Chemical and quality evaluation of Pacific white shrimp *Litopenaeus vannamei*: Influence of strains on flesh nutrition

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Abstract

The Pacific white shrimp, *Litopenaeus vannamei*, is an important fisheries resource in China. To investigate the differences in nutritional quality among strains, we analyzed and compared the basic muscle nutritional components, amino acid (hydrolyzed and free) compositions, and fatty acid compositions among four *L. vannamei* strains (Universal, KH-1, Syaqua, and common). The result showed that under an efficiency aquaculture model, all four strains had high protein (21.1%-22.3%) and low fat (0.8%-1.1%). The Universal strain was highest in protein and fat as well as essential amino acid score (147.97). The Syaqua strain had the highest levels of polyunsaturated fatty acids (44.88%). The KH-1 strain had the highest free amino acid content (2.68%), which contributes to the taste. Our findings revealed that strain-specific variability exists in chemical composition of the shrimp *L. vannamei* under controlled condition, which may provide buying reference for consumers.

**KEYWORDS**

amino acid, fat acid, *Litopenaeus vannamei*, nutritional component, strains

1 | INTRODUCTION

The Pacific white shrimp, *Litopenaeus vannamei*, is the dominant farmed shrimp worldwide, representing one of the most common aquaculture species (Zhang et al., 2014). *L. vannamei* is an important commercial species in China, with a catch volume exceeding 114,370 tons in 2019 (FBMA, 2020). Pacific white shrimp is widely favored due to its superior flesh quality, delicious taste, and nutritional properties, and ease of cooking. Given the high market value, *L. vannamei* has emerged as one of the most valuable globally traded seafood products (Blythe et al., 2015).

*L. vannamei* is a euryhaline shrimp that is suitable for high-density cultivation in seawater and salt-fresh water. Suitable aquaculture species possess the characteristics of stress resistance, strong disease resistance, rapid growth, low cost, and high benefit (Li et al., 2016). China depends on imported shrimp, such as Syaqua from Thailand and Universal from Indonesia to obtain improved parent varieties (Li et al., 2016). However, some new strains have been bred in China, such as Kehai No.1 (KH-1) and Zhongke No.1 (Chen et al., 2008; Huang et al., 2010). At present, research is mainly focused on germplasm selection (Hu et al., 2015; Luan et al., 2013). Few studies have documented the nutritional components of different *L. vannamei* strains.

Nutritional composition is an important index of germplasm evaluation for shrimp, providing a basis for resource development and genetic improvement (Ma et al., 2018). Different specifications, salinity conditions, aquaculture environment, and model have been reported to affect the nutritional composition and quality of *L. vannamei* (Li et al., 2020; Xu et al., 2015; Duan et al., 2017). However, these studies evaluated the same shrimp varieties under different conditions. Determining the nutritional components of different
strains under the same cultivated condition can provide novel nutri-
tional information to consumers.

The objective of this study is to evaluate and compare the basic
muscle nutritional components, amino acid (hydrolyzed and free)
compositions, and fatty acid compositions of four L. vannamei strains
(Universal, KH-1, Syaqua, and common) under the efficiency aqua-
culture model. Our findings will provide essential information for the
comprehensive development, utilization, and promotion of L. van-
namei strains.

2 | MATERIALS AND METHODS

2.1 | Experimental design

The 90-day feeding trial was performed from May 2020 to August
2020. The experiment was conducted in a shrimp cultural farm
(Binzhou, China). Prior to the experiment, juvenile shrimps (Universal,
KH-1, Syaqua, and common) with initial weights of 0.63 ± 0.02 g were
temporarily reared for seven days to acclimate. Next, the shrimps
were placed into 12 experimental ponds (30 m²) to constitute four
groups in triplicate. The stocking density was about 300 individuals
per square meter. There were no significant differences in survival
rate among the group (78.42% ± 1.29%).

The seawater used in the experiment was filtered using a com-
posite sand filter. The chamfer was shaded to preserve tempera-
ture and control light. The culture conditions were maintained at
29°C ± 1°C, pH 7.5–8.0, dissolved oxygen >5.0 mg/L, salinity 29
–31. Biological preparations, such as photosynthetic bacteria, were
added to the aquaria ponds every seven days (Li et al., 2016).

The special formula feed for shrimp (contain 40% crude protein,
8% crude lipid) was purchased from a local commercial feed com-
pany. This feed was mainly made of fish meal, fermented soybean
meal, vitamin, etc. All shrimp groups were fed daily at a rate of 6%–
10% of body weight, divided into two equal (at time 8:30 and 16:30).
The daily feeding dose was recalculated and adjusted every 15 d.
The feeding experiment lasted for 90 days. Diets were hand-fed until
apparent satiation. The feeding rates were selected to assure appar-
ent satiation was reached without overfeeding (Zhou et al., 2013).
Sewage was discharged from the central sump 2 hr after feeding,
followed by the addition of 10% fresh seawater.

2.2 | Sample collection

After the 90-day feeding trial, shrimps in each pond were sam-
ped 24 hr after the last feeding. 30 shrimps from each pond
(20.10 ± 2.30 g) were randomly selected to analyze approximate
meat composition. All samples were kept on ice until they reached
the laboratory. The abdominal meat was obtained from the shell, got
rid of the intestinal tract, pooled in triplicate, and homogenized using
a grinder. The samples were stored in PE bags in the dark at 20°C
until analysis (within 2 w).

All chemicals and solvents used were analytical grade
(Sinopharm, China). Fatty acid methyl esters (FAME, purity≥98%)
and mixed standards of amino acids (purity≥99%) were purchased from Sigma-Aldrich.

2.3 | The determination of proximate composition

Crude protein, crude lipid, moisture, and ash content in the shrimp
meat were determined following the procedures of the Association
of Official Analytical Chemists (AOAC, 1995). First, the samples
were oven-dried until a constant weight was reached at 105°C
to determine the moisture content. Crude protein content was esti-
imated using the Kjeldahl method (Nitrogen Analyzer 8,400, Foss,
Denmark), and a conversion factor of 6.25 was used to convert total
nitrogen to crude protein. Crude lipid was assayed by ether extrac-
tion method using the Soxhlet extraction method (Soxex-8000, Foss,
Denmark). The ash content was determined by dry ashing in a muffle
oven at 550°C for 24 hr.

2.4 | The determination of hydrolyzed amino acid
(HAA) and free amino acid (FAA)

HAA content was measured according to the GB/T 5,009.124–2016
in China (2016). The sample was hydrolyzed with 6 mol L mol/L HCl
at 110°C for 24 hr in sealed glass tubes filled with nitrogen; then,
1 ml of hydrolysate was evaporated to dryness at 45°C to remove
the HCl. The hydrolysate was dissolved in 5 ml of 0.02 mol/L HCl,
centrifuged (5,000 rpm, 10 min, 4°C), and then filtered. 1 μl aliquot of
the supernatant was used for the amino acid analysis. Cysteine and
methionine were determined as cystic acid and methionine sulfone,
respectively, by performic acid oxidation prior to their digestion in
6 N HCl. The content of tryptophan was determined after alkaline
hydrolysis (5 mol/L NaOH) of each sample. All determinations were
performed in triplicate.

Free amino acid (FAA) was carried out using the method of Li
et al., (2014) with some modification. The sample was mixed with
0.01 mol/L HCl, supersonic extracted for 30 min, and then filtered.
1 μl aliquot of the supernatant was used for the amino acid analysis.

The amino acid composition was analyzed using an automatic
amino acid analyzer (LA-8080, Hitachi, Tokyo, Japan) equipped
with a 4.6 mm ×60 mm Hitachi 2,622 column. The identity and
quantity of the amino acids were assessed by comparison with the
retention times and peak areas of amino acid standards. Each sam-
ple was measured thrice and presented as the average of three
replicates.

The essential amino acid score was calculated with respect to the
Food and Agriculture Organization/World Health Organization ref-
ence amino acid pattern of the preschool child (FAO/WHO/UNU,
1985) using the following equation:

\[
\text{Amino acid score} = \frac{\text{sample amino acid}}{\text{reference amino acid}} \times 100
\]
2.5 | The determination of fatty acid content

Fatty acids were extracted from the shrimp samples and analyzed according to the ISO 5509 method (2000) involving Soxhlet extraction, saponification, esterification, and finally fatty acid methyl ester (FAME) extraction in hexane. Gas chromatography was performed using an Agilent Technologies 6,890 gas chromatograph equipped with an HP-5 cross-linked methyl silicone-fused-silica capillary column (30 m × 0.32 mm I.D., 0.5 μm film thickness). Individual components were identified by comparing the mass spectral data and retention time data with those obtained for authentic and laboratory standards. Each sample value represents the mean of three measurements.

2.6 | Statistical analysis

All results were expressed as mean ± SD, and one-way analysis of variance (ANOVA) was performed using statistical analysis software (SPSS Version 16.0). Differences in the concentration of nutritional elements among shrimp strains were tested with ANOVA followed by a multiple comparison test (Tukey's HSD). Differences were considered to be significant at \( p < 0.05 \).

2.7 | Ethical statement

The Pacific white shrimp is an aquaculture species. All experiments in this study were approved by the Animal Care and Use guideline of the Marine Science Research Institute of Shandong Province.

3 | RESULTS AND DISCUSSION

3.1 | Proximate composition of four shrimp strains

The proximate composition of each strain is shown in Table 1. Crude protein content ranged from 21.1% to 22.3%, crude fat content ranged from 0.8% to 1.1%, and the crude ash did not differ among strains. These results are consistent with Ma et al. (2018) who found that crude protein and fat content were relatively uniform among shrimp strains. Among the four strains examined in the present study, crude protein content was the highest in Universal (22.3%). Crude fat content was the lowest in common shrimp, and crude ash content was the lowest in KH-1 and common shrimp. The samples came from the same culture area, but results were found to be comparable. A similar crude protein content was found in *Aristaeomorpha foliacea* (Bono et al., 2012) and *Penaeus monodon* (Sriket et al., 2007) (87.7 g 100g⁻¹ dry matter), while *Fenneropenaeus chinensis* had a low crude protein content of 20.60% (Wang et al., 2013). Shrimp cultured in pond had higher values of crude fat, as reported by Sriket et al. (2007). In general, the chemical composition analyses confirmed that the four strains were to be excellent food resources, with good balance of nutrients and good level of protein.

### TABLE 1 Proximate composition of four shrimp strains (mean±SD) (g 100g⁻¹ wet weight)

| Strains | Moisture | Protein | Fat     | Ash     | Energy |
|---------|----------|---------|---------|---------|--------|
| Universal | 74.6 ± 0.51b | 22.3 ± 0.30a | 1.1 ± 0.02a | 1.7 ± 0.02a | 425 ± 1.2a |
| KH-1     | 75.4 ± 0.39b | 21.8 ± 0.31ab | 1.0 ± 0.01b | 1.6 ± 0.03a | 411 ± 0.9b  |
| Syqua    | 75.2 ± 0.43ab | 21.7 ± 0.29ab | 1.0 ± 0.02b | 1.7 ± 0.02a | 413 ± 1.5b  |
| Common   | 76.5 ± 0.41a | 21.1 ± 0.34b | 0.8 ± 0.01c | 1.6 ± 0.03a | 388 ± 1.4c  |

Note: Values in the same column bearing different letters are significantly different (\( p < 0.05 \)).
| Amino acid       | Hydrolyzed amino acid | Free amino acid |
|------------------|-----------------------|-----------------|
|                  | Universal  | KH-1 | Syaqua | Common | Universal  | KH-1 | Syaqua | Common |
| Aspartic acid    | 6.16 ± 0.01b | 6.50 ± 0.01c | 6.73 ± 0.02b | 6.90 ± 0.01a | 0.201 ± 0.001b | 0.203 ± 0.001a | 0.161 ± 0.001b | 0.128 ± 0.000c |
| Threonine        | 3.14 ± 0.01a | 3.21 ± 0.01a | 3.27 ± 0.03a | 3.06 ± 0.02a | 0.406 ± 0.002a | 0.447 ± 0.009a | 0.403 ± 0.009a | 0.170 ± 0.001a |
| Serine           | 2.71 ± 0.02ab | 2.80 ± 0.02b | 2.74 ± 0.02ab | 2.86 ± 0.01a | 0.051 ± 0.006b | 0.122 ± 0.02a | 0.040 ± 0.001b | 0.043 ± 0.001b |
| Glutamine        | 13.98 ± 0.01ab | 14.19 ± 0.02b | 14.40 ± 0.05a | 13.88 ± 0.01ab | 2.028 ± 0.010b | 1.748 ± 0.009a | 1.573 ± 0.010b | 0.468 ± 0.009c |
| Glycine          | 5.47 ± 0.02c | 6.38 ± 0.01b | 5.65 ± 0.01c | 7.10 ± 0.01a | 1.976 ± 0.018c | 1.951 ± 0.015b | 1.853 ± 0.012b | 2.638 ± 0.014a |
| Alanine          | 5.95 ± 0.01c | 6.34 ± 0.01a | 6.21 ± 0.02b | 5.45 ± 0.01d | 1.874 ± 0.025b | 1.910 ± 0.031a | 1.694 ± 0.027ab | 0.851 ± 0.019c |
| Cysteine         | 4.42 ± 0.01a | 1.38 ± 0.02a | 1.37 ± 0.03a | 1.33 ± 0.01a | 0.201 ± 0.003a | 0.122 ± 0.004b | 0.121 ± 0.001b | 0.128 ± 0.001ab |
| Valine           | 3.78 ± 0.02a | 3.86 ± 0.01a | 3.91 ± 0.01a | 3.49 ± 0.02b | 0.457 ± 0.005b | 0.488 ± 0.009a | 0.444 ± 0.009a | 0.170 ± 0.005c |
| Methionine       | 2.76 ± 0.01b | 2.76 ± 0.01b | 2.74 ± 0.01b | 3.37 ± 0.01a | 0.201 ± 0.001c | 0.244 ± 0.001a | 0.202 ± 0.002b | 0.170 ± 0.001c |
| Isoleucine       | 3.62 ± 0.02a | 3.82 ± 0.02a | 3.75 ± 0.01a | 3.33 ± 0.03b | 0.303 ± 0.001a | 0.325 ± 0.001a | 0.282 ± 0.001a | 0.085 ± 0.001a |
| Leucine          | 6.50 ± 0.01a | 6.54 ± 0.03a | 6.69 ± 0.01a | 6.08 ± 0.02b | 0.559 ± 0.003c | 0.650 ± 0.008a | 0.565 ± 0.010b | 0.170 ± 0.002d |
| Tyrosine         | 2.60 ± 0.04a | 2.52 ± 0.01a | 2.66 ± 0.02a | 2.67 ± 0.01a | 0.051 ± 0.001b | 0.081 ± 0.001a | 0.041 ± 0.001b | 0.043 ± 0.001b |
| Phenylalanine    | 3.46 ± 0.01a | 3.54 ± 0.01a | 3.59 ± 0.03a | 3.49 ± 0.02a | 0.354 ± 0.002c | 0.447 ± 0.003a | 0.363 ± 0.004b | 0.128 ± 0.001d |
| Lysine           | 6.89 ± 0.02ab | 6.71 ± 0.02c | 6.94 ± 0.05bc | 7.10 ± 0.01a | 0.606 ± 0.005b | 0.691 ± 0.006a | 0.524 ± 0.007b | 0.298 ± 0.002c |
| Histidine        | 1.73 ± 0.02a | 1.75 ± 0.01a | 1.77 ± 0.02a | 1.73 ± 0.01a | 0.201 ± 0.001b | 0.203 ± 0.001a | 0.161 ± 0.001b | 0.085 ± 0.001c |
| Tryptophan       | 0.83 ± 0.01a | 0.81 ± 0.01a | 0.73 ± 0.01a | 0.74 ± 0.02a | 0.039 ± 0.000a | 0.041 ± 0.001a | 0.040 ± 0.001a | 0.043 ± 0.000a |
| Arginine         | 5.24 ± 0.01a | 4.80 ± 0.03c | 4.96 ± 0.01b | 5.22 ± 0.01a | 0.205 ± 0.001a | 0.122 ± 0.002b | 0.121 ± 0.001b | 0.043 ± 0.000c |
| Proline          | 3.39 ± 0.02b | 4.14 ± 0.01a | 3.39 ± 0.02b | 2.43 ± 0.03c | 0.472 ± 0.010b | 1.138 ± 0.012a | 0.766 ± 0.009c | 0.043 ± 0.001d |
| Total amino acids (TAA) | 80.08 ± 0.06ab | 82.07 ± 0.05c | 81.49 ± 0.06bc | 80.24 ± 0.05a | 7.992 ± 0.260c | 10.894 ± 0.180a | 9.315 ± 0.200ab | 5.600 ± 0.280d |
| Essential amino acids (EAA) | 30.98 ± 0.03a | 31.26 ± 0.02a | 31.61 ± 0.02a | 30.67 ± 0.02a |
| Delicious amino acids (DAA) | 32.01 ± 0.02c | 33.42 ± 0.05b | 32.98 ± 0.03bc | 33.33 ± 0.02a |
| EAA/TAA          | 38.69%    | 38.09%    | 38.79%    | 38.22%    |
| EAA/NEAA         | 63.11%    | 61.52%    | 63.38%    | 61.86%    |
| DAA/TAA          | 39.97%    | 40.71%    | 40.48%    | 41.54%    |

Note: indicates delicious amino acids; * indicates essential amino acids; △ indicates semi-essential amino acids. Values in the same column bearing different letters are significantly different (p < .05).
lysine, which is the limiting amino acid in the cereal-based diets of children in developing countries (Kim et al., 2000).

The EAA scores of each shrimp strain are presented in Table 3. When compared to the reference amino acid pattern of preschool children (2-5 years old), all amino acid scores were >100, except for tryptophan. Tryptophan had the lowest scores (especially in Syaqua), which would be considered the limiting amino acid in shrimp. However, in Chinese recipes, shrimp is often cooked with pork, mutton, and millet, which will supply the limiting amino acid (Jilin and Peck, 1995). Lysine and sulfur-containing amino acids (cysteine and methionine) had the highest scores in all strains. In general, the shrimp muscle protein was of high quality and exhibited well-balanced EAA compositions.

### 3.3 FAA profiles of four shrimp strains

The free amino acid (FAA) profiles of the four shrimp strains are presented in Table 2. The total FAA contents were 7.99 g 100g⁻¹ (DW), 10.89 g 100g⁻¹ (DW), 9.32 g 100g⁻¹ (DW), and 5.60 g 100g⁻¹ (DW), respectively. The most abundant FAA was glutamic acid, glycine, alanine, and lysine, which differed from the HAA profiles. These amino acids constituted 63.05%, 57.83%, 60.61%, and 75.10% of the total FAA, respectively. The least abundant FAA in the meat of all four shrimp strains was tryptophan.

The taste activity value (TAV) of the FAA identified in the four shrimp strains is presented in Table 4. Each amino acid has a unique taste, the flavor contribution of which is dependent on the TAV, the ratio between the taste substance contained in the sample and its threshold value (Chen et al., 2012; Li et al., 2014). A TAV >1 indicates an important contribution to the taste of food (Wang and Chen, 2014). However, TAV does not consider the interaction between the components, which may have a synergistic effect on food taste. Maybe sensory evaluation should be used in our future research. Among the four shrimp strains, glutamic acid, glycine, alanine, and aspartic acid greatly influence the shrimp flavor (Liu et al., 2017).

Figure 1 shows the comparative content model charts and TAV model charts of the major FAA in the four shrimp strains, respectively. All strains had the similar FAA compositions, except the common shrimp, which had higher glycine levels (Figure 1a). The FAA content model among the other three strains was similar, but the model area was highest for KH-1, followed by Syaqua, and then Universal, which indicates that the FAA content of KH-1 was higher.

The FAA content models were similar among strains, except for the common shrimp (Figure 1b). KH-1 had the largest model area. The top contributor to taste was glutamine, with a TAV of 14.33. The TAVs of alanine and glycine were 7.83 and 3.69, respectively, which also significantly influence the taste of shrimp meat. The models indicate that KH-1 would taste fresher and sweeter than the other strains.
3.4 Fatty acid profiles of four shrimp strains

The fatty acid profiles and levels, which varied among the four strains, are shown in Table 5. The profiles of all strains were dominated by polyunsaturated fatty acids (PUFA) except in the common shrimp, followed by saturated fatty acids (SFA), and monounsaturated fatty acids (MUFA). Among the SFAs, palmitic acid (C16:0) was the dominant and stearic acids (C18:0) were also abundant. The dominant MUFA was oleic acid (C18:1). The dominant PUFAs were linoleic acid (LA, C18:2–6), docosahexaenoic acid (DHA, C22:6–3), and eicosapentaenoic acid (EPA, C20:5–3).

Lipids store and provide energy to organisms. PUFAs are essential for the reproduction and growth of organisms; they can also increase the flavor of food during heating, reduce blood viscosity, and enhance human immunity (Cui et al., 2018). Compared with pomfret (Zhao et al., 2010), Pacific white shrimp have higher amounts PUFA contents, especially the Syaqua strain. In addition, all four strains had higher MUFA levels than Chinese white shrimp Fenneropenaeus chinensis (Li et al., 2017). LA is a fat acid typically found in plants; the high LA content observed in shrimp may attribute to their omnivorous diets. In fact, a previous study reported higher LA content in the muscle of L. vannamei fed diets supplemented with two species of marine algae (Ju et al., 2009). Dietary lipids have also been shown to affect the fatty acid composition of L. vannamei; whole body shrimps showed increases in MUFA and PUFA when fed diets with high levels of unsaturated fatty acids.

Among the most valuable FAs, DHA and EPA play important roles in the prevention of inflammatory and cardiovascular diseases due to their serum triglycerides-lowering effects (Bono et al., 2012). The EPA and DHA contents were moderately high in all the shrimp samples, especially KH-1. However, the EPA content measured in the present research was lower than that reported by Huang.

### Table 4: The taste attribute and TAV of free amino acid in four shrimp strains (mg g⁻¹)

| Amino acid  | Taste attribute     | Threshold value | TAV     |
|-------------|---------------------|-----------------|---------|
|             |                     |                 | Universal | KH-1 | Syaqua | Common |
| Aspartic acid | sweet/sour (+)  | 1               | 0.40     | 0.50  | 0.40   | 0.30    |
| Threonine    | sweet (+)           | 2.6             | 0.31     | 0.42  | 0.38   | 0.15    |
| Serine       | sweet (+)           | 1.5             | 0.07     | 0.20  | 0.07   | 0.07    |
| Glutamine    | sweet/sour (+)      | 0.3             | 13.33    | 14.33 | 13.00  | 3.67    |
| Glycine      | sweet (+)           | 1.3             | 3.00     | 3.69  | 3.54   | 4.77    |
| Alanine      | sweet (+)           | 0.6             | 6.17     | 7.83  | 7.00   | 3.33    |
| Valine       | sweet/bitter (-)    | 0.4             | 2.25     | 3.00  | 2.75   | 1.00    |
| Methionine   | bitter/sweet/ sulfurous (-) | 0.3 | 1.33 | 2.00 | 1.67 | 1.33 |
| Isoleucine   | bitter (-)          | 0.9             | 0.67     | 0.89  | 0.78   | 0.22    |
| Leucine      | bitter (-)          | 1.9             | 0.58     | 0.84  | 0.74   | 0.21    |
| Phenylalanine | bitter (-)         | 0.9             | 0.78     | 1.22  | 1.00   | 0.33    |
| Lysine       | sweet/bitter (-)    | 0.5             | 2.40     | 3.40  | 2.60   | 1.4     |
| Histidine    | bitter (-)          | 0.2             | 2.00     | 2.50  | 2.00   | 1.00    |
| Arginine     | bitter/sweet (-)    | 0.5             | 0.80     | 0.6   | 0.60   | 0.20    |
| Proline      | bitter/sweet (-)    | 3               | 0.4      | 0.93  | 0.63   | 0.03    |

### Figure 1: Comparative content and comparative TAV model charts of major free amino acids

Abbreviations: Glu, glutamine; Gly, glycine; Ala, alanine; Val, valine; Leu, leucine; Lys, lysine; His, histidine
| Fat acid | Universal | KH-1 | Syaqua | Common |
|---------|-----------|------|--------|--------|
| C4:0    | 0.04 ± 0.00a | 0.02 ± 0.00a | 0.03 ± 0.00a | 0.04 ± 0.00a |
| C6:0    | 0.02 ± 0.00a | -    | 0.02 ± 0.00a | 0.03 ± 0.00a |
| C10:0   | 0.05 ± 0.00a | 0.04 ± 0.00a | 0.06 ± 0.00a | 0.29 ± 0.00a |
| C11:0   | 7.29 ± 0.18c | 7.03 ± 0.05c | 9.47 ± 0.09b | 10.98 ± 0.05a |
| C12:0   | 0.06 ± 0.00b | 0.04 ± 0.00c | 0.06 ± 0.00b | 0.08 ± 0.01a |
| C14:0   | 0.61 ± 0.01a | 0.34 ± 0.00c | 0.31 ± 0.00d | 0.45 ± 0.01b |
| C15:0   | 0.77 ± 0.00b | 1.08 ± 0.09a | 0.66 ± 0.01bc | 0.63 ± 0.00c |
| C16:0   | 16.83 ± 0.10b | 16.75 ± 0.07b | 15.94 ± 0.09c | 17.46 ± 0.10a |
| C17:0   | 1.41 ± 0.01d | 1.99 ± 0.02b | 1.62 ± 0.01c | 2.64 ± 0.05a |
| C18:0   | 10.23 ± 0.19a | 10.32 ± 0.20a | 10.08 ± 0.21a | 9.05 ± 0.15b |
| C20:0   | 0.72 ± 0.01a | 0.67 ± 0.01b | 0.57 ± 0.02c | 0.65 ± 0.01b |
| C21:0   | 0.22 ± 0.00  | 0.20 ± 0.00  | 0.15 ± 0.00  | 0.22 ± 0.00  |
| C22:0   | 0.98 ± 0.01a | 0.76 ± 0.00b | 0.70 ± 0.01c | 0.98 ± 0.00a |
| C23:0   | 0.20 ± 0.00b | 0.21 ± 0.00b | 0.18 ± 0.00c | 0.29 ± 0.01a |
| C24:0   | 0.29 ± 0.00  | 0.28 ± 0.00  | 0.21 ± 0.00  | 0.36 ± 0.00  |
| ΣSFA    | 39.72 ± 0.26b | 39.73 ± 0.31b | 40.06 ± 0.41b | 44.15 ± 0.38a |
| C16:1(n-7) | 2.10 ± 0.02b | 1.37 ± 0.01c | 1.01 ± 0.00d | 3.77 ± 0.12a |
| C18:1(trans,n-9) | 0.56 ± 0.00 | 0.41 ± 0.00 | - | 0.61 ± 0.00 |
| C18:1(cis,n-9) | 13.89 ± 0.21a | 13.10 ± 0.09b | 12.71 ± 0.09c | 12.40 ± 0.07c |
| C20:1   | 0.69 ± 0.00b | 0.72 ± 0.00a | 0.72 ± 0.01a | 0.37 ± 0.00c |
| C24:1(n-9) | 0.43 ± 0.00  | 0.30 ± 0.00  | 0.35 ± 0.00  | 0.33 ± 0.00  |
| ΣMUFA n-9 | 14.88 ± 0.07a | 13.81 ± 0.08b | 13.06 ± 0.06d | 13.34 ± 0.10c |
| ΣMUFA   | 17.67 ± 0.09a | 15.90 ± 0.08b | 14.79 ± 0.11c | 17.48 ± 0.05a |
| C18:2(LA,n-6) | 16.12 ± 0.07a | 15.12 ± 0.07b | 16.14 ± 0.08a | 9.49 ± 0.11c |
| C20:2   | 1.34 ± 0.01c | 1.61 ± 0.05b | 1.85 ± 0.09a | 0.77 ± 0.06d |
| C22:2   | 0.04 ± 0.00a | 0.05 ± 0.00a | 0.07 ± 0.00a | 0.10 ± 0.00a |
| C18:3(GLA,n-6) | 0.05 ± 0.00  | 0.07 ± 0.00  | 0.04 ± 0.00  | 0.23 ± 0.00  |
| C18:3(ALA,n-3) | 1.89 ± 0.05c | 2.00 ± 0.04c | 2.22 ± 0.07b | 4.30 ± 0.05a |
| C20:3 (n-6) | 0.07 ± 0.00  | 0.10 ± 0.00  | 0.08 ± 0.00  | 0.46 ± 0.00  |
| C20:4 (ARA,n-4) | 2.92 ± 0.04d | 3.62 ± 0.05b | 3.25 ± 0.04c | 6.28 ± 0.09a |
| C20:5 (EPA,n-3) | 9.56 ± 0.07c | 10.35 ± 0.08a | 10.09 ± 0.09b | 9.93 ± 0.10b |
| C22:6(DHA,n-6) | 10.60 ± 0.10b | 11.44 ± 0.12a | 11.14 ± 0.21a | 6.55 ± 0.18c |
| ΣPUFA n-3 | 11.45 ± 0.22c | 12.35 ± 0.04b | 12.31 ± 0.08b | 14.23 ± 0.09a |
| ΣPUFA n-6 | 26.77 ± 0.28ab | 26.63 ± 0.19b | 27.32 ± 0.25a | 16.27 ± 0.19c |
| ΣPUFA  | 42.59 ± 0.45b | 44.36 ± 0.36a | 44.88 ± 0.47a | 38.11 ± 0.39c |
| ΣPUFA−3/ΣPUFA n-6 | 0.43 | 0.46 | 0.45 | 0.87 |
| ΣPUFA−6/ΣPUFA n-3 | 2.34 | 2.16 | 2.22 | 1.14 |

Note: Values in the same row bearing different letters are significantly different (p < 0.05), whereas values without letters indicate no significant differences.

Abbreviations: MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; SFA, saturated fatty acids.

et al. (2004) for *L. vannamei* (11.5 to 13.7 g 100 g⁻¹ FA), while the DHA content, which ranged from 8.9 to 10.4 g 100 g⁻¹ FA, was lower than that of our data.

The ratio of n-6/n-3 PUFA's found among the four strains in this study was lower than the threshold value recommended by the UK Department of Health (HMSO, 1994). Values >4.0 are considered to be harmful to health and may promote the development of cardiovascular disease (Moreira et al., 2001). Therefore, consuming these shrimp strains may contribute to maintenance of n-6/n-3 ratio recommended. The FA compositions among aquatic organisms are dependent on diet, size, age, reproductive conditions, and environmental conditions, especially water temperature, which can...
influence lipid content and FA composition (Zhao et al., 2010). Our results indicate that the shrimp strain influences FA content and composition.

4 CONCLUSION

The results from this study revealed that strain-specific variability exists in chemical composition of the shrimp L. vannamei under controlled condition. The Universal strain had the highest protein and fat content, and the highest overall EAA score. The Syaqua shrimps showed the highest levels of PUFA. And the KH-1 strain was highest in FAA taste-active components.

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CONFLICTS OF INTEREST

The authors declare that they have no conflict of interest.

DATA AVAILABILITY STATEMENT

The authors confirm that the data supporting the findings of this study are available within the article.

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