Statistical method to assess *Tachypleus gigas* and *Carcinoscorpius rotundicauda* (Xiphosura) allometry

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ABSTRACT: Morphology measurements could be used as a scale when converted into length-length or length-weight relationships. Size relationships could indicate variability for health and growth within horseshoe crab populations. However, in previous attempts, the selection of morphology units changed with every population. Basically, mean, and standard deviation was employed and median values became the baseline for normal classification. In this study, a linear equation was extracted for each morphology measurement. After inserting the mean values into the equation, a huge majority of Carcinoscorpius rotundicauda were within the normal or enlarged size scale. The similar was achieved for Tachypleus gigas except for the female group in which more crabs were indicated with normal body size. Comparatively, a greater number of males were scaled in the larger range. Meanwhile for other tests, the morphology measurements were square-root transformed. Resemblance was used to obtain a mirror expression for the transformed data. Draftsman plot revealed the data scattering while Link Tree analysis indicated dependable measurements and their range for allometry. Then, stepwise regression was employed and only matching variables were selected. Hence, the measurement units because reduced by 50%. This practice was generally introduced to minimize the management of large datasets. Therefore, the telson, prosoma length and opisthosoma width were selected for male horseshoe crabs whereas prosomal length was replaced with interorbit distance for the female crab. In relation to obtaining a huge majority of samples in the normal and positive allometry category, northern shores of Java could be indicated with sufficient resource supply. This study highlights revision in mean values which could become baseline for each morphology measurement during the assessment of allometry in populations of Java, Indonesia.

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KEY WORDS: morphology; arthropod; linear; population; size

Статистический метод для изучения аллометрии мечехвостов *Tachypleus gigas* и *Carcinoscorpius rotundicauda* (Xiphosura)

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РЕЗЮМЕ: Морфологические промеры могут быть использованы как шкала будучи конвертированы в соотношения длина-длина и длина-вес. Соотношения размеров могут указывать на изменения состояния здоровья и степени роста в популяциях мечехвостов. Тем не менее, в предыдущих исследованиях выбор морфологических единиц различался между популяциями. Исходно, в качестве основы нормальной классификации использовали средние величины, т.е. среднее и стандартное отклонение. В данном исследовании, для каждого морфологического промеры выведено линейное уравнение. После введения в уравнение средних величин, подавляющее большинство особей Carcinoscorpius rotundicauda оказалось внутри нормальной или увеличенной размерной шкалы. Сходные результаты были получены для *Tachypleus* gigas за исключением группы самок, в которых больше особей было указано для нормального размера тела. Соответственно, большее число самцов было отнесено к шкале большего размера. В сравнении с другими тестами, морфологические промеры были трансформированы при помощи уравнения квадратного корня. Для зеркального отображения трансформированных данных была использована мера подобия. Чертежный редактор Draftsman показал разброс данных, тогда как анализ Link Tree выявил зависимые измерения и их уровень для аллометрии. Таким образом, была использована пошаговая регрессия и выбраны только согласованные переменные. При этом единицы измерения были редуцированы на 50%. Эта практика обычно используется для минимизации управления большими данными. Для самцов мечехвостов были выбраны длина тельсона, длина просомы и ширина опистосомы, а для самок длина просомы была заменена на межорбитальное расстояние. Северное побережье Явы может рассматриваться как удовлетворительный источник мечехвостов, подавляющее большинство которых относятся к нормальной и позитивной аллометрическим категориям. Настоящее исследование указывает на необходимость ревизии средних величин, которые могут стать основой каждого морфологического промера для оценки аллометрии в популяциях мечехвостов на Яве, Индонезия.

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КЛЮЧЕВЫЕ СЛОВА: морфология; членистоногие; линейное уравнение; популяция; размер.

Introduction

The exoskeleton structure of horseshoe crabs has remained unchanged throughout their existence. However, the arthropods were thought to shrink in size with every generation cycle. For instance, the total length of 500-millionyear-old fossils that measured 84 cm (Moreau et al., 2014) were then replaced by smaller surviving generations that age 280-450 million years. These include the Carcinoscorpius rotundicauda (Latreille, 1802) with total length of 40 cm, it is 69 cm for Tachypleus gigas (O.F. Müller, 1785), 62 cm for Limulus polyphemus (Linnaeus, 1758) and 79.5 cm for T. tridentatus (Leach, 1819) (Srijaya et al., 2010; Mohamad et al., 2016; Jawahir et al., 2017). Size reductions were perhaps an evolutionary response as each younger generation adapts with the changing environment. Meanwhile, horseshoe crabs take about 17 molt cycles to reach maturity; the male has one molt short and ends at the 16th molt cycle. Therefore, sexually mature male horseshoe crabs would generally occur in the smaller size range if compared to its suitor. In L. polyphemus, a single female would measure 22% larger than a male and individuals from southern waters were appearing larger than individuals from the North (Botton, Loveland, 1992). Meanwhile, the prosoma of T. tridentatus and C. rotundicauda measured larger for populations in Hong Kong when compared to individuals retrieved from the mainland in Fujian, China. Interestingly, the variations were not limited to sexually mature adults but it did occur in samples from different life stages; such as sixth-molt juveniles and onwards (Chiu, Morton, 2003). This indicates that not all horseshoe crabs end up in standard or similar size after completing the final molt or when reaching maturity.

In early periods of research concerning the biology of horseshoe crabs, retrieving horseshoe crabs in different sizes did not receive much attention because literature was scarce as well as inadequate to make viable comparisons. In addition, researchers assumed these arthropods endured a series of fixed annual molt cycles that give each individual uniform size appearance upon reaching sexual maturity. However, literature begun to emerge with mentions on size variations in the arthropod. First observations emerged for both, the American (Botton, Loveland, 1992) and Asian species (Vijayakumar et al., 2000). With this, the influence of size towards fitness became another mode in exploring the biology of horseshoe crabs. Yet, visual inspections alone were somewhat focused on epibiont infestation, degeneration, and deformities, and carapace damage (John et al., 2018). Disease does not occur in horseshoe crabs unless they became weak or fatigue from dehydration. Since horseshoe crabs were only encountered during mating where they emerge into shallow waters in amplexus (Nelson et al., 2015), their participation in this monthly routine overrides any form of understanding produced from visual inspections alone. Basically, for researchers, if the arthropod could attract a mate, they were assumed with good health.

Like geospatial scaling, the body plan of horseshoe crabs could be mapped and measured using a series of morphology units. However, obtaining these units is not easy because horseshoe crabs have an uneven 3-dimentional body plan and therefore, every measurement needs to be short and the measuring points must be near. Interestingly a total of 36 length and width measurements were proposed (Wardiatno et al., 2021). Unfortunately, specialists in big dataset were needed to manage a high number of measurements. Basically, fewer keys and small set of data were preferred for the length-length and length-weight analysis. Then, a range of body scale or allometry could be proposed in the form of negative, normal, or positive definitions (Vijayakumar et al., 2000). Again, researchers such as Sahu & Dey (2013), Mohamad et al. (2016), Jawahir et al. (2017), Razak & Kassim (2018) and Agustriani & Putri (2021) were challenged by inconsistencies in

choosing the most influencing morphology units to indicate allometry. Since the study of Vijayakumar *et al.*, 2000, the 8–9 morphology units were maintained and it followed with descriptive analysis such as average, percentage and standard deviation values (Mohamad *et al.*, 2016). Generally, any outliers from this range would be considered with negative (if below the range) or positive (larger exhibits in value) allometry.

This idea was retained in setting a new approach that used statistics. In the first attempt, Mohamed et al. (2021) indicated the differences of using the descriptive methodology and compared it with a series of data treatments that used linear equation, correlation, and regression. Stepwise regression was essential to limit the morphology keys to fewer measurements that have the best validation. Only then a baseline median value could be proposed for each of the morphology unit. It follows with organizing large and small values into classifications like positive, normal, or negative for the allometry. In the second attempt, Chan et al. (2022) used a larger set of samples and divided the entire group into male and female.

Stepwise analysis was reliable in both studies when applied to select morphology units that influence allometry. Interorbit distance and prosoma length were respectively suitable for female and male while samples containing juveniles could rely on telson and carapace width measurements. Correct allometry suggestions could have added support in studies of Fairuz-Fozi et al. (2018), Zauki et al. (2019), Pati et al. (2021) and Pramanik et al. (2021) that examined feeding habits and size variations. To this point, the published method was only tested on crabs from Malaysia. The aim of this study is to carry out similar assessments on T. gigas and C. rotundicauda from northern shores of Java, Indonesia. These arthropods were measured from local mongers in Semarang who associated with suppliers. Hence, the only awareness concerning location source is the regional waters of northern Java, Indonesia. Based on the aim of this study, if the morphology keys such as telson, carapace width, interorbit distance (female) and prosoma length (male) were still indicated after the stepwise analysis, this approach could be the breakthrough in analyzing the scale (or allometry) of these arthropods.

Materials and Methods

DESCRIBING THE MORPHOLOGY. The dorsal section of a horseshoe crab is divided into prosoma, opisthosoma and telson. With an uneven 3-dimentional shape, each section could be measured by using a flexible measuring tape. The starting point for each section whether plotted diagonally or horizontally implies a single measurement for the morphology. For instance, the interorbit distance is considered the length between each of the false-eye sockets whereas carapace width is the measurement between two prosoma spines. Therefore, a total of 9 length measurements could be proposed to measure the body plan for a single horseshoe crab (Fig. 1).

SCALE METHODOLOGY. A total of 115 *C. rotundicauda* and 89 *T. gigas* were collected from northern shores of Jawa, Indonesia. The morphology of these crabs was measured by using length and width dimensions to scale their body plan (Fig. 1, Suppl. Tables S1, S2). Every dimension was arranged by species and separated by gender in an ascending order before the extraction of mean and standard deviation. This was the descriptive analytical method which was introduced by Vijayakumar *et al.* (2000). After setting a baseline (the median value for a series of data), relevant morphology measurements were compared to develop allometry relationships. Any size below the baseline value was classified as negative whereas values larger than the baseline was positive.

THEANALYTICAL PROCEDURES. In another Microsoft Excel sheet, a linear graph was developed from each set of morphology measurements. Then, linear equations (y = mx + c) and regression (R^2) scores were extracted and compiled. Meanwhile, a new Microsoft Excel sheet was created before exported into Primer v.7. In this dataset, the samples were already divided by species (C. rotundicauda and T. gigas) and gender (male and female). The protocols of Mohamad et al. (2021) and Chan et al. (2022) were adopted for the following analyses. Square root (\sqrt{Xi}) transformation was carried out on the data before Bray-Curtis cluster analysis to generate the Resemblance matrix. The first analysis was Draftsman's plot for observations related to scatter of data. Second, Link Tree analysis was carried out to identify relative subgroup separation and absolute measure of group differentiation (through the Similarity Percentage). This information could be retrieved from indicative values that associate with each set of morphology variable. In the last step, a stepwise regression amalgamated with Pearson's correlation was developed. The highest stepwise regression scores (value ~ 1) were used in the final selection of measurements. These scores were assumed with reliability for exact indication of allometry. In the second sheet, only the standard deviation (σ) was used to produce a revised range for



Fig. 1. The body plan of a female *Tachypleus gigas* and basic morphological measurements.
1 — prosoma length, 2 — carapace length, 3 — opisthosoma length, 4 — telson length, 5 — interorbit width, 6 — prosoma width, 7 — opisthosoma width, 8 — carapace width, 9 — total length.
Рис. 1. Строение тела самки *Tachypleus gigas* и основные морфологические промеры.
1 — длина просомы, 2 — длина карапакса, 3 — длина опистосомы, 4 — длина тельсона, 5 — интерорбитальная

1 — длина просомы, 2 — длина карапакса, 9 — длина опистосомы, 4 — длина тельсона, 5 — интерроитальная ширина, 6 — ширина просомы, 7 — ширина опистосомы, 8 — ширина карапакса, 9 — общая длина тела.

each set of morphology. These values were manually inserted as x-value into the previously extracted linear equation (y = mx + c). The range of values whether large or small was determined by the mean (\bar{x}) value which was the new baseline for each morphology cluster Only them, it is possible to organize the final output into a body scale reservation c.f. (Vijayakumar *et al.*, 2000) classified as negative, normal, or positive.

Results

The horseshoe crab body plan was assessed by each species and in the first assessment, there were 47 female and 68 male *C. rotundicauda*. A total of 9-morphometric indicators were selected to represent the exoskeleton dimensions of this arthropod (Suppl. Table 3). Length-length and length-width relationships via Draftsman's plot indicated 1–2 asymmetrical measurements for female *C. rotundicauda* that involved prosoma, opisthosoma, carapace and telson (Fig. 2A). It was 1–5 asymmetrical measurements between each morphological variable in the male crab (Fig. 2B). The linear equations produced regression scores (\mathbb{R}^2) that ranged 0.633–0.991. Through descriptive analysis ($\bar{x}\pm\sigma$), 6–11 female crabs could be considered with negative allometry. The ascending order for measurements were opisthosoma length<prosoma width, telson length, total length, carapace length<prosoma length, opisthosoma width, interorbit length<carapace width. A huge majority between 29 and 37 female crabs were having normal allometry. In fact, 37 female crabs could be considered with normal allometry if opisthosoma length was used and it reduced to 29 crabs if the total length and prosoma length was considered.

Comparatively, between 4 and 10 female crabs were considered with positive allometry when the morphology measurements were arranged into an ascending order from opisthosoma length<carapace length, carapace width<prosoma width, interorbit length<telson length, opisthosoma width<prosoma length<total length. Only the carapace length and opisthosoma length were reliable for having closely associated organization for the number of crabs. In another analysis, 47–59 male horseshoe crabs were indicated with normal allometry with 4-10 individuals having negative allometry. Only the interorbit length,



Fig. 2. Draftsman's plot for series of resemblance involving (A) female and (B) male *Carcinoscorpius rotundicauda* morphology values.

CL — carapace length, CW — carapace width, IOL — interorbit length, OL — opisthosoma length, OW — opisthosoma width, PL — prosoma length, PW — prosoma width, Tel — telson, TL — total length.

Рис. 2. Результаты использования редактора Draftsman для подобия морфологических показателей самок (А) и самцов (В) *Carcinoscorpius rotundicauda*.

CL — длина карапакса, CW — ширина карапакса, IOL — интерорбитальная длина, OL — длина опистосомы, OW — ширина опистосомы, PL — длина просомы, PW — ширина просомы, Tel — тельсон, TL — общая длина тела.

carapace width and carapace length could be considered with reliability.

Link Tree cluster of female *C. rotundicauda* was indicated with relative = 0.97 and absolute similarity percentage = 98% for the prosoma width (130-159 mm), interorbit length (65-80 mm), prosoma length (75-88 mm), carapace width (115–135 mm), total length (286–312 mm), opisthosoma length (64–71 mm), opisthosoma width (100–105 mm) and telson length (165–167 mm; Fig. 3). It was relative = 0.82 and absolute similarity percentage = 93% and only the carapace width with medial range (baseline) at 99–105 mm was indicated for the



Fig. 3. Link Tree analysis for each female *Carcinoscorpius rotundicauda* morphology separated by relative and absolute measures of its values. Abbreviations as is Fig. 2.

Рис. 3. Анализ Link Tree для морфологии каждой самки *Carcinoscorpius rotundicauda*, отделенной относительными и абсолютными данными ее показателей. Сокращения как на рис. 2.



Fig. 4. Link Tree analysis for each male *Carcinoscorpius rotundicauda* morphology separated by relative and absolute measures of its values. Abbreviations as is Fig. 2.

Рис. 4. Анализ Link Tree для морфологии каждого самца *Carcinoscorpius rotundicauda*, отделенного относительными и абсолютными данными его показателей. Сокращения как на рис. 2.

male C. rotundicauda (Fig. 4). However, after the stepwise analysis, only telson and opisthosoma width were indicated with best reliability. If the telson was considered since it had the highest regression score (0.964), 31 female crabs were demarcated with normal allometry. It became reduced to 23 if the opisthosoma width was considered. Comparatively, if the analysis was specific towards female crabs, the interorbit length was preferred. Therefore, about 18 horseshoe crabs could be considered with normal allometry whereas the remaining 29 were demarcated with positive allometry for having larger size than the baseline value. Percentage values were added into morphometric revisions to indicate changes after resetting the baseline values for morphology measurements. It could lead to drastic reorganization of male and female allometry (Suppl. Table 3). For example, the changes between descriptive analysis and

baseline corrections were large that it could vary from -29.8 to -2.1% for the normal allometry of female crabs.

Although telson length was the second largest measurement ($\bar{x} = 129.1 \text{ mm}$) for the male horseshoe crab, but the range of \bar{x} became reduced to 114.6 mm in the linear equation (Suppl. Table 3). Alike the female, the male was indicated with 0.956 for their stepwise regression score of the telson. From this, 1 male crab was indicated with negative allometry, 62 crabs were having normal allometry and only 5 crabs were having positive allometry. If the opisthosoma width was considered, the percentage of male crabs with positive allometry increased by 47.1% or by 32 individuals. Overall, the prosomal length was selected as preferred morphology to scale the size of male horseshoe crab (stepwise regression score = 0.953). With this, 31 crabs could be considered with normal allometry whereas most



Fig. 5. Draftsman's plot for series of resemblance involving (A) female and (B) male *Tachypleus gigas* morphology values. Abbreviations as is Fig. 2.

Рис. 5. Результаты использования редактора Draftsman для серии подобий включая морфологические показатели самок (А) и самцов (В) *Tachypleus gigas*. Сокращения как на рис. 2.

of them (37 individuals) were demarcated with positive allometry.

The abundance of *T. gigas* was slightly less in northern shores of Java during the sampling period. Only 50 female and 39 male crabs were retrieved. The *T. gigas* is roughly 28% larger than *C. rotundicauda* and has a telson-to-carapace ratio of 1 : 0.96; somewhat with symmetrical body dimensions. However, the *T. gigas* were occurring in wide range of measurements for each morphology unit. Values for opisthosoma length, prosoma length and telson length of the female *T. gigas* were scattered in resemblance relationships (via Draftsman's plot) (Fig. 5A). Comparatively, the values of all male *T. gigas* morphology units were horizontally aligned and it implies that x/y>1 (Fig. 5B). The male *T. gigas* could be considered with disproportional body plan for its length and width scale. In addition, the \bar{x} total length for both, female and male were 327.0 and 319.8 mm and σ were large in range, at ±97.1 mm for the female and ±30.3 mm for



Fig. 6. Link Tree analysis for each female *Tachypleus gigas* morphology separated by relative and absolute measures of its values. Abbreviations as is Fig. 2.

Рис. 6. Анализ Link Tree для морфологии каждой самки *Tachypleus gigas*, отделенной относительными и абсолютными данными ее показателей. Сокращения как на рис. 2.

the male. Perhaps, the disproportional body plan between male crabs was responsible for the R^2 scores that range 0.5653–0.9903 (Suppl. Table 4).

If descriptive statistics were considered for the female, between 24 and 35 crabs would be classified with normal allometry, between 3 and 13 crabs with negative allometry and between 9 and 13 crabs with positive allometry. The ascending order for negative allometry would be opisthosoma length<prosoma width<telson length<total length, prosoma length, carapace width<carapace length, interorbit length, opisthosoma width; for normal allometry it would be carapace length<interorbit length<opisthosoma width, prosoma length<total length<carapace width<telson length<opisthosoma length, prosoma width and; for positive allometry it would be organized as telson length, carapace width<total length, opisthosoma width<opisthosoma length, interorbit length<carapace length, prosoma length (Suppl. Table 4).

There was contrasting difference for the male as 3-8 crabs were demarcated with negative allometry, 27-34 crabs with normal allometry and 1-7 crabs with positive allometry. However, based on the R² scores, only total length (0.9162) and carapace width (0.9288) could be accepted for the descriptive statistics. As such, 6 crabs were both indicated with negative and positive allometry whereas the remaining 27 crabs were having normal allometry; n = 39 (Suppl. Table 4). Link Tree clustering of female T. gigas morphology was indicated with relative = 0.91and absolute similarity percentage = 97% for its interorbit length (70-80 mm), carapace width (115–125 mm), carapace length (142–154 mm), opisthosoma width (95-100 mm) and total length (296-304 mm; Fig. 6). It was relative = 0.98 and absolute similarity percentage = 99% for the male T. gigas in which, the interorbit length (54-66 mm), carapace width (102-112 mm), total length (245-267 mm), prosoma length (61-65 mm) and carapace length (110-113) were best to indicate the allometry (Fig. 7).

The stepwise regression could be considered the best protocol in choosing measurements that have the most relevance with allometry of horseshoe crabs. The telson and carapace width was indicated with highest regression scores in the range of 0.880–0.945. Meanwhile, the stepwise regression was consistent for interorbit length and prosomal length measurements



Fig. 7. Link Tree analysis for each male *Tachypleus gigas* morphology separated by relative and absolute measures of its values. Abbreviations as is Fig. 2.

Рис. 7. Анализ Link Tree для морфологии каждого самца *Tachypleus gigas*, отделенного относительными и абсолютными данными его показателей. Сокращения как на рис. 2.

when tested to select measurements that were most desired for horseshoe crab size analysis according to their gender. After revising the \bar{x} (as median baseline) measurement, between 9 and 32 female crabs were indicated with positive allometry (Suppl. Table 4). However, if interorbit length was solely considered, only 28 female crabs were having normal allometry. It was 16 male crabs if prosoma length was considered. Comparatively, 14 female crabs were indicated with negative allometry if interorbit length was observed whereas only 2 male crabs were having negative allometry when prosoma length was considered. About -8.0% female crabs or reduction of 4 individuals and +35.9% or surplus of 14 crabs were associated with positive allometry for the same indicators. This shows revision in baseline values produced consistent results especially in samples comprising of sexually mature adult horseshoe crabs that occur in broad range of body dimensions.

Discussion

Previously, pairs in length-length, lengthwidth, length-weight, and width-weight relationships were used for horseshoe crab allometry analysis (Jawahir *et al.*, 2017). Generally, raw data were consecutively matched but the measurement pairs were inconsistent. This was generally the treatment seen in Draftsman's plot where for the male *T. gigas*, the plot areas became horizontal instead of being linear. In comparison, this study used the protocol of Mohamad *et al.* (2021) to set medial measurement (perhaps a baseline) for *T. gigas* and *C. rotundicauda* morphology. The populations of northern Java, Indonesia were assessed. Stepwise regression was used to screen gender-exclusive measurements. For instance, about 23–31 female and 25–62 male *C. rotundicauda* were normal sized whereas 11–24 female and 37–43 male crabs were oversized. By revising the mean baseline, this study corrects an opinion (*cf.* Syuhaida *et al.*, 2019) that horseshoe crabs of Java were mostly in the negative allometric range. For populations of northern Java, 40% were having normal allometry and 35% were having positive allometry.

Compared to Link Tree analysis and other multivariate analysis, stepwise regression could identify predictors and is applicable for large datasets (Bain et al., 1988). Link Tree analysis was used for categorizing samples with independent and dependent variables but mostly, it involved a series of biological and environmental attributes (Lloyd et al., 2020). Based on the outcome, stepwise regression was a preferred choice for analysis that involves morphometric datasets (Dibble et al., 2015; Prather, Kaspari, 2019). Previously, stepwise regression was useful to identify predictors in both, abundance, and edaphic conditions. However, log-transformation and Kendall's resemblance was used (Nelson et al., 2016). Another study used log-transformation and Bray-Curtis's resemblance in predicting the influence of environment conditions towards organism size (Sari et al., 2020; Meilana et al., 2021; Maulana et al., 2023). At present, by using square-root transformation and Bray-Curtis's resemblance, the prosoma length and interorbit length were best to ascertain gender-wise allometry. General measurements such as carapace width and telson length could result in false readings when horseshoe crabs were discovered damaged or deformed.

With similarities to Chan *et al.* (2022), firstly, stepwise regression screened the nine measurements and only indicated four as most influential units for allometry analysis. Secondly, there was consistency in the selection; prosoma length, carapace width, interorbit length and telson length exhibit the highest scores ($\mathbb{R}^2 \sim 1$). Thirdly, mean baseline measurements for *C. rotundicauda* and *T. gigas* morphology were revised and the number of crabs associated with positive allometry became increased. Fourthly, this approach sets a nominal size baseline in comparison to descriptive statistics that only use mean and standard deviation. Lastly, by being able to screen baseline size measurements of geographical isolated populations, this universal approach is novel and breakthrough for horseshoe crab allometry. With 1 : 1 ratio for its length-to-width (Buhler, Grey, 2017) and asymmetrical aperture (Chamberlain, Barlow, 1987), this approach could be used in *L. polyphemus* for the understanding of retrogressive edaphic adaptation with modernization.

The samples in Java were mostly skewed towards normal size or otherwise a small portion were having larger dimensions for their body plan. These samples have already reached the final 16th and 17th molt (Sekiguchi et al., 1988). Number of molts are responsible for dimorphic observations between their genders. Basically, the morphological dimensions classify these T. gigas and C. rotundicauda as sexually active in the mature size class. These crabs were discovered in mating pairs (or in amplexus). While the horseshoe crabs were not demarcated with deformities or damage, these arthropods were assumed to have occurred naturally with their existing body size. Parental genetics could be responsible. It was indicated with populations of L. polyphemus (Botton, Loveland, 1992) and both, C. rotundicauda as well as T. tridentatus (Chiu, Morton, 2003). Similarly, these arthropods (or current samples) were from northern Java and both species co-existed as a single population.

With telemetry conformation in T. tridentatus that a single female has smaller range than the male (Watanabe et al., 2022), the chances of populations to have mixed constituents could be rare because sperm competition does not occur entirely in Java, Indonesia. Recent findings stipulate between 4-5 female crabs for every male crab encountered (Supadminingsih et al., 2022). Meanwhile, though segregated by a large peninsula, genetic information revealed that populations of horseshoe crabs do not mix unless, they were intentionally discarded after becoming entangled in fishermen nets (Fairuz-Fozi et al., 2021). Therefore, in this circumstance concerning the populations from northern Java, capturing normal and enlarged sizes would generally mean that resources (or sustenance) were beyond adequate in supporting all life stages during the horseshoe crab development. The richness or diversity in food sources have provided sufficient nourishment to T. gigas and C. rotundicauda and this demarcates northern waters of Java with stable food network.

Conclusion

The population of horseshoe crabs from northern Java, Indonesia was inspected for their allometry using statistics that involve mean size revision and only predictive morphology measurements were selected after stepwise regression analysis. Initially, mean values demarcate C. rotundicauda and T. gigas in the normal allometry but with the median baseline, the number of individuals having negative allometry became reduced and those having positive allometry was increased. Firstly, the assessment method is a breakthrough for allometry analysis in horseshoe crabs. It was useful for populations that have 1 : ~1 body plan. Secondly, by having a greater number of crabs in normal and positive allometry, there is possibility that northern shores of Java, Indonesia have diverse assemblages of food sources that support healthy feeding habits for horseshoe crabs.

Compliance with ethical standards

CONFLICTS OF INTEREST: The authors declare that they have no conflicts of interest.

Supplementary data.

The following supplemental tables are available online.

Suppl. Table S1. Morphology measurements for female and male *Carcinoscorpius rotundicauda*.

Suppl. Table S2. Morphology measurements for female and male *Tachypleus gigas*.

Suppl. Table S3. Morphology measurements, baseline revisions, allometry and statistical support concerning *Carcinoscorpius rotundicauda*.

Suppl. Table S4. Morphology measurements, baseline revisions, allometry and statistical support concerning *Tachypleus gigas*.

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