stage and larval dispersal together form the genetic structure of an organism (Awise 1998; Grantham et al. 2003; Madduppa et al. 2014).

The study of morphometric, genetic diversity, population structure and connectivity of *T. sparverius* and *T. bruneus* in West Papua has not been previously reported. These kinds of studies are necessary for marine management and conservation (Japaud et al. 2013). Therefore, this study aimed to analyze length-weight relationship, genetic diversity, population structure, and connectivity of *T. sparverius* and *T. bruneus* in West Papua.

MATERIALS AND METHODS

Studied species

Turbo is marine gastropod mollusk in the family Turbinidae (Williams 2007). *Turbo sparverius*, common

name the corded turban, is a species of sea snail, characterized by their shell. The solid, imperforate shell has an ovate-conic shape with a dirty white or greenish and grows to a length of 75 mm. This marine gastropod species is distributed in the southwest Pacific and off the Philippines (Rosenberg 2015). *Turbo bruneus*, common name the Brown (Pacific) dwarf turban or the little burnt *Turbo*, has a length of the shell varies between 20 mm and 50 mm. This gastropod occurs in the Red Sea, in the Central Indo-Pacific, in the Western Pacific Ocean, off East India, the Philippines and off Western Australia (Rajagopal and Mookherjee 1978; Williams 2007).

Sample collection and morphometric measurement

A total of 179 specimens from four localities throughout the West Papua (Manokwari, Sorong, Raja Ampat and Teluk Wondama) were collected expeditions from October 2014 to January 2015 (Figure 1). *Turbo sparverius* were collected from Manokwari (72 specimens), Teluk Wondama (30), Sorong (3) and *T. bruneus* were collected from Raja Ampat (52), and Manokwari (22). The sample was collected from the rocky intertidal area during low tide. Indonesian Shells II (Dharma 1992) and Recent & Fossil Indonesian Shell (Dharma 2005) were used to identify samples morphologically. The total length and total weight of gastropod shell were measured for each sampled individual. Foot muscle tissues from *T. sparverius* and *T. bruneus* were collected, and preserved in 96% ethanol for subsequent analysis.

DNA extraction, amplification and sequencing

Genomic DNA for each sample was extracted using extraction kit (Qiagen kit. Cat No. 69504) or Chelex (Walsh et al. 1991). A fragment of mitochondrial Cytochrome Oxidase subunit-I gene (COI) was amplified using the following primer set: LCO1490 5'-GGTCAACAAATCATAAAGATATTGG-3' and HCO2198 5'-TTAACTTCAGGGTGACAAAAAATCA-3' (Folmer et al. 1994). Polymerase Chain Reaction (PCR) was conducted in 25 µL reaction volume containing 1-4 µL template DNA, 2.5 µL of 10x PCR buffer (Applied Biosystems), 2.5 µL dNTP (8 mM), 2 µL MgCl₂ (25 mM), 0.125 µL AmplyTaq Red™ (Applied Biosystems), 1.25 µL of each primer (10 mM), 1 µL 1x BSA, and 13.5 µL ddH₂O. PCR conditions were: initial denaturation at 94 °C for 15 s, followed by 40 cycles of denaturation at 95 °C for 30 s, annealing at 50 °C for 30 s, and extension at 72 °C for 45 s. The final extension step was conducted at 72 °C for 10 min. The quality of PCR products was assessed by agarose gel electrophoresis and ethidium bromide staining and visualized using UV transilluminator. All good PCR products were sent to Berkeley Sequencing Facility, USA.

Data analysis

Length-Weight Relationship of *T. sparverius* and *T. bruneus* were analyzed using linear regression. The length-weight relationship is the most widely used method for estimating biomass of benthic invertebrates. This analysis

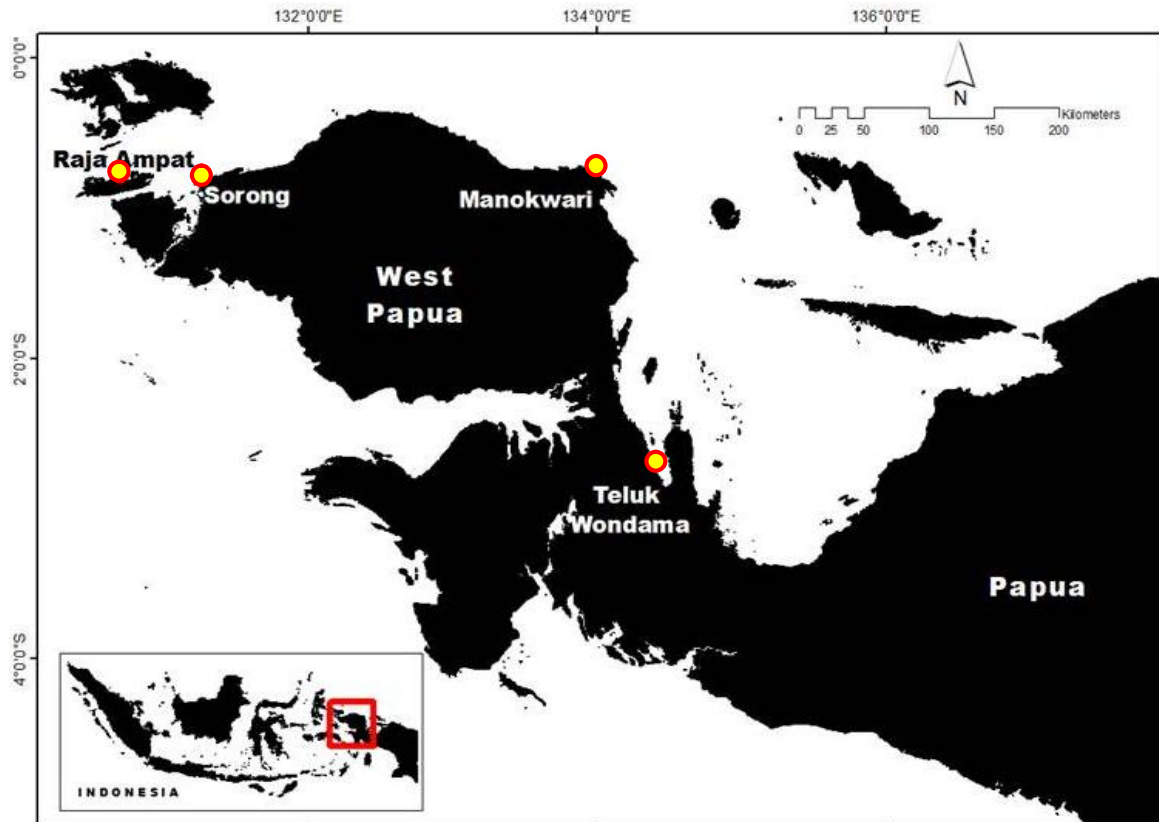


Figure 1. Sampling location (●) of *T. sparverius* dan *T. bruneus* in West Papua, Indonesia: Raja Ampat, Sorong, Manokwari, and Teluk Wondama, Papua, Indonesia

could presume whether there was a difference in size due to differences in environmental conditions (Scheffler 1987; Benke et al. 1999). The length-weight relationships of these species were described by the following equation $W = aL^b$, where W is body weight (gram), L is body length (mm) and a and b are constant values (Effendie 1979). If $b = 3$ indicated an isometric growth, which means the length and weight increase equally. If $b \neq 3$ indicated an allometric growth, which $b < 3$ indicated an increase in length was faster than weight, and $b > 3$ indicated an increase in the weight was faster than the length (Effendie 1979).

Sequences were aligned and edited in Mega 6 (Tamura et al. 2013). Genetic distance (D) was calculated within and between populations. A Neighbour-Joining (NJ) tree was constructed in Mega 6 (Tamura et al. 2013) based on Kimura 2-parameter model, and 1,000 bootstrap replicates. Additional sequences data of *T. sparverius*, *T. bruneus*, and *T. setosus* were added from GeneBank (Table 1). *T. setosus* was utilized as an outgroup in phylogenetic reconstruction. DnaSP 5.10 (Rozas et al. 2003) was used to analyzed a number of the haplotype (H), haplotype diversity (Hd) (Nei, 1987), and nucleotide diversity (π) (Lynch and Creasef 1990). Population differentiation was assessed with Fixation index (F_{st}) (Excoffier et al. 1992) using Arlequin 3.5 (Excoffier and Lischer 2009). Consider investigating the phylogenetic relationship among haplotype, a minimum spanning tree was constructed in Network 4.6.1 (<http://www.fluxusengineering.com>).

RESULTS AND DISCUSSION

Length-weight relationship

The growth pattern of *Turbo sparverius* and *Turbo bruneus* were presented in Table 2. The result from the length-weight calculation of the *T. sparverius* produced equation $W = 0.001L^{2.654}$ with $R^2 = 0.847$ (Manokwari), $w = 0.017L^{1.939}$ with $R^2 = 0.553$ (Teluk Wondama), and $W = 0.00017L^{3.091}$ with $R^2 = 0.996$ (Sorong). The analysis of total length and weight showed a linear relationship with the line equation $Y = 2.4672x - 2.6569$ with $R^2 = 0.799$. Figure 2 presented the linear regression graph of the total length and weight of the *T. sparverius*. Based on obtained r^2 values, the contribution of shell length to weight was 84.7% (Manokwari), 55.3% (Teluk Wondama), 99.6 % (Sorong), and 79.9 % (all populations). These values suggested that body weight can be used to estimate the size of the shell length. The b values were less than 3 indicated the growth pattern of the *T. sparverius* was negative allometric, which means weight gain was slower than the length. *T. sparverius* from Sorong showed positive allometric growth pattern ($b > 3$), which means weight gain were faster than the length. This value could be due to low sample size (3 samples).

Length-weight relationship of *T. bruneus* described by equation $W = 0.00054L^{2.802}$ with $R^2 = 0.983$ (Raja Ampat) and $W = 0.05004L^{1.548}$ with $R^2 = 0.734$ (Manokwari). The analysis of total length and weight showed a linear

relationship with the line equation $y = 2.2954x - 2.4604$ with $R^2 = 0.8724$. Linear regression graph of the total length and weight of the *T. bruneus* was presented in Figure 2.

Based on obtained R^2 values, the contribution of shell length to weight was 98.30% (Raja Ampat), 73.4 % (Manokwari) and 87.2 % (all populations). These values also suggest that body weight can be used to estimate the size of the shell length.

Phylogenetic relationship

Phylogenetic analysis of *T. bruneus* resulted in two main clades with high bootstrap support (99). Clade 1 consisted of *T. bruneus* from West Papua and Clade 2 was *T. bruneus* from Malaysia. The close relationship between *T. bruneus* population from West Papua might be due to high sequence similarities. Phylogenetic tree of *T. sparverius* showed a group of all population into 2 main

Table 1. GenBank data information of the *T. sparverius*, *T. bruneus* and *T. setosus*, included in this analysis, location and accession number from National Center for Biotechnology Information (NCBI)

Species	Location	Acc. GenBank	References
<i>Turbo bruneus</i>	Sabah, Malaysia	AM403930	Williams 2007
<i>Turbo bruneus</i>	Sabah, Malaysia	AM403931	Williams 2007
<i>Turbo sparverius</i>	Longkang, Taiwan	AM403911	Williams 2007
<i>Turbo setosus</i>	Longkang, Taiwan	AM403910	Williams 2007

Table 2. Length-weight relationship of *T. sparverius* and *T. bruneus* showing the number of samples (n), constant values (a), the index of the growth values (b), correlation values (r), determinant values (R^2) and the growth pattern.

Species	Site	n	a	b	r	R^2	Growth pattern
<i>T. sparverius</i>	Sorong	3	0.00017	3.091	0.998	0.996	Positive allometric
	Manokwari	72	0.00104	2.654	0.921	0.847	Negative allometric
	Teluk Wondama	30	0.01678	1.939	0.744	0.553	Negative allometric
	All populations	105	0.0022	2.467	0.894	0.799	Negative allometric
<i>T. bruneus</i>	Raja Ampat	52	0.00054	2.802	0.992	0.983	Negative allometric
	Manokwari	22	0.05004	1.548	0.857	0.734	Negative allometric
	All populations	74	0.00346	2.295	0.934	0.872	Negative allometric

Table 4. Genetic distance (D) within and between population of *T. sparverius* and *T. bruneus*

Species	Genetic distance	Site	Manokwari	Teluk Wondama	Sorong
<i>T. sparverius</i>	Within population	Manokwari	0.002	-	-
		Teluk Wondama	-	0.002	-
		Sorong	-	-	0.002
	Between population	Manokwari	-	-	-
		Teluk Wondama	0.002	-	-
		Sorong	0.002	0.002	-
<i>T. bruneus</i>	Within population	Manokwari	0.004	-	-
		Raja Ampat	-	0.003	-
	Between population	Manokwari	-	-	-
		Raja Ampat	0.003	-	-

Table 5. Pairwise F_{ST} values of *T. sparverius* and *T. bruneus*

Species	Population	Manokwari	Teluk Wondama	Sorong
<i>T. sparverius</i>	Manokwari	-	-	-
	Teluk Wondama	0.037	-	-
	Sorong	0.201	0.146	-
<i>T. bruneus</i>	Raja Ampat	-	-	-
	Manokwari	0.031	-	-

clades, supported by high bootstrap values (99). Clade 1 composed of the population from Papua and clade 2 consisting of the population from Taiwan. Low gene flow possibly caused genetic differentiation between Papua and Taiwan due to distant geographic location. Overall, phylogenetic analysis revealed that all population of *T. sparverius* and *T. bruneus* lacked in genetic structuring indicated by low geographic partition between all samples (Figure 3). These were also supported by the low genetic distance between population (Table 4) and low F_{ST} values (Table 5).

Genetic diversity

A 656 bp fragment from Cytochrome Oxidase I (COI) was obtained from all samples (*T. sparverius* and *T. bruneus*) with a similarity of 98-99%. Similar fragment length was also found in family Turbinidae (Williams, 2007). In 656 bp DNA fragment of *T. sparverius* and *T. bruneus* there are many nucleotide difference (polymorphism) caused by point mutation. It is called point mutation because the mutation only occurs at a single nucleotide (Xiao et al. 2007). Transitions are substitution mutation between A and G (purines) or between C and T (pyrimidines), transversion occurs when nucleotide of purines changed to pyrimidines or vice versa (Graur 2003). There were five transition mutations found in *T. sparverius* consist of 1 synonymous substitution and four non-synonymous substitutions. The numbers of codons in *T. sparverius* were 218 with four mutated amino acids at codon position of 13, 35, 110, and 138. Meanwhile, in *T. bruneus*, 15 point mutations were found; consist of 14 transition mutations and one transversion mutation. The nucleotide substitution in *T. bruneus* consists of nine non-synonymous substitutions and six synonymous substitutions. The number of codons in *T. bruneus* was 218 with nine amino acid mutations at codon position of 51, 73, 132, 138, 168, 198, 201, 203, and 211. The occurrence of transition mutation are more often found than transversion mutation (Santos et al. 2003) and the transitional rate between pyrimidines (C and T) are higher than that between purines (A and G) (Castro et al. 1998). Mutations

can occur in either somatic or germ-line cells. Somatic mutations are not inherited so that they can be disregarded in an evolutionary or genetic context (Graur 2003).

The number of haplotypes and various types of haplotype were influenced genetic diversity of a population (Akbar et al. 2014). A total number of haplotype found in *T. sparverius* and *T. bruneus* were 7 and 13 haplotypes, respectively (Table 3). *T. sparverius* from Manokwari had six haplotypes (20 samples), Teluk Wondama had four haplotypes (15 samples) and two haplotypes (3 samples) from Sorong. *T. bruneus* from Raja Ampat had eight haplotypes (17 samples) and Manokwari had six haplotypes (18 samples).

Each population showed a high level of haplotype diversity (H_d) ranged from 0.657 to 0.816 (Table 3). The highest haplotype diversity of the *T. sparverius* was found in Teluk Wondama (0.705) and the lowest was found in Manokwari (0.657). The highest haplotype diversity of the *T. bruneus* was found in Raja Ampat (0.816) and the lowest was found in Manokwari (0.739). Nucleotide diversity (π) of *T. sparverius* ranged from 0.0018 (Manokwari) to 0.0021 (Teluk Wondama and Sorong). Meanwhile, nucleotide diversities of *T. bruneus* ranged from 0.0027 (Raja Ampat) to 0.0037 (Manokwari). This study showed that nucleotide diversities of *T. sparverius* and *T. bruneus* were lower than other gastropod species such as *Lunnella gradulata* ($\pi = 0.0046$) (Chiu et al. 2013).

Table 3. Genetic diversity of *T. sparverius* and *T. bruneus* accessed from the number of the haplotype (H_n), haplotype diversity (H_d), and nucleotide diversity (π), N indicated the number of samples for each site

Species	Population	N	Genetic diversity		
			H_n	H_d	π
<i>T. sparverius</i>	Manokwari	20	6	0.657	0.0018
	Wondama Bay	15	4	0.705	0.0021
	Sorong	3	2	0.667	0.0021
	All populations	38	7	0.691	0.0020
<i>T. bruneus</i>	Raja ampas	17	8	0.816	0.0027
	Manokwari	18	6	0.739	0.0037
	All populations	35	13	0.785	0.0032

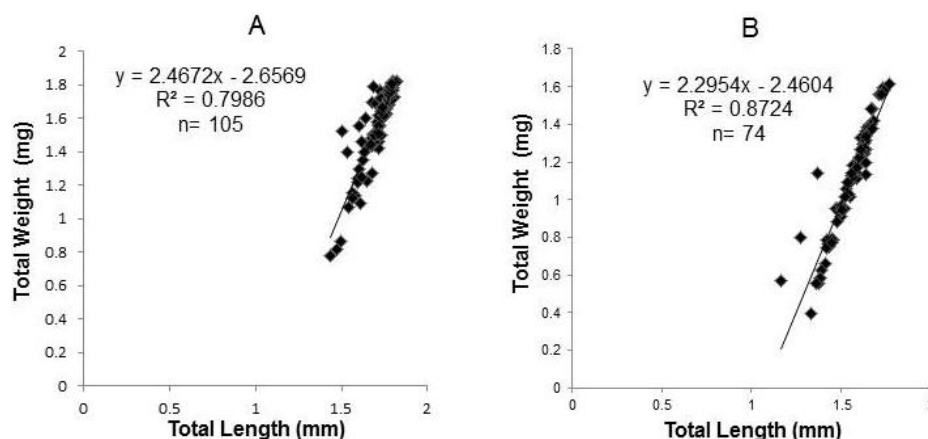


Figure 2. Linear regression of total length and weight from 105 individuals *T. sparverius* (A) and 74 individuals *T. bruneus* (B)

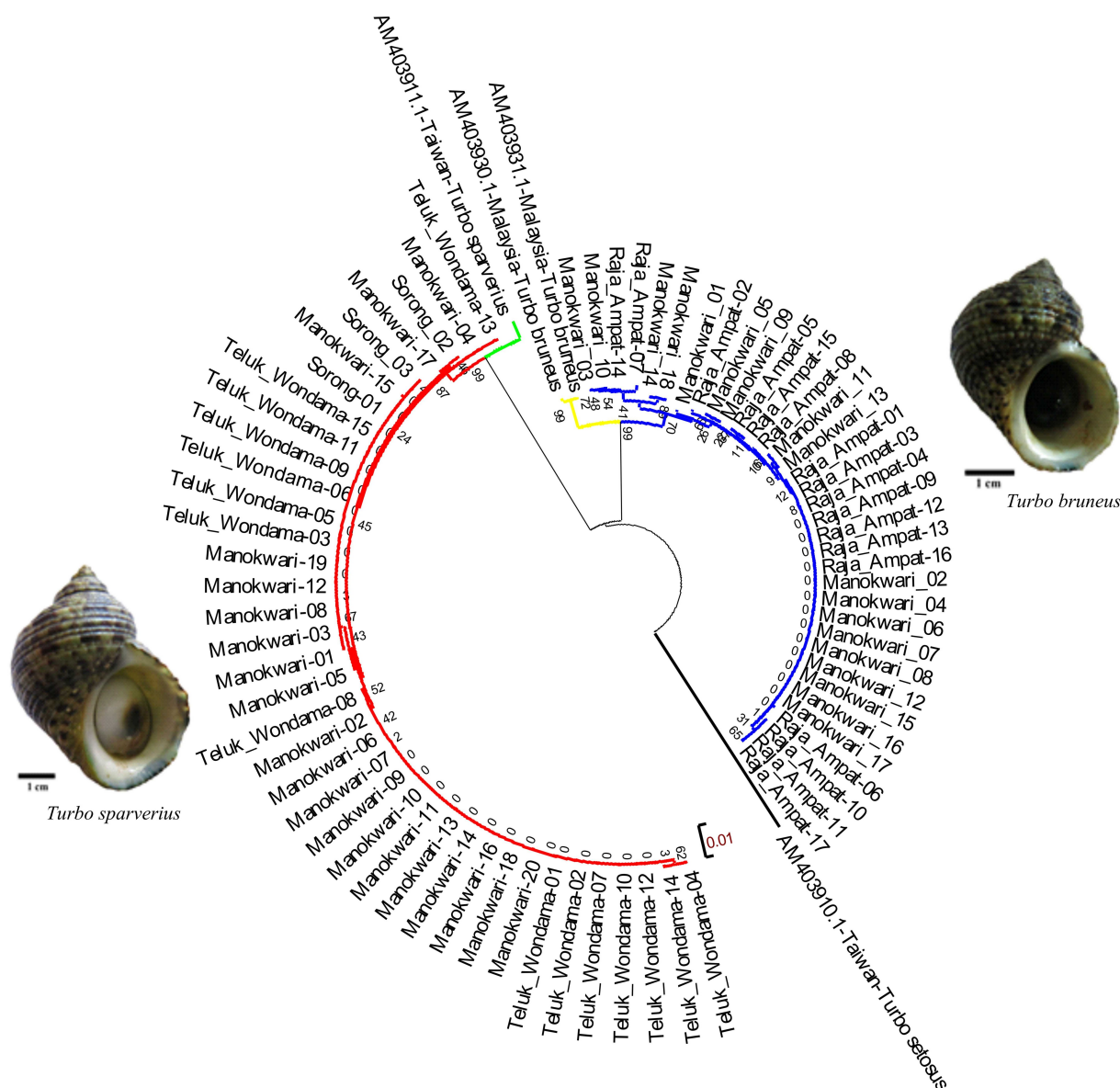


Figure 3. Phylogenetic tree of *T. sparverius* (39 sequences) and *T. bruneus* (37 sequences) using Neighbour-Joining (NJ) method with Kimura 2-parameter model and 1,000 bootstraps.

Population structure

Genetic distance within individuals of *T. sparverius* and *T. bruneus* were 0.0-0.6 % and 0.0-1.1 %, respectively. Genetic distance between *T. sparverius* and *T. bruneus* was 10.6 %. Genetic distance within individual was less than 2% while genetic distance among species ranged from 7-12% (Jusmaldi et al. 2014). Meanwhile, according to Brown et al. (1982), the genetic distance among species ranged from 9-19%.

Genetic distance within and between population of the *T. sparverius* in Manokwari, Teluk Wondama, and Sorong was 0.002 (Table 4). Meanwhile, genetic distance within population of *T. bruneus* in Manokwari and Raja Ampat were 0.004 and 0.003, respectively. Genetic distance between populations of *T. bruneus* was 0.003 (Table 4).

Pairwise F_{ST} test showed low level of genetic differentiation with F_{ST} values ranged from 0.037 to 0.201

(Table 5). AMOVA indicated that P-value of *T. sparverius* and *T. bruneus* were 0.23 and 0.17, which mean these population showed non-significance genetic differentiation among population ($P > 0.05$).

Population connectivity

The highest number of haplotype of the *T. sparverius* was found in Manokwari (Figure 4). Among these populations, there were four shared haplotypes such as, H1, H2, H3, and H6. Private haplotypes were found in Teluk Wondama (H7) and Manokwari (H4 and H5). The haplotype network of the *T. bruneus* showed that Raja Ampat has the highest number of haplotype, and there was only one shared haplotype (H1) (Figure 4). Genetic distance and F_{ST} showed that all populations of *T. sparverius* and *T. bruneus* had close genetic relationship.

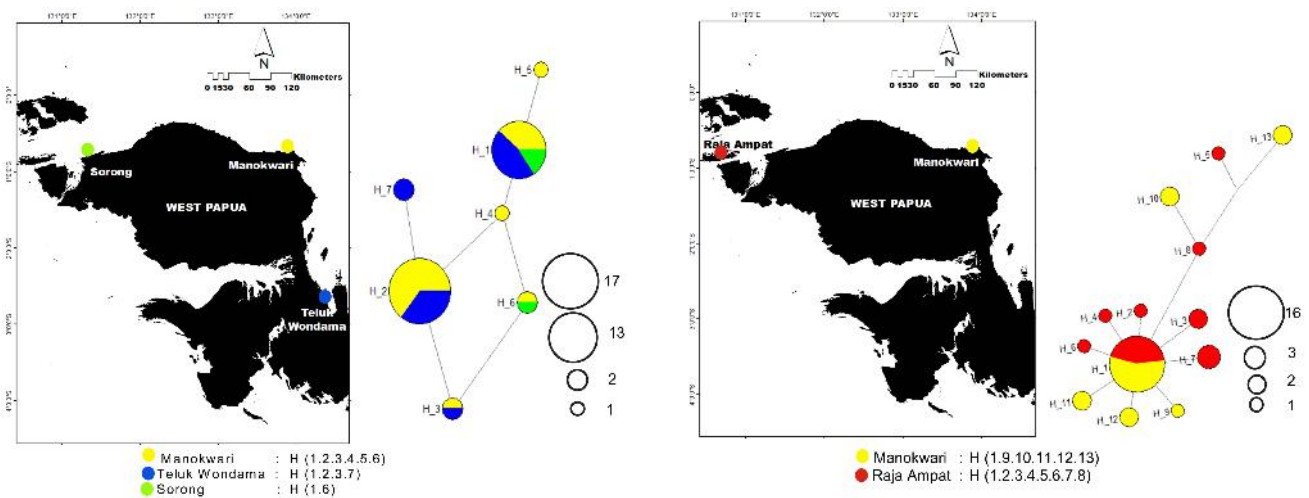


Figure 4. Haplotype network of the *T. sparverius* (left) and *T. bruneus* (right) from different locations in Papua. Each haplotype represents by a circle, whereas the size indicated the haplotype frequencies. Colors filling correspond to different sampling locations: Manokwari (yellow), Teluk Wondama (blue), Sorong (green)

Discussion

Length-weight relationship

The length-weight relationship are widely used in biological fisheries research for describing the change in the size of the individual, showing the growth pattern of an organism, obtaining the index of physical condition of populations and evaluate habitat quality (Gayon 2000; Albuquerque et al. 2009). This study showed that the growth pattern of *T. sparverius* and *T. bruneus* from West Papuan were negative allometric. The *b* values were less than 3, indicated the growth pattern of the *T. bruneus* was negative allometric, which means weight gain was slower than the length. A different result was obtained from the *T. sparverius* from Sorong which showed positive allometric growth pattern. *T. sparverius* were exploited by local people in Sorong and the sampling site was near the tourism object, these facts might be responsible for the low sample size found in this area. Negative allometric growth pattern means that weight gain was slower than the length. It is indicated that the collected individuals are the young individual. The Growth in younger individuals more focused on the growth of the shell so that the shell growth is faster than the growth in weight (Mulki et al. 2014). Differences of the growth patterns on the same species is caused by several factors such as the number of samples, sex differences, and other external factors such as environmental conditions suitable for the development of the growth of these species (Innal et al. 2015).

This study has a consistent result with Ramesh et al. (2009), which also found negative allometric growth pattern in *T. bruneus*. Various gastropod species also showed negative growth pattern such as *Lambis lambis* (Jaykumar et al. 2011), *Achatina fulica* (Albuquerque et al. 2009), *Litorina* sp. (McKinney et al. 2004), and *Tympanotonus fuscatus* (Udo 2013). The morphometric variation found in mollusks seemingly triggered by various factor such as, tidal variation, food availability, changes in seasonality, and sexual maturity (Ramesh et al. 2009).

Population genetic

Genetic distance analysis showed that all population of *T. sparverius* and *T. bruneus* were closely related. Genetic similarities of these species are probably triggered by ocean currents that act as a medium for gene transfer among those species. Lin and Liu (2008) found genetic similarities may exist due to ocean currents, high larval dispersal, and an appropriate habitat condition. Genetic diversity of marine biota in North Papua probably affect by New Guinea Coastal Current (Kashino et al. 2007) because planktonic larval dispersal and ocean current influence genetic exchange between populations (Chiu et al. 2013). Differences in environmental condition resulted in morphological changes, anatomical, and phylogenetic of a population (Twindiko et al. 2013). According to Chiu et al. (2013), genetic diversity can be influenced by two factors such as over-exploitation and habitat condition. High genetic diversity of individual within the population, increase the ability of the population to respond to environmental changes or exploitation (Akbar et al. 2014). *T. sparverius* and *T. bruneus* are widely used by local people for food or merchandise, which could reduce the genetic diversity of these species.

Pairwise F_{ST} test showed a low level of genetic differentiation in the current study, implied that those populations were genetically similar. Similar results was found in *Echinolittorina ziczac* (Diaz-Ferguson et al. 2011) and *Cittarium pica* (Diaz-Ferguson et al. 2010) which showed low F_{ST} values ranged from 0.007 to 0.04, and from 0.07 to 0.106, respectively. They also found that adjacent populations tend to have a low-value F_{ST} , while the greater distances tend to have higher F_{ST} value (Diaz-Ferguson et al. 2011). Genetic heterogeneity increases with increasing distance between populations (Wolf et al. 2000). *Coralliophila violacea* showed low average F_{ST} values (0.078), this is probably caused by the ability of larval dispersal and the pattern of ocean current (Lin and Liu 2008).

Gene flow and geographic isolation were affected by geographical distance and environment complexity. Genetic homogeneity of *T. sparverius* and *T. bruneus* seems to be caused by short distance between all sampling sites. Other possible explanation related to New Guinea Coastal Current (NGCC), which might facilitate larval dispersal across study areas. Genetic similarities might also exist due to the similarity of habitats in each population. Urta et al. (2003) found that gastropods originating from different habitat can have different both in genetic and morphology.

Shared haplotypes could be due to larval dispersal following ocean currents. *Turbo* sp. experienced a larval stage in its life cycle. *T. marmoratus* required 4 days to change from egg phase until larval settlement (Yamaguchi 1993). Dwiyono et al. (2001) revealed that the required time of *T. marmoratus* from the egg stage to become benthic organisms was about 60 hours. Such a long time larval duration provides an opportunity for this species to distribute widely via New Guinea Coastal Current (NGCC) (Kashino et al. 2007). New Guinea Coastal Current (NGCC) is a surface current that flows along the northern coast of Papua (Kuroda 2000). Genetic connectivity between populations of the benthic organism mainly occurred at pelagic larval stage (Cowen and Sponaugle 2009).

Analysis of genetic distance and F_{ST} showed that all populations of *T. sparverius* and *T. bruneus* had a close genetic relationship, possibly caused by the short distance between sampling sites (63-415 km) and geographic condition that are relatively open. Wyrski (1961) found that circulation pattern in the northern coast of Papua has a strong seasonal variability, flowing continuously to the Philippines. Ocean current condition and pelagic larval stage were potential factors that play a role in the dispersal of organisms, for example, dispersal distance of *Gaimardia trapesina* could reach 1300-2000 km (Helmuth et al. 1994). Isolated population tends to have low population size and high extinction risk compared to connected populations (Noreen et al. 2009). Ecological isolation and geographic structure were also affected population genetic structure (Crispo and Chapman 2008). Adjacent populations usually showed more genetic similarities than distant populations (Palumbi 2003). Geographical isolation, population history, oceanographic condition, and ecological traits can lead to high variations in the genetic diversity among populations (Chiu et al. 2013; Silva et al. 2013). Similar microhabitat (rocky intertidal) contribute to the occurrence of the genes mixing between populations *T. sparverius* and *T. bruneus*. Albaina et al. (2012) stated that microhabitat was an important factor in the dispersal of species, even though these species possess similar life cycle and dispersal potential.

We conclude that growth pattern in all populations of *T. sparverius* and *T. bruneus* was negative allometric, which means that weight gain was slower than length. All populations showed high haplotype diversity and genetic diversity. Phylogenetic reconstruction and population structure analysis indicated that genetic homogeneity was dominant among the population of *T. sparverius* and *T.*

bruneus, which possibly caused by gene flow between populations.

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