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ORIGINAL RESEARCH ARTICLE

Proximate and Amino Acid Profiles of Chelipede Variants of Freshwater Prawn (*Macrobrachium vollenhovenii*) in Southwestern Nigeria

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ABSTRACT

The need for precise information on nutritional implications of novel strains of fish species necessitated the assessment of chelipede variants of Macrobrachium vollenhovenii, for proximate and amino acid content, for effective utilization in food and nutrition. Pooled fleshy tissue from 30 individuals each of the chelipede variants, being individuals possessing equal length of left and right sides', longer left sides' and shorter left sides' chelipede representing EA(novel), LL(novel) and SL(erstwhile), of differing allozyme marker (12.5% SDSPAGE) fingerprints were characterized for proximate values (dry matter-DM, crude protein-CP, crude fibre-CF, ether extract-EE, ash-AC, Nitrogen free extract-NFE and profile of essential amino acids-EAA and non-essential amino acids-NEAA following standard laboratory procedures. Values across variants were compared for significant differences at p<0.05. Significantly, CP, EE, AC and NFE varied at 78.08±3.56%-LL to 81.83±0.94%-EA, 8.70±0.28%-LL to 9.84±0.23%-SL, 2.91±0.12%-SL to 3.10±0.29%-EA, and 1.42±0.09%-EA to 3.68±0.02%-LL respectively. Total NEAA was between 45.76±3.25mg/g(LL) and 47.32±1.26mg/g(EA); Cysteine-LL (1.34±0.05mg/g) was lowest; Glutamate-EA (14.46±0.07mg/g) was highest. Total EAA ranged from 44.09±0.90mg/g(LL) to 48.71±1.07mg/g(EA); Tryptophan-EA(1.11±0.05mg/g) was lowest; Lysine-EA(9.72±0.06mg/g) was highest. The variants possessed tissues of desirable nutritional quality. Variant EA was superior in protein, mineral/ash, total NEAA and EAA, while SL and LL were superior in oil and carbohydrate (NFE) content respectively. Cognizance of the superior attributes of each variant would facilitate their optimum utilization for food and nutrition.

Keywords: Crustacean, Meat quality, Intra-specific variants, Food chemical, *Macrobrachium vollenhovenii*

INTRODUCTION

Macrobrachium vollenhovenii are the freshwater prawns belonging to the genus Macrobrachium. According to New (2002), *M. vollenhovenii* and *M. Macrobrachium* are the largest species of Macrobrachium known. These freshwater prawns are decapod crustaceans of high economic importance found in diverse inland and estuary ecosystems, such as ponds, lakes, rivers, irrigation ditches, and estuaries throughout the West Africa region (Udo and Opeh, 2013). The *M. Macrobrachium* is the brackish water strains, while the *Macrobrachium vollenhovenii* are widely distributed in freshwater rivers; hence, they are commonly referred to as African River Prawns. Ajuzie and Fagade (1992) reported that *M. vollenhovenii* and *M. Macrobrachium* have the highest commercial potential among the Macrobrachium species. The species has prospect of being a means to mitigate food insecurity, especially, in riverine communities of developing countries. They are classified as potential species for commercial aquaculture (Marioghae, 1982).

There is a growing interest towards aquaculture development of the indigenous freshwater prawns, such as the *M. vollenhovenii* in developing African countries. Meanwhile, sustainable aquaculture development would require adequate information on existing fish breeds and their specific contributions to nutrition. Information on intra and inter population diversity of species may help in developing efficient stock management and improvement (Khan and Jafri, 1991). In the meantime, genetic diversity can highlight potential strains for specific nutritional utilization.

A study revealed potential diverse strains among *M. vollenhovenii* in Nigeria. Presence of chelipede

morphotypes in *M. vollenhovenii* at both inland Lake and River environments in southwestern Nigeria was observed (Oyebola 2015). Discovery of specific allozyme fingerprints of the morphotypes implied that they were genetically divergent, being separable at specific allozyme locus (Oyebola *et al.,* 2017). The morphotypes possessed shorter left (SL) sides' arm/chelipede compared to right arm, longer left (LL) compared to right arm and equal length of left and right sides arms/chelipede (EA). The SL was the earlier reported specimens of the freshwater prawn (Holthuis, 1980; Bello-Olusoji *et al*., 2004, 2006; Jimoh *et al.*, 2012, Lawal-Are and Owolabi, 2012), while the rest were newly observed at the freshwater environments. There is the need to understand the implications of the diversity with respect to aquaculture and nutritional potentials.

The FAO/UNDP (1989), asserted that individual food item should be assessed for fitness for human consumption. Food could be analysed for proximate qualities, and profiles of biochemical nutrient compounds including minerals, vitamins and energy content. Nutritionally, protein is the most prominent biochemical component of crustaceans (Dinakaran *et al*., (2009). However, proteineous food must also be analyzed for proximate and amino acid compositions at the first instance. Meanwhile, these biochemical parameters are of prime relevance in assessment of nutritional qualities of any food item. According to Mayr (1969), biochemical polymorphism could be highlighted through allozyme techniques and this could have correlation with phenotypic qualities. It is opined that the observed morphologic/genetic divergent subgroups/genotypes of *M. vollenhovenii* could have correlation with nutritional quality; and each of the genotypes could constitute potential breeds of the species.

Therefore, it is of interest to investigate the nutritional qualities of the discovered divergent chelipede subgroups of *M. vollenhovenii*, using proximate and amino acid contents as biochemical indicators. It is expected that such knowledge would reveal specific nutritional relevance of the morphologic subgroups, and subsequently facilitate their aquaculture development for local and international trade.

MATERIALS AND METHODS

Experimental Site

Samples of freshwater prawn were collected from Asejire Lake, in Southwest Nigeria. Asejire Lake lies at borderline between Oyo and Osun States of Nigeria, on 04^0 07'E and $07^0$21'N, at an altitude of 137 m above sea level. It is a major artificial dam constructed on River Osun which links the Ogun River and drains ultimately to the Lagos Lagoon in South Western Nigeria. Asejire River is one of the series of West African Rivers that do not drain into Niger system but discharge into coastal lagoons and creeks bordering the Atlantic Ocean (Omoike, 2004). Map of the sample location, the Asejire Lake, is presented in Figure 1.

Sampling Procedure

Samples of *M. vollenhovenii* were collected from Asejire Lake being one of the reported habitats of the discovered genotypes (Oyebola, 2015). Fresh and healthy captured samples of the freshwater prawn were collected from fisher-folks at the main landing site of the Lake during June to August, (being period of their abundance). Taxonomic tools provided by Holthuis (1980) was utilised for identification to species level. Samples of the species were transported inside iced containers to the Department of Aquaculture and Fisheries Management, University of Ibadan, Nigeria, where they were separated to chelipede genotypic subgroups following the description of Oyebola *et al*., (2017). Samples possessing equal length of chelipede on the left and right sides, referred to as Equal Arm were denoted as EA, those with longer left side, referred to as Long Left were denoted as LL and those with shorter left side, referred to as Short Left were denoted as SL. During each sampling period, identified samples of each genotype were selected, well labeled and preserved in separate containers inside freezer at -4ºC. Thirty (30) individuals of each of the genotypes were selected for the study. Image of the chelipede genotypes is presented in Figure 2.

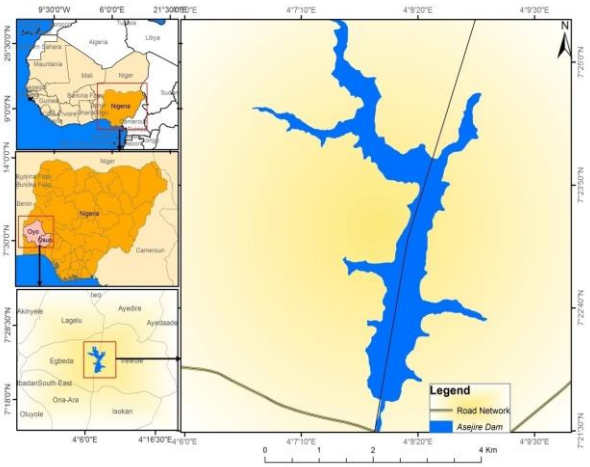

Figure 1:Map showing the location of the sample collection site, Asejire Lake, Nigeria
Source: Oyebola (2014)

Figure 2: Chelipede genotypes of *M. vollenhovenii* (Oyebola 2015, Oyebola *et al*., 2017)
**EA, LL, and SL indicate samples possessing equal length of left and right side chelipede, longer left side chelipede and shorter left side chelipede genotypes respectively*

Sample Preparation

Preserved samples of each of the genotype (11.6 to 15.6cm length and 22-32grammes weight) were thawed and deveined (removal of exoskeleton) to separate the fleshy edible tissues. The pooled fleshy tissues of each genotype was homogenized and subjected to proximate and amino acid analyses following standard laboratory procedures.

Assessment of Nutritional Qualities of the Fleshy Tissue of the Genotypes

Determination of the Proximate Qualities

Subsamples of homogenized fleshy tissues of each genotype were chemically assessed for proximate values following A.O.A.C (2000). Homogenized wet samples were oven dried at 105^0C for 5hours to obtain dry matter (DM) content. Crude protein content was analyzed using the Kjeldahl method, following standard procedures for digestion, distillation, and titration. The determined total nitrogen in samples (N) was converted to percentage crude protein achieved by multiplying N by a constant of 6.25. Subsamples were ashed in furnace at 600^0C for 2hours to determine ash content, while ether extract (fat content) was assessed through Soxhlet extraction method. To determine the crude fiber content, homogenized fleshy tissues of each genotype were macerated, homogenized and digested in 100ml of trichloroacetic acid digestion reagent (500ml glacial acetic acid, 450ml of water, 50ml conc. Nitric acid), boiled, filtered in Whatman paper, dried overnight at 105^0C, weighed and ashed at 600^0C (overnight) in muffle furnace. Crude protein, crude fat, crude ash, crude fibre and NFE contents were expressed as percentage of dry matter (%DM). The NFE/Carbohydrate content was taken as the difference between DM and the sum of values of other analyzed parameters following Ehigiator and Oterai (2012).

Determination of Amino Acid Profiles

Ten (10) grams of dry matter of each of the fleshy tissues of the genotypes (SL, LL, and EA) were measured and utilized for the amino acid profiling following the Gas-liquid chromatography (GLC) method (Moore and Stein, 1963). Samples were hydrolyzed with 6M HCl for 22 h at 110 °C followed by separation and quantification of amino acids through the gas-liquid chromatography medium. The GLC (HP 6890 powered with HP Chemstation Rev. A 09.01 [1206] Software) system utilized for the analysis uses split injection technique with Hydrogen as the carrier gas. Flow rate was maintained 1.0ml/min. while inlet temperature was 250^0C. Oven was programmed at 60^0C initial temperature, first ramp at 8^0C / min. for 20 min., maintained for 2 mins. The second ramp was at 12^0C / min for 6 mins. Detection was carried out under hydrogen pressure at 20psi and compressed air at 35psi. Data were automatically generated and printed out from the computer system attached to the amino acid auto analyzer. Tryptophan was determined through enzymatic hydrolysis of sample with Pronase at

40°C for 24 h, followed by a colorimetric reaction with 4-Dimethyl-Amino-Benzaldehyde (DAB) in sulfuric acid. Values were read at 590 nm,

following the procedures of Arruda *et al*. (2006).

Statistical Analysis

Data were described using mean, standard deviation, and percentages. Significant differences ($p<0.05$) across treatments (genotypes)' data on proximate and amino acid profile, were tested through One-Way Analysis of variance (ANOVA). The PAST statistical software (Hammer *et al*., 2005) was utilized for data analysis.

RESULTS

Proximate Composition of Fleshy Tissues of the Genotypes

The results of proximate composition of fleshy tissues of chelipede genotypes are presented in Table 1. The dry matter ranged from 21.45±0.07% (EA) to 21.97±0.10% (LL), while crude fibre ranged from 2.40±0.01% (SL) to 2.49±0.16% (EA). The dry matter and crude fiber content were statistically ($p>0.05$) similar across the genotypes. Crude protein (% dry matter) ranged from 78.08±3.56% in LL to 83.83±0.94% in EA. The EA was significantly higher than LL, but similar to SL. Ash content ranged from 2.91±0.12% (SL) to 3.10±0.29% (EA), the EA was significantly ($p<0.05$). higher than SL, while LL and SL were similar. The NFE ranged from 1.42±0.09% (EA) to 3.68±0.02% (LL), the EA was significantly ($p<0.05$). lower to LL, while SL was intermediate. Ether extract (EE) ranged from 8.70±0.28% (LL) to 9.84±0.23% (SL), the LL was significantly lowest, SL significantly highest, while EA was intermediate.

Amino Acid Profile of the Fleshy Tissues of the Genotypes/Variants

Profile of the Non-Essential Amino Acids (NEAA)

As presented in Table 2, the EA had significantly highest total content of NEAA (47.32±1.26 mg/g) while LL had the lowest (45.76±3.25 mg/g), Meanwhile, SL and LL were statistically similar ($p>0.05$) in total content of NEAA. Specifically, values of NEAA ranged from 1.34±0.05 mg/g (cysteine) to 14.11±0.02 mg/g (glutamate) in LL, 1.42±0.07 mg/g (cysteine) to 14.46±0.07 mg/g (glutamate) in EA, and 1.36±0.17 mg/g (cysteine) to 14.16±0.03 mg/g (glutamate) in SL. Least alanine content (5.74±0.26 mg/g) was observed in SL while the highest value (6.30±0.05 mg/g) occurred in EA. Glycine was least in SL (4.11±0.73 mg/g), highest in EA (4.22±0.21 mg/g); Serine was least in LL (4.10±0.80 mg/g), highest in SL (4.38±0.04 mg/g); Proline was least in LL (2.85±0.21 mg/g) but highest in EA (3.03±0.28 mg/g); Aspartate was least in SL (10.37±0.40 mg/g), but highest in EA (10.65±0.14 mg/g); Glutamate was least (14.11±0.02 mg/g) in LL, but highest (14.46±0.07 mg/g) in EA; The least Tyrosine content (2.81±0.07 mg/g) occurred in LL, while the highest (3.03±0.04 mg/g) occurred in SL; Cysteine was least in LL (1.34±0.05 mg/g) but highest in EA (1.42±0.07 mg/g).

Table 1: Proximate Composition of Fleshy Tissues from Chelipede Genotypes/Variants of Freshwater Prawn, *Macrobrachium vollenhovenii*

Proximate Parameters (%)	Genotype/Variants LL	EA	SL
Dry matter	21.97±0.10	21.45±0.07	21.83±0.04
Crude protein	78.08±3.56^{b}	81.83±0.94^{a}	80.76±1.03^{a}
Crude fiber	2.45±0.07	2.49±0.16	2.40±0.01
Ether Extract	8.70±0.28^{b}	9.40±0.28^{ab}	9.84±0.23^{a}
Ash	2.95±0.21^{b}	3.10±0.29^{ab}	2.91±0.12^{b}
NFE	3.68±0.02^{a}	1.42±0.09^{b}	2.15±0.55^{ab}

Mean with different superscript along the same row are significantly different ($p<0.05$)

EA, LL, and SL indicate samples possessing equal length of left and right side chelipede, longer left side chelipede and shorter left side chelipede genotypes respectively

Table 2: Profile of Non-Essential Amino Acids (mg/g) of the Fleshy Tissues from Chelipede Genotypes/Variants of Freshwater Prawn, *Macrobrachium vollenhovenii*

Amino Acids	Genotypes/Variants		
	LL	EA	SL
Alanine	6.04±1.90^{b}	6.30±0.05^{a}	5.74±0.26^{c}
Glycine	3.85±0.14^{b}	4.22±0.21^{a}	4.11±0.73^{ab}
Serine	4.10±0.80^{b}	4.33±0.20^{ab}	4.38±0.04^{a}
Proline	2.97±0.07^{a}	3.03±0.28^{a}	2.85±0.21^{b}
Aspartate	10.54±0.07^{ab}	10.65±0.14^{a}	10.37±0.40^{b}
Glutamate	14.11±0.02^{b}	14.46±0.07^{a}	14.16±0.03^{b}
Tyrosine	2.81±0.07^{c}	2.92±0.14^{b}	3.03±0.04^{a}
Cysteine	1.34±0.05^{b}	1.42±0.07^{a}	1.36±0.17^{b}
Total	45.76±3.25^{b}	47.32±1.86^{a}	46.00±1.98^{b}

Means with different superscripts along the same row are significantly different ($p<0.05$)
EA, LL, and SL indicate samples possessing equal length of left and right side chelipede, longer left side chelipede and shorter left side chelipede genotypes respectively.

Table 3: Profile of Essential Amino Acids (mg/g) of the Fleshy Tissues from Chelipede Genotypes/Variants of Freshwater Prawn, *Macrobrachium vollenhovenii*

Amino Acids	Genotypes/Variants		
	LL	EA	SL
Valine	4.36±0.03^{b}	4.65±0.04^{a}	4.36±0.06^{b}
Threonine	3.74±0.11^{b}	4.34±0.12^{a}	4.15±0.10^{a}
Isoleucine	4.18±0.05^{b}	4.60±0.14^{a}	4.19± 0.06^{b}
Leucine	8.21±0.07^{b}	8.98± 0.06^{a}	8.03±0.05^{b}
Phenylalanine	3.78±0.21	3.91±0.41	3.98± 0.28
Histidine	2.75±0.08^{c}	3.36±0.07^{a}	3.02±0.01^{b}
Arginine	5.47±0.03^{b}	6.55±0.06^{a}	5.73±0.02^{b}
Tryptophan	1.12±0.05	1.11±0.05	1.15±0.06
Lysine	9.24±0.05^{b}	9.72±0.06^{a}	8.95±0.05^{b}
Methionine	1.24±0.31	1.49±0.33	1.29±0.24
Total	44.09±0.90^{b}	48.71±1.07^{a}	44.85±0.95^{b}

***EAA: NEAA were 0.96, 1.03 and 0.98 in LL, EA and SL respectively**
Means with different superscripts along the same row are significantly different ($p<0.05$)

Profile of the Essential Amino Acids (EAA)

In Table 3, the total content of EAA was significantly lowest (44.09±0.90 mg/g) in LL, but highest (48.71±1.07 mg/g) in EA, while SL and LL had statistically similar value. Specifically, EAA values ranged from 1.12±0.05 mg/g (tryptophan) to 9.24±0.05 mg/g (lysine) in LL, 1.11±0.05 mg/g (tryptophan) to 9.72±0.06 mg/g (lysine) in EA, and 1.15±0.06 mg/g (tryptophan) to 8.95±0.05 mg/g (lysine) in SL. The EAA: NEAA ratio was 0.96 in LL, 0.98 in SL and 1.03 in EA.

DISCUSSIONS

Proximate Composition of the Genotypes of *M. vollenhovenii*

Dry Matter Content

Dry matter is normally obtained after a drying process (Vaieretti *et al*., 2007). The obtained value of dry matter can be deduced as the quantity of the dehydrated mass of wet meat samples. This could otherwise be referred to as the dried meat yield of the wet samples. The obtained dry matter content in the specimens agrees with the reported values of dry matter /moisture content in *Cryphiops caementarius* (Moreno-Reyes *et al*., 2015); muscle tissues of wild, cultured and frozen *Macrobrachium rosenbergii* (Ferdose and Hossain, 2011), *Macrobrachium amazonicum* (Meireles *et al*., 2013), *M. amazonicum and M. rosenbergii* (Portella *et al*., 2013).

This indicates that the relative dry meat content of the genotypes compared favorably with values in the highlighted commercially important freshwater prawns species of other regions of the world. Values of dry matter were similar across the genotypes, thus implying that the *M. vollenhovenii* genotypes were not divergent in this regard. The similarity of dry matter contents across the studied genotypes indicates uniformity of the genotypes' tissues. Also, the comparability of the dry matter of all the genotypes with other commercially important freshwater prawn could indicate that the meat yield of these genotypes would also be comparable with that of the highlighted freshwater prawn species.

Crude Fibre

Fibre intake is critical for optimal health and can reduce the risk of diseases and disorders (Kuo, 2012). Crude fibre in diet can improve bowel activities and digestion (Pituch-Zdanowska *et al*., 2015). Range of crude fibre in the studied genotypes indicates that the prawns have appreciable quantity of fibre content. Although, Bernard and Adeyeye (2016) reported lower value (1.21±0.12 %) in *P. monodon* but higher value (2.88±0.06 %) in *Peneaus notialis* (Similarly, crude fibre of 1.0% in *M. macrobrachium* (Ehigiator and Nwangwu, 2011) and 0.45±0.01% in *M. vollenhovenii* (Ehigiator and Oterai, (2012) were obtained. This trend of values indicates that the obtained values in the genotypes fell within the reported range of 0.45±0.01% to 2.88±0.06% crude fibre in the above cited prawn species. Meanwhile, crude fiber content was statistically similar across the genotypes, thus following similar scenario with dry matter contents. This indicates that the genotypes were not divergent with respect to these two parameters.

Crude Protein

Shellfishes are known as sources of cheap proteineous food, useful for international trade (Wang and Reed, 2014). The range of crude protein content of the genotypes were similar to that of *Macrobrachium idea* (Ngoan *et al.*, 2000) and *M. vollenhovenii* (Ehigiator and Oterai, 2012), but better than the reported values (73.2 - 78.0%) in *M. rosenbergii* (Santos *et al*., 2007), and 68.27±0.23%, 74.85±0.65% and 60.8±0.12% respective crude protein contents in muscle tissue of wild, cultured and frozen samples of *M. rosenbergii* (Ferdose and Hossain, 2011). The values were higher compared to that of the commercially important *P. notialis* (Adeyeye *et al*., 2008), *Peneaus indicus* (Ravichandra *et al*., 2009), *Macrobrachium jelskii* (Ramirez *et al*., 2010) and *Cryphiops caementarius* (Moreno-Reyes *et al*., 2015) and. This implies that the crude protein content of the studied genotypes is comparable to most of the listed commercially important prawn species, indicating that the fleshy tissues of all the genotypes could be seen as potentially desireable source of protein in food, similar to the other species.

The result also showed that EA had significantly superior protein content than either of the SL and LL. This implies that content of protein could vary across intra species genotypes in *M. vollenhovenii*. Moreno-Reyes *et al*. (2015) observed that abundance of protein compound and proximate values in tissues of freshwater prawn could indicate habitat biasness. Although, the superior protein content in the EA compared to the rest genotypes could emanate based on this assumption; this may not be applicable in the case of the studied genotypes since samples of the genotypes (SL and LL) were equally obtained from the same environment/habitat as with EA, and all the genotypes would have interacted with this same environment in their capacities.

Ideally; the epistasis of genotype X environment interaction will produce corresponding phenotypes. It could therefore be insinuated that the superiority of EA would be the influence of intrinsic ability of the genotype (EA) to efficiently utilise the genotypes X environment nuances, which could have resulted in its achievement of comparatively superior crude protein content. The trend of divergence in crude protein content among the genotypes could be another dimension of the morpho/genetic divergence of the genotypes, since morphologic and genetic differences between the EA and the other genotypes as expressed in Oyebola *et al*. (2017) could co-vary with crude protein content.

Ether Extract/Lipid Content: Lipids/ether extract are major food reserve along with protein (Nagabhushanam and Farooqui 1982). Lipids are highly efficient energy source, containing twice the energy of carbohydrates and proteins (Okuzumi and Fujii, 2000). Fishes including

shellfishes are known to contain desire-able fat compounds, such as the omega-3 and 6-fatty acids (Abulude *et al*., 2006). The range of values for ether extract in the genotypes was similar to the reported values in *Peneaus notialis* (Adeyeye *et al*., 2008), *P. indicus* (Ravichandra *et al*., 2009) and *P. monodon* (Karuppasamy *et al.,* 2014). It is also similar to the values in muscle tissues of wild, cultured and frozen samples of *M. rosenbergii* (Ferdose and Hossain, 2011). Ether extract in the studied genotypes fell within the highlighted values for the listed commercially important freshwater prawns; thus indicating that the fleshy tissues of the genotypes would favorably compete with majority of these counterpart prawns, with respect to lipid content per unit of fleshy tissue. Ether extract was significantly highest in SL, and lowest in LL, with EA being intermediate. Conventionally, relatively low fat content is an indication of better lean meat yield. It could therefore be inferred that the relatively lowest ether extract in LL is an indication that it could have superior potentials for lean meat yield when compared to the rest of the two genotypes (EA and SL). This would be an advantage because meat products of low fat content (lean meat) are usually preferred by consumers as presence of some grades of fatty acid could encourage rancidity and reduced shelf life in some instances. In other words, the highest ether extract, as reflected in SL implies that it has the relatively least potentials for lean meat production among the studied genotypes. Consumption of shellfishes such as shrimps and prawns is considered healthy for circulating system because of the lack of significant levels of saturated fat, while the high cholesterol content in shrimps improves the ratio of desireable cholesterol and lowers triglycerides (Karuppasamy *et al*., 2014). However, future research would need to confirm the specific fatty acid profiles of the genotypes. Such action would highlight specific profile of fatty acids in each genotype, thus establishing their strengths or weaknesses in this regard. Considering sources of the variation, Karapanagiolidis *et al*. (2010) reported that prawns' fat content could be species-specific. It could be deduced from the current study that variation in fat content may also occur at sub-species/intra-specific level. The genetic potential for synthesis of fatty acid could have been highest in SL and lowest in LL, while EA would be intermediate.

Ash Content

Proximate ash content is an indicator for mineral nutrients when a food substance is ingested. According to Wardlaw and Smith (2009), ash helps in immune function and it is essential for healing of wounds, development of sexual organs and bones, storage or release of insulin, and cell membrane structure and function. Ash content in the studied genotypes was low when compared with data from previous studies; 19.9±0.1 in flesh of *P. notialis* (Adeyeye *et al*., 2008), 26.6±0.0% in *P. indicus* (Ravichandra *et al*., 2009),16.30 ± 0.65 and 10.14 ± 0.55 in respective muscle tissues of wild, and cultured *M. rosenbergii* (Ferdose and Hossain, 2011), 23.09 ± 0.39% in muscle tissues of frozen samples of *M. rosenbergii* (Ferdose and Hossain, 2011), 21.1-21.4% in *M. amazonicum* (Meireles *et al*., 2013) and 13.81-28.61% in *C. caementarius* (Moreno-Reyes *et al*., 2015),., and the relatively low ash content in the studied genotypes could indicate potential limitation in obtaining large quantity of minerals when fleshy portion of the prawns are consumed. Generally, in shellfishes, fleshy tissues are mainly protein source, while the exoskeleton and appendages could be good source of minerals. It has been demonstrated that the exoskeleton and appendages of the studied prawn genotypes contain high level of ash ranging from 11.36±0.07% in EA to 19.56±0.08% in SL (Oyebola, 2016). This opportunity of the mineral ash in the genotypes' wastes could be taken for mineral supplementation by consumers. More so, shells of prawns contain chitin and chitosan derivatives which have anti-cancer, antioxidant, and immune-enhancing activities (Ahmed *et al*., 2016).

Divergence of ash content across the genotypes, EA having the highest value, while lowest value occurred in SL implies significant superiority of EA over the other genotypes with respect to this proximate parameter. The genotypes were of the same species, located within the same habitat, yet, they reflected divergence in ash content. This result indicates that genotype factor would have also played out in divergence of ash content, similar to the observations on crude protein and ether extracts.

NFE Content

Carbohydrate/NFE content of the genotypes was comparable to most of the values in previous studies on freshwater prawns. The values were within the ranges of values in *P. notialis* (Adeyeye *et al*., 2008), *P. indicus* (Ravichandra *et al.,* 2009), *M. jelskii* (Ramirez *et al*., 2010), *M. vollenhovenii* (Ehigiator and Oterai, 2012)) and *C. caementarius* (Moreno-Reyes *et al*., 2015), . However, it was lower than the reported values in muscle tissues of wild and cultured *M. rosenbergii* (Ferdose and Hossain, 2011). Content of carbohydrate in the studied genotypes were within the range of values for the listed prawns, except that of *M. rosenbergii* (Ferdose and Hossain, 2011). The result thus indicates that the genotypes' carbohydrate content would be in tandem with majority of counterpart prawns across the regions of the world.

With respect to the intra specific genotypes, the genotypes reflected divergence in which LL was superior; having had the highest value, while the EA was relatively the inferior, having had the least value. This implies that although EA was superior in most of the proximate parameters, it would have relatively low carbohydrate yield when consumed; meanwhile, LL would be superior in this regard. Conventionally, carbohydrates contribute to sweetness, appearance and textural characteristics of food materials and are important sources of energy and dietary fibre. It follows that the EA would reflect relatively lowest potentials in this regard, while the LL would be the superior. However, since carbohydrates are usually in grades, it would be necessary to investigate the profile of carbohydrate content in the genotypes in another study.

In summary, the proximate characteristic of the studied genotypes indicates that utilization of the freshwater prawn genotypes for enhanced nutrition and food security would be attractive since the prawns have desireable proximate qualities. The comparative values with other commercially available prawns from other regions of the world would favor their patronage at both the local and international markets. The studied specimens of the genotypes were divergent in some of the proximate parameters, thus implying that the earlier observed morpho-genetic divergence in the *M. vollenhovenii* population could have relationship with divergence in nutritionally important parameters. Specifically, the proximate analysis implies that at statistically similar dry matter and crude fibre content across the genotypes, EA would have significantly highest crude protein and mineral (ash) content, it would be intermediate in crude fat (ether extract) content, and would be lowest in carbohydrate (NFE) content. Optimal utilization of the genotypes would therefore require cognizance of their divergence in this regard.

Amino Acid Profile and Chemical Scores of the Genotypes

The total NEAA in the genotypes compares favorably with the reported values by Ngoan *et al*., (2000) who observed total NEAA content of 42.1 mg/g, 44.6 mg/g and 46.7 mg/g in respective *Metapeneaus affiris*, *P. semisulcatus* and *P. monodon.* The range of values of NEAA in each of the genotypes indicates that cysteine and glutamate consistently had the respective lowest and highest values in all the genotypes. This result indicates that cysteine could be the limiting NEAA while glutamate could be the predominant NEAA in all of the genotypes. The pattern of result in which cysteine and glutamate had the lowest and the highest among the NEAA agreed with the report of Mukundan (1981) in other prawns. Values of glutamate in all the genotypes fell within the reported 14.01mg/g in prawns (Mukundan, 1981). However, the values were higher than 10.4 mg/g, 11.4 mg/g and 11.9 mg/g in respective *Metapeneaus affiris*, *P. semisulcatus* and *P. monodon* (Ngoan *et al*., 2000) and 10.8mg/g in *M. vollenhovenii* (Ehigiator and Oterai 2012).

Konosu (1979) reported that glutamate and glycine are the main contributors to palatability of dried shrimps. Cysteine in the genotypes was similar to the reported 1.78mg/g for prawns (Mukundan (1981). Walkins *et al*. (1982) listed glutamate as one of the amino acids of relatively high content in shrimps. The values of glutamate as observed in all the genotypes and the comparability of these values with that of the highlighted shrimp species indicate their potential importance as palatable prawn food item, similar to the species.

Across genotypes, EA demonstrated superior quality of NEAA having had the significantly

highest total NEAA content, while SL and LL were statistically lower and similar to each other.. It could therefore be inferred that, while EA was the relatively superior genotype, LL was the relatively most inferior. This implies that the genotypes followed the pattern EA>SL>LL in order of superiority in content of NEAAs. Coincidentally, this pattern is in congruent with the pattern of their crude protein content. Values of each of the NEAA in each of the genotypes are an indicator for the specific area of strength of each of the genotypes in terms of delivery of the specific NEAAs to consumers.

The range of total EAA in the studied genotypes were within the reported 43.1 mg/g, 46.0 mg/g and 45.4 mg/g in respective *Metapeneaus affiris*, *P. semisulcatus* and *P. monodon* (Ngoan *et al*., 2000) and 52.81 mg/g in prawns (Mukundan, 1981).The result showed that tryptophan consistently had the lowest values in all genotypes, while lysine consistently had the highest. This could imply that tryptophan was the most limiting EAA, while lysine is the most abundant in all the genotypes. This trend is similar to that of the values on NEAA in which same amino acid that occurred as the limiting and the most abundant were consistent for all the genotypes. The range of EAA values in all the genotypes agrees with the report of Mukundan *et al*., (1981) who reported 0.98 mg/g tryptophan and 9.49 mg/g lysine contents in prawns.

Tryptophan contributes to growth and protein synthesis and participates in several biochemical processes (Umezawa, 1989). The obtained value of tryptophan in the genotypes was higher than the tryptophan content in *P. monodon*, *F. indicus*, and *A. virilis* (Karuppasamy *et al*., (2014). Usydus *et al*., (2009) reported that fish products are good sources of lysine, which is severely restricted in cereals, the most important staple foodstuff in the world. The obtained values of lysine in the genotypes were higher than the reported values in *Metapeneaus affiris*, *P. semisulcatus* and *P. monodon* (Ngoan *et al*., 2000), *M. vollenhovenii* (Ehigiator and Oterai, 2012) and *P. indicus* (Abdel-Salam, 2013). The relatively high values of this amino acid content could indicate its relative advantage with respect to the issues raised by Usydus *et al*. (2009).

Amino acids plays prime role in human nutrition and health (Karupassamy *et al.,* 2014). The results showed that all the genotypes had essential amino acid composition that could appreciably contribute to normal functioning of human body. Meanwhile, values of total EAA in the genotypes followed similar trend with that of the NEAA, in which EA was superior. The fact that the EA also contains significantly highest values in most of the EAAs implies that the superiority of EA in some proximate qualities and the content of NEAA are maintained in the content of EAA.

The EAA:NEAA ratio is an indication of the contribution of the essential amino acid relative to the content of non-essential amino acids in a protein. The EAA:NEAA ratio of the genotypes were similar to the obtained 1.15 and 1.00 obtained in respective *F. indicus* and *A. virilis* (Karupassamy *et al*., 2014), but were higher than 0.70 and 0.83 obtained in *P. monodon* as reported by respective Sriket *et al*. (2007) and (Karupassamy *et al*., 2014). The values were also higher than the 0.60 in *P. semisulcatus* (Yanar and Celik, 2006). This result implies that the structure of amino acids (EAA:NEAA) in each of the genotypes compares favorably with the highlighted similar prawn species. Meanwhile, across the genotypes, EA was still superior in this regard.

CONCLUSION

The current study revealed nutritional quality intra–specific variants/genotypes in *M. vollenhovenii*. The study discovered that the genotypes have potentials as good protein source for human nutrition; however, the genotypes were divergent in some nutritional qualities, in which EA was the most nutritious. Precision in the utilization of *M. vollenhovenii* would require recognition of the genotypes as nutritional entities with cognizance of the parameters in which each of the genotype is superior/inferior. The information from this study would enhance utilization of the prawns in human nutrition, and their aquaculture development. It is therefore recommended that the freshwater prawn, *M. vollenhovenii* and its discovered genotypes should be promoted as valuable proteineous food sources for human. Aquaculture of the prawn should be

with cognisance of the highlighted nutritional potentials of each of the genotypes.

CONFLICT OF INTEREST

Authors declare that there is no conflict of interest on the article.

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