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Research Article

Characterization of Amino Acid Composition, Nutritional Value, and Taste of Fruits from Different *Actinidia arguta* Resources

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The nutritional value and flavor and texture characteristics of fruits from different *Actinidia argute* resources were scientifically evaluated and compared. Using 35 *A. arguta* fruits as materials, the amino acid composition and content were determined by an automatic amino acid analyzer, and differentiation analysis, amino acid nutritional value evaluation, TAV flavor analysis, correlation analysis, PCA comprehensive evaluation, and cluster analysis were conducted to clarify the diversity of *A. arguta* resources in terms of amino acid content, composition, and flavor characteristics. Analysis of differential results showed that the *A. arguta* resource fruits contained 17 amino acids with a total amino acid content of 384.20~2590.56 mg/100 g. The results of the nutritional value evaluation showed that the Leu of the fruits of the *A. arguta* resources all conformed to the ideal model proposed by FAO/WHO, and the Leu content of all the resources exceeded the human body's needs, and it was also found that the first limiting amino acid of the Actinidia argute resources was Ile and the second limiting amino acid was Lys. TAV of the flavor-presenting amino acids was calculated to evaluate the flavor-presenting taste characteristics, and the amino acids that influenced the flavor of *A. arguta* fruit were Glu and Cys. PCA showed that the 2 principal components could better reflect the comprehensive information of amino acids in *A. arguta*, and the cumulative variance contribution rate was 87.88%, which could represent the main trend of amino acids in *A. arguta*. A comprehensive amino acid evaluation model was established, and the composite scores indicated that the top 5 excellent resources were S4, S10, S18, S25, and S30. Hierarchical cluster analysis classified the 35 *A. arguta* resources into 4 categories, which better reflected the differences in amino acid content and composition, nutritional value, and taste characteristics among *A. arguta* fruits from different collection sites.

1. Introduction

The *Actinidia argute* ((Sieb. & Zucc) Planch. ex Miq.) belongs to the kiwifruit family (Actinidiaceae Gilg & Werderm.), the kiwifruit genus (Actinidia Lindl), alias soft jujube, kiwifruit, and kiwifruit pear, which is a large deciduous vine [1, 2]. Its wild germplasm resources are mainly distributed in China, Japan, the Korean Peninsula, and the Russian Far East [3, 4], and in China, it is distributed in the northeast, north, and northwest of China in the Yangtze River Basin as well as in Taiwan [5, 6]. Its fruits are crisp, juicy, and tasty when eaten fresh and are rich in nutrients such as vitamin C, protein, amino acids, minerals, and dietary fiber [2, 7]. In addition to this, it is also of extremely high medicinal value, and its fruits are rich in active ingredients such as polysaccharides, polyphenols, alkaloids, volatile oils, and proanthocyanidins [8], which are antitumor, antiradiation, antioxidant, antiaging, hypoglycemic, anti-inflammatory, insomnia inhibitor, immunity enhancement, laxative, and other effects [9–12]. Wojdylo and Nowicka [13] found that *A. arguta* polyphenolic compounds could play a role in the treatment of diabetes after an in vitro antidiabetic experimental study. Xu [14] et al. found that *A. arguta* can significantly improve the constipation caused by montelukast in mice and increase the amount of food intake and the number of defecation, with a laxative effect.

Nowadays, *A. arguta* is loved by the public and welcomed by the market because of its rich nutritional and medicinal value, and its fruit is often used to make processed foods such as dried fruit, dried fruit, fruit wine, fruit jam, canned food, fruit juice, fruit vinegar, or pectin oral liquid [15].

Amino acids, as an important compound in the body, are mainly involved in protein synthesis, metabolism, and immune response. In addition, it is an important bioactive component that can be used as a pharmacological component to regulate various physiological activities, and it has been shown that amino acids not only have a role in cancer metabolism but also have important roles such as redox balance, energy regulation, and homeostasis maintenance [16], and even preventive and therapeutic functions, and they can also act in coordination with hormones and play an important role in the control of gene expression [17–20]. For example, alanine, aspartate, and glutamate play a variety of roles as the main substrates for glucose synthesis in the liver, influencing the immune function in humans and animals [21]. Proline is an essential component of collagen and extracellular matrix and plays an important role in gene expression, cellular signaling, cellular redox, synthesis of polyamines, glutamate, and collagen [22], and it plays an important role in the regulation of dehydration stress, redox, and cell proliferation [23]. Glycine is a potent antioxidant that scavenges free radicals required for leukocyte proliferation and antioxidant activity, reducing inflammatory responses and pathogens in animals [24]. Amino acids often exist in two forms in plants: one is in the form of a bound state in peptides and proteins; the other is in the form of a free state [25], which can help plants to form organs and a variety of active substances during the growth process [26]. At the same time, plant amino acid crops, components of plant-based proteins, are an important source of dietary protein for humans and are recognized as a continuous source of nutrients to meet human needs, and the intake of plant-based proteins has potential benefits for the health of the human organism in terms of lowering the risk of chronic diseases, reducing deaths due to disease, and increasing the intake of plant proteins may also slow down unhealthy aging. Among them, free amino acids can be directly absorbed by the human body, and their content and composition can not only reflect the nutritional value of food, which is an important indicator for evaluating the nutritional value of food; they also have a close relationship with the flavor quality of food [27, 28]. At present, there have been some studies on the amino acids of *A. arguta* fruits, but they are mainly focused on their contents and components [29, 30], and there are almost no reports on the evaluation of their nutritional value and flavor characteristics; at the same time, there is a lack of systematic and rigorous statistical and comprehensive evaluation of amino acids of *A. arguta* resource fruits. Therefore, in-depth research on the types and contents of amino acids and their nutritional value of *A. arguta* resources is not only of great significance to the systematic and comprehensive evaluation of *A. arguta* resources but also of theoretical significance to the development of functional products that are beneficial to human health.

At present, for the analysis of fruit amino acid detection and analysis of commonly used methods are ninhydrin colorimetric method, HPLC, GC, GC-MS, near-infrared spectroscopy, amino acid analyzer, and electrochemical analysis [31–36]. The amino acid analyzer is a fully automated special analytical instrument for amino acid separation, derivatization, and detection, using cations in the exchange column separation, postcolumn ninhydrin derivatization, and diode photometer detection, with the ability to be able to be equipped in the general laboratory, good selectivity, specificity, high sensitivity, easy to operate, separation and reproducibility of the better, simple sample pretreatment, and the ability to carry out the advantages of batch testing [37–39]. Methodology for statistical analysis of data such as principal PCA modeling, TAV, and HCA is commonly used when testing and analyzing fruit amino acids using an amino acid analyzer. PCA is based on the principle of KL transformation, and through the way of dimensionality reduction, multiple variables are simplified into a few composite variables, so that the existing few composite variables can directly reflect the information of the original variables [40]. TAV can be used to assess the contribution of individual components to the flavor, and compounds with a TAV value greater than 1 can be regarded as components that contribute significantly to the overall flavor [41, 42]. HCA is the process of calculating the similarity between samples by means of criteria that have been determined, simplifying and combining them by means of the degree of correlation, and dividing the similar analyzed samples into different groups for a comprehensive evaluation based on their respective characteristics [43]. Currently, amino acid analyzer testing combined with PCA, TAV, and HCA multiple regression analysis has been widely used for amino acid testing and comprehensive evaluation of food quality [27, 44–47]. Jian [48] et al. used PCA to analyze the hydrolyzed amino acids and free amino acids of five edible mushroom powders and established a comprehensive evaluation model, and the comprehensive evaluation found that the comprehensive amino acid quality of the edible mushroom powder of tea tree mushroom was the best. Lin [49] et al. used PCA and HCA to analyze the free amino acids of the fruits of 15 hybrid citrus varieties, and the results showed that the results of the two analytical methods were basically the same and could better reflect the variability of amino acid fractions among varieties.

Amino acid analyzer assay combined with PCA, TAV, and HCA multiple regression analysis has rarely been reported in the detection and evaluation of amino acids in *A. arguta* resource fruits. Therefore, in this study, the amino acid analyzer was used to isolate and detect the amino acids of 35 different *A. arguta* resource fruits, to analyze the differences in their contents, to evaluate the changes in their nutritional value by using the amino acid ratio coefficient method, and to analyze and comprehensively evaluate the amino acid quality indexes by using the taste activity value (TAV), correlation analysis, PCA, and HCA, to compare the differences between the different resources in the nutrient composition and taste characteristics of the fruits. The results of the study provide a scientific basis for revealing the

nutritional value and taste characteristics of *A. arguta*, a theoretical reference for the screening of excellent *A. arguta* resources and product development and utilization.

2. Materials and Methods

2.1. Materials and Reagents

2.1.1. Materials. The 35 resources selected for this study were harvested in September 2022 at the fruit ripening stage from the National Forest Germplasm Resource Bank of *A. arguta* and Schisandra chinensis. About 300 g of fruit was picked from each resource, and the samples were placed in separate corresponding sampling bags and transported back to the laboratory in an insulated box. After testing the relevant indexes on the same day, the remaining part of the sample was frozen and ground into powder with liquid nitrogen and then stored at −80°C in ultralow temperature for amino acid testing.

2.1.2. Reagents. The reagents are hydrochloric acid, phenol, and sodium citrate analytical purity (Shanghai, Sinopharm Chemical Reagent Co., Ltd.), sodium hydroxide and sodium chloride superior purity (Beijing, Beijing Beihua Fine Chemicals Co., Ltd.), and 17 kinds of L-amino acid mixed standards (Wako, Japan).

2.2. Instruments and Equipment. Instruments and equipment are as follows: DFT-50A 50 g portable high-speed pulverizer (Wenling Linda Machinery Co., Ltd.); L-8900 amino acid auto-analyzer (Hitachi, Japan); MS204S electronic analytical balance (Mettler Toledo, Switzerland); DZF6090 vacuum drying oven (Shanghai Pudong Rongfeng Scientific Instrument Co., Ltd.); DHG-9240A temperature drying oven (Shanghai Yihang Science & Technology Co., Ltd.); Milli-Q Advantage A1 ultrapure water apparatus (Millipore Corporation, U.S.A.).

2.3. Methodology

2.3.1. Chromatographic Detection Conditions. Column is 4.6 mm × 60 mm ion exchange column; flow rate is 0.40 mL/min (pump1) and 0.35 mL/min (pump2); detection wavelengths are 570 nm and 440 nm; column temperature is 135°C; injection volume is 20 μL, mobile phase eluted according to the gradient table (Table 1), and analysis time is 40.2 min.

2.3.2. Amino Acid Assay of A. arguta Samples. Refer to GB/T 5009.124-2016 [50]. Accurately weighed 2.50 g of *A. arguta* sample, added 20 mL of hydrochloric acid solution with a concentration of 6 mol/L, and hydrolyzed in a constant temperature oven at 110°C for 22 h. Then, all the hydrolyzed solution was transferred to a 50 mL volumetric flask, and the volume was fixed with primary water. After taking 2 mL of the above solution and evaporating it under reduced pressure, it was dissolved with 2 mL of hydrochloric acid solution at a concentration of 0.02 mL/L and then filtered through an aqueous filter membrane of 0.22 μm and analyzed. Each sample was separated and detected by an L-8900 amino acid autoanalyzer, and all samples were repeated three times.

2.3.3. Nutritional Evaluation of Amino Acids. According to the International Standard Reference Model for the needs of older children, young people, and adults aged >3 years proposed by the Food and Agriculture Organization of the United Nations (FAO) and World Health Organization (WHO) in 2013 [51], E/T (%) = EAA/TAA, E/N (%) = EAA/NEAA [52], E/N (%) = EAA/NEAA [53], E/T (%) = EAA/TAA, E/N (%) = EAA/NEAA [52], M/T (%) = MAA/TAA, BC/E (%) = BCAA/EAA, and BC/A = BCAA/AAA [21].

The amino acid ratio coefficient method was proposed by Shengtao and Kun [53] to calculate the ratio of amino acid (RAA), the ratio coefficient of amino acid (RC), and the score of RC and SRC [51].

$$\begin{aligned} \mathrm{RAA} &= \frac{\text{content of an essential amino acid in the protein to be measured/ (mg/}g)}{\text{corresponding amino acid content in the reference protein pattern/ (mg/}g)}, \\ \mathrm{RC} &= \frac{\text{amino acid RAA}}{\text{RAA average}}, \\ \mathrm{SRC} &= 100 - 100 \times \mathrm{CV}. \end{aligned} \tag{1}$$

Eq: CV is the coefficient of variation of the RC and CV = standard deviation/average number.

Table 1: Gradient elution program.

Time (min)	PH-1	PH-4	PH-RG	PH-2
0	100	0	0	0
0.1	0	100	0	0
14.2	0	100	0	0
14.3	0	0	100	0
20.2	0	0	100	0
20.3	0	0	0	100
21.2	0	0	0	100
21.3	100	0	0	0
40.2	100	0	0	0

2.3.4. Taste-Presenting Amino Acid Analysis. Taste-presenting amino acids can be classified as fresh, sweet, bitter, and aromatic amino acids, and taste active value (TAV) refers to the ratio of the value of the content of taste-presenting substances to the taste threshold of taste-presenting substances [54].

2.4. Statistical Analysis of Data. The experimental data were organized for statistics using Excel 2016, and ANOVA, principal component analysis, was performed using SPSS (version 23.0, IBM, Armonk, NY, USA). PCA, correlation analysis, and HCA were performed using Origin 2021 and OmicShare tools.

3. Results and Discussion

3.1. Chromatographic Analysis. According to the chromatographic detection conditions, the chromatographic separation of 17 amino acid standards using amino acid autoanalyzer is shown in Figure 1. Chromatogram of 17 amino acid standard samples, proline, was measured at the wavelength of 440 nm, and the rest of 16 amino acids were measured at the wavelength of 570 nm, and the 17 amino acids achieved a very good separation effect under the separation conditions. The samples to be tested were processed for amino acid determination as shown in Figure 2. Amino acid chromatogram of *A. arguta*, a comparison of the chromatographic separations of the samples with those of the amino acid standards, revealed that the *A. arguta* fruit samples contained 17 amino acid species.

3.2. Analysis of Amino Acid Composition and Content of Fruits of Different A. arguta Resources. The different amino acids of 35 *A. arguta* resources were statistically analyzed, and the results are shown in Table 2. Amino acid composition and content of different resources of*A. arguta* mg/100 g. All 35 *A. arguta* contained 17 amino acids, including 7 EAAs, 10 NEAAs, 2 CEAAs, and 9 MAAs. The 7 EAAs are Thr, Val, Met, Ile, Leu, Phe, and Lys, the 10 NEAAs are Asp, Ser, Glu, Gly, Ala, Cys, Tyr, His, Arg, and Pro, the 2 CEAAs are His and Arg, and the 9 MAAs are Asp, Glu, Gly, Met, Ile, Lue, Phe, Lys, and Arg. The variation of standard deviation of 17 amino acids was 9.68~146.87, and the coefficient of variation was 40.94%~77.74%, which indicated that the content of different amino acids differed significantly among resources, among which the coefficient of variation of Pro was the largest, and the coefficient of variation of Gys was the smallest, and at the same time, the results of the analysis of variance showed that each amino acid differed significantly among most of the A. arguta resources; the variation of the mean value was 18.16~222.22 mg/100 g, with the lowest content of Met and the highest content of Glu. Glu, as an indispensable amino acid during the critical period of life, including the period of fast-growing newborns, has the ability to enhance the immune function of the immune cells [55], and it can also be used to treatment of liver-related diseases such as hepatic coma and hepatic insufficiency [56], and glutamine, which is formed by combining with blood ammonia, also contributes to the repair of traumatized organisms and the treatment related to peptic ulcers [57], so appropriate consumption of *A. arguta* fruits can improve immunity, while, in the future, it can be developed as a healthcare product for liver protection and repair of ulcers.

The results of the variance analysis showed that there were differences in the content of various amino acids among the different *A. arguta* resources. The resources with the highest content of Thr, Ser, Glu, Ala, Val, Ile, Tyr, Lys, His, and Arg were S4; the resources with the highest content of Phe were S4 and S27, and the resources with the highest content of Asp were S8; the resources with the highest content of Gly, Met, and Leu were S10; the resources with the highest content of Pro were S30; the resources with the highest content of Cys were S28 and differed from other resources. Leu content was S10; the highest Pro content was S30; the highest Cys content was S28, and it was significantly different from other resources. The TAA content was 384.20~2590.56 mg/100 g, and the highest content was 674.27% of the lowest content. The resource with the highest TAA content was S4, and the resource with the lowest content was S34. The EAA content was 140.23~901.54 mg/100 g, with a mean value of 391.48 mg/100 g; the NEAA content was 237.41~1689.02 mg/100 g, with a mean value of 797.68 mg/100 g; the CEAA content was 47.89~480.52 mg/100 g, with a mean value of 101.82 mg/100 g; the content of MAA was 219.81~1640.16 mg/100 g, with a mean value of 741.23 mg/100 g; the content of BCAA was 78.86~496.36 mg/100 g, with a mean value of 213.55 mg/100 g; the total amino acid content was 384.20~2590.56 mg/100 g. In comparison, the mean contents of NEAA and MAA were higher than the others, so NEAA and MAA were the main components of TAA in *A. arguta*.

3.3. Evaluation of Amino Acid Nutritional Value of Fruits of Different A. arguta Resources. The WHO and FAO proposed a standard model for evaluating essential amino acids in food in 1973, and it has been suggested that the closer the variety of essential amino acids in the proteins of each substance and the ratio of their composition is to the FAO/WHO standard model of amino acids, the higher the nutritional value of proteins and the better the quality of the proteins in the substance, and vice versa, and the worse the nutritional quality [30]. Comparing the essential amino acids in 35 *A. arguta* resources with the amino acid pattern

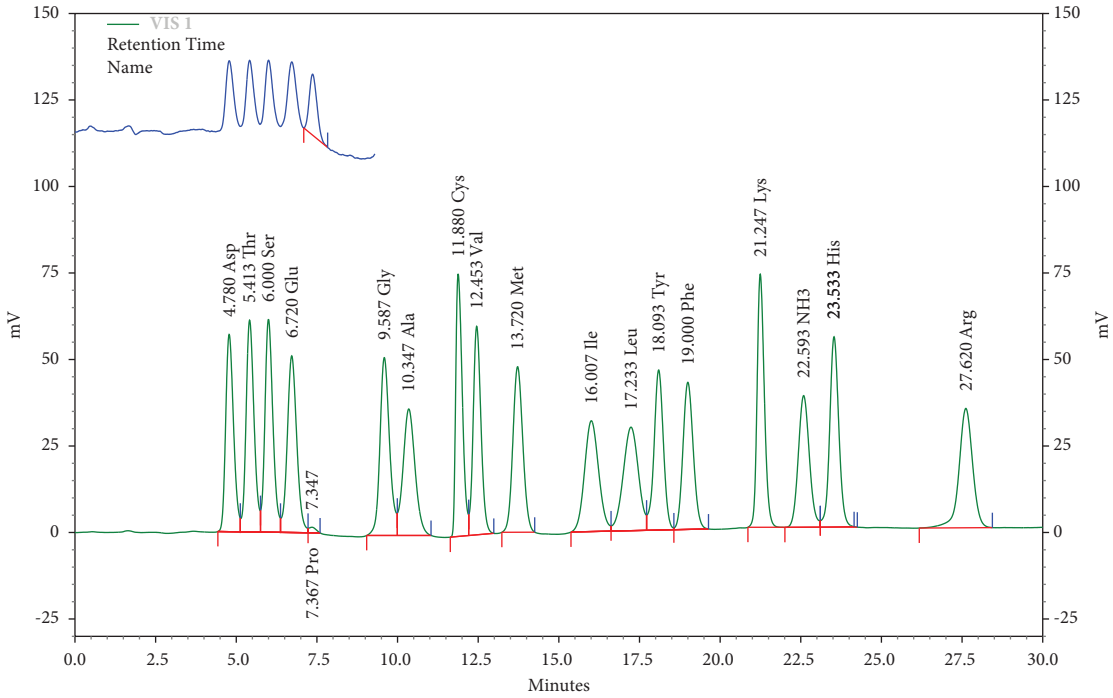

Figure 1: Chromatogram of 17 amino acid standard samples.

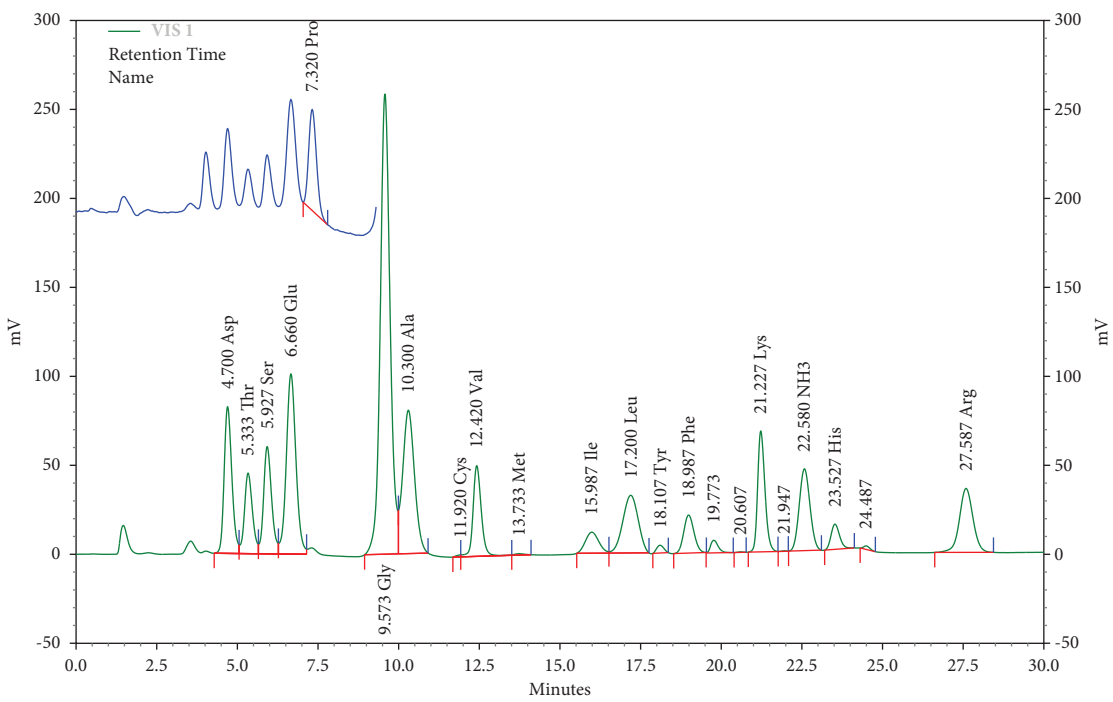

Figure 2: Amino acid chromatogram of *A. arguta*.

spectrum of FAO/WHO is shown in Table 3. Comparison of essential amino acids and FAO/WHO amino acid patterns in different resource fruits of *A. arguta* shows that the Leu of 35 *A. arguta* resources meets the ideal pattern proposed by FAO/WHO, and Leu, as an essential amino acid, is commonly used in the treatment of idiopathic hyperglycemia in young children, as well as liver disease, anemia, and muscular dystrophy caused by the imbalance of glucose metabolism accompanied by a decrease in bile secretion [58, 59], and therefore, studies on the regulation of glucose and lipid metabolism by the *A. arguta* may be carried out in the subsequent studies. There were 2 resources that did not fit

Table 2: Amino acid composition and content of different resources of *A. arguta* mg/100 g.

Name	Content mg/100 g							
	Asp	Thr	Ser	Glu	Gly	Ala	Cys	Val
S1	71.87 ± 2.26pq	37.76 ± 0.72kl	35.47 ± 0.65l	113.03 ± 5.71no	13.00 ± 0.18p	34.62 ± 0.20no	9.28 ± 0.24opq	44.75 ± 2.11pq
S2	69.18 ± 2.47q	40.28 ± 1.54k	34.66 ± 1.48lm	75.43 ± 3.29rs	13.02 ± 0.49p	27.10 ± 1.27p	9.40 ± 0.06opq	42.82 ± 1.51qr
S3	39.60 ± 0.52vw	22.17 ± 1.16qr	20.43 ± 0.72s	52.19 ± 0.65t	8.52 ± 0.11q	18.51 ± 0.07q	8.32 ± 0.19qr	30.34 ± 0.90w
S4	312.88 ± 4.55b	134.31 ± 1.47a	127.57 ± 2.04a	534.73 ± 6.69a	8.32 ± 0.01q	185.33 ± 2.99a	33.70 ± 1.33cd	177.77 ± 1.24a
S5	80.87 ± 1.64no	35.60 ± 0.74lm	35.88 ± 0.95l	127.68 ± 2.85m	40.28 ± 0.94j	52.97 ± 1.94k	9.12 ± 0.30opqr	44.53 ± 0.20pq
S6	36.28 ± 0.73vwx	20.72 ± 0.99r	27.31 ± 0.22pq	94.77 ± 2.14pq	23.21 ± 0.63mn	24.63 ± 0.61p	22.97 ± 0.24m	32.16 ± 0.48vw
S7	42.72 ± 2.11uv	24.35 ± 0.32pq	28.74 ± 0.18op	106.38 ± 1.54op	25.90 ± 0.03m	35.25 ± 0.93no	20.47 ± 0.26n	34.85 ± 1.48uv
S8	355.31 ± 12.59a	82.36 ± 0.77de	92.32 ± 2.09c	408.42 ± 10.31c	99.66 ± 0.91f	132.68 ± 1.56c	25.36 ± 0.41kl	99.45 ± 2.83j
S9	109.87 ± 5.76k	45.46 ± 0.89j	50.02 ± 0.61j	251.86 ± 7.02hi	55.11 ± 0.32i	87.05 ± 0.23h	33.52 ± 1.09cde	70.36 ± 3.09lm
S10	219.45 ± 7.22e	96.87 ± 3.06b	100.81 ± 3.54b	407.83 ± 15.32c	146.36 ± 5.88a	145.62 ± 5.30b	30.86 ± 1.08f	155.96 ± 2.25b
S11	30.16 ± 1.42x	17.23 ± 0.19s	20.65 ± 0.79s	87.52 ± 3.81qr	21.07 ± 0.46no	25.16 ± 0.48p	33.17 ± 0.15de	42.34 ± 1.30qr
S12	51.86 ± 2.57st	24.37 ± 0.24pq	24.97 ± 0.86qr	153.76 ± 3.18l	24.87 ± 0.94mn	27.93 ± 0.89p	26.56 ± 0.03ijk	39.16 ± 0.75rst
S13	68.86 ± 3.28q	26.87 ± 1.46op	32.52 ± 0.89mn	126.92 ± 0.01m	34.11 ± 1.57kl	38.56 ± 0.29mn	23.32 ± 0.29m	40.41 ± 1.22rs
S14	149.91 ± 6.80i	69.81 ± 2.49f	79.07 ± 3.36g	351.21 ± 11.28fg	98.72 ± 3.61f	105.26 ± 3.38f	26.12 ± 0.80jkl	104.61 ± 2.18j
S15	198.07 ± 9.35f	80.77 ± 3.26e	88.91 ± 3.78de	378.82 ± 15.11d	110.21 ± 6.13e	118.16 ± 6.05e	32.26 ± 1.03e	115.07 ± 4.16g
S16	242.42 ± 7.40d	96.52 ± 3.40b	99.01 ± 2.49b	421.17 ± 12.46b	122.42 ± 3.10c	130.46 ± 3.15c	26.97 ± 0.75ij	127.71 ± 4.77e
S17	98.22 ± 4.19l	50.82 ± 2.11h	55.18 ± 1.96i	200.86 ± 6.95j	66.67 ± 3.05h	63.46 ± 2.87i	30.77 ± 1.76f	81.42 ± 1.40k
S18	271.47 ± 7.65c	93.52 ± 5.30c	101.87 ± 2.85b	361.17 ± 2.76ef	136.76 ± 5.43b	124.77 ± 2.26d	27.77 ± 1.05hi	145.27 ± 5.65c
S19	38.12 ± 1.31vwx	19.86 ± 0.93rs	22.52 ± 0.71rs	112.86 ± 5.15no	18.42 ± 0.20o	24.51 ± 0.00p	34.57 ± 0.24bc	37.46 ± 1.08stu
S20	91.02 ± 0.20lm	46.72 ± 1.79ij	48.91 ± 0.29j	168.16 ± 7.55k	51.32 ± 0.61i	63.97 ± 1.06i	26.91 ± 0.00ij	69.22 ± 1.40m
S21	58.92 ± 2.40rs	33.32 ± 2.21mn	32.07 ± 0.96mn	107.26 ± 0.43op	37.47 ± 1.35jk	33.07 ± 0.25o	25.17 ± 0.55l	44.76 ± 1.37pq
S22	182.87 ± 5.25g	84.92 ± 2.90d	87.52 ± 2.21e	374.21 ± 10.18de	115.27 ± 3.65d	105.71 ± 2.90f	30.81 ± 1.22f	117.82 ± 2.30g
S23	60.57 ± 1.25r	32.42 ± 1.01n	39.12 ± 0.31k	124.87 ± 3.14mn	41.37 ± 0.66j	44.01 ± 0.90l	34.96 ± 0.17b	55.47 ± 1.25o
S24	134.42 ± 2.61j	71.97 ± 1.75f	78.52 ± 1.59g	262.66 ± 5.76h	90.37 ± 0.55g	107.61 ± 1.50f	25.71 ± 0.52jkl	84.37 ± 1.56k
S25	177.87 ± 3.25g	82.57 ± 0.46de	89.87 ± 2.06cde	382.06 ± 12.47d	118.97 ± 4.26cd	123.02 ± 5.00d	29.57 ± 0.95g	131.56 ± 2.85d
S26	31.41 ± 1.00wx	19.06 ± 0.82rs	21.26 ± 0.25s	70.86 ± 1.04s	20.87 ± 0.84no	20.06 ± 0.12q	22.47 ± 0.05m	24.57 ± 0.86x
S27	159.17 ± 8.86h	80.42 ± 0.90e	84.06 ± 0.47f	249.16 ± 1.55i	97.51 ± 3.83f	95.32 ± 0.70g	25.26 ± 0.67l	108.87 ± 3.74h
S28	164.17 ± 7.84h	71.72 ± 0.51f	90.86 ± 2.63cd	342.22 ± 17.81g	89.47 ± 2.34g	114.81 ± 4.97d	38.37 ± 0.25a	99.87 ± 4.54j
S29	143.17 ± 7.05i	57.96 ± 2.77g	63.87 ± 2.66h	364.07 ± 16.65ef	70.42 ± 0.51h	86.41 ± 0.12h	32.46 ± 1.13de	73.67 ± 2.65l
S30	203.18 ± 2.95f	91.77 ± 0.74c	99.37 ± 1.06b	528.36 ± 4.53a	117.57 ± 1.84d	134.17 ± 1.95c	28.57 ± 1.24gh	123.26 ± 0.78f
S31	77.68 ± 0.56op	32.39 ± 0.25n	36.39 ± 0.45kl	106.97 ± 0.73op	38.97 ± 0.56j	58.78 ± 0.65j	10.14 ± 0.20o	47.14 ± 1.75p
S32	88.19 ± 0.04mn	28.14 ± 0.01o	31.21 ± 0.02no	100.82 ± 0.01opq	31.52 ± 0.07l	40.19 ± 0.13m	7.98 ± 0.64r	36.32 ± 1.11tu
S33	50.24 ± 1.19tu	20.59 ± 0.46r	22.52 ± 0.71rs	78.56 ± 2.53rs	26.52 ± 0.11m	26.86 ± 0.33p	6.48 ± 0.14s	28.98 ± 0.06w
S34	42.42 ± 0.21uv	21.27 ± 0.05qr	22.70 ± 0.13rs	53.92 ± 0.51t	25.57 ± 0.26m	34.03 ± 0.88o	8.67 ± 0.05pqr	29.65 ± 0.21w
S35	78.78 ± 0.35op	48.83 ± 0.08hi	50.58 ± 0.46j	97.08 ± 0.14pq	17.47 ± 0.04o	45.30 ± 0.27l	9.87 ± 0.15op	60.77 ± 0.76n
Stdeva	85	30.41	31.63	146.87	42.58	45.8	9.68	42.35
Average	120.89	52.68	56.48	222.22	58.78	72.44	23.65	74.36
CV%	70.31	57.73	56	66.09	72.43	63.22	40.94	56.95

Table 2: Continued.

Name	Content mg/100 g							
	Met	Ile	Leu	Tyr	Phe	Lys	His	Arg
S1	7.32 ± 0.11o	45.51 ± 1.27lm	44.83 ± 2.01opq	47.88 ± 1.64j	35.66 ± 0.87n	39.33 ± 1.59mn	14.33 ± 0.30n	45.72 ± 1.90l
S2	7.38 ± 0.14o	44.82 ± 1.80lm	42.02 ± 1.99pq	37.73 ± 1.30lmn	35.03 ± 1.22n	39.66 ± 1.39mn	18.82 ± 0.60m	45.07 ± 2.24l
S3	5.82 ± 0.00p	30.93 ± 0.11op	32.22 ± 0.69t	23.92 ± 1.11p	23.33 ± 0.81q	26.35 ± 0.49p	10.78 ± 0.26op	35.12 ± 1.60no
S4	39.16 ± 1.48b	132.77 ± 2.04a	185.82 ± 5.81b	159.75 ± 7.37a	99.03 ± 0.79a	132.68 ± 1.67a	92.30 ± 5.26a	194.77 ± 3.36a
S5	7.57 ± 0.04o	35.95 ± 0.17n	48.63 ± 0.09no	24.32 ± 0.00p	29.26 ± 0.54o	41.17 ± 1.14lm	17.62 ± 0.99m	40.81 ± 0.48lm
S6	4.14 ± 0.21q	15.85 ± 0.72w	35.03 ± 0.71st	18.18 ± 0.15q	11.02 ± 0.11t	21.31 ± 0.27q	18.93 ± 0.10m	30.13 ± 0.79op
S7	5.98 ± 0.04p	27.30 ± 0.43qr	52.93 ± 0.79mn	40.77 ± 1.16kl	57.60 ± 0.74i	32.52 ± 1.49o	17.97 ± 0.63m	28.73 ± 1.30pqr
S8	16.11 ± 0.38k	77.72 ± 1.89g	118.96 ± 6.39h	76.27 ± 2.66f	66.32 ± 0.92h	70.61 ± 1.58gh	29.76 ± 1.09ij	96.42 ± 1.39g
S9	25.36 ± 0.18h	46.98 ± 0.97l	77.87 ± 0.34k	46.90 ± 0.54j	52.36 ± 2.17k	43.82 ± 2.01kl	19.16 ± 0.13m	53.36 ± 0.57k
S10	49.11 ± 1.77a	110.55 ± 2.82b	193.23 ± 6.99a	57.81 ± 2.02i	91.91 ± 2.44b	118.47 ± 0.14b	60.61 ± 1.17c	187.17 ± 7.86b
S11	15.71 ± 0.14k	20.52 ± 0.50uv	40.96 ± 1.38qr	28.77 ± 0.95o	18.56 ± 0.43r	12.27 ± 0.36r	9.98 ± 0.14p	20.35 ± 0.16st
S12	12.38 ± 0.45mn	24.26 ± 0.93st	43.17 ± 0.56pq	34.11 ± 0.18n	49.17 ± 0.24l	26.67 ± 0.16p	9.91 ± 0.13p	23.82 ± 0.61rs
S13	6.12 ± 0.11p	27.06 ± 0.68qrs	52.32 ± 1.61mn	40.07 ± 2.05klm	34.21 ± 0.22n	26.97 ± 1.24p	14.16 ± 0.12n	33.12 ± 0.41op
S14	39.22 ± 1.11b	72.81 ± 1.08h	136.72 ± 4.00fg	41.71 ± 0.68k	69.31 ± 3.84g	73.22 ± 1.01g	47.07 ± 1.66e	130.07 ± 5.16e
S15	27.47 ± 0.25g	83.51 ± 3.92f	140.81 ± 4.54ef	40.00 ± 0.91klm	73.98 ± 3.06ef	68.32 ± 3.11h	50.51 ± 1.98d	126.06 ± 5.99e
S16	29.82 ± 1.10f	92.92 ± 2.81d	145.06 ± 5.27de	64.32 ± 2.59h	80.76 ± 1.55d	87.54 ± 3.90e	47.21 ± 2.33e	119.32 ± 3.01f
S17	29.56 ± 0.23f	52.83 ± 2.49k	88.86 ± 3.47j	68.96 ± 2.42g	49.62 ± 1.50l	46.77 ± 1.16k	30.61 ± 0.49ij	84.27 ± 4.46h
S18	37.01 ± 1.32c	97.92 ± 4.60c	170.61 ± 2.32c	54.47 ± 0.56i	92.36 ± 0.48b	104.16 ± 4.67d	64.76 ± 1.55b	146.77 ± 3.24d
S19	13.21 ± 0.07m	22.01 ± 0.40tu	39.57 ± 0.46qrs	39.72 ± 0.29klm	17.62 ± 0.80rs	13.16 ± 0.72r	5.27 ± 0.16q	24.50 ± 1.31qrs
S20	19.87 ± 0.76j	44.02 ± 0.81m	73.81 ± 1.40k	37.42 ± 0.59lmn	42.97 ± 0.54m	36.16 ± 0.53n	18.22 ± 0.50m	55.62 ± 1.81jk
S21	4.91 ± 0.00pq	29.41 ± 0.30opq	55.21 ± 0.48m	36.32 ± 0.09mn	36.62 ± 1.21n	27.56 ± 0.27p	11.22 ± 0.40op	29.56 ± 0.65pq
S22	30.62 ± 0.30ef	86.42 ± 2.31e	146.86 ± 4.97d	81.92 ± 2.50e	83.86 ± 2.95c	86.72 ± 3.70e	38.87 ± 0.36g	161.52 ± 4.61c
S23	21.22 ± 0.02i	31.77 ± 0.26o	61.72 ± 1.59l	41.77 ± 1.96k	58.22 ± 0.71i	31.07 ± 0.96o	13.57 ± 0.05n	28.57 ± 0.54pqr
S24	12.47 ± 1.95mn	68.22 ± 0.31i	115.86 ± 1.36hi	84.36 ± 2.87e	76.32 ± 1.20e	79.11 ± 3.93f	31.87 ± 1.35i	87.17 ± 1.15h
S25	40.02 ± 0.51b	90.96 ± 2.23d	165.92 ± 4.90c	84.97 ± 0.85e	93.32 ± 1.62b	89.16 ± 2.79e	42.22 ± 1.60f	185.46 ± 7.35b
S26	2.62 ± 0.11r	18.07 ± 0.26vw	36.22 ± 0.39rst	19.62 ± 0.23q	8.32 ± 0.31u	13.97 ± 0.56r	4.88 ± 0.05q	17.47 ± 0.75t
S27	3.92 ± 0.11q	73.67 ± 1.36h	116.67 ± 5.15hi	100.97 ± 1.64c	97.17 ± 4.35a	109.41 ± 4.98c	35.42 ± 0.90h	77.26 ± 2.79i
S28	31.46 ± 0.33e	66.17 ± 1.35i	112.52 ± 1.99i	90.01 ± 1.30d	71.92 ± 0.20f	72.77 ± 2.74g	28.47 ± 1.16j	88.26 ± 1.63h
S29	11.52 ± 0.30n	51.32 ± 2.29k	89.17 ± 4.15j	128.38 ± 6.16b	55.02 ± 1.20j	58.12 ± 1.90i	25.91 ± 0.32k	96.37 ± 4.15g
S30	33.52 ± 1.50d	82.27 ± 0.86f	134.52 ± 0.40g	126.37 ± 0.85b	90.86 ± 0.71b	106.01 ± 3.60cd	39.57 ± 0.25g	128.27 ± 1.96e
S31	15.39 ± 0.74kl	28.62 ± 0.49pqr	46.69 ± 0.34op	19.43 ± 0.31q	26.74 ± 0.50p	42.03 ± 0.18lm	17.68 ± 0.55m	41.64 ± 0.20lm
S32	5.44 ± 0.01p	25.81 ± 0.08rs	42.32 ± 0.31pq	20.13 ± 0.22q	23.34 ± 0.10q	32.13 ± 0.02o	12.62 ± 0.09no	38.73 ± 0.35mn
S33	5.52 ± 0.51p	19.97 ± 0.36uv	35.11 ± 0.57st	8.14 ± 0.10r	18.57 ± 0.35r	25.01 ± 0.52p	10.08 ± 0.24p	39.33 ± 0.81mn
S34	4.18 ± 0.16q	19.56 ± 0.37uv	31.13 ± 0.49t	9.78 ± 0.15r	15.22 ± 0.09s	25.78 ± 0.36p	9.12 ± 0.11p	20.32 ± 0.09st
S35	14.47 ± 0.05l	59.50 ± 0.02j	60.18 ± 0.04l	43.36 ± 0.58k	48.62 ± 0.41l	54.07 ± 0.04j	22.92 ± 0.63l	60.12 ± 0.89j
Stdeva	13.23	30.61	50.43	35.46	28.16	33.09	19.36	53.52
Average	18.16	53.09	86.1	53.67	52.41	54.69	26.93	74.89
CV%	72.85	57.66	58.58	66.07	53.73	60.51	71.92	71.47

Table 2: Continued.

Name	Content mg/100 g						
	Pro	EAA	NEAA	CEAA	MAA	BCAA	TAA
S1	13.21 ± 0.07v	255.16	398.41	60.05	416.27	135.09	653.57
S2	18.23 ± 0.21u	252.01	348.64	63.89	371.61	129.66	600.65
S3	10.12 ± 0.30v	171.16	227.51	45.9	254.08	93.49	398.67
S4	39.67 ± 0.76s	901.54	1689.02	287.07	1640.16	496.36	2590.56
S5	19.88 ± 0.57tu	242.71	449.43	58.43	452.22	129.11	692.14
S6	14.01 ± 0.17v	140.23	310.42	49.06	271.74	83.04	450.65
S7	49.51 ± 0.73p	235.53	396.44	46.7	380.06	115.08	631.97
S8	184.99 ± 0.17c	531.53	1501.19	126.18	1309.53	296.13	2032.72
S9	111.27 ± 1.16j	362.21	818.12	72.52	716.59	195.21	1180.33
S10	34.17 ± 0.34r	816.1	1390.69	247.78	1524.08	459.74	2206.79
S11	76.32 ± 1.59m	167.59	353.15	30.33	267.12	103.82	520.74
S12	67.22 ± 0.99n	219.18	445.01	33.73	409.96	106.59	664.19
S13	75.81 ± 0.01m	213.96	487.45	47.28	409.69	119.79	701.41
S14	155.46 ± 1.98h	565.7	1184.6	177.14	1121.19	314.14	1750.3
S15	175.66 ± 0.75e	589.93	1318.66	176.57	1207.25	339.39	1908.59
S16	191.61 ± 5.91b	660.33	1464.91	166.53	1341.43	365.69	2125.24
S17	91.91 ± 2.68k	399.88	790.91	114.88	717.66	223.11	1190.79
S18	160.31 ± 2.17g	740.85	1450.12	211.53	1418.23	413.8	2190.97
S19	60.81 ± 1.98o	162.89	381.3	29.77	299.47	99.04	544.19
S20	73.17 ± 2.94m	332.77	634.72	73.84	582.95	187.05	967.49
S21	58.56 ± 0.55o	231.79	429.62	40.78	386.92	129.38	661.41
S22	170.06 ± 2.05f	637.22	1348.76	200.39	1268.35	351.1	1985.98
S23	81.41 ± 2.50l	291.89	510.22	42.14	459.38	148.96	802.11
S24	119.97 ± 4.86i	508.32	1022.66	119.04	926.6	268.45	1530.98
S25	179.47 ± 6.54d	693.51	1413.48	227.68	1343.74	388.44	2106.99
S26	44.47 ± 1.05q	122.83	273.37	22.35	219.81	78.86	396.2
S27	118.33 ± 2.81i	590.13	1042.46	112.68	983.94	299.21	1632.59
S28	156.27 ± 2.96h	526.43	1202.91	116.73	1038.96	278.56	1729.34
S29	172.81 ± 3.72ef	396.78	1183.87	122.28	939.18	214.16	1580.65
S30	256.67 ± 1.34a	662.21	1662.1	167.84	1424.56	340.05	2324.31
S31	23.39 ± 0.75t	239	431.07	59.32	424.73	122.45	670.07
S32	18.83 ± 0.31u	193.5	390.22	51.35	388.3	104.45	583.72
S33	13.02 ± 0.59v	153.75	281.75	49.41	298.83	84.06	435.5
S34	10.88 ± 0.26v	146.79	237.41	29.44	238.1	80.34	384.2
S35	22.83 ± 0.91t	346.44	448.31	83.04	490.29	180.45	794.75
Stdeva	68.19	221.82	488.31	71.68	455.23	122.46	702.91
Average	87.72	391.48	797.68	101.82	741.23	213.55	1189.16
CV%	77.74	56.66	61.22	70.4	61.42	57.35	59.11

Means with different letters in the same column express significant differences (Duncan's test $p < 0.05$).

Table 3: Comparison of essential amino acids and FAO/WHO amino acid patterns in different resource fruits of *A. arguta*.

Name	%						
	Leu	Val	Met + Cys	Ile	Thr	Phe + Tyr	Lys
S1	6.86	6.85	2.54	6.96	5.78	12.78	6.02
S2	7	7.13	2.79	7.46	6.71	12.11	6.6
S3	8.08	7.61	3.55	7.76	5.56	11.85	6.61
S4	7.17	6.86	2.81	5.13	5.18	9.99	5.12
S5	7.03	6.43	2.41	5.19	5.14	7.74	5.95
S6	7.77	7.14	6.02	3.52	4.6	6.48	4.73
S7	8.38	5.51	4.19	4.32	3.85	15.57	5.15
S8	5.85	4.89	2.04	3.82	4.05	7.01	3.47
S9	6.6	5.96	4.99	3.98	3.85	8.41	3.71
S10	8.76	7.07	3.62	5.01	4.39	6.78	5.37
S11	7.87	8.13	9.39	3.94	3.31	9.09	2.36
S12	6.5	5.9	5.86	3.65	3.67	12.54	4.02
S13	7.46	5.76	4.2	3.86	3.83	10.59	3.85
S14	7.81	5.98	3.73	4.16	3.99	6.34	4.18
S15	7.38	6.03	3.13	4.38	4.23	5.97	3.58
S16	6.83	6.01	2.67	4.37	4.54	6.83	4.12
S17	7.46	6.84	5.07	4.44	4.27	9.96	3.93
S18	7.79	6.63	2.96	4.47	4.27	6.7	4.75
S19	7.27	6.88	8.78	4.04	3.65	10.54	2.42
S20	7.63	7.15	4.84	4.55	4.83	8.31	3.74
S21	8.35	6.77	4.55	4.45	5.04	11.03	4.17
S22	7.39	5.93	3.09	4.35	4.28	8.35	4.37
S23	7.69	6.92	7	3.96	4.04	12.47	3.87
S24	7.57	5.51	2.49	4.46	4.7	10.5	5.17
S25	7.87	6.24	3.3	4.32	3.92	8.46	4.23
S26	9.14	6.2	6.33	4.56	4.81	7.05	3.53
S27	7.15	6.67	1.79	4.51	4.93	12.14	6.7
S28	6.51	5.78	4.04	3.83	4.15	9.36	4.21
S29	5.64	4.66	2.78	3.25	3.67	11.6	3.68
S30	5.79	5.3	2.67	3.54	3.95	9.35	4.56
S31	6.97	7.04	3.81	4.27	4.83	6.89	6.27
S32	7.25	6.22	2.3	4.42	4.82	7.45	5.5
S33	8.06	6.65	2.76	4.59	4.73	6.13	5.74
S34	8.1	7.72	3.34	5.09	5.54	6.51	6.71
S35	7.57	7.65	3.06	7.49	6.14	11.57	6.8
FAO/WHO standard mode	4	5	3.5	7	4	6	5.5

the Val ideal model, 17 resources that fit the Met + Cys ideal model, 3 resources that fit the Ile ideal model, 10 resources that did not fit the Thr ideal model, 1 resource that did not fit the Phe + Tyr ideal model, and 24 resources that did not fit the Lys ideal model.

In accordance with the ideal amino acid composition proposed by WHO/FAO, EAA/TAA is 40%, EAA/NEAA is ≥60%, and BCAAs should account for 40% of the daily EAA requirement for adults, 41% for children, and 45% for infants [60–62].

Figure 3(a) shows the distribution range of amino acid nutritional value of different *A. arguta* resources, and it can be seen that the range of EAA/TAA of fruits of different *A. arguta* resources was 26.15%~43.59%, among which there were three resources that met the EAA/TAA standard, with a value of 41%~44%; meanwhile, Figure 3(b) shows the distribution range of amino acid nutritional value of different *A. arguta* resources and the range of EAA/NEAA ranged from 33.52% to 77.28%, among which there were five resources that met the EAA/NEAA standard, and S2 (A040103), S3 (A060902), and S35 (SH5) met the standard for both EAA/TAA and EAA/NEAA.

The higher the ratio of medicinal amino acids/total amino acids (MAA/TAA), the higher the medicinal value of the substance. Figure 3(c) shows the distribution range of amino acid nutritional value of different *A. arguta* resources, the MAA/TAA ratios of 35 *A. arguta* resources were all in the range of 51.30%~69.06%, and the MAA/TAA ratios of 28 of the resources were more than 60%, which are the results that indicate that the *A. arguta* has a high medicinal value.

Branched-chain amino acids, collectively known as leucine, valine, and isoleucine, are not only important components of human proteins but also regulators of protein, glucose, energy metabolism, and brain functions [63]. Figure 3(d) shows the distribution range of amino acid nutritional value of different *A. arguta* resources, all the resources achieved ≥40% BCAA/EAA, the range is 48.63%~64.20%, and three of the BCAA/EAA were more than 60%, which were 61.95% for S11, 60.80% for S19, and 64.20% for S26.

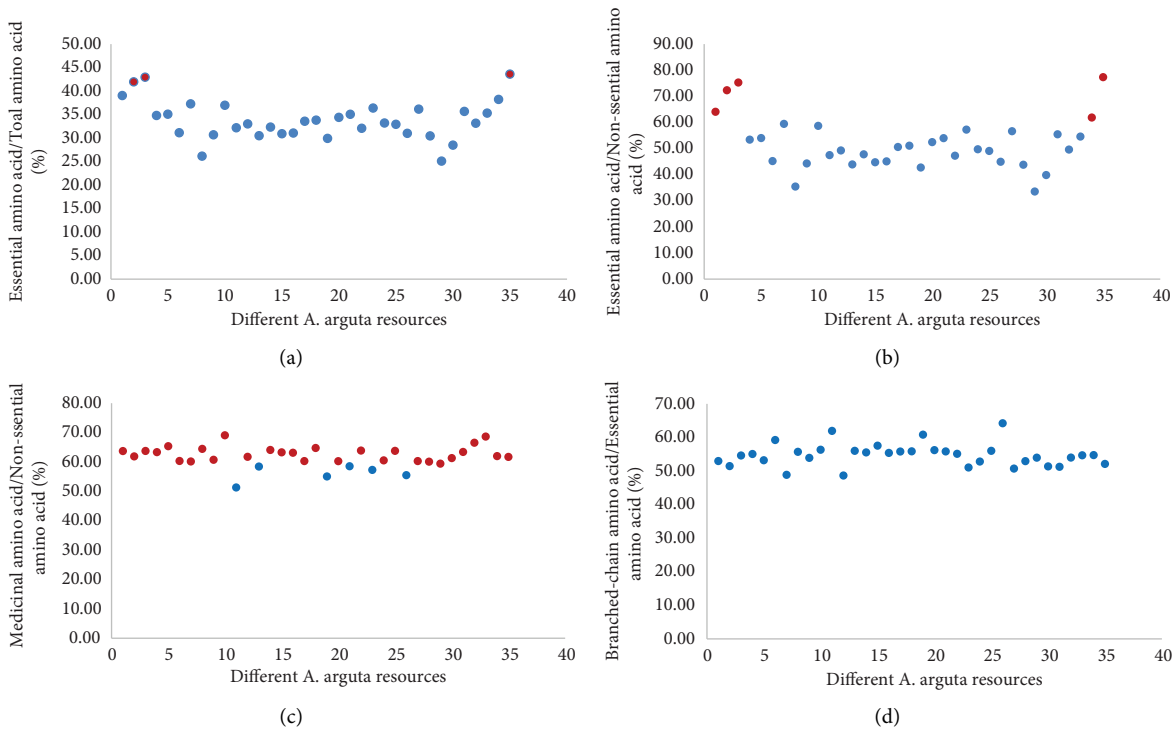

Figure 3: Distribution range of amino acid nutritional value of different *A. arguta* resources. (a) Essential amino acids/total amino acids (%). (b) Essential amino acids/nonessential amino acids (%). (c) Medicinal amino acids/total amino (%). (d) Branched-chain amino acids/essential amino acids (%).

3.4. Comparison of Amino Acid RAA, RC, and SRC in Fruits of Different A. arguta Resources. Amino acid balance theory suggests that the closer the amino acid composition of a food protein is to the pattern amino acid composition, the higher its nutritional value [51]. Based on the amino acid balance theory, RC and SRC were calculated to evaluate the quality of proteins based on the dispersion of various essential amino acids from the amino acid pattern, which is closer to the biological price [53, 54]. The RAA values of the fruits of different soft date kiwifruit resources are shown in Table 4. Values of RAA of different *A. arguta* resources and the RAA values of the two amino acids Leu and Val were greater than 1 in 35 resources. Whether the proportion of essential amino acids in a food conforms to the human essential amino acid pattern profile is closely related to the size of the RC, with $RC = 1$ conforming, whereas $RC < 1$ indicates a relative deficiency, and the amino acid with the lowest content is considered to be the limiting amino acid of the substance. Figure 4 shows the range of RC values of 9 amino acids, and the Leu of all 35 *A. arguta* resources is greater than 1, indicating that the content of this amino acid in *A. arguta* fruits exceeds the human body's needs; the RC values of Ile and Lys are less than 1, and the content of Ile is lower than that of Lys, indicating that the first limiting amino acid of *A. arguta* resource fruits is Ile, and the second limiting amino acid is Lys, so when consuming *A. arguta*, it is necessary to eat food rich in isoleucine and lysine with it, such as spinach, potatoes, bean curd, soya bean milk, and eggs.

Modern scientific research has identified that amino acid deficiency can negatively affect the nutritional value of food. In order to measure whether the amino acid composition of a food is reasonable or not, the SRC value was introduced, which is a measure of how well the amino acids in a food match the model, and the closer the value is to 100, the closer the amino acid composition of the food is to the ideal model, and, therefore, the higher the nutritional value of the meal can be. Figure 5 shows the distribution of SRC value in different *A. arguta* resources. The SRC values of 35 *A. arguta* resources' fruits were between 40 and 80, of which 20 resources had SRC values of 60~70, which accounted for 57.14% of the samples supplied for testing, and three resources had SRC values of more than 70, with the highest score being S3.

3.5. Analysis of Taste-Presenting Amino Acids in Fruits of Different A. arguta Resources

3.5.1. Taste-Presenting Amino Acids Content and Radar Chart Analysis. *A. arguta* fruit has a unique sweet and sour taste when eaten fresh, which is closely linked to its rich amino acid content. Based on the flavor-presenting characteristics, the flavor-presenting amino acids can be classified into four groups, namely, fresh amino acids (Glu, Asp, and Lys), sweet amino acids (Thr, His, Ser, Pro, Gly, and Ala), bitter amino acids (Val, Met, Leu, Ile, and Arg), and aromatic amino acids (Cys, Tyr, and Phe) [49], and the contents of the four taste-presenting amino acids of different

Table 4: Values of RAA of different *A. arguta* resources.

Name	Leu	Val	Met + Cys	Ile	Thr	Phe + Tyr	Lys
S1	1.71	1.37	0.73	0.99	1.44	2.13	1.09
S2	1.75	1.43	0.8	1.07	1.68	2.02	1.2
S3	2.02	1.52	1.01	1.11	1.39	1.98	1.2
S4	1.79	1.37	0.8	0.73	1.3	1.66	0.93
S5	1.76	1.29	0.69	0.74	1.29	1.29	1.08
S6	1.94	1.43	1.72	0.5	1.15	1.08	0.86
S7	2.09	1.1	1.2	0.62	0.96	2.59	0.94
S8	1.46	0.98	0.58	0.55	1.01	1.17	0.63
S9	1.65	1.19	1.43	0.57	0.96	1.4	0.68
S10	2.19	1.41	1.04	0.72	1.1	1.13	0.98
S11	1.97	1.63	2.68	0.56	0.83	1.51	0.43
S12	1.62	1.18	1.68	0.52	0.92	2.09	0.73
S13	1.86	1.15	1.2	0.55	0.96	1.77	0.7
S14	1.95	1.2	1.07	0.59	1	1.06	0.76
S15	1.84	1.21	0.89	0.63	1.06	1	0.65
S16	1.71	1.2	0.76	0.62	1.14	1.14	0.75
S17	1.87	1.37	1.45	0.63	1.07	1.66	0.71
S18	1.95	1.33	0.84	0.64	1.07	1.12	0.86
S19	1.82	1.38	2.51	0.58	0.91	1.76	0.44
S20	1.91	1.43	1.38	0.65	1.21	1.38	0.68
S21	2.09	1.35	1.3	0.64	1.26	1.84	0.76
S22	1.85	1.19	0.88	0.62	1.07	1.39	0.79
S23	1.92	1.38	2	0.57	1.01	2.08	0.7
S24	1.89	1.1	0.71	0.64	1.18	1.75	0.94
S25	1.97	1.25	0.94	0.62	0.98	1.41	0.77
S26	2.29	1.24	1.81	0.65	1.2	1.18	0.64
S27	1.79	1.33	0.51	0.64	1.23	2.02	1.22
S28	1.63	1.16	1.15	0.55	1.04	1.56	0.77
S29	1.41	0.93	0.79	0.46	0.92	1.93	0.67
S30	1.45	1.06	0.76	0.51	0.99	1.56	0.83
S31	1.74	1.41	1.09	0.61	1.21	1.15	1.14
S32	1.81	1.24	0.66	0.63	1.21	1.24	1
S33	2.02	1.33	0.79	0.66	1.18	1.02	1.04
S34	2.03	1.54	0.96	0.73	1.38	1.08	1.22
S35	1.89	1.53	0.88	1.07	1.54	1.93	1.24

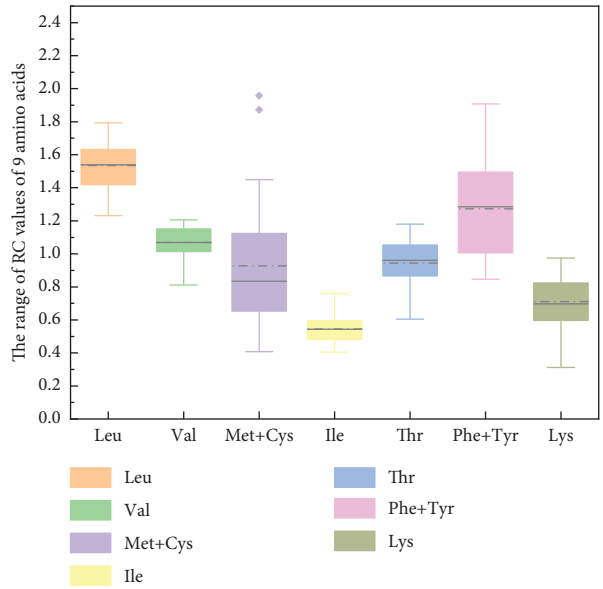

Figure 4: The range of RC values of 9 amino acids.

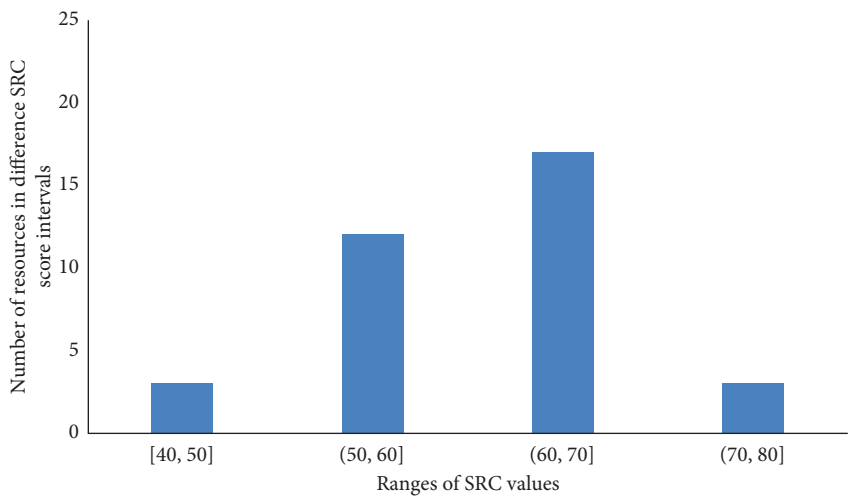

Figure 5: Distribution of SRC value in different *A. arguta* resources.

A. arguta resources are shown in Figure 6. Figure 6 shows the contents of flavored amino acids in different *A. arguta* resources mg/100 g, the variation of the fresh amino acid content was 116.24~980.29 mg/100 g, the variation of the sweet amino acid content was 90.53~687.23 mg/100 g, the variation of the bitter amino acid content was 98.95~730.29 mg/100 g, and the variation of aromatic amino acid content was 33.19~292.48 mg/100 g. The resource with the highest content of fresh, bitter, and aromatic amino acids was S4, and the resource with the highest content of sweet amino acids was S16.

Radar plot analysis of the flavor-presenting amino acids of different A. arguta resources shows that, as can be seen from Figure 7, those that contribute more to the flavor of A. arguta are fresh amino acids and sweet amino acids, and the larger area of the pattern plot of S4 compared with the other resources indicates that the content of flavor amino acids in S4 is generally higher than that of the other resources 7. Figure 7 shows the flavor amino acid radar map of different *A. arguta* resources, the greater contribution in the flavor of *A. arguta* was made by fresh taste amino acids and sweet taste amino acids, and the larger area of the pattern plot of S4 compared with other resources indicated that the taste amino acid content of S4 was generally higher than that of other resources. The unique flavor of *A. arguta* may be closely related to its high content of gustatory amino acids. The high percentage of fresh and sweet amino acids such as Glu, Asp, and Ala gives the *A. arguta* its fresh, sweet, and sour flavor characteristics, while effectively reducing the bitterness of the rind and alleviating the undesirable taste brought about by the rind.

3.5.2. TAV Analysis. Different amino acids have different taste perception thresholds, so higher amino acid content does not necessarily contribute more to food flavor [54], further analysis of the effect of each presenting amino acid on fruit flavor quality by TAV values is needed, and the TAV of different *A. arguta* resources presenting amino acids is shown in Table 5. When TAV > 1 is present, then the amino acid contributes to flavor quality. As shown in Table 5, the amino acids with TAV values greater than 1 in all 35 *A. arguta* were Glu and Cys, the amino acids with TAV values less than 1 in all were Thr and Tyr, and the remaining amino acids had TAV values greater than 1 in some resources. Thus, Glu and Cys were the main contributors to the flavor of the 35 *A. arguta* resources, but in comparison, the mean TAV of Cys was greater than that of Glu, so Cys was the main influence on the flavor of *A. arguta*.

3.6. Correlation Analysis of Amino Acid Content of Different A. arguta Resources. The correlation analysis of 17 of the 35 *A. arguta* was carried out, and the results are shown in Figure 8. Correlation analysis of amino acid content in different *A. arguta* resources is shown in Figure 8. 17 amino acids were all highly significant and positively correlated, of which the correlation coefficient between Ser and Thr was as high as 0.99; the correlation coefficient between Cys and Pro was higher, 0.63, and the correlation coefficients with the other amino acids were all below 0.6; in short, the correlation of the amino acid fractions was strong, which was similar to the results of the study by Min et al. [64].

3.7. PCA Analysis. The PCA method can simplify multiple indicators with correlation into several relatively independent and representative indicators, retaining the vast majority of the original information, which is faster and more accurate compared with a single evaluation, and at the same time, it can also avoid the influence of correlation between traits on the evaluation results [65, 66], and it has been widely used in the evaluation of the quality of agricultural products such as jujube [21], *A. arguta* [19], black fungus [67], and peach [68]. PCA of the amino acids of different *A. arguta* resources is shown in Figure 9. PCA scores of amino acid content in different *A. arguta* resources revealed that S4, S10, S18, and S27 were located in quadrant 1, but all of them were located in scattered locations, indicating that the amino acid contents of these four resources were not similar; there were 10 resources located in quadrant 2, of which S8, S15, S22, S16, and S25 were closer to each

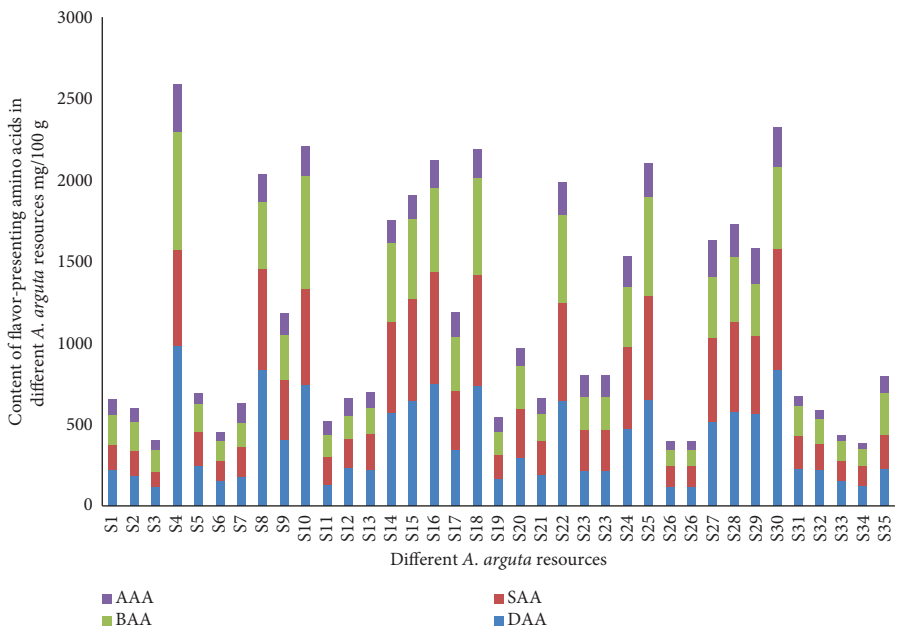

Figure 6: Contents of flavored amino acids in different *A. arguta* resources mg/100 g.

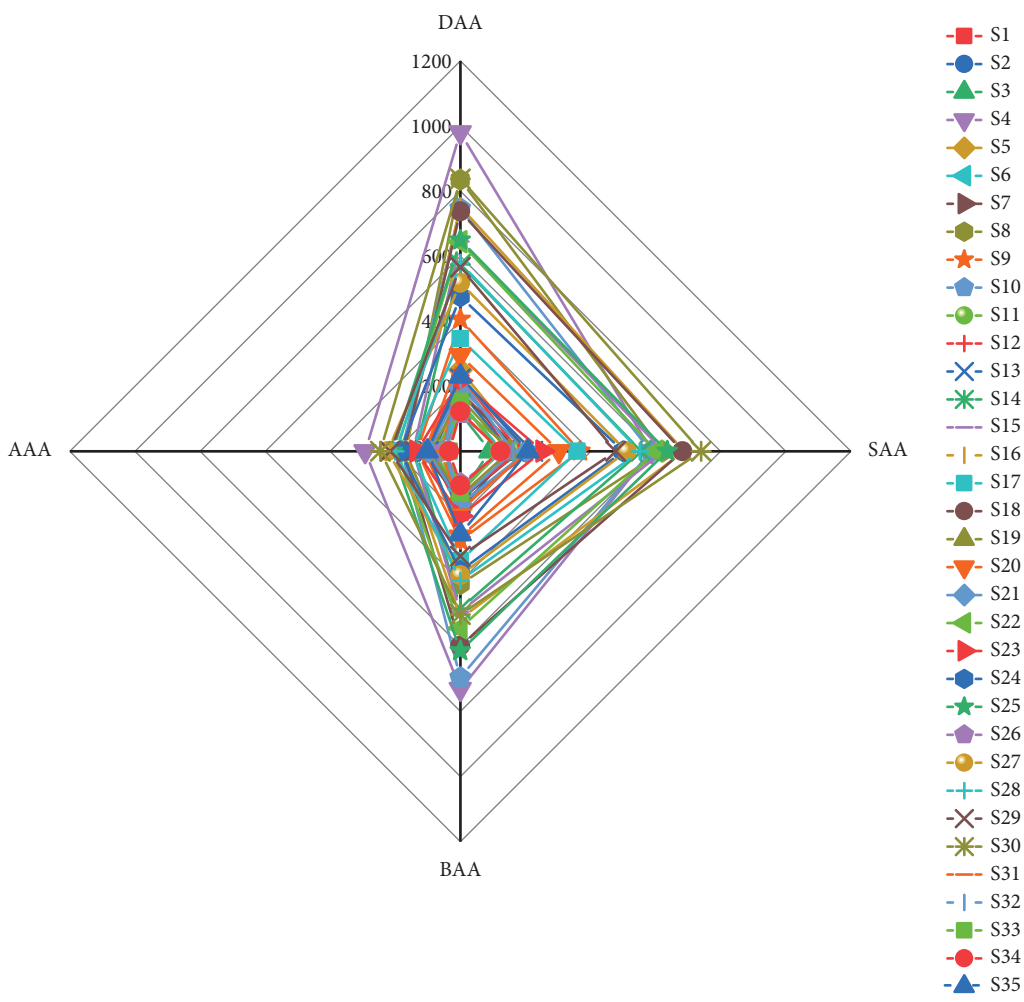

Figure 7: Flavor amino acid radar map of different *A. arguta* resources.

Table 5: Taste activity values of flavor amino acids in different *A. arguta* resources.

Sort	Amino acid	Taste threshold (mg/g) [49]	TAV																	
			S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15	S16	S17	S18
DAA	Asp	1	0.72	0.69	0.4	3.13	0.81	0.36	0.43	3.55	1.1	2.19	0.3	0.52	0.69	1.5	1.98	2.42	0.98	2.71
	Glu	0.3	3.77	2.51	1.74	17.82	4.26	3.16	3.55	13.61	8.4	13.59	2.92	5.13	4.23	11.71	12.63	14.04	6.7	12.04
	Lys	0.5	0.79	0.79	0.53	2.65	0.82	0.43	0.65	1.41	0.88	2.37	0.25	0.53	0.54	1.46	1.37	1.75	0.94	2.08
SAA	Thr	2.6	0.15	0.15	0.09	0.52	0.14	0.08	0.09	0.32	0.17	0.37	0.07	0.09	0.1	0.27	0.31	0.37	0.2	0.36
	His	0.2	0.72	0.94	0.54	4.62	0.88	0.95	0.9	1.49	0.96	3.03	0.5	0.5	0.71	2.35	2.53	2.36	1.53	3.24
	Ser	1.5	0.24	0.23	0.14	0.85	0.24	0.18	0.19	0.62	0.33	0.67	0.14	0.17	0.22	0.53	0.59	0.66	0.37	0.68
	Pro	3	0.04	0.06	0.03	0.13	0.07	0.05	0.17	0.62	0.37	0.11	0.25	0.22	0.25	0.52	0.59	0.64	0.31	0.53
	Gly	1.3	0.1	0.1	0.07	0.06	0.31	0.18	0.2	0.77	0.42	1.13	0.16	0.19	0.26	0.76	0.85	0.94	0.51	1.05
	Ala	0.6	0.58	0.45	0.31	3.09	0.88	0.41	0.59	2.21	1.45	2.43	0.42	0.47	0.64	1.75	1.97	2.17	1.06	2.08
BAA	Val	0.4	1.12	1.07	0.76	4.44	1.11	0.8	0.87	2.49	1.76	3.9	1.06	0.98	1.01	2.62	2.88	3.19	2.04	3.63
	Met	0.3	0.24	0.25	0.19	1.31	0.25	0.14	0.2	0.54	0.85	1.64	0.52	0.41	0.2	1.31	0.92	0.99	0.99	1.23
	Ile	0.9	0.51	0.5	0.34	1.48	0.4	0.18	0.3	0.86	0.52	1.23	0.23	0.27	0.3	0.81	0.93	1.03	0.59	1.09
	Leu	1.9	0.24	0.22	0.17	0.98	0.26	0.18	0.28	0.63	0.41	1.02	0.22	0.23	0.28	0.72	0.74	0.76	0.47	0.9
	Arg	0.5	0.91	0.9	0.7	3.9	0.82	0.6	0.57	1.93	1.07	3.74	0.41	0.48	0.66	2.6	2.52	2.39	1.69	2.94
AAA	Tyr	2.6	0.18	0.15	0.09	0.61	0.09	0.07	0.16	0.29	0.18	0.22	0.11	0.13	0.15	0.16	0.15	0.25	0.27	0.21
	Phe	0.9	0.4	0.39	0.26	1.1	0.33	0.12	0.64	0.74	0.58	1.02	0.21	0.55	0.38	0.77	0.82	0.9	0.55	1.03
	Cys	0.02	4.64	4.7	4.16	16.85	4.56	11.49	10.24	12.68	16.76	15.43	16.59	13.28	11.66	13.06	16.13	13.49	15.39	13.89

Sort	Amino acid	Taste threshold (mg/g) [49]	TAV																
			S19	S20	S21	S22	S23	S24	S25	S26	S27	S28	S29	S30	S31	S32	S33	S34	S35
DAA	Asp	1	0.38	0.91	0.59	1.83	0.61	1.34	1.78	0.31	1.59	1.64	1.43	2.03	0.78	0.88	0.5	0.42	0.79
	Glu	0.3	3.76	5.61	3.58	12.47	4.16	8.76	12.74	2.36	8.31	11.41	12.14	17.61	3.57	3.36	2.62	1.8	3.24
	Lys	0.5	0.26	0.72	0.55	1.73	0.62	1.58	1.78	0.28	2.19	1.46	1.16	2.12	0.84	0.64	0.5	0.52	1.08
SAA	Thr	2.6	0.08	0.18	0.13	0.33	0.12	0.28	0.32	0.07	0.31	0.28	0.22	0.35	0.12	0.11	0.08	0.08	0.19
	His	0.2	0.26	0.91	0.56	1.94	0.68	1.59	2.11	0.24	1.77	1.42	1.3	1.98	0.88	0.63	0.5	0.46	1.15
	Ser	1.5	0.15	0.33	0.21	0.58	0.26	0.52	0.6	0.14	0.56	0.61	0.43	0.66	0.24	0.21	0.15	0.15	0.34
	Pro	3	0.2	0.24	0.2	0.57	0.27	0.4	0.6	0.15	0.39	0.52	0.58	0.86	0.08	0.06	0.04	0.04	0.08
	Gly	1.3	0.14	0.39	0.29	0.89	0.32	0.7	0.92	0.16	0.75	0.69	0.54	0.9	0.3	0.24	0.2	0.2	0.13
	Ala	0.6	0.41	1.07	0.55	1.76	0.73	1.79	2.05	0.33	1.59	1.91	1.44	2.24	0.98	0.67	0.45	0.57	0.76
BAA	Val	0.4	0.94	1.73	1.12	2.95	1.39	2.11	3.29	0.61	2.72	2.5	1.84	3.08	1.18	0.91	0.72	0.74	1.52
	Met	0.3	0.44	0.66	0.16	1.02	0.71	0.42	1.33	0.09	0.13	1.05	0.38	1.12	0.51	0.18	0.18	0.14	0.48
	Ile	0.9	0.24	0.49	0.33	0.96	0.35	0.76	1.01	0.2	0.82	0.74	0.57	0.91	0.32	0.29	0.22	0.22	0.66
	Leu	1.9	0.21	0.39	0.29	0.77	0.32	0.61	0.87	0.19	0.61	0.59	0.47	0.71	0.25	0.22	0.18	0.16	0.32
	Arg	0.5	0.49	1.11	0.59	3.23	0.57	1.74	3.71	0.35	1.55	1.77	1.93	2.57	0.83	0.77	0.79	0.41	1.2
AAA	Tyr	2.6	0.15	0.14	0.14	0.32	0.16	0.32	0.33	0.08	0.39	0.35	0.49	0.49	0.07	0.08	0.03	0.04	0.17
	Phe	0.9	0.2	0.48	0.41	0.93	0.65	0.85	1.04	0.09	1.08	0.8	0.61	1.01	0.3	0.26	0.21	0.17	0.54
	Cys	0.02	17.29	13.46	12.59	15.41	17.48	12.86	14.79	11.24	12.63	19.19	16.23	14.29	5.07	3.99	3.24	4.34	4.94

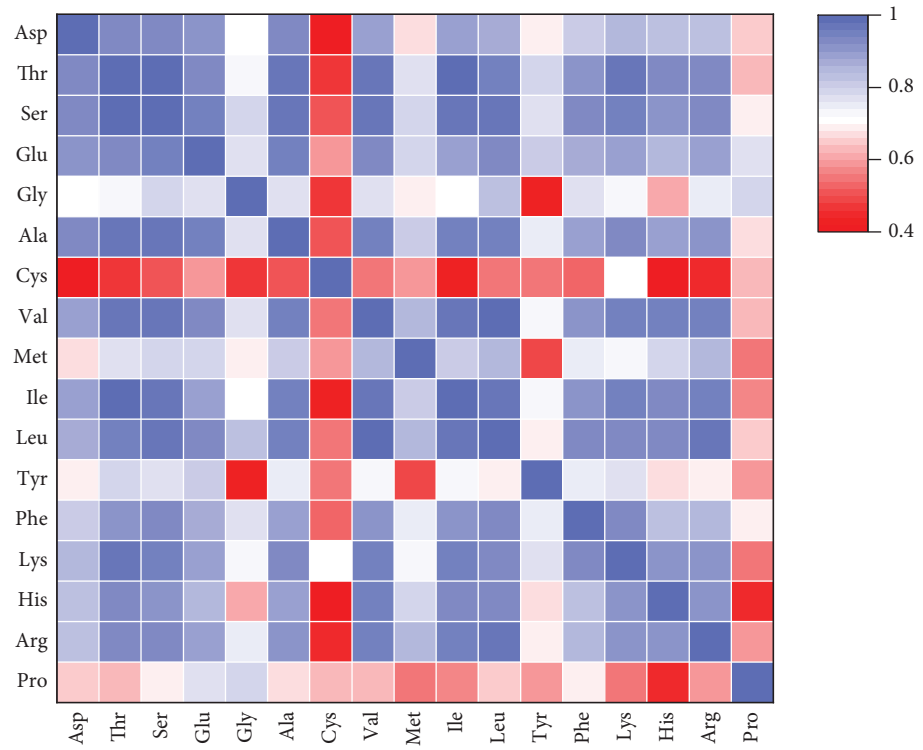

Figure 8: Correlation analysis of amino acid content in different *A. arguta* resources.

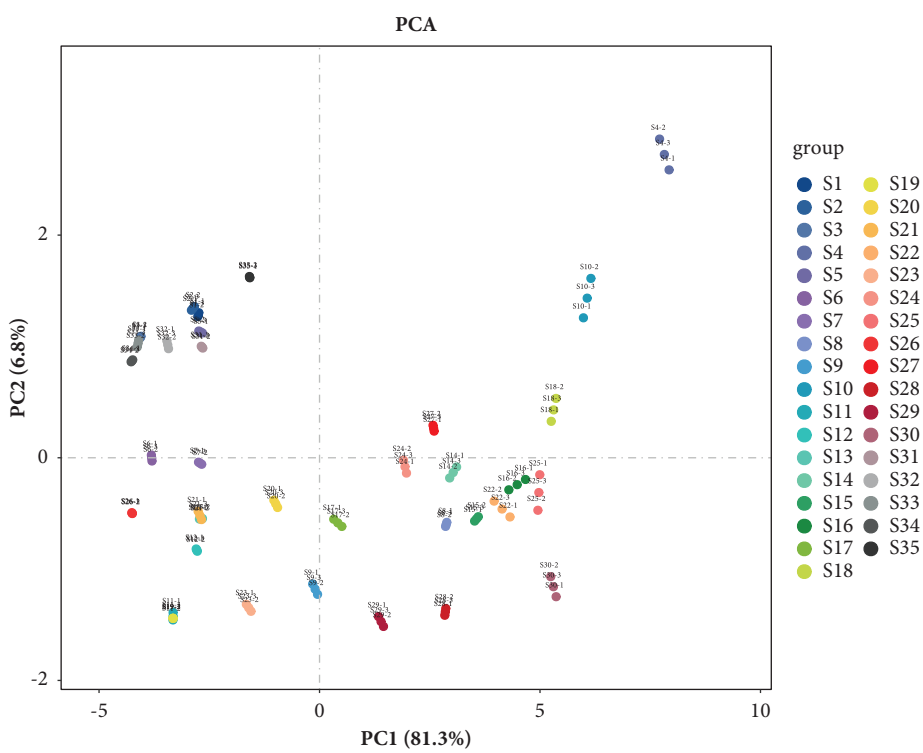

Figure 9: PCA scores of amino acid content in different *A. arguta* resources.

other, indicating that the amino acid contents of these five resources were similar; S11, S12, S20, S21, S23, and S26 are located in quadrant 3; S1, S2, S5, S31, S32, S33, S34, and S35 are located in quadrant 4, but S35 is far away from the other resources, indicating that the amino acid content is similar among the resources except for S35; S6, S7, and S24 are

Table 6: Factor loading matrix and contribution rate after rotation.

PC	Asp	Thr	Ser	Glu	Gly	Ala	Cys	Val	Met	Ile	Leu	Tyr	Phe	Lys	His	Arg	Pro	Eigenvalue	Contribution rate (%)	Cumulative contribution rate (%)
1	0.848	0.927	0.891	0.792	0.585	0.879	0.175	0.903	0.698	0.946	0.877	0.636	0.807	0.936	0.937	0.899	0.345	10.846	63.797	63.797
2	0.353	0.348	0.432	0.562	0.61	0.428	0.863	0.408	0.47	0.289	0.446	0.453	0.474	0.269	0.196	0.334	0.851	4.094	24.083	87.880

Table 7: Comprehensive evaluation results of amino acids of different *A. arguta* resources.

No.	$F1$	$F2$	F	Rank
S1	−0.06	−1.45	−0.44	19
S2	−0.06	−1.51	−0.46	22
S3	−0.48	−1.45	−0.74	29
S4	3.16	−1.19	1.97	1
S5	−0.11	−1.32	−0.44	20
S6	−0.93	−0.51	−0.81	32
S7	−0.70	−0.31	−0.60	25
S8	0.65	0.76	0.68	9
S9	−0.58	0.98	−0.15	16
S10	2.07	−0.32	1.42	2
S11	−1.49	0.75	−0.87	34
S12	−1.07	0.32	−0.69	28
S13	−0.89	0.08	−0.63	26
S14	0.62	0.55	0.60	10
S15	0.61	0.93	0.70	8
S16	1.01	0.78	0.95	6
S17	−0.22	0.57	0.00	15
S18	1.52	0.35	1.20	3
S19	−1.49	0.76	−0.87	33
S20	−0.44	0.22	−0.26	18
S21	−0.90	0.06	−0.64	27
S22	0.76	0.96	0.81	7
S23	−1.05	0.93	−0.51	23
S24	0.41	0.33	0.39	13
S25	0.99	0.97	0.99	4
S26	−1.25	−0.17	−0.96	35
S27	0.74	0.12	0.57	11
S28	0.03	1.55	0.45	12
S29	−0.34	1.40	0.14	14
S30	0.73	1.68	0.99	5
S31	−0.17	−1.19	−0.45	21
S32	−0.31	−1.34	−0.59	24
S33	−0.50	−1.42	−0.75	30
S34	−0.61	−1.31	−0.80	31
S35	0.35	−1.55	−0.17	17

located in the horizontal axis, which indicates that they are mainly influenced by PC1; S9 is located in the vertical axis, which indicates that it is importantly influenced by PC2.

3.8. Comprehensive Evaluation of Amino Acids of Different A. arguta Resources. As can be seen from Table 6, a total of 2 principal components were extracted using factor analysis, the contribution of the first principal component was 63.979%, the contribution of the second principal component was 24.083%, and the cumulative variance of the first 2 PCs reached 87.88%, Gly, Cys, and Pro were the principal component 2, and the remaining 14 amino acids were the principal component 1. Table 6 shows the factor loading matrix and contribution rate after rotation that a comprehensive evaluation of different *A. arguta* resources using the first 2 PCs is feasible.

With 17 amino acid indicators as the initial independent variables, the equation expressions for the three PC factors were finally derived by PCA as follows:

$$\begin{aligned} F1 &= 0.102X1 + 0.125X2 + 0.086X3 + \ldots + 0.182X15 + 0.123X16 - 0.208X17, \\ F2 &= -0.049X1 - 0.080X2 - 0.008X3 + \ldots - 0.191X15 - 0.080X16 + 0.482X17. \end{aligned} \tag{2}$$

The relative contribution of the variance of the two PCs was used as the weight, and the PC scores of each resource and the corresponding weights were linearly weighted and summed to establish a comprehensive evaluation function $F = 0.726F1 + 0.274F2$. The comprehensive score of each *A. arguta* resource was calculated to reflect its comprehensive amino acid quality, and the higher the comprehensive score, the better the amino acid quality of the resource. As shown in Table 7, comprehensive evaluation results of amino acids of different *A. arguta* resources, the

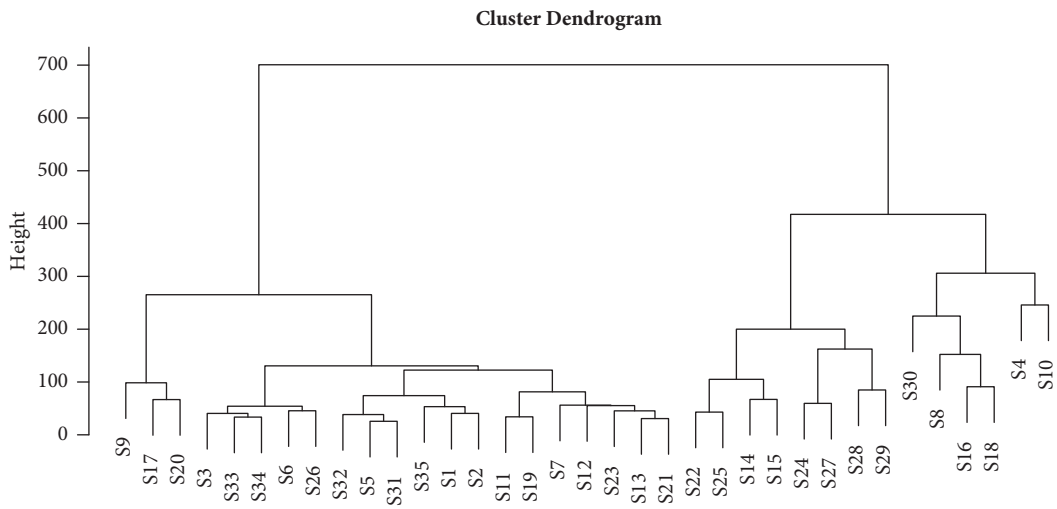

Figure 10: Hierarchical cluster analysis of amino acid contents of *A. arguta* resources.

top 5 resources in terms of the overall score were S4, S10, S18, S25, and S30, indicating that these five *A. arguta* resources had relatively good overall amino acid evaluations.

3.9. Hierarchical Clustering Analysis of Amino Acids in Different A. arguta Resources. The results of the hierarchical cluster analysis of 17 amino acids in 35 *A. arguta* resources are shown in Figure 10. All *A. arguta* resources could be classified into four categories when the transect line took the value of 300, category 1 contained S4 and S10, category 2 contained S30, S8, S16, and S18, category 3 contained S22, S25, S14, S15, S24, S27, S28, and S29, and the remaining 21 resources were all in category 4, among which S4 and S10 in category 1 had the highest amino acid content and better quality. The clustering results were consistent with the comprehensive evaluation results of PCA. Therefore, it can provide a good reference for the introduction and promotion of excellent resources of *A. arguta*, the development and utilization of products, and the evaluation of amino acid nutritional value.

4. Conclusion

In this study, an amino acid analyzer was used to separate and determine the amino acid composition and content of 35 *A. arguta* resource fruits from the Zuojia Town *Actinidia arguta* and *Magnolia vine* National Forest Germplasm Resource Bank in Jilin Province, and the results showed that *A. arguta* fruits contained 17 amino acids, with a total amino acid content of 384.20~2590.56 mg/100 g and that the average contents of NEAA and MAA had higher average contents than others, which were the main components of TAA in *A. arguta*. The analysis of the variance results showed that the standard deviation of the 17 amino acids had a variance of 9.68~146.87, the coefficient of variation was 40.94%~77.74%, and the content of different amino acids differed significantly among resources, of which the coefficient of variation of Pro was the largest and the coefficient of variation of Gys was the smallest. Meanwhile, the amino acids varied significantly among most of the A. arguta resources, with mean values ranging from 18.16~222.22 mg/100 g.Among them, the lowest content was Met, and the highest content was Glu. The results of amino acid nutritional value evaluation showed that the Leu of 35 *A. arguta* resources conformed to the ideal model proposed by FAO/WHO, and the RAA value of Leu of all resources was greater than 1, which indicated that the content of this amino acid in *A. arguta* fruits exceeded the human body's needs; the RC values of Ile and Lys were both less than 1, and the content of Ile was lower than that of Lys, which indicated that the first limiting amino acid of the fruits of the *A. arguta* resources was Ile and the second limiting amino acid was Lys, and the SRC value of their fruits was in the range of 40~80. The analysis of the results of flavor-presenting amino acids showed that Glu and Cys had the main contribution to the fruit flavor of *A. arguta* resources, and Cys was the main amino acid factor for *A. arguta* flavor in comparison. However, the effect of amino acids on fruit flavor was limited, and the volatile flavor components of the fruit need to be analyzed and determined at a later stage. The principal component analysis extracted 2 principal components from 17 amino acids, and the cumulative variance contribution rate was 87.88%, which better reflected the comprehensive information of amino acids in *A. arguta.* A comprehensive amino acid evaluation model was established, and the top 5 excellent resources with comprehensive scores were S4, S10, S18, S25, and S30. Hierarchical cluster analysis classified the 35 *A. arguta* resources into 4 categories, which better reflected the differences in amino acid content and composition, nutritional value, and taste characteristics among *A. arguta* fruits from different collection sites. This study provides a scientific basis for revealing the nutritional value and taste characteristics of *A. arguta*, a theoretical reference for the screening of excellent *A. arguta* resources and the development and utilization of products, and a theoretical basis for guiding people to establish a scientific and healthy dietary structure. Further research will test and analyze the volatile flavor quality of *A. arguta* and establish a more detailed evaluation system of *A. arguta* fruit quality by

combining the nutritional quality, amino acid composition and content, and volatile flavor quality, to lay a theoretical foundation for the development of excellent *A. arguta* resources. In addition, we will further study the effects of amino acids of *A. arguta* on human health to provide a theoretical basis for the provision of a scientifically balanced diet for human beings and the development of *A. arguta* functional products.

Data Availability

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

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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