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Short Communication: Biometric of freshwater crayfish (*Cherax* spp.) from Papua and West Papua, Indonesia

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Abstract. *Abinawanto, Hamidah H, Bowolaksono A, Eprilurahman R. 2018. Short Communication: Biometric of freshwater crayfish (*Cherax *spp.) from Papua and West Papua,, Indonesia. Biodiversitas 19: 489-495.* Freshwater crayfish, *Cherax* spp. is a native crayfish species in Papua, Indonesia. Biometric information of this crayfish species in Indonesia is limited. Hence, this study aimed to provide these data. Specimens were collected from West Papua Province, i.e., from Uter Lake (Atinjo Subdistrict, Maybrat) and Seremuk River (Haha Village, Seremuk Subdistrict, South Sorong), respectively. Besides, the specimens were also collected from Papua Province in Baliem River at Pike Village, Hubukiak Subdistrict, and Wesaput Village, Wesaput Subdistrict, Jayawijaya. Data were analyzed using canonical discriminant function (CDF). The results showed that the longest carapace of *Cherax* spp. was 97.83 mm found in Baliem River at Pike Village. CDF analysis showed that there were three population groups of *Cherax* spp. from four locations. The first group originated from Uter Lake (Atinjo Subdistrict) and Seremuk River (Haha village). The second group was from Baliem River (Pike Village; Hubukiak Subdistrict, Jayawijaya and the third group from Baliem River (Wesaput Village; Wesaput Subdistrict).

Keywords: Biometric, *Cherax,* crayfish, Papua

INTRODUCTION

Freshwater crayfish is a widespread local fishery commodity in Papua, including South Sorong, Maybrat, and Jayawijaya Districts. According to Lukhaup and Pekny (2006), the freshwater crayfish found in South Sorong, Maybrat and Jayawijaya Districts belongs to the Parastacidae family and *Cherax* genus. Twenty species of Papua's endemic freshwater crayfish (*Cherax* spp.) had been identified using both morphological characters (Roux 1911; Holthuis 1949; 1950; Lukhaup and Pekny 2006; 2008; Lukhaup and Herbert 2008) and molecular approach (Lukhaup 2015; Lukhaup et al. 2015; Patoka et al. 2015a,b; Lukhaup et al. 2017).

Cherax spp. has an important ecological role for freshwater ecosystems; one of them is as a component of the food chain. In the freshwater ecosystem, the larva of *Cherax* spp. serves as food for larger aquatic animals such as fish while the adult of this freshwater crayfish has a cannibal trait that makes it preys on each other, as well as a carcass and detritus eaters in the waters. The food chain will be disrupted if one of its components is lost (Wowor et al. 2009). Preservation of *Cherax* spp. is vital to maintaining the ecosystem equilibriummaintained, more particularly in the freshwater regions of South Sorong, Maybrat, and Jayawijaya Districts. In addition to its ecological functions, *Cherax* spp. is also classified as an important commodity, and has a relatively higher price compared to other types of shrimp (Kusrini 2008; Dewi and Nugraha 2015). *Cherax* spp. is utilized by local communities for consumption and as an ornamental fish commodity (Tanjung 2013). *Cherax* spp. demands for consumption come from Japan, Malaysia, Hongkong, China, Taiwan, Korea, Singapore, USA, Canada, France, Netherlands, Germany, Belgium, New Zealand and Australia as this commodity has been a favorite food for consumers in these countries due to its healthier food properties as compared to seafood (Kurniasih 2008). The high demand for *Cherax* causes overexploitation of this freshwater commodity through continuous capture, which leads to the drastic accelerated decline of the stock in nature. IUCN (2015) classified the status of *Cherax* spp. in Papua as "*Data Deficient, Vulnerable,* and *Endangered*". According to Sari et al. (2011), the existence of *Cherax* spp. population is in a threatening condition. The decline in *Cherax* spp. population can also be caused by the destruction of their habitat, as a result of mining, the use of improper fishing methods and the use of non-selective fishing gear. *Cherax* spp. is one of the superior commodities that need to be elucidated and preserved to ensure its optimal utilization (Kurniasih 2008).

Studies related to *Cherax* spp. had been carried out but were still limited to the biological types and aspects. Meanwhile, specific studies related to inventory, identification, and characterization, and evaluation of *Cherax* spp. have not been done at present. *Cherax* spp. is widely distributed in South Sorong, Maybrat, and Jayawijaya Districts, so that this research was done in various stages of inventory, identification and characterization of the *Cherax* spp. types exist in these regions. Conditions of the population that live in nature as a wild population needs to be determined as valuable information for integrated fishery management and conservation activities. One of the efforts to study the population of *Cherax* spp. is by conducting inventory, characterization, and identification of *Cherax* spp. through morphometric analysis.

The objective of the study was to identify the diversity of freshwater crayfish (*Cherax* spp.) through morphometric analysis.

MATERIALS AND METHODS

The research was conducted during August 2016 to April 2017. A purposive sampling technique was used to determine the sample locations, based on the previous ecological study results which revealed that freshwaters in the southern part of Papua shared a common characteristics/conditions. South Sorong (Seremuk River), Maybrat (Uter Lake), and Jayawijaya (Baliem-Wamena River) are districts located in the southern part of Papua (Sukmajaya and Suharjo 2003; Kurniasih 2008; Kartikasari et al. 2012; RKPD West Papua 2016). Also, these three districts represent the endemic area and are the center of *Cherax* spp. diversity in Papua. The districts of South Sorong (Seremuk River), Maybrat (Uter Lake), and Jayawijaya (Baliem-Wamena River) share similar ecological conditions and water parameters that support the optimal growth of *Cherax* spp. (Sukmajaya and Suharjo 2003; Kurniasih 2008; Kartikasari et al. 2012) allowing the research team successfully collected *Cherax* spp. at any spot in the three districts as a sampling site. *Cherax* spp. was collected from Uter Lake (Maybrat District) (1°26'07.1"S and 132°22'56.7 " E), Seremuk River (South Sorong District) (1°31'55.6" and 131° 58'33.0" E), Baliem River (Pike Village, Jayawijaya District) (04 03'18.3" S and 138°56'13.8" E), and Baliem River (Wesaput Village, Jayawijaya District) (04°05'40.1" S and 138°57'54.7" E) (Figure 1). Three sampling spots were taken at each location, two spots were close to each other, and the other spot was far apart.

Morphometric measurements of freshwater crayfish were conducted at the Genetic Laboratory, Department of Biology FMIPA UI, Depok. The tools used in the study consisted of field equipment (plastic sample bottles, scissors, tissue, gloves, cutter, 1.5 ml tube, digital camera, digital caliper, meter, ruler, stationery, specimen tray, and GPS) as well as and laboratory equipment.

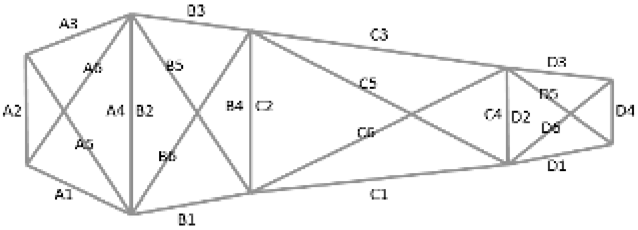

Figure 2. *Truss* morphometric method modified from Bookstein et al. (1985)

Figure 1. Location of sampling in Papua and West Papua provinces, Indonesia

Specimens collected in Uter Lake were three samples, Seremuk River were ten samples, and Baliem River (Pike Village) were seven samples, Baliem River (Wesaput Village) were 11 samples. *Truss* morphometric method employed was modified from Bookstein et al. (1985) as presented in Figure 2. The measured morphometric characters were head, abdominal, and telson based on Brezky and Doyle (1988). The measurements were carried out using digital calipers with 0.01 mm accuracy.

The discriminant canonical function was used to determine the distribution of *Cherax* spp. (Suparyanto et al. 1999). All data analysis was performed using SPSS software (version 19). Species identification was conducted based on FAO species catalog (Holthuis 1991).

RESULTS AND DISCUSSION

Diversity of freshwater crayfish

Thirty-one individuals (adults) of freshwater crayfish were obtained from four research locations (Uter Lake, Seremuk River, Baliem River-Pike Village, Baliem River-Wesaput Village) within three districts (South Sorong, Maybrat, and Jayawijaya), consisted of eight females and 23 males. Morphology of the 31 freshwater crayfish was characterized and analyzed to study the crayfish morphological diversity, population structure, and its distribution.

Morphological characterization employing the *truss* morphometric method revealed that morphological characters of crayfish from the four locations differed significantly ($P<0.05$) based on "Test of Equality of Group Means," for the following variables/characters: Carapace Lenght, Body Lenght, and A1-D6 (Figure 2). The length of carapace ranged from 31.21 to 97.83 mm with an average of 50.36 mm. Freshwater crayfish with the longest carapace was found in Baliem River-Wesaput Village. The freshwater crayfish with the longest A1-D6 characters were also found in Baliem River-Wesaput Village.

Table 2. Function at group centroid

Location	Function		
	1	2	3
Uter Lake	-1.919	-3.069	1.037
Seremuk River	-1.398	0.246	-1.078
Baliem River-Pike Village	-0.785	1.378	1.238
Baliem River-Wesaput Village	2.294	-0.264	-0.091

Note: Unstandardized canonical discriminant functions; evaluated at group means

Table 1. Observed parameters of *truss* morphometric of *Cherax* spp.

Parts of the body	Symbol	Explanation
Front part of the head	A1	The distance between the broadest left point of the carapace to the base of the left eyes
	A2	The distance between stalks of the right and left eyes
	A3	The distance between the broadest right point of the carapace to the base of the left eyestalk
	A4	The distance between the widest point of the carapace point
	A5	Diagonal of left point of carapace to the right eye
	A6	Diagonal of right point of carapace to the left eye
Back part of the head	B1	The distance between the back point of the carapace to the leftmost portion of the carapace
	B2	The distance between the largest carapace points
	B3	The distance between the back point of the carapace to the leftmost portion of the carapace
	B4	The distance between the two left and right points of the back part of carapace
	B5	The diagonal from the point of left rear of carapace point to the broadest rightmost point of carapace
	B6	The diagonal from the point of right rear carapace to leftmost widest point of carapace
Abdomen	C1	The distance between the back point of the left abdomen to front point of the left abdomen
	C2	The distance between the two left and right points of the rear carapace
	C3	The distance between the back point of right abdomen to the front point of right abdomen
	C4	The distance between the left point to the right point of back abdomen
	C5	The diagonal of the point at the back-left side of the abdomen to the point at the front-right side of the abdomen
	C6	The diagonal of the left back of abdomen to the right front of abdomen
Telson	D1	The distance between the left rear telon point, to the left front telson point
	D2	The distance between the two left and right points of the back abdomen
	D3	The distance between the back point of the right telson to the front point of right telson
	D4	The distance between right side and the left side of back telson
	D5	The diagonal of back-left side telson to the front-right side telson
	D6	The diagonal of back-right side telson to the front-left side telson

Table 3. Tests of equality of group means

	Wilks' Lambda	F	df1	df2	Sig.
Body length	0.860	1.467	3.000	27.000	0.246
Carapace length	0.587	6.340	3.000	27.000	0.002
A1	0.664	4.564	3.000	27.000	0.010
A2	0.633	5.209	3.000	27.000	0.006
A3	0.676	4.314	3.000	27.000	0.013
A4	0.660	4.629	3.000	27.000	0.010
A5	0.639	5.089	3.000	27.000	0.006
A6	0.665	4.540	3.000	27.000	0.011
B1	0.608	5.815	3.000	27.000	0.003
B2	0.624	5.415	3.000	27.000	0.005
B3	0.592	6.192	3.000	27.000	0.002
B4	0.586	6.361	3.000	27.000	0.002
B5	0.589	6.289	3.000	27.000	0.002
B6	0.586	6.347	3.000	27.000	0.002
C1	0.610	5.750	3.000	27.000	0.004
C2	0.625	5.402	3.000	27.000	0.005
C3	0.612	5.698	3.000	27.000	0.004
C4	0.596	6.091	3.000	27.000	0.003
C5	0.643	5.003	3.000	27.000	0.007
C6	0.633	5.209	3.000	27.000	0.006
D1	0.622	5.458	3.000	27.000	0.005
D2	0.614	5.658	3.000	27.000	0.004
D3	0.593	6.186	3.000	27.000	0.002
D4	0.592	6.206	3.000	27.000	0.002
D5	0.621	5.490	3.000	27.000	0.004
D6	0.617	5.591	3.000	27.000	0.004

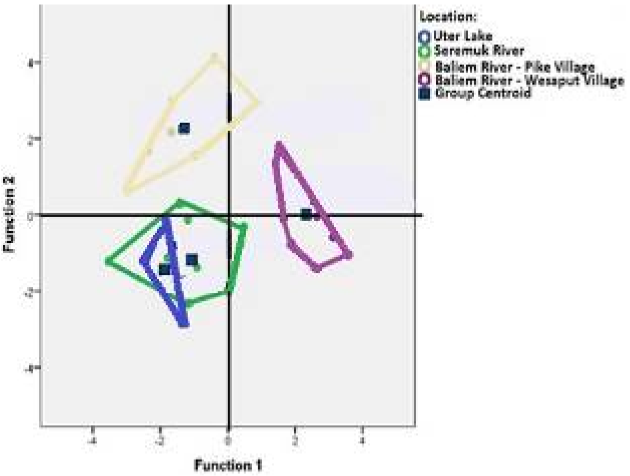

Figure 3. Distribution of morphological character of freshwater crayfish from South Sorong, Maybrat, and Jayawijaya Districts based on *truss* morphometric with canonical discriminant analysis

Results of the morphometric analysis showed that morphological characters of crayfish from Uter Lake (Maybrat Regency) and Seremuk River (South Sorong District) were grouped in one cluster and overlapped, while that of other populations were separated. The group centroids of these four populations are in the area around the zero/horizontal line of X and Y axis (Figure 3).

Table 4. Matrix value of genetic distance among freshwater crayfish populations

Population	Uter Lake	Seremuk River	Baliem River-Pike Village	Baliem River-Wesaput Village
Uter Lake	0			
Seremuk River	0.2408	0		
Baliem River-Pike Village	0.2775	0.1634	0	
Baliem River-Wesaput Village	0.2640	0.1631	0.1037	0

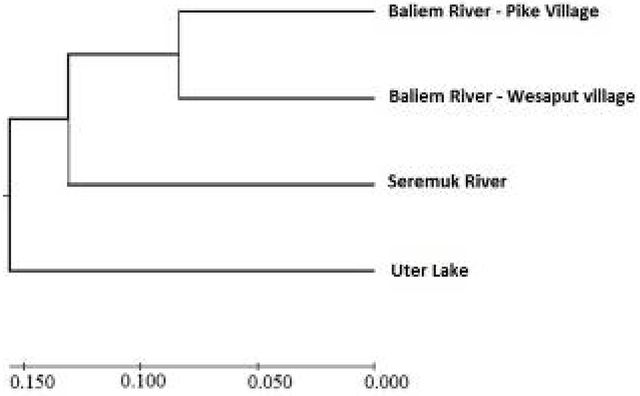

Figure 4. Dendrogram of genetic distance among freshwater crayfish populations from South Sorong, Maybrat, and Jayawijaya Districts based on *truss* morphometric

Phenotypic distribution and genetic distance of freshwater crayfish based on *truss* morphometric characters

The genetic matrix value was obtained from measurement of the truss morphometric parameters. PCA analysis of morphological characteristics resulted in matrix value of genetic distance as presented in Table 4.

The present study results show that the largest genetic distance (0.2775) was found between population of Uter Lake and Baliem River-Pike Village population; followed by the genetic distance between Baliem River-Pike Village population and Baliem River-Wesaput Village population (0.2640); Uter Lake population and Seremuk River population (0.2408); Baliem River-Wesaput Village population and Seremuk River population (0.1634); Baliem River-Wesaput Village population and Seremuk River population (0.1631); and between Baliem River-Wesaput Village population and Baliem River-Pike Village population (0.1037) (Table 4).

The genetic distance matrix among *Cherax* spp. populations presented in Table 4 was used as the basis for clustering those populations in a dendrogram (Figure 4) to explain their genetic relatedness based on truss morphometric. The furthest genetic distance did occur between Uter Lake population and Baliem River-Pike Village population while the nearest genetic distance was observed between the populations of River Baliem-Wesaput Village and Baliem River-Pike Village.

Figure 5. Freshwater crayfish collected from Papua and West Papua Provinces, Indonesia. Bar = 3 cm

Freshwater crayfish collected from Papua and West Papua provinces, Indonesia with different physical appearance is presented in Figure 5.

Figure 5 shows three groups of *Cherax* spp. that were collected from four locations based on canonical discriminant function analyses. The first group was freshwater crayfish originated from Uter Lake and Seremuk River while the second group was those originated from the Baliem River-Hubukiaki District. Meanwhile, the third group was freshwater crayfish originated from Baliem River-Wesaput District.

Discussion

Information on the diversity of freshwater crayfish based on morphometrics in South Sorong, Maybrat and Jayawijaya Districts is lacking. Therefore, this research was important to be carried. Freshwater crayfish is an endemic species (Sukmajaya and Suharjo 2003; Kartikasari et al. 2012) of the Parastacidae family and the *Cherax* genus (Roux 1911; Holthuis 1949; 1950; Lukhaup and Pekny (2006, 2008) that is widely distributed in aquatic waters of southern part of Papua, such as South Sorong District (Seremuk River), Maybrat District (Uter Lake) and Jayawijaya District (Baliem River-Wamena) (Kartikasari et al. 2012; Eprilurahman 2014). The morphometric analysis used to reveal the crayfish diversity (*Cherax* spp.) are the *truss* morphometric and sexual dimorphism.

The study results show that the truss morphometric can be used to identify differences in freshwater crayfish morphological characters, population structure, and distribution. Truss morphometric analysis revealed that morphological characteristics of freshwater crayfish from Uter Lake (Maybrat District) and Seremuk River (South Sorong District) were grouped in one cluster and overlapped each other, while those of other populations were separated. Overlapping among the morphological characters of the two populations indicates their high morphological similarities.

Distribution of freshwater crayfish is divided into several populations, which then further split into several groups based on several geographical factors. These geographic factors caused the populations become isolated and may form different characters (Hadie 1997). According to Suparyanto et al. (1999), the tight relatedness between groups is indicated by an inter-sample allusion/ overlapping. The distribution of Uter Lake and Seremuk River populations was closely related, but that of Baliem River-Pike Village (Jayawijaya District) and Baliem River-Wesaput Village (Jayawijya District) population was distantly related (Figure 4).

Observed morphological characters of freshwater crayfish through truss morphometric can be used to differentiate populations as depicted in genetic distance matrix (Table 4). The genetic distance matrix between populations in Table 4 was used to construct the dendrogram (Figure 4). The most distant genetic relatedness was observed between Uter Lake population and Baliem River-Pike Village (Jayawijaya District) population while the closest genetic distance was found between Baliem River-Wesaput Village (Jayawijaya District) population and Baliem River-Pike Village (Jayawijaya District) population.

The genetic distance value is used as a reference in the crossing of individuals within the population. Crossings of individuals within distantly related populations will more likely increase the diversity significantly than those of closely related populations. This is because, in crossings of individuals from closely related populations, the heterozygosity is only derived from one single population while in the distantly related population crossings, the genetic diversity can be obtained from both populations (Suparyanto et al. 1999).

Implication of the calculated genetic distance values is that crossings of individuals of: Uter Lake population x Baliem River-Pike Village population, Uter Lake population x Baliem River-Wesaput Village population, and Seremuk River population x Baliem River-Pike Village population will more likely increase the diversity more significantly as compared to that of Uter Lake population x Seremuk River population or Baliem River-Pike Village population x Baliem River-Wesaput Village population. The genetic relatedness among the four natural populations of freshwater crayfish is described in three main clusters. The freshwater crayfish of Baliem River-Pike Village population and the Baliem River-Wesaput Village population were placed in one cluster while the other two clusters consisted of Seremuk River population and Uter Lake population, respectively (Figure 4).

Two or more populations can be grouped in a single cluster due to their close geographical position. The phenotype of an individual is an expression of genotype by environment interaction. The same geographic location is suspected to have similar conditions of water quality. Figure 3 shows that individuals within each population shared almost the same characters and body size. According to Hadie et al. (2002), growth and development of specific body parts are influenced by environmental stress such as water population. Thus, environmental factors can affect the growth rate of specific organs.

In conclusion, morphometric analysis was successfully used to identify the diversity and genetic relatedness of freshwater crayfish (*Cherax* spp.). The truss morphometric analysis revealed three groups of *Cherax* spp. that were distributed separately in Papua. PCA analysis placed the four *Cherax* spp. populations into three main clusters, i.e., Baliem River-Pike Village population and Baliem Village-Wesaput Village population in one cluster while Seremuk River population and Uter Lake population were each in a separate cluster.

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