

Research Article

Determination of Free Amino Acids in Three Species of Duckweed (Lemnaceae)

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In this study, a fast, simple, precise, and sensitive hydrophilic interaction liquid chromatography (HILIC) method was established for simultaneous determination of free amino acids in three different varieties of duckweed including *Spirodela polyrhiza* (L.) Schleid., *Landoltia punctata* (G. Mey.) Les & D. J. Crawford, and *Lemna aequinoctialis* Welwitsch by ultrahigh performance liquid chromatography coupled with tandem mass spectrometry (UHPLC-MS/MS). Method validation was processed in terms of linearity, precision, stability, repeatability, and accuracy as well as limits of detection and quantification. The developed method was applied for quantification of 59 batches of samples. Then chemometric analysis was used to evaluate different duckweeds by principle component analysis (PCA) and orthogonal partial least squares-discriminant analysis (OPLS-DA). The results demonstrated that there was no significant difference in FAAs' profile among three varieties of duckweed.

1. Introduction

Amino acids are kinds of nitrogenous components that play vital and diverse roles in metabolism and have attracted significant attention in food, feedstuff, and alimentary supplements. Amino acids are basic units and important ingredients of proteins and involved in the progress of biosynthesis for glycoprotein, porphyrins, neurotransmitters, polyamines, and nitric oxide [1–5]. Nutritional studies show that amino acids can modulate gene expression and enhance the growth of skeletal muscle and small intestine [6].

The family of Lemnaceae colloquially known as duckweed has been consumed as human food since long [7]. Duckweeds have the striking capacity of explosive reproduction [8]. They can grow almost everywhere with appropriate temperature and nutrition in water. But their greatest potential is to produce large quantities of protein-rich biomass that is a promising food resource for humans [9] and is suitable for

feeding a wide range of animals including fish, poultry, and cattle [10–12]. The contents of free amino acids (FAAs) are very important for the evaluation of the protein-rich food. Fresh duckweed contains a large amount of water with moisture content of 86%–94%. But for dried samples, their protein concentration ranges from 25% to 40% with much lower fibrous material than that of land forage [13]. The habitat influences the content of proteins and fibers dramatically. Content of amino acids and protein always depend on their species pattern and growth environment, such as sunshine, nutrition media, and their growth pattern: gregarious or solitary. Under high nutritional conditions, more proteins and fewer fibers are accumulated in duckweed and vice versa. The amino acid type of duckweed is very close to that of animals and thus could be used by animals efficiently [7, 14]. The first limited amino acid (lysine) is similar to soybean and is more superior to that in other food such as sorghum and maize.

There are several methods reported in literature for analysis of free amino acids. In general, the FAAs are extracted with solvents water, formic acid, hydrochloric acid, or ethanol, followed by filtration or centrifugation before analysis [15–17]. Several techniques have been described for detection of free amino acids including ion-exchange chromatography [18], precolumn derivatization followed by reversed high-performance liquid chromatography coupled with diode array or fluorescence detector [19, 20], gas chromatography, mass spectrometry, and capillary electrophoresis [21]. In recent years, determination of FAAs using ultrahigh performance liquid chromatography hyphenated to mass spectrometry has gained great notice because of the merit of selective separation for the polar underivatized analytes under HILIC condition with acetonitrile-dominated mobile phase [22–25].

In present study, a feasible and reliable UPLC-QTRAP-MS/MS method was developed and validated for quantitative analysis of 24 underivatized FAAs simultaneously. Multivariate statistical analysis was employed to assess the differences in the profiles of FAAs among three species of duckweed. This simple and fast analytical method would be used for quality control of duckweeds.

2. Materials and Methods

2.1. Reagents and Materials. 59 batches of duckweed were collected from different regions in China as shown in Table 1. The samples were identified and classified by PCR [26–28], and the number of populations was as follows: 25 populations from species *Spirodela polyrhiza*, 16 populations from species *Landoltia punctata* (its another previously invalid name is *Spirodela oligorrhiza* (Kurz) Hegelm.), and 18 populations from *Lemna aequinoctialis*. Fresh materials were washed by tap water, dried in sunshine, and pulverized, and the powder was screened through 60-mesh sieve. Reference standards of tyrosine (Tyr), alanine (Ala), glutamic acid (Glu), phenylalanine (Phe), histidine (His), isoleucine (Ile), aspartic acid (Asp), lysine (Lys), glycine (Gly), valine (Val), citrulline (Cit), cystine (Cys2), proline (Pro), tryptophan (Trp), leucine (Leu), arginine (Arg), cysteine (Cys), hydroxyproline (Hpro), methionine (Met), threonine (Thr), asparagine (Asn), and serine (Ser) were purchased from National Institutes for Food and Drug Control (Beijing, China) with the purity more than 98%. Reference standards of γ -aminobutyric (GABA) and glutamine (Gln) with the purity more than 98% were obtained from Aladdin Industrial Corporation (Shanghai, China). Acetonitrile (HPLC grade) was purchased from Merk (Darmstadt, Germany). Formic acid and ammonium formate (HPLC grade) were provided by Mreda Technology Incorporation (USA). Deionized water used for analysis procedure was produced by a Milli-Q Academic ultrapure water system (Millipore, Bedford, MA, USA).

2.2. Instrumentation and Chromatographic and Mass Conditions. Chromatographic analysis was performed on a Shimadzu LC-30 ultrahigh performance liquid chromatography system (Shimadzu, Japan), which consisted of a

TABLE 1: Information of duckweeds from different regions.

Sample	Species	Site
SP1-7	<i>Spirodela polyrhiza</i>	Yangzhou City of Jiangsu Province
SP8-9	<i>Spirodela polyrhiza</i>	Yancheng City of Jiangsu Province
SP10-11	<i>Spirodela polyrhiza</i>	Nanjing City of Jiangsu Province
SP12-13	<i>Spirodela polyrhiza</i>	Huaian City of Jiangsu Province
SP14-17	<i>Spirodela polyrhiza</i>	Lianyungang City of Jiangsu Province
SP18-19	<i>Spirodela polyrhiza</i>	Linyi City of Shandong Province
SP20-21	<i>Spirodela polyrhiza</i>	Hefei City of Anhui Province
SP22-23	<i>Spirodela polyrhiza</i>	Hangzhou City of Jiangsu Province
SP24-25	<i>Spirodela polyrhiza</i>	Baoding City of Hebei Province
LP1-11	<i>Landoltia punctata</i>	Yangzhou City of Jiangsu province
LP12-16	<i>Landoltia punctata</i>	Huaian City of Jiangsu province
LA1-3	<i>Lemna aequinoctialis</i>	Yangzhou City of Jiangsu Province
LA4-8	<i>Lemna aequinoctialis</i>	Yancheng City of Jiangsu Province
LA9-14	<i>Lemna aequinoctialis</i>	Nanjing City of Jiangsu Province
LA15-16	<i>Lemna aequinoctialis</i>	Lianyungang City of Jiangsu Province
LA17-18	<i>Lemna aequinoctialis</i>	Linyi City of Shandong Province

communication bus module (CMB-20A), a vacuum degasser, binary gradient pumps (LC-30AD), an autosampler (SIL-30A), and a column oven (CTO-30A) coupled with an AB Sciex QTRAP 5500 (AB SCIEX, USA). A Waters XBridge Amide column (2.1 mm \times 150 mm, 2.5 μ m, Waters, USA) was used for chromatographic separation. The binary mobile phase was composed of acetonitrile (A) and 10 mM ammonium formate with 0.2% (v/v) formic acid (B) at a flow rate of 0.4 mL/min. The linear gradient elution was carried out as follows: 0–5 min, 90%–85.5% A; 5–11 min, 85.5%–54% A; 11–12 min, 54%–10% A; 12–14 min, 10% A; 14–15 min, 10%–90% A; 15–20 min, and 90% A. The reequilibration time was 4 min with a total running time of 20 min. The column compartment was kept at 20°C, while the autosampler trial was maintained at 15°C, and injection volume was 2 μ l. The needle was washed with mixtures of acetonitrile and water.

The mass spectrometry assay was performed on a triple quadruple mass spectrometer equipped with an electrospray ionization source. The spectra were recorded under positive-ion type with the multiple reaction monitoring (MRM) mode. The capillary voltage was 5500 V, and desolvation gas temperature was 550°C. The curtain gas was 35 psi with both nebulizer and drying gas of 55 psi. Nitrogen was used as source gas with purity more than 95% and collision gas with purity over 99.999%. The 24 components of amino acids were optimized in the tuning mode with mass only to obtain the mass of the precursor and product ion, the best declustering potential (DP), and collision energy (CE), respectively. The details are shown in Table 2. The entrance potential (EP) and collision cell exit potential (CXP) were set as default value. The typical LC-QTRAP-MS/MS chromatograms are shown in Figure 1.

TABLE 2: The precursor ions, product ions, declustering potential, and collision energy of amino acids.

Number	Compound	Precursor ion	Product ion	DP (V)	CE (V)
1	Tyr	182.0	91.1	60	37
2	Ala	90.0	44.1	50	14
3	Glu	148.1	84.0	60	21
4	Phe	166.1	120.1	60	19
5	His	156.1	110.3	80	20
6	Ile	132.1	86.1	50	14
7	Asp	134.1	74.0	50	19
8	Lys	147.0	84.1	60	23
9	Gly	76.1	29.9	40	16
10	Val	118.1	71.9	50	15
11	Cit	176.2	70.0	60	31
12	GABA	104.1	86.8	50	14
13	Cys2	241.1	73.9	80	40
14	Pro	116.0	70.1	60	22
15	Trp	205.1	146.0	50	24
16	Leu	132.1	86.1	50	14
17	Arg	175.2	70.2	90	30
18	Cys	122.1	59.0	40	32
19	Hpro	132.1	86.1	60	20
20	Met	150.1	103.9	60	14
21	Thr	120.1	74.1	40	14
22	Asn	133.1	74.0	60	21
23	Gln	147.0	84.1	60	23
24	Ser	106.0	60.1	60	15

2.3. Preparation of Reference Compound Solution. Stock solutions of individual standards were made by dissolving accurately weighed components in 0.5% formic acid at a concentration of 0.2 mg/mL approximately and stored at 4°C before use. The mixed working solutions of all the standards were diluted with 0.5% formic acid solution to a series of appropriate concentrations immediately before analysis and used to attain the calibration curves.

2.4. Preparation of Sample Solution. Each sample powder was weighed 0.2 g accurately and transferred into a 25 mL stainless tube with 6 stainless beads with a diameter of 0.6 mm. Then, the sample was extracted in a high-throughput tissue-grinding apparatus with vibrating frequency of 70 kHz for 120 s with 15 mL 0.5% formic acid. The sample solution was centrifuged at 15000 rpm for 10 min, and then the supernatant was screened through a 0.22 µm polytetrafluoroethylene membrane filter and stored in a glass bottle at 4°C for later LC-MS/MS analysis.

2.5. Method Validation. For each reference substance, the calibration curve was confirmed by linear regression of the peak area versus concentration. The limits of detection (LOD) and limits of quantification (LOQ) were determined by diluting the standard solution till the signal-to-noise ratios were about 3 and 10, respectively. Precision was determined by intraday and interday variability. The intraday variability was conducted by determining the same standard solution in six replicates on the same day. The interday variability was conducted by determining the same solution for three

consecutive days. The relative standard deviation (RSD) values were calculated to denote the precision. Stability of the sample solution was analysed by peak areas of analytes at 0, 2, 4, 8, 12, and 24 h at room temperature. To evaluate the repeatability of the developed method, the same sample was analysed in six replicates and variations were expressed as RSD. The recovery test was performed to assess the accuracy of the method. For the test, a known amount of the 24 standard components was spiked into a certain amount (0.1 g) of sample. Then, the spiked sample was extracted and analysed as described. The recovery rate was calculated by using the following formula: recovery (%) = (measured amount – original amount)/spiked amount × 100%. Six replicates were performed for the recovery test.

2.6. Data Analysis. The quantitative analyses of acquired data were processed by MultiQuant 3.0.2 (AB SCIEX, USA). Multivariate statistical analysis including PCA and OPLS-DA was used to classify the sample. SIMCA-P 14.1 (Umetrics AB, Sweden) was used to perform statistical analysis for the data of 59 batches of duckweed.

2.7. Analysis of Minerals and Total Proteins. Twenty-four minerals of each environment water where duckweed lived were quantified by ICP-MS. Total nitrogen and phosphorus of the water body were measured according to the alkaline potassium persulfate digestion method GB11894-89 and the ammonium molybdate spectrophotometric method GB11893-89 published by the State Bureau of Technological Supervision of China. Total proteins of each duckweed were determined by the Kjeldahl method. Each sample of duckweeds was hydrolyzed in acidic conditions, and then total amino acids were quantified by the HPLC-MSMS method mentioned above.

3. Results and Discussion

3.1. Optimization of Extraction Procedure. Free amino acids can dissolve in methanol, ethanol, water, diluted acid, and so on. In order to acquire an efficient extraction strategy of amino acids from duckweed, variables of the extraction process were investigated. The solvents (methanol, ethanol, water, 0.1% formic acid, and 0.5% formic acid), methods (heating reflux, ultrasonication, and tissue-grinding), and time (20, 30, and 40 min for ultrasonication; 60, 90, and 120 s for tissue-grinding) were studied. The results showed that the amount of amino acids had no significant difference between the ultrasonication time of 30 min in 0.5% formic acid and tissue-grinding time of 120 s in 0.5% formic acid. The amounts of extraction by other methods were not more than that by these two modalities. From the viewpoint of working efficiency, the tissue-grinding method was much more time-saving than the ultrasonication method by the extracting time of 120 s versus 30 min.

3.2. Optimization of UPLC Condition. Chromatographic conditions were optimized to attain a satisfactory separation for amino acid especially for isomeric molecules. Columns

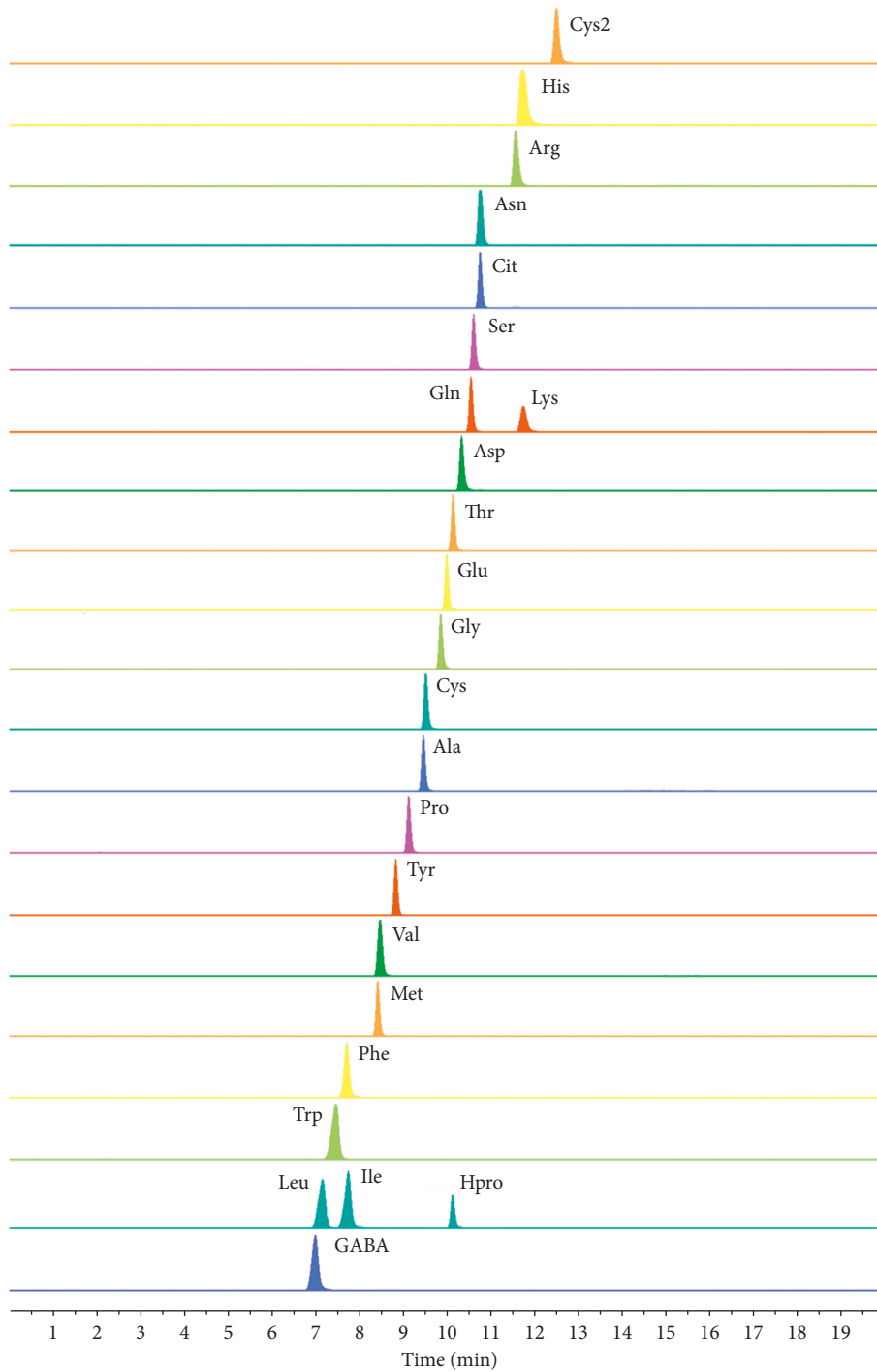


FIGURE 1: Typical MRM chromatograms of the 24 amino acids.

(Waters XBridge Amide, $2.5\ \mu\text{m}$, $2.1 \times 150\ \text{mm}$ and Agilent Poroshell 120 HILIC, $2.7\ \mu\text{m}$, $2.1 \times 150\ \text{mm}$), column temperature (20, 25, 30, 35, and 40°C), mobile phase (acetonitrile-0.1% formic acid, acetonitrile-0.2% formic acid, acetonitrile with 0.2% formic acid-0.2% formic acid, and acetonitrile-10 mM ammonium formate with 0.2% formic acid), and different kinds of gradient elution were investigated.

The results demonstrated that the peak shape of amino acids became good when the concentration of

formic acid rose, but retention time would be shortened significantly especially if some formic acid was complemented into the acetonitrile. The buffers such as ammonium formate increased the resolution degrees of amino acids. Better retention times and separations were observed by conducting analysis on Waters Amide column than on Agilent Poroshell 120 HILIC column, and the best chromatograms were gained with temperature controlled at 20°C . Especially for the isomers of leucine and isoleucine, baseline separation was

TABLE 3: Calibration curves, LODs, and LOQs for the 24 compounds.

Number	Compound	Calibration curve	R^2	Linear range (ng/mL)	LOQ (ng/mL)	LOD (ng/mL)
1	Tyr	$y = 6534.1x + 6063.4$	0.9984	1.16–5780	0.92	0.46
2	Ala	$y = 7168.9x + 4932.8$	0.9969	5.30–5300	3.71	1.24
3	Glu	$y = 12796x + 47334$	0.9960	6.41–2564	4.49	1.50
4	Phe	$y = 59157x + 42917$	0.9965	0.99–992.0	0.79	0.40
5	His	$y = 20263x + 247917$	0.9962	5.57–5570	3.90	1.30
6	Ile	$y = 70857x + 46587$	0.9957	1.07–1074	0.86	0.43
7	Asp	$y = 7084.7x + 86152$	0.9963	5.43–5430	3.80	1.27
8	Lys	$y = 4305.1x + 17648$	0.9980	5.53–5530	3.87	1.94
9	Gly	$y = 1063.0x + 3407.3$	0.9990	0.94–4680	0.75	0.37
10	Val	$y = 31972x + 35728$	0.9962	1.11–1112	0.89	0.44
11	Cit	$y = 8520.8x + 9811.0$	0.9980	1.01–5070	0.81	0.41
12	GABA	$y = 18495x + 14623$	0.9981	1.10–5490	0.88	0.44
13	Cys2	$y = 2389.7x + 3146.6$	0.9978	1.09–5440	0.87	0.44
14	Pro	$y = 51204x + 58539$	0.9981	1.02–510.0	0.82	0.41
15	Trp	$y = 19030x + 4465.3$	0.9977	1.24–2476	0.99	0.50
16	Leu	$y = 56715x + 40047$	0.9974	1.01–1012	0.81	0.40
17	Arg	$y = 11505x + 84828$	0.9974	5.96–5960	4.17	1.39
18	Cys	$y = 2496.6x + 1017.5$	0.9988	1.20–6012	0.96	0.48
19	Hpro	$y = 15783x + 3968.1$	0.9977	0.95–1892	0.76	0.38
20	Met	$y = 8626.4x + 1545.9$	0.9984	1.05–5250	0.84	0.42
21	Thr	$y = 8807.8x + 19073$	0.9957	4.46–4460	3.12	1.56
22	Asn	$y = 4939.9x + 22367$	0.9967	1.20–5980	0.96	0.48
23	Gln	$y = 7733.9x + 8338.4$	0.9961	0.93–4650	0.74	0.37
24	Ser	$y = 7731.3x + 54859$	0.9977	5.09–5090	3.56	1.19

TABLE 4: Precision, stability, repeatability, and accuracy of the investigated analytes ($n = 6$).

Number	Compound	Precision		Stability RSD (%)	Repeatability RSD (%)	Accuracy	
		Intraday RSD (%)	Interday RSD (%)			Recovery (%)	RSD (%)
1	Tyr	1.36	1.85	0.94	3.05	98.56	1.33
2	Ala	2.60	3.31	3.47	3.09	102.49	2.18
3	Glu	2.07	2.56	2.10	2.11	106.94	3.76
4	Phe	0.66	1.03	2.60	1.66	97.23	4.03
5	His	1.07	3.30	1.58	1.17	98.32	2.20
6	Ile	0.97	3.21	3.82	0.71	99.09	3.57
7	Asp	1.96	3.98	2.42	1.84	97.86	2.36
8	Lys	2.70	3.51	1.44	0.99	102.30	3.02
9	Gly	1.66	2.65	3.43	3.74	104.48	3.07
10	Val	2.42	2.89	3.30	0.83	107.51	1.52
11	Cit	1.47	1.88	3.12	3.86	99.14	2.21
12	GABA	3.14	2.32	2.27	0.82	102.54	3.41
13	Cys2	2.53	4.27	3.24	1.49	96.60	1.27
14	Pro	1.21	3.39	1.09	2.09	101.94	3.20
15	Trp	0.37	3.93	1.36	1.39	99.11	3.46
16	Leu	1.50	3.90	3.40	1.50	95.27	3.61
17	Arg	2.72	4.15	3.72	1.45	102.37	1.79
18	Cys	2.82	3.63	1.16	0.53	103.65	3.82
19	Hpro	3.05	2.23	0.87	2.38	97.55	3.91
20	Met	1.57	3.02	1.26	0.52	104.89	2.14
21	Thr	2.11	2.13	1.77	3.01	95.97	3.00
22	Asn	2.93	2.85	1.48	3.68	105.35	2.95
23	Gln	0.97	1.87	1.22	2.72	102.33	2.16
24	Ser	2.71	2.86	0.98	1.48	97.44	1.88

successfully achieved when using the mobile phase consisting of acetonitrile-10 mM ammonium formate with 0.2% formic acid. Under other abovementioned conditions, these two isomeric amino acids were not well separated reciprocally.

3.3. Optimization of MS/MS Conditions. Primary experiments were conducted to acquire the best mass spectrometry conditions of amino acids individually. For this purpose, each reference component of amino acids with the concentration of approximate 100 ng/mL was delivered into the

TABLE 5: Continued.

Sample	Hpro			Met			Thr			Asn			Gln			Ser			Total free amino acids	Total proteins (%)
	Free	Total	Ratio	Free	Total	Ratio	Free	Total	Ratio	Free	Total	Ratio	Free	Total	Ratio	Free	Total	Ratio		
LP9	2.85	15395.17	0.0185	1.09	2611.93	0.0417	95.31	6079.19	1.5678	135.68	5800.10	2.3393	21.02	2847.50	0.7382	160.76	6714.80	2.3941	1620.64	20.09
LP10	3.15	12510.19	0.0252	0.19	2294.16	0.0083	139.99	5986.95	2.3388	316.13	4149.54	7.6184	20.34	2755.14	0.7383	126.41	9249.73	1.3666	1408.67	18.88
LP11	2.02	11304.83	0.0179	0.44	1616.02	0.0272	92.06	7087.95	1.2988	100.62	3134.85	3.2097	9.67	2255.64	0.4287	81.26	7479.28	1.0865	735.57	14.11
LP12	1.26	11500.95	0.0110	0.34	1721.63	0.0197	24.77	6419.44	0.3859	25.52	4463.29	0.5718	3.93	2645.29	0.1486	15.06	7598.99	0.1982	291.40	16.46
LP13	6.41	13163.18	0.0487	0.30	2716.29	0.0110	172.44	9432.07	1.8282	143.41	4225.29	3.3941	134.72	2932.22	4.5945	169.75	8497.59	1.9976	1667.79	19.79
LP14	3.64	16225.57	0.0224	0.17	2793.92	0.0061	175.47	6457.65	2.7172	140.65	5052.79	2.7836	118.28	3874.56	3.0527	171.21	9352.55	1.8306	1529.56	21.15
LP15	1.70	11614.17	0.0146	0.09	2501.01	0.0036	89.92	6615.18	1.3593	269.56	3725.94	7.2347	3.34	2877.91	0.1161	82.11	8616.92	0.9529	900.44	18.46
LP16	0.94	11631.20	0.0081	0.99	1651.61	0.0599	95.46	5189.08	1.8396	201.46	3964.71	5.0813	106.74	2083.97	5.1220	89.52	5649.83	1.5845	1381.04	15.81
LA1	0.75	10525.37	0.0071	0.33	1722.41	0.0192	119.80	5747.08	2.0845	146.08	4354.39	3.3548	117.79	2828.86	4.1639	99.93	8354.17	1.1962	1262.44	15.27
LA2	0.71	11050.46	0.0064	2.14	2075.76	0.1031	88.95	5755.14	1.5456	114.22	4714.20	2.4229	113.30	2590.48	4.3737	128.49	8446.54	1.5212	1057.50	16.42
LA3	1.58	14292.88	0.0111	—	2387.79	—	85.96	9803.09	0.8769	129.12	5651.48	2.2847	172.44	2107.17	8.1835	147.16	11408.14	1.2900	1716.54	20.72
LA4	0.78	11457.33	0.0068	—	2109.40	—	75.39	7598.12	0.9922	177.20	4225.71	4.1934	34.18	2341.13	1.4600	45.77	7073.90	0.6470	778.32	15.58
LA5	6.18	11098.92	0.0557	0.60	1527.50	0.0393	127.09	6426.35	1.9776	196.17	4798.09	4.0885	29.66	2500.29	1.1863	66.00	7750.15	0.8516	1332.28	16.58
LA6	1.69	11256.40	0.0150	0.14	1485.02	0.0094	92.57	6651.83	1.3916	129.99	4328.83	3.0029	86.79	1722.57	5.0384	157.13	8406.98	1.8690	1547.66	16.04
LA7	2.07	11307.16	0.0183	—	1577.93	—	92.43	4656.66	1.9849	145.34	4362.67	3.3314	135.71	1877.25	7.2292	170.21	8033.47	2.1188	1517.92	14.71
LA8	10.79	15918.39	0.0678	0.19	2259.56	0.0084	117.78	7883.83	1.4939	154.15	5792.38	2.6613	216.67	2621.75	8.2643	61.37	7941.33	0.7728	1171.00	21.30
LA9	0.76	14178.74	0.0054	0.14	2618.77	0.0053	6.51	6538.81	0.0996	7.87	4624.51	0.1702	2.68	2321.32	0.1155	6.76	10561.97	0.0640	189.02	21.46
LA10	1.44	11088.93	0.0130	0.26	1806.72	0.0144	62.25	6942.43	0.8967	53.97	4802.60	1.1238	47.46	2041.76	2.3245	36.17	5403.37	0.6694	775.54	16.41
LA11	0.84	15220.71	0.0055	1.65	2528.91	0.0652	8.60	7038.75	0.1222	1.31	5236.37	0.0250	4.91	2429.40	0.2021	7.80	6092.24	0.1280	289.21	19.05
LA12	2.55	9164.65	0.0278	0.18	1894.44	0.0095	174.89	4404.00	3.9712	138.27	3675.47	3.7620	72.48	1770.28	4.0943	85.28	5128.63	1.6628	1294.14	14.54
LA13	2.16	13906.13	0.0155	—	2514.70	—	116.52	7070.17	1.6481	294.15	3964.62	7.4194	42.77	2727.93	1.5679	65.75	7050.95	0.9325	1282.38	18.31
LA14	9.08	13760.74	0.0660	0.60	2297.56	0.0261	164.90	9014.10	1.8294	131.85	5045.39	2.6133	63.90	2704.59	2.3627	144.27	5601.90	2.5754	1371.90	17.81
LA15	3.69	8467.71	0.0436	0.30	1826.09	0.0164	135.18	5450.03	2.4804	62.94	3497.92	1.7994	46.02	1747.54	2.6334	51.56	4656.58	1.1073	1020.37	13.89
LA16	2.78	16217.53	0.0171	0.29	2603.75	0.0111	97.73	8455.20	1.1559	22.61	5055.17	0.4473	18.70	2206.25	0.8476	48.71	9026.29	0.5396	811.03	20.42
LA17	0.68	12202.21	0.0056	2.23	2011.22	0.1109	81.41	5966.49	1.3645	207.86	3770.32	5.5131	55.84	3327.23	1.6783	76.89	7660.33	1.0037	1027.14	18.44
LA18	0.55	9875.86	0.0056	2.42	1754.15	0.1380	76.82	5468.75	1.4047	143.75	3704.63	3.8803	52.67	1760.52	2.9917	90.61	6192.83	1.4631	1068.96	14.93

—, analytes were not detected.

TABLE 6: Contents of 26 minerals in living water of three species of duckweed ($\mu\text{g/L}$).

Sample	Ti	V	Cr	Mn	Co	Ni	Cu	Zn	As	Se	Sr	Mo	Cd	Sn	Sb	Ba	Tl	Pb
SP1	22.831	2.900	2.178	47.015	0.181	1.860	1.061	90.405	1.530	1.578	261.614	2.840	0.007	0.087	0.440	96.840	0.003	0.058
SP2	27.277	1.017	2.922	36.990	0.177	1.648	0.806	80.395	2.091	1.288	199.006	3.275	0.006	0.007	0.516	60.613	0.003	0.001
SP3	35.621	1.915	1.838	41.295	0.162	2.899	1.500	56.437	1.127	1.983	172.960	3.017	0.016	0.168	0.386	70.196	0.002	0.024
SP4	22.183	3.099	1.687	55.683	0.214	1.767	1.690	63.717	3.164	1.935	178.985	0.407	0.014	0.168	0.487	77.659	0.001	0.041
SP5	45.839	3.162	1.413	24.431	0.189	2.829	0.615	71.741	0.920	1.861	275.418	2.211	0.011	0.098	0.542	63.126	0.004	0.074
SP6	41.446	1.783	2.371	2.110	0.240	2.157	2.805	87.665	2.146	1.464	193.120	0.577	0.002	0.121	0.536	39.704	0.004	0.046
SP7	37.099	2.423	2.068	13.993	0.219	2.583	1.424	88.936	2.601	1.747	165.967	1.562	0.010	0.095	0.316	69.916	0.003	0.050
SP8	28.377	2.251	2.276	54.028	0.197	1.709	2.941	46.581	2.262	2.139	249.180	2.345	0.015	0.125	0.359	110.809	0.004	0.047
SP9	17.084	1.069	2.452	40.559	0.192	3.140	1.247	29.974	2.770	1.664	163.694	2.659	0.015	0.139	0.637	60.895	0.004	0.018
SP10	37.166	3.316	1.705	35.254	0.184	1.793	2.040	78.451	1.247	1.407	174.872	0.632	0.002	0.137	0.720	86.360	—	0.003
SP11	24.163	1.033	1.368	60.738	0.190	3.261	2.894	66.981	1.135	2.291	207.084	1.840	0.003	0.160	0.488	117.603	0.004	0.046
SP12	38.630	2.597	1.146	53.768	0.252	2.550	1.505	76.263	1.772	2.126	180.679	0.626	0.003	0.124	0.628	142.280	0.001	0.062
SP13	39.728	2.347	1.577	26.733	0.173	3.173	2.882	75.098	1.628	1.112	225.261	0.323	0.012	0.106	0.550	95.230	0.001	0.001
SP14	39.483	2.488	2.539	3.742	0.249	2.137	1.427	55.271	1.670	1.581	154.375	3.214	0.019	0.135	0.338	119.138	0.003	0.043
SP15	19.629	2.734	2.326	22.405	0.198	3.153	1.427	55.631	1.175	2.065	247.855	2.928	0.011	0.011	0.633	136.536	0.004	0.030
SP16	34.619	1.068	2.064	52.250	0.163	2.169	3.017	54.488	3.221	1.985	253.553	2.155	0.002	0.120	0.377	68.487	0.001	0.022
SP17	28.672	3.244	2.192	31.414	0.159	1.880	2.871	91.946	1.444	1.287	175.165	1.721	0.018	0.138	0.669	91.883	0.004	0.030
SP18	25.018	1.789	2.378	45.984	0.183	2.570	2.365	24.786	1.877	2.146	194.164	3.450	0.007	0.049	0.318	95.469	0.002	0.057
SP19	22.802	2.136	2.199	53.284	0.212	2.704	1.054	85.613	0.913	2.073	269.684	3.174	0.014	0.043	0.423	111.149	0.003	0.004
SP20	40.638	1.682	1.746	14.621	0.180	1.611	2.705	73.740	3.221	2.055	225.646	3.023	0.013	0.159	0.450	137.841	0.004	0.019
SP21	23.513	1.413	2.811	12.908	0.236	1.959	0.607	22.616	2.711	1.170	227.681	3.187	0.005	0.037	0.205	62.615	0.003	0.016
SP22	32.010	1.755	2.461	56.750	0.202	2.515	1.114	80.116	1.210	2.322	223.754	1.075	0.015	0.155	0.573	96.469	0.002	0.012
SP23	17.817	2.259	2.391	43.452	0.219	1.903	0.700	88.007	3.277	1.855	155.450	2.793	0.014	0.164	0.311	82.020	0.002	0.010
SP24	24.306	2.384	1.841	32.935	0.253	1.896	3.027	63.243	1.975	1.109	214.325	2.979	0.008	0.044	0.642	47.431	0.003	0.061
SP25	30.842	2.878	1.693	29.377	0.254	2.786	1.811	69.276	1.082	1.349	218.438	0.896	0.011	0.125	0.474	126.036	0.001	0.032
LP1	37.974	1.441	2.756	42.898	0.251	1.828	2.325	46.010	2.655	2.264	162.610	0.298	0.004	0.049	0.368	106.287	0.002	0.055
LP2	25.601	3.144	1.914	10.035	0.173	2.425	2.422	53.173	1.031	1.740	211.860	0.256	0.017	0.153	0.596	73.995	0.002	0.001
LP3	40.576	2.424	1.579	36.158	0.203	2.635	1.373	32.781	1.839	1.363	234.793	1.450	0.001	0.145	0.697	107.956	0.001	0.032
LP4	29.919	1.451	2.468	31.060	0.239	3.221	2.253	43.918	2.873	1.754	193.086	2.154	0.013	0.027	0.249	36.637	0.001	0.015
LP5	43.240	2.466	2.331	46.991	0.209	3.218	1.577	26.153	1.994	2.211	234.265	1.895	0.010	0.017	0.224	84.449	0.004	0.006
LP6	29.925	2.796	2.933	11.764	0.248	2.974	2.174	43.896	2.394	1.784	247.178	3.487	0.012	0.017	0.336	125.785	0.003	0.016
LP7	28.783	1.090	2.067	41.129	0.244	2.388	1.514	76.640	1.923	1.886	157.760	2.486	0.003	0.031	0.241	87.240	0.004	0.053
LP8	45.076	3.030	1.857	7.724	0.247	2.328	2.152	87.415	2.455	2.044	225.691	2.976	0.011	0.009	0.607	111.718	0.003	0.023
LP9	20.651	2.339	2.731	42.403	0.257	1.681	1.012	89.960	1.066	1.855	210.521	2.237	0.007	0.052	0.424	32.520	—	0.033
LP10	23.769	1.646	1.288	52.927	0.243	2.319	2.950	93.752	2.929	1.882	217.655	2.496	0.017	0.165	0.196	135.624	0.003	0.051
LP11	32.364	2.560	3.084	33.335	0.208	3.219	2.180	82.812	1.451	1.918	269.769	3.250	0.019	0.008	0.406	66.278	0.003	0.051
LP12	24.918	1.470	2.999	37.041	0.243	1.893	1.928	95.305	2.415	1.698	224.103	1.906	0.008	0.041	0.570	64.033	0.004	0.008
LP13	33.468	1.704	2.451	45.575	0.176	2.507	1.882	38.837	2.524	1.580	187.087	1.245	0.003	0.133	0.285	44.075	0.003	0.030
LP14	28.614	2.426	1.879	39.614	0.209	3.272	1.963	74.622	2.875	1.962	261.572	2.514	0.013	0.136	0.287	100.138	0.002	0.048
LP15	35.617	2.088	2.116	42.214	0.162	2.284	1.641	39.037	1.412	1.185	244.588	0.489	0.007	0.158	0.512	110.953	0.003	0.032
LP16	32.522	2.845	1.545	41.087	0.186	2.100	1.860	94.105	3.060	1.921	165.053	1.398	0.015	0.008	0.451	69.796	0.002	0.066
LA1	36.451	2.711	1.271	38.156	0.233	2.893	0.909	65.183	3.041	1.926	194.455	3.342	0.005	0.055	0.262	51.502	0.002	0.023
LA2	43.394	2.188	2.067	17.427	0.165	2.206	1.564	58.425	3.159	1.247	254.469	1.789	0.006	0.146	0.280	33.628	0.003	0.052
LA3	24.311	1.120	2.917	35.712	0.247	2.359	2.087	59.228	3.345	2.092	247.432	1.778	0.010	0.108	0.362	105.945	—	0.069

TABLE 6: Continued.

Sample	Ti	V	Cr	Mn	Co	Ni	Cu	Zn	As	Se	Sr	Mo	Cd	Sn	Sb	Ba	Tl	Pb	
LA4	26.794	1.110	1.710	13.192	0.232	1.909	1.963	25.002	3.351	1.618	198.614	1.801	—	0.011	0.452	33.107	0.003	0.024	
LA5	39.248	2.722	1.585	24.608	0.203	2.755	2.186	68.836	1.896	1.634	279.990	3.413	0.016	0.037	0.213	37.247	0.004	0.077	
LA6	20.981	2.024	1.392	25.368	0.248	2.878	2.542	45.526	1.863	1.095	215.126	3.019	0.009	0.148	0.651	117.017	0.003	0.010	
LA7	30.279	1.148	2.330	62.335	0.231	2.772	2.791	44.135	2.816	1.556	187.777	3.290	0.012	0.151	0.436	36.940	0.003	0.041	
LA8	39.053	0.971	3.084	15.630	0.243	3.097	1.738	42.571	2.567	1.411	231.825	2.281	0.010	0.013	0.499	33.670	0.003	0.053	
LA9	41.198	2.925	2.254	52.257	0.230	2.490	2.132	95.196	2.872	2.220	170.239	1.302	0.002	0.132	0.395	80.576	0.003	0.015	
LA10	16.833	1.384	2.832	34.567	0.188	2.044	1.951	62.570	0.922	1.571	169.715	0.952	0.001	0.110	0.496	81.418	0.002	0.044	
LA11	38.564	2.900	3.171	30.344	0.257	2.860	2.083	37.280	1.155	1.073	172.207	1.959	0.008	0.117	0.433	108.524	0.002	0.014	
LA12	43.364	1.975	2.442	7.660	0.253	1.986	0.775	85.359	2.247	1.143	237.191	0.673	0.009	0.155	0.201	41.025	—	0.002	
LA13	30.181	3.229	1.146	53.644	0.230	2.341	2.091	77.183	0.842	2.028	177.614	2.395	0.009	0.105	0.689	97.023	0.001	0.022	
LA14	31.940	3.492	1.508	64.537	0.181	2.947	2.883	24.336	3.049	2.137	243.782	1.989	0.017	0.117	0.272	125.192	0.003	0.021	
LA15	22.170	2.327	3.077	51.812	0.175	3.050	0.998	60.176	2.860	1.716	206.597	0.281	0.006	0.058	0.397	108.215	—	0.025	
LA16	42.638	1.570	1.978	49.228	0.258	1.959	0.924	88.563	2.498	1.683	201.422	3.242	0.014	0.029	0.295	80.373	0.003	0.075	
LA17	39.670	1.249	2.650	27.755	0.259	2.112	2.250	55.219	2.830	1.217	154.053	1.978	0.006	0.099	0.561	116.452	—	0.047	
LA18	23.423	2.528	2.932	10.179	0.199	2.743	2.953	66.269	3.199	1.527	209.326	3.075	0.016	0.116	0.306	79.441	0.001	0.040	
Sample	Na	Mg	Al	Ca			Fe	N	P	Total									
SP1	410579.062	209771.718	18661.431	178472.536	591631.101	334974.476	4.303	0.914	1744628.970										
SP2	546214.809	232797.639	9209.284	416708.514	386703.829	349989.801	2.389	0.675	1942044.979										
SP3	384732.341	302374.639	16864.219	351597.651	645593.344	330485.336	18.804	5.589	2032063.470										
SP4	763978.060	217006.139	24174.116	515345.319	525036.011	165789.077	19.687	4.182	2211765.493										
SP5	498927.575	304758.187	29743.190	617594.946	663524.773	200323.584	25.750	23.839	2315416.327										
SP6	568688.625	219822.814	31062.346	305039.982	486491.766	202085.631	25.562	22.681	1813617.704										
SP7	815621.400	203217.299	32660.784	559562.408	566642.730	171755.702	2.565	1.507	2349855.405										
SP8	704283.730	188285.004	23602.584	315772.349	624642.806	439955.497	23.372	6.689	2297077.677										
SP9	876213.262	151574.474	27629.879	516294.381	409003.501	35506.241	18.458	4.258	2016572.669										
SP10	873643.979	294027.085	21164.307	737471.818	383002.078	37324.576	33.550	19.033	2347111.719										
SP11	491391.823	256934.016	10147.423	610308.309	636084.667	367347.644	31.694	25.205	2372762.062										
SP12	796497.255	269227.175	17999.811	414658.818	512138.780	171064.616	16.646	2.703	2182110.814										
SP13	366808.463	156147.673	11576.232	471660.374	756208.109	347515.518	11.647	4.202	2110408.155										
SP14	512150.165	243500.636	31493.169	641312.090	499270.353	208734.109	11.077	1.602	2136861.051										
SP15	533557.790	280721.134	16614.646	267728.355	378226.451	306162.902	13.593	4.564	1783528.184										
SP16	644403.624	276057.049	21110.856	521532.157	583524.045	59176.189	11.942	25.264	2106319.987										
SP17	751229.025	173163.933	10495.020	625004.125	472688.229	345116.023	8.458	5.204	2378144.753										
SP18	522140.520	176639.957	29371.612	557932.109	690911.336	157124.877	29.906	10.221	2134563.150										
SP19	579415.759	238453.094	30677.565	439717.245	686006.551	382672.972	10.823	3.662	2357515.153										
SP20	476281.317	182915.790	9070.049	325811.742	373586.252	432553.750	34.616	21.891	1800784.763										
SP21	760676.992	188574.381	12126.295	619462.993	550226.213	88795.927	20.170	9.877	2218626.941										
SP22	709408.940	239417.173	10783.138	51694.267	732144.084	326876.462	34.159	26.699	2164823.520										
SP23	513303.754	213899.504	26441.948	351694.267	679154.325	297001.594	14.031	10.796	2788075.528										
SP24	824465.276	238490.190	31283.397	717257.458	508251.297	371174.761	24.650	2.494	2478087.325										
SP25	815267.536	215764.623	30718.721	536395.881	696960.175	327232.239	17.263	7.080	2699502.116										
LP1	897950.747	158686.979	27871.364	590366.194	648189.841	273059.464	15.536	1.239	2333208.859										
LP2	531566.916	294929.433	14640.021	570417.870	648189.841	273059.464	15.536	1.239	2333208.859										

TABLE 6: Continued.

Sample	Na	Mg	Al	K	Ca	Fe	N	P	Total
LP3	858626.936	266231.149	32272.481	727712.714	480257.660	348345.090	12.319	1.894	2713926.251
LP4	431098.253	221743.162	34467.794	311381.975	785570.359	339960.811	26.584	17.225	2124617.501
LP5	818404.736	237360.411	25820.309	683695.992	566015.946	406722.563	20.219	7.521	2738498.958
LP6	614726.783	203772.151	23626.598	170198.351	715325.262	132978.487	8.402	1.447	1861115.202
LP7	498622.492	200069.361	34249.218	182114.487	450498.128	213156.897	26.337	12.664	1579155.065
LP8	407734.217	308322.609	12414.630	462642.984	726996.054	273473.025	23.952	9.428	2192112.264
LP9	591923.425	196758.141	20795.603	169080.807	379447.395	244832.850	24.638	15.719	1603288.325
LP10	506188.280	278745.249	26183.977	548614.526	619327.368	71487.282	27.250	10.475	2051124.319
LP11	484360.416	252740.828	27267.497	394747.762	420528.173	411590.345	15.427	3.462	1991756.825
LP12	755545.368	290158.455	18713.693	269669.218	653034.467	303936.794	26.120	0.889	2291545.587
LP13	644431.270	171083.444	14922.153	701260.007	799614.153	241821.499	27.383	10.915	2573534.387
LP14	855511.785	226105.300	11812.507	382201.190	657443.790	421778.147	4.108	0.257	2553378.850
LP15	840333.425	261183.216	19461.126	468066.062	568653.040	96502.984	17.469	12.422	2254714.244
LP16	662138.232	247763.574	23217.103	653430.420	481555.835	52632.672	16.297	0.242	2121172.397
LA1	542867.038	291631.774	16101.327	208393.119	534546.718	287585.245	20.487	11.217	1881559.346
LA2	768502.457	174767.313	34293.763	538598.282	767009.154	130620.652	24.093	8.098	2414246.025
LA3	836100.485	232547.859	8383.317	197659.044	475008.913	70420.274	26.668	18.771	1820654.452
LA4	554969.006	231606.445	11451.728	365538.304	505163.079	269818.459	11.932	3.908	1938873.753
LA5	794677.014	293809.893	30832.050	293530.490	510493.154	262663.280	12.498	6.307	2186491.358
LA6	704360.729	287183.610	31019.483	189142.179	384371.287	327789.933	12.239	4.852	1924324.212
LA7	894339.623	204701.453	27985.214	281212.437	595254.900	371594.312	24.934	18.350	2375510.268
LA8	427283.433	184599.086	23700.009	211637.098	596714.072	325251.967	22.097	1.616	1769588.097
LA9	879491.821	180076.383	12682.543	611024.725	416252.729	426535.290	22.887	10.851	2526553.669
LA10	712373.467	297199.560	9966.649	218385.532	678770.388	129164.596	32.940	4.216	2046274.948
LA11	625486.302	275066.946	25810.603	496586.040	470812.328	438093.869	14.927	1.233	2332275.197
LA12	796469.226	199565.531	26532.869	616737.846	538184.180	286481.065	25.413	16.087	2464438.679
LA13	587462.535	234893.095	16533.152	573600.610	441381.833	215218.753	5.375	3.154	2069549.281
LA14	598797.362	200101.308	32285.037	179408.885	737688.278	321911.868	10.937	7.808	2070719.888
LA15	775176.535	182419.544	9875.652	375172.731	686178.073	146549.529	20.767	18.862	2175875.636
LA16	486462.514	269482.486	19514.461	382028.835	385846.710	419515.606	25.566	4.690	1963357.619
LA17	397975.248	220647.104	20225.722	404790.872	406870.509	69049.196	25.782	16.448	1520009.288
LA18	852308.317	145491.528	11612.476	499143.838	570244.949	84828.689	23.929	16.569	2164078.568

—, analytes were not detected.

mass spectrometer directly via a syringe pump with the velocity of 7 $\mu\text{L}/\text{min}$. While tuning the standard dissolved in water, most response of amino acids was very low when the sodium-adducted ion, $[\text{M}+\text{Na}]^+$, was relatively high. On the contrary, when dissolving the standard in 0.1% or higher concentration of formic acid solution, the response of protonated molecule, $[\text{M}+\text{H}]^+$, was dramatically higher and the metal-adducted ion was barely observed. Consequently, precursor ion (Q1), product ion (Q3), declustering potential (DP), and collision energy (CE) of each amino acid were acquired and optimized.

3.4. Method Validation. As shown in Table 3, the calibration curves of twenty-four amino acids showed good linear regression (all correlation coefficients > 0.995) within a wide range of concentration. The LOD and LOQ of each analyte with the signal-to-noise ratio (S/N) of 3 and 10 were in the range of 0.37–1.94 ng/mL and 0.74–4.49 ng/mL, respectively. The RSD values of intraday and interday precision are summarized in Table 4. From the results, the present method was found to be precise with intraday variability less than 3.14% and interday variability less than 4.27%. The sample solutions were stable within 24 h with stability RSD < 3.82%. The RSD values of repeatability were 0.52%–3.86%. The recoveries of 24 amino acids ranged from 95.27%–107.51% with RSD < 4.03%.

3.5. Quantitative Analysis for Samples. The developed UPLC-MS/MS method was applied for simultaneous determination of 24 free amino acids in 59 batches of three species of duckweed. All the contents are displayed in Table 5. The results showed that the total amount of amino acids varied dramatically among each sample from different regions and species. Total content of AAs in SP25 from Baoding City of Hebei Province reached as high as 1899.50 $\mu\text{g}/\text{g}$, which was much more than that in SP17 of 166.05 $\mu\text{g}/\text{g}$ from Lianyungang City of Jiangsu Province. For each amino acid, the content also varied significantly even in the same sample. Coincidentally, the contents of free amino acids that include sulfur in their molecules were much less than others, including cysteine, cystine, and methionine with the concentration of 0.24, 4.25, and 4.20 $\mu\text{g}/\text{g}$ in maximum, respectively. Especially for cysteine, it was not found in all of *Spirodela polyrrhiza* and only detected in several samples of other two species. The putative reason was that the thiol in cysteine was not stable and easily oxidized. But in general, there was no significant difference observed in the total content of all FAAs among different species.

Twenty-six minerals, total proteins, and the content of amino acids after hydrolysis are shown in Tables 5 and 6. From the tables, it could be found that the total protein contents in 59 samples ranged from 13.61% to 21.46%. The relative contents of amino acids such as Lys, Ala, Ser, Thr, GABA, Gln, and Asn were all a little higher than other components based on the average value of each species among three different varieties of duckweed. The contents of Cys, Cys2, and Met were higher after hydrolysis. Obviously, it could be seen that the contents of free amino acids in duckweed were much lower than that of protein-bound

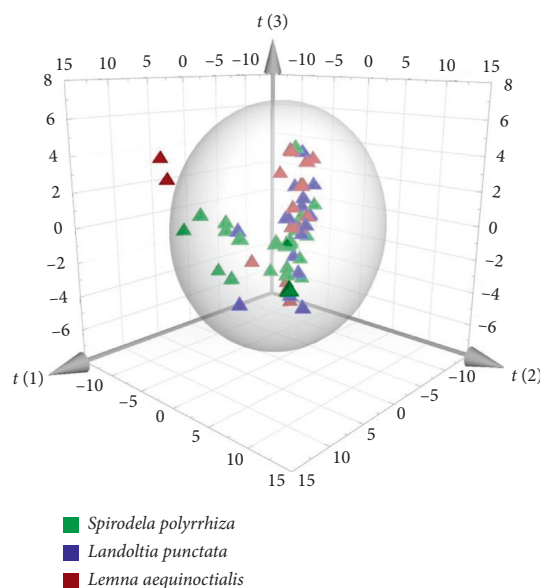


FIGURE 2: Three-dimensional score plot of principle component analysis (PCA) based on the content of free amino acids.

amino acids. Moreover, the data showed that the contents of free amino acids in duckweed were negatively correlated with binding amino acids.

The elements with higher content in the samples were sodium, calcium, potassium, iron, magnesium, and aluminum. Their concentration ranges were 366808.463–897950.747, 373586.252–799614.153, 169080.807–737471.818, 35506.241–439955.497, 145491.528–308322.609, and 8383.317–34467.794 $\mu\text{g}/\text{L}$, respectively. The concentration ranges of strontium, barium, zinc, manganese and titanium were 154.053–279.990, 32.520–142.280, 22.616–95.305, 2.110–64.537, 16.833–45.839 $\mu\text{g}/\text{L}$. The concentrations of vanadium, chromium, cobalt, nickel, copper, arsenic, selenium, molybdenum, cadmium, tin, antimony, thallium, and lead are very low. It ranged from 0.0 to 3.492 $\mu\text{g}/\text{L}$. Evidently, the contents of macroelements in the samples were higher while they contained much lower trace elements.

3.6. Statistical Analysis. As one of the most important multivariate analysis techniques, PCA was employed to evaluate the variation among three species of duckweed. PCA is an unsupervised pattern recognition method without prior information of the data set and retained maximum variance of multidimensional data while reducing its dimensionality into two- or three-dimension [29–31]. Furthermore, all of the data information about amino acids was subjected to a supervised method, OPLS-DA [32], to get more information about different duckweeds. All the raw data were processed by normalization and Pareto scaling (Par) before modeling. Three dimensions were established in both the PCA and OPLS-DA models based on the content of free amino acids and the ratio of free to total amino acids with R2X (cum) value of 0.628, 0.596 and 0.758, 0.676, respectively. As shown in Figures 2–5, both PCA and OPLS-DA methods demonstrated that *Spirodela polyrrhiza*,

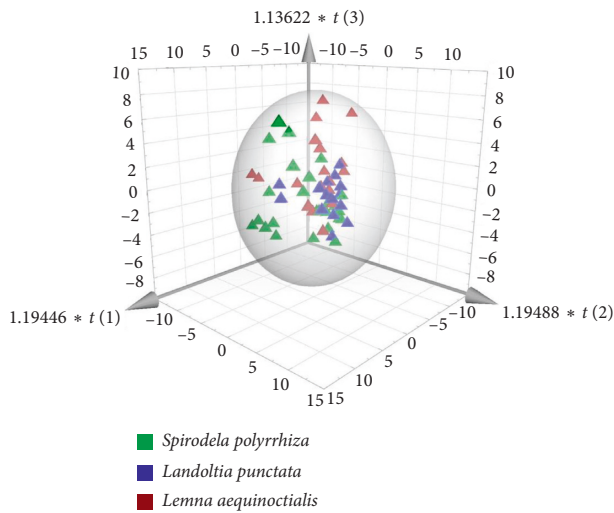


FIGURE 3: Three-dimensional score plot of orthogonal partial least square-discriminant analysis (OPLS-DA) based on the content of free amino acids.

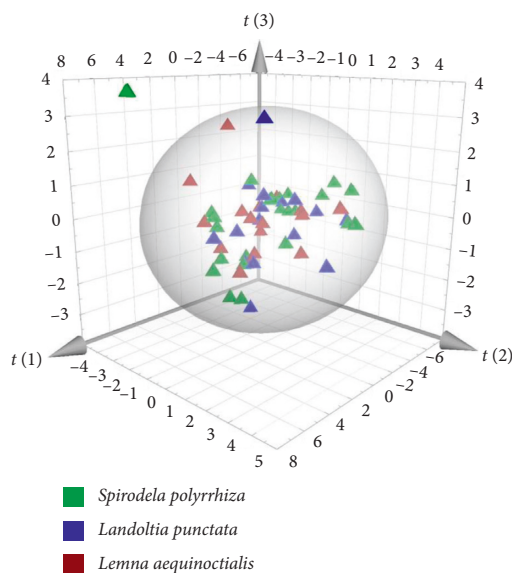


FIGURE 4: Three-dimensional score plot of principle component analysis (PCA) based on the ratio of free to total amino acids.

Landoltia punctata, and *Lemna aequinoctialis* were clustered together with each other in the score plot. There was no remarkable difference in different duckweeds.

4. Conclusions

In this study, a simple, fast, and convenient method with UPLC-QTRAP-MS/MS was established for the identification and quantification control of duckweeds by HILIC separation without derivatization. The results of method validation suggested that the developed method was sensitive, accurate, and precise for determination of 24 free amino acids. 59 batches of sample in three species were quantified, and then the data were statistically analysed by using PCA and OPLS-DA. The multivariate analysis

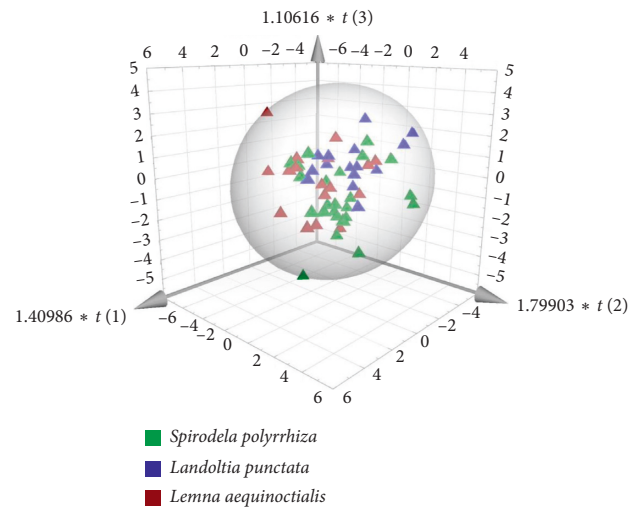


FIGURE 5: Three-dimensional score plot of orthogonal partial least squares-discriminant analysis (OPLS-DA) based on the ratio of free to total amino acids.

illustrated that the content of free amino acids was not significantly different among *Spirodela polyrrhiza*, *Landoltia punctata*, and *Lemna aequinoctialis* in pattern recognition. But as a food, more amino acids mean more nutrition it has and more valuable it is. In other words, all of the three species of duckweed could be used as food equally if the absolute amount of AAs was more or less the same. In conclusion, a reliable and feasible method was developed for the nutritional evaluation of duckweeds.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

Acknowledgments

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References

- [1] E. Ernst and G. Legler, “The role of the hydroxy amino acid in the triplet sequence Asn-Xaa-Thr(Ser) for the N-glycosylation step during glycoprotein biosynthesis,” *Biochemical Journal*, vol. 195, no. 3, pp. 639–644, 1981.
- [2] C. P. S. Badenhorst, E. Erasmus, R. van der Sluis, C. Nortje, and A. A. van Dijk, “A new perspective on the importance of glycine conjugation in the metabolism of aromatic acids,” *Drug Metabolism Reviews*, vol. 46, no. 3, pp. 343–361, 2014.

- [3] R. J. Ward, D. T. Dexter, and R. R. Crichton, "Neurodegenerative diseases and therapeutic strategies using iron chelators," *Journal of Trace Elements in Medicine and Biology*, vol. 31, pp. 267–273, 2015.
- [4] G. Mondanelli, S. Ugel, U. Grohmann, and V. Bronte, "The immune regulation in cancer by the amino acid metabolizing enzymes ARG and IDO," *Current Opinion in Pharmacology*, vol. 35, pp. 30–39, 2017.
- [5] P. J. Murray, "Amino acid auxotrophy as a system of immunological control nodes," *Nature Immunology*, vol. 17, no. 2, pp. 132–139, 2016.
- [6] T. Themelis, R. Gotti, and R. Gatti, "A novel hydrophilic interaction liquid chromatography method for the determination of underivatized amino acids in alimentary supplements," *Journal of Pharmaceutical and Biomedical Analysis*, vol. 145, pp. 751–757, 2017.
- [7] K. J. Appenroth, K. S. Sree, V. Bohm et al., "Nutritional value of duckweeds (Lemnaceae) as human food," *Food Chemistry*, vol. 217, pp. 266–273, 2017.
- [8] P. Ziegler, K. Adelmann, S. Zimmer, C. Schmidt, and K. J. Appenroth, "Relative in vitro growth rates of duckweeds (Lemnaceae)-the most rapidly growing higher plants," *Plant Biology*, vol. 17, no. 1, pp. 33–41, 2015.
- [9] M. F. A. de Beukelaar, G. G. Zeinstra, J. J. Mes, and A. R. H. Fischer, "Duckweed as human food. The influence of meal context and information on duckweed acceptability of Dutch consumers," *Food Quality and Preference*, vol. 71, pp. 76–86, 2019.
- [10] J. P. Goopy and P. J. Murray, "A review on the role of duckweed in nutrient reclamation and as a source of animal feed," *Asian-Australasian Journal of Animal Sciences*, vol. 16, no. 2, pp. 297–305, 2003.
- [11] K. E. Anderson, Z. Lowman, A. M. Stomp, and J. Chang, "Duckweed as a feed ingredient in laying hen diet and its effect on egg production and composition," *International Journal of Poultry Science*, vol. 10, no. 1, pp. 4–7, 2011.
- [12] L. Landesman, C. Fedler, and R. Duan, "Plant nutrient phytoremediation using duckweed," in *Eutrophication: Causes, Consequences and Control*, pp. 341–354, Springer, Dordrecht, Netherlands, 2011.
- [13] L. L. Rusoff, E. W. Blakeney Jr., and D. D. Culley Jr., "Duckweeds (Lemnaceae family): a potential source of protein and amino acids," *Journal of Agricultural and Food Chemistry*, vol. 28, no. 4, pp. 848–850, 1980.
- [14] E. Yilmaz, İ. Akyurt, and G. Günel, "Use of duckweed, *Lemna minor*, as a protein feedstuff in practical diets for common carp, *Cyprinus carpio*, fry," *Turkish Journal of Fisheries and Aquatic Sciences*, vol. 4, no. 2, pp. 105–109, 2004.
- [15] F. Tezcan, S. Uzasci, G. Uyar, N. Öztekin, and F. B. Erim, "Determination of amino acids in pomegranate juices and fingerprint for adulteration with apple juices," *Food Chemistry*, vol. 141, no. 2, pp. 1187–1191, 2013.
- [16] G. V. V. Liyanaarachchi, K. R. R. Mahanama, H. Somasiri, and P. A. N. Punyasiri, "Validation of a reversed-phase high-performance liquid chromatographic method for the determination of free amino acids in rice using l-theanine as the internal standard," *Food Chemistry*, vol. 240, pp. 196–203, 2018.
- [17] Y. Q. Jing, B. L. Zhang, X. X. Yuan et al., "Determination of free amino acids in burley tobacco by high performance liquid chromatography," *Saudi Journal of Biological Sciences*, vol. 23, no. 1, pp. S64–S68, 2016.
- [18] J. A. Hogenboom, P. D'Incecco, F. Fuselli, and L. Pellegrino, "Ion-exchange chromatographic method for the determination of the free amino acid composition of cheese and other dairy products: an inter-laboratory validation study," *Food Analytical Methods*, vol. 10, no. 9, pp. 3137–3148, 2017.
- [19] Y. C. Zhu, Y. H. Luo, P. P. Wang et al., "Simultaneous determination of free amino acids in Pu-erh tea and their changes during fermentation," *Food Chemistry*, vol. 194, pp. 643–649, 2016.
- [20] Z. L. Dai, Z. L. Wu, S. C. Jia, and G. Y. Wu, "Analysis of amino acid composition in proteins of animal tissues and foods as precolumn o-phthaldialdehyde derivatives by HPLC with fluorescence detection," *Journal of Chromatography B*, vol. 964, pp. 116–127, 2014.
- [21] T. Luo, J. Ke, Y. F. Xie, and Y. M. Dong, "Determination of underivatized amino acids to evaluate quality of beer by capillary electrophoresis with online sweeping technique," *Journal of Food and Drug Analysis*, vol. 25, no. 4, pp. 789–797, 2017.
- [22] X. Y. Lai, J. A. Kline, and M. Wang, "Development, validation, and comparison of four methods to simultaneously quantify l-arginine, citrulline, and ornithine in human plasma using hydrophilic interaction liquid chromatography and electrospray tandem mass spectrometry," *Journal of Chromatography B*, vol. 1005, pp. 47–55, 2015.
- [23] H. C. M. T. Prinsen, B. G. M. Schiebergen-Bronkhorst, M. W. Roeleveld et al., "Rapid quantification of underivatized amino acids in plasma by hydrophilic interaction liquid chromatography (HILIC) coupled with tandem mass spectrometry," *Journal of Inherited Metabolic Disease*, vol. 39, no. 5, pp. 651–660, 2016.
- [24] K. Inoue, Y. Miyazaki, K. Unno et al., "Stable isotope dilution HILIC-MS/MS method for accurate quantification of glutamic acid, glutamine, pyroglutamic acid, GABA and theanine in mouse brain tissues," *Biomedical Chromatography*, vol. 30, no. 1, pp. 55–61, 2016.
- [25] T. Nemkov, A. D'Alessandro, and K. C. Hansen, "Three-minute method for amino acid analysis by UHPLC and high-resolution quadrupole orbitrap mass spectrometry," *Amino Acids*, vol. 47, no. 11, pp. 2345–2357, 2015.
- [26] N. Borisjuk, P. Chu, R. Gutierrez et al., "Assessment, validation and deployment strategy of a two-barcode protocol for facile genotyping of duckweed species," *Plant Biology*, vol. 17, no. 1, pp. 42–49, 2015.
- [27] Y. L. Xu, S. Ma, M. Huang et al., "Species distribution, genetic diversity and barcoding in the duckweed family (Lemnaceae)," *Hydrobiologia*, vol. 741, no. 1, pp. 75–87, 2015.
- [28] H. L. Xue, Y. Xiao, Y. L. Jin et al., "Genetic diversity and geographic differentiation analysis of duckweed using inter-simple sequence repeat markers," *Molecular Biology Reports*, vol. 39, no. 1, pp. 547–554, 2012.
- [29] I. Abdel-Qader, S. Pashaie-Rad, O. Abudayyeh, and S. Yehia, "PCA-based algorithm for unsupervised bridge crack detection," *Advances in Engineering Software*, vol. 37, no. 12, pp. 771–778, 2006.
- [30] W. Gao, H. Yang, L. W. Qi et al., "Unbiased metabolite profiling by liquid chromatography-quadrupole time-of-flight mass spectrometry and multivariate data analysis for herbal authentication: classification of seven *Lonicera* species flower buds," *Journal of Chromatography A*, vol. 1245, pp. 109–116, 2012.
- [31] B. Worley, S. Halouska, and R. Powers, "Utilities for quantifying separation in PCA/PLS-DA scores plots," *Analytical Biochemistry*, vol. 433, no. 2, pp. 102–104, 2013.
- [32] J. Boccard and D. N. Rutledge, "A consensus orthogonal partial least squares discriminant analysis (OPLS-DA) strategy for multiblock Omics data fusion," *Analytica Chimica Acta*, vol. 769, pp. 30–39, 2013.



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