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Microbiological load evaluation of white shrimp (*Nematopalaemon hastatus* Aurivillius, 1898) in the coastal waters of Ondo state, Nigeria

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Abstract. *This study investigated the condition factor with microbial load of Nematopalaemon hastatus (Aurivillius, 1898) collected for two years from four coastal towns in Ilaje communities of Ondo State, Nigeria. Shrimps' weight, length and condition factor were determined using standard methods while estimation of microbial load (Total heterotrophic bacteria, coliform, Escherichia coli, Salmonella/Shigella, and fungal counts) was done using standard microbiological methods. The correlation between microbial load and condition factor was thereafter determined using regression analysis. N. hastatus exhibited allometric growth, with low but consistent condition factor. Mean heterotrophic bacteria count was 1.107×10² CFU/g and 1.079×10² CFU/g during the dry and wet season, respectively. Mean coliform count, total Salmonella-Shigella and E. coli counts were 0.398×10² CFU/g, 0.218×10² CFU/g and 0.303×10² CFU/g, respectively, during the wet season. A significant increase in counts (mean) was observed in the dry season for the coliform (0.404×10² CFU/g), total Salmonella-Shigella (0.234×10² CFU/g) and E. coli (0.326×10² CFU/g). The mean fungal count was 0.604×10² SFU/g and 0.563×10² SFU/g during the wet and dry seasons, respectively. The microbial loads were below acceptable limits; therefore, shrimps of the study area are safe for consumption. Conclusively, the condition factor of the shrimps was non-significantly influenced by the microbes. However, there is a need to regulate and/or prevent untreated sewage and effluent discharge into natural water bodies to reduce the environmental hazards it may portend and also obtain relatively safe aquatic products for consumption*.

Keywords: aquatic life, condition factor, food safety, microorganisms, pollution, shrimps

Introduction

About 60% of the world's supply of protein is contributed by fish while over 2/3 of the developing countries get more than 30% of their animal protein from fish (Emikpe et al., 2011). However, World Health Organisation reported that fishes (which are generally regarded as safe, nutritious and beneficial) have been linked with certain food safety issues due to contamination from human and animal sources (WHO, 2007). Adebayo-Tayo et al. (2012) also reported that fish (including other seafood) can be involved in the transmission of pathogenic microorganisms and toxins. Thus, consumption of fish and shellfish may cause diseases that have been specifically associated with pathogens that are resistant to antibiotics (Olugbojo and Ayoola, 2015).

Microorganisms exist on the gills, skin/slime and gut of living and newly caught fish. Adebayo-Tayo et al. (2012) also stated that the microbiological flora in seafood (fin and shellfishes) is psychotropic, and is assumed to reflect the general contamination of the aquatic environment. Several studies including Emikpe et al. (2011) have also reported different species of bacteria (such as *Streptococcus* spp. and *Pseudomonas angulluseptica* which are potentially pathogenic under certain conditions) in fish.

The tendencies of water to accommodate microbial pathogens and therefore causing illnesses have been documented for developing and developed countries (Ajibare, 2018). The coastal area of Ondo State, Nigeria (which is located between the densely populated Lagos and Delta coasts) is affected by several human activities which may lead to the inputs of harmful/hazardous substances through the atmosphere, rivers as well as direct domestic and industrial discharges. Aquatic animals accumulate microbes in their tissues in a considerable amount over a long time (Duru and Nwanekwu, 2012; Nwachukwu et al., 2013; Olugbojo and Ayoola, 2015; Olawusi-Peters and Akinola, 2018) and human dependence on the water (for domestic purposes) and its organisms (for food) makes it imperative to assess the microbial load (total heterotrophic bacterial counts, total salmonella/shigella counts, total fungal counts, total coliform counts and *E. coli*) of *N. hastatus* to determine the relationship between these parameters and the well-being of the shrimps to ensure the safety of this ecosystem.

Ofor (2002), Zabbey (2007) Olawusi-Peters et al. (2017),

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and Ajibare (2018) reported that *N. hastatus* (which makes up about 75% of the total shrimp catch of artisanal fishermen) dominate artisanal catches from coastal waters and marketed over a majority of inland Nigeria as a condiment in cooking. Apart from the unique taste/flavour imparted to foods, *N. hastatus* has a protein content of almost 70% dry matter. Olawusi-Peters et al. (2014, 2017) also recorded low condition factor for *N. hastatus* and called for pollution study on its sustainability of biodiversity. Thus, there is a need to assess the effect of microbial contamination on aquatic life and the ecosystem in general. The specific objective was to determine the microbial loads of *N. hastatus* and relate them with the condition factor of the shrimp.

Material and methods

Study area

The study was carried out in four coastal communities of the Ilaje Local Government Area of Ondo State, Nigeria. The coastal area of Ondo State (which is at the extreme southern part of the State) empties to the Atlantic Ocean and some other parts of the country. The area is known for seafood (Adebowale et al., 2008), an indication that its pollution may portend ecological, national and global health issues. The coastal communities have two seasons (dry and wet) and experience consistently high temperatures (about 32°C) throughout the year (Adeparusi et al., 2003). Adebowale et al. (2008) reported that all domestic wastes are discharged directly into the coast untreated.

Ayetoro (Station I: 06°06'N 04°46'E), Idiogba (Station II: 06°05'N 04°47'E), Bijimi (Station III: 06°04'N 04°49'E), and Asumogha (Station IV: 06°03'N 04°39'E) were chosen for this study because of extensive shrimp fishing activities, accessibility and anthropogenic inputs from activities such as oil exploration, farming practice, boat transportation and discharges which finally empty into the Atlantic Ocean (Ajibare et al., 2017)

Samples collection

Shrimps were collected monthly from each location with the assistance of local fishermen for 24 months (April 2014 to March 2016). The shrimps were identified according to FAO (1981) and Ajibare et al. (2020) before being preserved in an ice chest and transferred to the laboratory.

Determination of length, weight, length-weight relationship and condition factor

At the Fisheries and Aquaculture Laboratory of the Federal University of Technology Akure, samples were allowed to thaw before the total length (i.e. tip of the rostrum to the edge of telson) was measured with a measuring board (to the nearest 0.01 cm) while weight was measured with a sensitive weighing balance (Model BL100001) to the nearest 0.01 g.

The length-weight relationship of the shrimps was determined by the equation of Ajibare et al. (2020):

$$W = a.L^b \quad (1)$$

The condition factor (K) of the shrimps was calculated by the formula of Ajibare et al. (2020):

$$K = (100.W)/L^3 \quad (2)$$

Where: W= Weight (g); L= Total length (cm); a= Constant (intercept); b= The Length exponent (slope).

Microbiological analysis

The shrimp samples (50 g) were surface sterilized with 70% ethanol, after which, they were homogenized using sterile mortar. 1 g was aseptically weighed into 99 mL sterile distilled water and used as stock, for the analysis. 1 mL was taken from the stock into 9 mL sterile distilled water and subsequent 10-fold serial dilutions were made. Standard pour plates were prepared using 0.1 mL diluent of each selected dilution into Nutrient agar (LabM, UK) medium for total heterotrophic bacterial counts (THBC), Salmonella/Shigella (LabM, UK) agar for total *Salmonella/ Shigella* counts (TSSC), MacConkey agar (LabM, UK) for total coliform counts (TCC), Eosin Methylene Blue agar (LabM, UK) for *Escherichia coli* counts (ECC), and Sabouraud Dextrose agar (LabM, UK) for total fungal counts (TFC). Triplicate bacterial and fungal plates were incubated at 37°C for 24 hours and at room temperature (26±1°C) for 3 to 5 days, respectively (APHA, 1992; Adebayo-Tayo et al., 2012). Microbial enumeration on the plates was carried out, using a colony counter (J-2 Wincom). The colony-forming unit (CFU/g) and spore-forming unit (SFU/g) were determined by multiplying the number of units formed by the dilution factor. Confirmation of presumptive colonies was done using API® (bioMerieux, Marcy-l'Etoile, France). The tests were carried out according to the manufacturer's instructions. All growth media and glassware used in this study were sterilized by autoclaving at 121°C for 15 minutes.

Statistical analysis

Analysis of Variance (ANOVA) was used to evaluate the significant difference in respect to stations while the relationship between condition factor and the microbial loads was determined with regression analysis at p=0.05. Descriptive analysis was also used to present means and standard deviations in tables and figures.

Results

Shrimp samples collected were identified as *Nematopalaemon hastatus* and Table 1 revealed that the exponential (*b*) values obtained in the wet season ranged between 1.43 (a=-2.78, R^2=0.89, n=584) and 1.77 (a=-3.49, R^2=0.87, n=608) in Station II and Station I, respectively, while the '*b*' obtained in the dry season ranged from 1.33 (a=-2.62, R^2=0.80, n= 662 at Station II) and 1.66 (a=-3.23, R^2= 0.80, n=551 at Station III). The table further shows that the lowest 'K' (0.42) in the wet season was recorded in Station I and the highest (0.52) in Station II while it ranged from 0.43 (n=604 at Station I; n=551 at Station III) to 0.53 (n=662 at Station II) during the dry season.

The seasonal variation of microbial load of *N. hastatus* in the study area over two successive seasons for two years is presented in Table 2.

Table 1. Length-Weight relationship and Condition factor of *N. hastatus* in the coastal waters of Ondo state

Season	Indicators				
	n	*a*	*b*	R^2	K
			Station I		
Dry	604	-2.94	1.43	0.81	0.43
Wet	608	-3.49	1.77	0.87	0.42
			Station II		
Dry	662	-2.62	1.33	0.80	0.53
Wet	584	-2.78	1.43	0.89	0.52
			Station III		
Dry	551	-3.23	1.66	0.80	0.43
Wet	595	-3.05	1.56	0.72	0.44
			Station IV		
Dry	623	-3.00	1.51	0.73	0.44
Wet	611	-3.04	1.55	0.80	0.45

**a*= Constant (intercept); *b*=The Length exponent (slope); R^2= Regression coefficient; n= Number of individuals; K= Condition factor.

Table 2. Seasonal variation in microbial load of *N. hastatus* in coastal waters of Ondo state (mean±SDx10^2 CFU/g), n=3

Parameter	Sampling stations	Wet season	Dry season	T stat	T crit	*p* value
THBC	I	1.086±0.042^a	1.125±0.052^b	3.51	1.99	0.00
	II	1.078±0.043^a	1.109±0.055^b	2.75	1.99	0.01
	III	1.077±0.038^a	1.095±0.073^a	1.32	1.99	0.19
	IV	1.076±0.038^a	1.101±0.056^b	2.19	1.99	0.03
TCC	I	0.404±0.032^a	0.413±0.044^a	0.97	1.99	0.33
	II	0.403±0.030^a	0.409±0.048^a	0.62	1.99	0.54
	III	0.394±0.028^a	0.395±0.050^a	0.03	1.99	0.98
	IV	0.391±0.023^a	0.401±0.041^a	1.21	1.99	0.23
TSSC	I	0.222±0.027^a	0.239±0.043^b	2.11	1.99	0.04
	II	0.218±0.027^a	0.238±0.044^b	2.38	1.99	0.02
	III	0.220±0.027^a	0.232±0.043^a	1.34	1.99	0.19
	IV	0.214±0.026^a	0.230±0.047^a	1.73	1.99	0.09
TFC	I	0.611±0.064^b	0.568±0.069^a	2.73	1.99	0.01
	II	0.604±0.066^b	0.562±0.071^a	2.63	1.99	0.01
	III	0.601±0.062^b	0.567±0.067^a	2.24	1.99	0.03
	IV	0.601±0.057^b	0.556±0.076^a	2.81	1.99	0.01
E. coli	I	0.310±0.015^a	0.334±0.047^b	2.93	1.99	0.00
	II	0.308±0.020^a	0.328±0.041^b	2.61	1.99	0.01
	III	0.303±0.017^a	0.324±0.063^a	1.91	1.99	0.06
	IV	0.293±0.029^a	0.321±0.049^b	2.89	1.99	0.01

*THBC- total heterotrophic bacterial counts, TCC- total coliform counts, TSSC- total *Salmonella/Shigella* counts, TFC- total fungal counts; Mean±SD in the same row with homogenous superscript are not significantly different (p>0.05).

Total heterotrophic bacterial counts (THBC) in the wet season, ranged from 1.076±0.038×10^2 CFU/g to 1.086±0.042×10^2 CFU/g, while the range was between 1.095±0.073×10^2 CFU/g and 1.125±0.052×10^2 CFU/g in the dry season, across the four stations. However, station I had the highest THBC in both wet (1.086±0.042×10^2 CFU/g) and dry (1.125±0.052×10^2 CFU/g) seasons. Mean THBC among the four stations was not significantly different at p<0.05 (as presented in Figures 1 and 2). Furthermore, the result showed a significant difference (p<0.05) in THBC recorded in the wet and dry seasons of each sampling station except Station III where p=0.19.

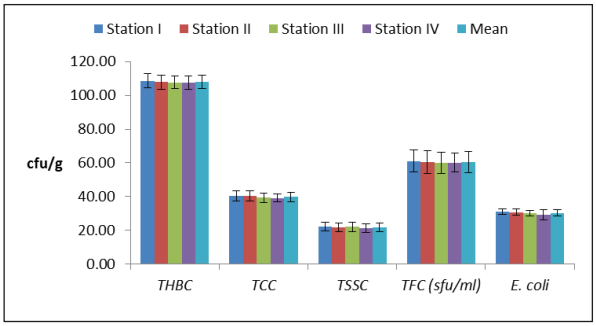

Figure 1. Locational variation in microbial load of *N. hastatus* during the wet season

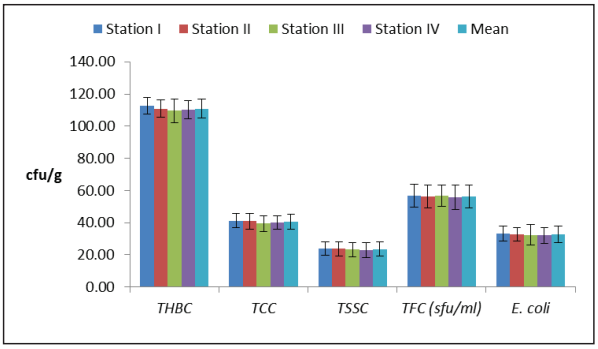

Figure 2. Locational variation in microbial load of *N. hastatus* during the dry season

Total coliform counts (TCC) ranged from 0.391±0.023×10^2 CFU/g to 0.404±0.032×10^2 CFU/g in the wet season and between 0.395±0.050×10^2 CFU/g and 0.413±0.023×10^2 CFU/g in the dry season. As reported for THBC, the highest TCC (0.404±0.032×10^2 CFU/g and 0.413±0.023×10^2 CFU/g) was also observed at Station I in both wet and dry seasons, respectively. The result also indicated that the TCC of the wet season was not significantly different (p>0.05) from that of the dry season in the four sampling stations. The mean TCC recorded also showed no locational variation (p>0.05) in both dry and wet seasons (Figures 1 and 2).

Total *Salmonella/Shigella* counts (TSSC) in the wet season ranged from 0.214±0.026×10^2 CFU/g to 0.222±0.047×10^2 CFU/g, while it ranged between 0.230±0.047×10^2 CFU/g and 0.239±0.043×10^2 CFU/g in the dry season. Sampling station I had the highest counts in both wet and dry seasons while the least count was observed at Station IV. The result further showed that TSSC in the wet season was not significantly different (p>0.05) from the counts recorded in the dry season at stations III and IV. However, TSSC showed seasonal variation (p<0.05) at stations I and II. The mean TSSC recorded among the four sampling stations were not significantly different at p>0.05 as shown in Figures 1 and 2.

The highest total fungal count (TFC) in the wet season was 0.611±0.064×10^2 SFU/g, while it was 0.568±0.069×10^2 SFU/g in the dry season. Both values were recorded from sampling station I. It was also observed that station IV had the least counts (0.601±0.057×10^2 SFU/g and 0.556±0.076×10^2 SFU/g) in both seasons. Furthermore, TFC in the four sampling stations showed seasonal variation at p<0.05 while no significant difference was recorded across the sampling stations in both wet and dry seasons (Figures 1 and 2).

The *E. coli* count in the wet season was between 0.293±0.029×10^2 CFU/g in Station IV and 0.310±0.015×10^2 CFU/g in Station I, while it ranged between 0.321±0.049×10^2 CFU/g (Station IV) and 0.334±0.047×10^2 CFU/g (Station I) in the dry season. Furthermore, there was a significant difference (p<0.05) between the *E. coli* counts recorded in wet and dry seasons in the sampling stations except at station III where the values recorded in both seasons were not significantly different (p=0.06). It was also observed that there was a significant difference between the mean *E. coli* counts recorded at stations IV and I at p<0.05 in the wet season (Figure 1), however, in the dry season, the counts among the four sampling stations were not significantly different at p>0.05 (Figure 2).

The relationship between the condition factor (K) and the microbial loads of the shrimps is presented in Table 3. The table revealed that the microbial loads of the shrimps did not collectively have a significant effect (p>0.05) on the condition factor. However, the R^2 (which ranged between 0.15-0.59) revealed that the condition factor of the shrimps was being influenced to a good extent by the microbes. In addition, the regression values of *E. coli* revealed that it consistently affected the condition factor/well-being of the shrimps across the stations.

Table 3. Relationship between Condition factor and Microbial loads

Station	Season	Regression Equation	R^2	P
I	Wet	*K* = -0.19 + 0.01*THBC* + 0.00*TCC* + 0.02*TSSC* - 0.01*TFC* + 0.01*E.coli*	0.26	0.82
	Dry	*K* = -2.03 - 0.02*THBC* + 0.02*TCC* + 0.02*TSSC* - 0.01*TFC* + 0.01*E.coli*	0.31	0.74
II	Wet	*K* = -0.42 + 0.01*THBC* + 0.00*TCC* + 0.01*TSSC* - 0.00*TFC* + 0.03*E.coli*	0.15	0.95
	Dry	*K* = 1.14 - 0.01*THBC* - 0.00*TCC* - 0.02*TSSC* + 0.00*TFC* + 0.28*E.coli*	0.38	0.62
III	Wet	*K* = 0.11 + 0.00*THBC* + 0.01*TCC* + 0.01*TSSC* - 0.00*TFC* + 0.01*E.coli*	0.44	0.52
	Dry	*K* = 0.80 - 0.00*THBC* - 0.01*TCC* - 0.00*TSSC* + 0.00*TFC* + 0.01*E.coli*	0.48	0.45
IV	Wet	*K* = 0.22 + 0.00*THBC* + 0.00*TCC* - 0.01*TSSC* - 0.01*TFC* + 0.01*E.coli*	0.29	0.78
	Dry	*K* = 1.24 - 0.01*THBC* + 0.01*TCC* + 0.01*TSSC* - 0.01*TFC* - 0.01*E.coli*	0.59	0.26
Mean	Wet	*K* = 0.08 + 0.00*THBC* + 0.00*TCC* + 0.00*TSSC* - 0.01*TFC* + 0.01*E.coli*	0.34	0.70
	Dry	*K* = 0.57 + 0.00*THBC* - 0.00*TCC* - 0.01*TSSC* + 0.00*TFC* + 0.00*E.coli*	0.39	0.61

*THBC- total heterotrophic bacterial counts, TCC- total coliform counts, TSSC- total *Salmonella/Shigella* counts, TFC- total fungal counts.

Discussion

The results obtained in this study showed that growth in white shrimp was negative allometry (i.e. the values of 'b' were less than 3, Table 1), indicating that the rate of increase in body length was not proportional to the rate of increase in body weight (Ajibare, 2018). This confirms the observations of Yakubu and Ansa (2007) on *F. notialis* in Buguma; Deekae and Abowei (2010) on *M. Macrobrachion* in Luubara Creeks, Olawusi-Peters et al. (2014) on white shrimps in the coastal waters of Ondo state and Ajibare et al. (2020) on berried *M. vollenhovenii* in Asejire Reservoir, Nigeria.

Our findings showed a range of condition factors (K=0.42-0.53, Table 1) that falls within the observations of previous researchers (Enin and Enidiok, 2002; Ekelemu and Zelibe, 2006; Abowei, 2010; Ajibare et al., 2017). Moreso, the low

but consistent value of 'K' in both seasons indicated that hydrological seasons did not influence the wellbeing of the shrimps (and other organisms) in the study area, but other environmental conditions (such as water quality, competition, predation, among others) did. Moreover, the observed condition factor may indicate stress from low food availability or unfavourable/adverse ecological conditions as earlier reported (George et al., 2013 and Olawusi-Peters et al., 2014).

The range of THBC in shrimps (1.076 to 1.125x10^2 CFU/g) slightly exceeded the limit of 1.10^2 CFU/g set by FAO/WHO (2007). However, according to the International Commission on Microbial Specification for Foods (ICMSF, 1998), the acceptable upper limit of total bacterial load in food is 1.0×10^6 CFU/g. Thus, the examined shrimps were under the acceptable limit according to ICMSF and FDA guidelines (ICMSF, 1998; FDA, 2001). Even though findings from this study showed higher coliform (i.e. *Salmonella/Shigella, E.coli* and total coliform) counts than the FAO/WHO (2007) limit of zero CFU/g, the results were lower than the 1.10^2 CFU/g limits stated by ICMSF (1998) and FDA (2001). Hence, the shrimps are safe for human consumption.

Adebayo-Tayo et al. (2012) had earlier stated that high THBC might be due to poor hygiene, contamination from the water and general sanitation condition of the coastal area. The generally high total heterotrophic bacterial count reported in our findings was similar to the observations of Facklam and Peterson (2004), Yousuf et al. (2008) and Nwachukwu et al. (2013), who all noted that a wide range of organisms which include indigenous and saprophytic species, as well as a pathogenic contaminant and other species are present in an aquatic environment. Nwachukwu et al. (2013) observed that a significant increase in bacteriological load in the aquatic environment could lead to a higher risk of infectious diseases, considering that Crowther et al. (2001) reported that higher bacterial concentrations were strongly linked to total coliform and fecal coliform, a few species of which are opportunistic pathogens that may be responsible for diseases in fish, especially under immune deficiency and/or conditions of stress. Such diseases often present as poor feeding and erratic swimming in infected fishes (Oyhakilome et al., 2012).

Considering that there is a dearth of information in scientific works of literature to prove that microorganisms affect the growth, health, reproduction, or even survival of fish, our findings showed that microbial loads of shrimps have positive and negative impacts (as revealed by the positive and negative regression values in Table 3) on the health (condition factor) of the examined shrimps. The same was observed by Nwachukwu et al. (2013) in Njaba River. Moreover, this study revealed that all the considered microbiological properties had a minimal non-significant influence on the shrimps (Table 3). The reason for this observation may be that the parameters considered were not the sole determinant of the wellness of the shrimps since several biotic and abiotic factors (predation, competition, sex difference (George et al., 2013) changes in season, gonad maturity level, availability of food (Ajibare et al., 2017), stomach fullness, length-weight relationship/growth pattern, stress, loss of habitat, reduction in breeding and nursery grounds (Olawusi-Peters et al., 2014 and Ajibare et al., 2020, etc.) influence the well-being of aquatic organisms. Also, Oyhakilome et al. (2012) stated that the presence of microbes may not have a direct negative effect on aquatic organisms since most aquatic bacteria are free living. However, most organisms have been implicated as a causative agent of diseases (Nwachukwu et al., 2013), hence, the organisms enumerated in this study become important when their impacts are considered in terms of ecological implications (Duru and Nwanekwu, 2012).

The microbial load of *N. hastatus* did not exhibit locational variation but exhibited seasonal variation, however, the fact that total coliform counts (which is a clear indication of anthropogenic impact) did not show seasonal variation in all the stations can be linked to the consistent introduction of wastes from the alimentary canal of man/animals into the water body both in wet and dry seasons. This was supported by Olugbojo and Ayoola (2015), who stated that the occurrence of coliforms is evidence of feacal contamination of the environment through man, animals and that such activities (defeacating) were carried out all year round. The presence of *E. coli, Salmonella* and *Shigella* sp. (pathogenic organisms) in the studied shrimp is of public health concern because according to ICMSF (1998) and FAO/WHO (2007) S*almonella* and *Shigella* should not be present in food. However, the total *Salmonella-Shigella* count (TSSC) for the shrimps was below the limit of 1.10^2 CFU/g as recommended (FSRI, 2003; FDA, 2007). A similar trend was documented by Yousuf et al. (2008) in *Penaeus monodon* and *Macrobrachium rosenbergii* from Bangladesh. Adebayo-Tayo et al. (2012) also stated that the presence of *Salmonella sp.* and *Shigella sp.* in shrimp products mainly instigated from the environment rather than from poor sanitation or standards of hygiene. Even though the observed TFC was below the FAO/WHO (2007) limit of 100 SFU/g, the high fungal load could be due to the degree of hygiene of the study area. Moreso, it could be an aftermath of the effect of food particles, vegetables and oil which are the major source of organic matter in the water body (Akpor and Muchie, 2011).

It had earlier been reported that the microbial load of shrimps has a very strong relationship with its condition factor or health. The human and animal waste emanating from inhabitants of the aquatic environments strongly influences the health of aquatic life (Nwachukwu et al., 2013). Since it has been established that THBC and TCC are results of feacal contamination from man and other animals, it can be said that the health of the shrimps as well as other aquatic life in the environment is directly and indirectly influenced by anthropogenic activities in the area (Nwachukwu et al., 2013; Njoku et al., 2015). Hence, the low condition factor (K) recorded for shrimps in this study was strongly influenced by the microbial load of the environment among other factors. The observed low and positive regression coefficients indicated that a beneficial association exists between the shrimps and microorganisms. This corroborates earlier documentation that microorganisms of the normal flora

may be in a mutualistic relationship with their host (Olugbojo and Ayoola, 2015).

Conclusion

This study has shown that *N. hastatus* exhibited allometric growth and a low but consistent condition factor which may be generally attributed to pollution in the study area. Also, the analysis of the influence of microorganisms on the wellbeing/ condition factor of *N. hastatus* revealed that all the considered microbiological properties were important factors that influence shrimps in both wet and dry seasons, even though they were found to have only a minimal non-significant influence on the shrimps. The values of total heterotrophic bacteria count in the study area were below the acceptable limit of ICMSF and FDA guidelines while the total fungal counts and the coliform counts were below the FAO/WHO and ICMSF limit, respectively. Therefore, shrimps of the study area are safe for consumption. However, there is a need to regulate, and prevent untreated sewage and effluent discharged from households or industries into natural water bodies to reduce the environmental hazards it may portend and to also obtain relatively safe products for consumption.

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