

Research Article

Biochemical Characterization of Some Taro (*Colocasia esculenta* L. Schott) Germplasm in Ghana

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Corms of eighteen (18) genotypes comprising twelve (12) introduced and six (6) local genotypes were studied for their nutrient quality to provide information on their nutrient characteristics for a holistic development of the crop. The crop is known for its edible corms and leaves. Corms are boiled before eating and take a short time to cook as their carbohydrate structure is not complex. The leaves are eaten as vegetables. The crops were planted at Nobewam in the Ejisu-Juaben Municipality in the Ashanti Region of Ghana using the Randomized Complete Block Design (RCBD). The biochemical or nutritional analysis was done at Crop and Soil Sciences laboratory at Kwame Nkrumah University of Science and Technology (KNUST). Data were collected on the chemical and mineral compositions of the genotypes (corms). Variations were observed in both chemical and mineral characteristics. Carbohydrate content of the genotypes ranged from 62% to 76%; protein ranged from 13% to 25%; fibre ranged from 1% to 2%; calcium ranged from 0.29% to 0.72% and iron content ranged from 0.18 mg/100 g to 1.18 mg/100 g. Significant differences ($P < 0.05$) were observed in both chemical and mineral traits, indicating a higher degree of variability in the genotypes. Significant ($P < 0.01$) and positive correlations were observed between protein and energy levels; magnesium and iron; magnesium and calcium; and potassium and ash. The Principal Component Analysis (PCA) showed that the first component (PC1) accounted for 96% of variation. Some genotypes including; BL/SM/10, BL/SM/132, KA/019, SAO/020, BL/SM/151, BL/SM/80, BL/SM/116, BL/SM/16, and KA/035 possess desirable nutrient levels such as protein, fibre, carbohydrate, and iron which could be exploited for further development of taro in Ghana.

1. Introduction

Taro (*Colocasia esculenta* L. Schott) is a major root crop belonging to the family *Araceae*, subfamily *Aroideae* [1, 2]. It is one of the oldest crops known to man and it originated from Asia [1]. The crop is a monocotyledonous crop that has the character of being an underground stem [3]. Taro is a herbaceous plant, which grows to a height of about 1-2 m. The plant consists of a central corm lying just below the soil surface, with leaves growing from the lower portion [4]. It is different from yam as it is not a tuber but a corm [5]. Taro is important for food security since many tropical areas often experience unfavourable environmental conditions. It is the fourth most consumed tuber crop worldwide [6]. Taro is cultivated mainly in developing countries using low input production systems. It is generally considered as an easy crop to grow provided there is adequate rainfall [7]. The crop has several characters such

as corms, leaves, and flowers as well as chemical nutrients [3]. According to [3], the diversity among the varieties can be distinguished based on morphological and biochemical markers. Taro is especially useful to people allergic to cereals and can be consumed by children who are sensitive to milk and as such, taro flour is used in infant food formulae, and canned baby foods [8]. Taro leaves contain large amounts of vitamin A, are good source of vitamin C and B₂ (riboflavin), and contain vitamin B₁ [9]. Taro serves as an important food during the dry season or before yam and cassava harvest in West Africa [10]. According to [11], Ghana produced 900 and 1,707 tonnes of taro in the years 1990 and 2000, respectively. In Ghana, the taro germplasm is found in farmers' fields and forest areas. Nevertheless, this germplasm is being lost because the crop is being replaced by cereals as well as drought and human interference such as deforestation. Little or no work has been done on taro germplasm by Agricultural Research Centers and for

TABLE 1: Source of taro genotypes used for the studied.

Genotype	Name	Origin	TLB	Taste
CE/MAL/32	<i>Klang</i>	Malaysia	Resistant	Very good
CE/MAL/14	<i>Klang</i>	Malaysia	Resistant	Poor
BL/SM/10	<i>Samoa 10</i>	Samoa	Tolerant	Very good
BL/SM/16	<i>Samoa 11</i>	Samoa	Tolerant	Very good
BL/SM/116	<i>Manu</i>	Samoa	Tolerant	Very good
BL/SM/80	<i>Alafua</i>	Samoa	Tolerant	Very good
BL/SM/115	<i>Mandela</i>	Samoa	Tolerant	Very good
BL/SM/151	<i>Letogo</i>	Samoa	Tolerant	Very good
BL/SM/132	<i>Fanuatapu</i>	Samoa	Tolerant	Very good
BL/SM/158	<i>lalomanu</i>	Samoa	Tolerant	Very good
CE/IND/12	<i>IND 237</i>	Indonesia	Susceptible	Good
CE/IND/16	<i>Lebak</i>	Indonesia	Susceptible	Good
SAO/006	<i>Kooko</i>	Ghana	Tolerant	Good
SAO/020	<i>Kooko</i>	Ghana	Tolerant	Good
ELO/002	<i>Kooko</i>	Ghana	Tolerant	Very good
KA/019	<i>Kooko</i>	Ghana	Tolerant	Very good
KA/035	<i>Kooko</i>	Ghana	Tolerant	Very good
EX BUNSO	<i>Kooko</i>	Ghana	Tolerant	Very good

TLB = Taro leaf blight, MAL = Malaysia, SM = Samoa, IND = Indonesia.

that matter these germplasm/genotypes have not been properly characterized and evaluated, and their attributes still remain unknown by breeders. Detailed description of genotypes based on biochemical characters have tremendous impact on the use of the crop and the need to characterize, conserve, and maintain the germplasm to serve as a source of desired genotypes for further breeding purposes and to reduce further genetic erosion. Therefore, the objective of this study was to characterize taro germplasm using biochemical traits.

2. Materials and Methods

2.1. Description of the Study Area. The plants were planted at Nobewam in the Ejisu-Juaben Municipality.

The site is situated at latitude 06° 41'N and longitude 01° 23'W with an altitude of 228.7 m above sea level. The area has a bimodal rainfall pattern and receives mean annual rainfall of 2000 mm with maximum and minimum temperatures of 32.1°C and 21.8°C, respectively [12, 13]. The soil of the area has a pH of 5.3–6.5 [13, 14]. The environmental conditions are conducive for the production of *Colocasia esculenta* L. Schott. The biochemical or nutritional analysis was done at the Crop and Soil Sciences laboratory at Kwame Nkrumah University of Science and Technology (KNUST).

2.2. Genotypes Evaluated. Eighteen *Colocasia esculenta* L. Schott genotypes were used in the study. The genotypes used consisted of 12 exotic genotypes from South-East Asia and 6 locals obtained from the Crops Research Institute (CRI) in Fumesua, Kumasi, Ghana (Table 1) [13].

2.3. Experimental Design. The genotypes were planted in the field using Randomized Complete Block Design (RCBD) with 20 m × 12 m plots and three replications. The methods of [13]

were followed for planting with a single row in a plot, with each row 10 m long. Ten plants were spaced 1 m between rows and 1 m between plants within a row. The planting materials were raised from tissue culture at the Crop Research Institute and planted. They were then harvested after seven months and taken to the laboratory for analysis [13].

2.4. Data Collection. Fresh corms of taro genotypes were harvested and taken to the laboratory for analysis.

For chemical composition of genotypes, the samples were analyzed for moisture, ash, crude fat, crude protein, crude fibre, and nitrogen free extracts using Association of Official Analytical Chemists' Approved Methods [15]. For mineral analysis, standard [15] method was used to digest 100 g of flour samples. One hundred milliliter (100 ml) standard solutions were prepared from the digest and used for mineral analysis. The minerals (Ca, P, K, Fe, Cu, and Mg) were determined using standard analytical methods.

2.5. Statistical Data Analysis. Data were subjected to Analysis of Variance (ANOVA) using Genstat Release 12.1 was used to examine the presence of statistically significant difference among the genotypes for biochemical traits.

Least Significant Difference (LSD) was used to identify genotypes that are significantly different from each other at 5% probability level ($P < 0.05$). Correlation Matrix was also carried out for all traits using Genstat Release 12.1. Pearson correlation, principal component, and clustering of genotypes were carried out to assess the diversity between genotypes for the traits measured by using Genstat Release 12.1 statistical package.

3. Results

3.1. Analysis of Variance

3.1.1. Chemical Composition. Table 2 shows the chemical composition of the taro genotypes that were studied.

The analysis of variance for the chemical composition showed significant differences ($P < 0.05$) among the genotypes that were studied. The protein content of the genotypes ranged from 13.1% to 25.7% with genotype BL/SM/132 recording the highest protein content (25.7%) and genotype BL/SM/32 had the least (3.1%). The moisture content ranged from 5.7% to 6.3%. Genotype BL/SM/115 recorded the highest moisture content of 6.39% and genotype EX-BUNSO recorded the lowest moisture content of 5.7%. The percentage ash for the genotypes ranged from 1.06% to 1.84%. Genotype SAO/006 had the highest amount of percentage ash (1.84%). Genotype BL/SM/151 recorded the lowest amount of percentage ash (1.06%). The percentage crude fat ranged between 1.04% and 3.6% with genotype BL/SM/16 recording the highest amount of 3.6%. Genotype KA/019 recorded the least amount of 1.04%. The percentage crude fibre of the genotypes ranged from 1.02% to 2.12%. Genotype KA/035 had the highest amount of crude fibre of 2.12% and the least amount of percentage crude fibre was recorded in genotype BL/SM/132 (1.02%). The carbohydrate content ranged from 62.43% to 76.08%. Genotype CE/MAL/32 had the highest carbohydrate content of 76.08%. However, the lowest carbohydrate content

TABLE 2: Chemical composition of the 18 taro genotypes.

Genotype	Protein (%)	Moisture (%)	Ash (%)	Fat (%)	Fibre (%)	Carbohydrate (%)	Energy (%)
CE/MAL/32	13.06	6.12	1.59	1.43	1.71	76.08	34.56
BL/SM/10	22.52	6.07	1.41	2.87	1.71	65.42	35.34
BL/SM/16	24.54	5.93	1.39	3.60	2.11	62.43	35.58
BL/SM/116	13.95	5.84	1.58	1.33	1.58	75.71	34.56
BL/SM/80	23.62	6.13	1.50	1.64	1.05	66.05	34.93
CE/IND/12	21.14	6.27	1.77	2.50	1.65	66.67	35.06
BL/SM/115	19.76	6.39	1.28	1.37	1.15	70.04	34.83
BL/SM/151	23.31	6.11	1.06	1.44	1.43	66.65	34.85
CE/MAL/14	19.24	5.99	1.62	2.55	1.23	69.36	35.28
SAO/006	19.85	6.13	1.84	1.38	1.45	69.34	34.53
CE/IND/16	19.06	5.99	1.35	1.85	1.46	70.29	34.94
BL/SM/132	25.70	6.17	1.11	1.73	1.02	64.26	35.12
BL/SM/158	19.86	6.12	1.29	1.72	1.14	69.88	35.01
EX-BUNSO	15.73	5.73	1.25	2.19	1.20	73.91	35.24
SAO/020	25.43	6.25	1.16	2.73	1.65	62.78	35.38
ELO/002	19.95	5.89	1.20	1.80	1.67	69.50	34.90
KA/019	23.19	5.99	1.15	1.04	1.24	67.38	34.68
KA/035	14.93	6.12	1.32	1.21	2.12	74.30	34.40
LSD(<0.05)	0.81	0.23	0.21	0.26	0.18	0.86	0.15

TABLE 3: Mineral composition of the 18 taro genotypes.

GENOTYPE	P (%)	K (%)	Ca (%)	Mg (%)	Cu (mg/100 g)	Fe (mg/100 g)
CE/MAL/32	0.17	0.66	0.49	0.38	0.43	0.67
BL/SM/10	0.14	0.66	0.47	0.37	0.49	0.47
BL/SM/16	0.19	0.65	0.43	0.34	0.53	0.18
BL/SM/116	0.15	0.68	0.53	0.39	0.35	0.57
BL/SM/80	0.12	0.71	0.58	0.43	0.42	0.71
CE/IND/12	0.16	0.77	0.47	0.41	0.87	0.73
BL/SM/115	0.13	0.70	0.60	0.44	0.48	0.76
BL/SM/151	0.15	0.48	0.50	0.42	0.15	0.65
CE/MAL/14	0.16	0.83	0.49	0.42	0.47	0.62
SAO/006	0.18	0.78	0.72	0.53	0.31	0.85
CE/IND/16	0.14	0.34	0.62	0.47	0.15	1.03
BL/SM/132	0.17	0.59	0.58	0.48	0.35	0.71
BL/SM/158	0.16	0.71	0.67	0.47	0.26	0.81
EX-BUNSO	0.17	0.66	0.44	0.43	0.47	0.84
SAO/020	0.17	0.49	0.59	0.46	0.78	0.77
ELO/002	0.19	0.66	0.29	0.28	0.36	0.51
KA/019	0.23	0.65	0.33	0.29	0.45	0.82
KA/035	0.21	0.69	0.51	0.41	0.30	1.18
LSD (<0.05)	0.03	0.02	0.02	0.01	0.66	0.49

P (%) = Percentage phosphorus, K (%) = Percentage potassium, Ca (%) = Percentage calcium, Mg (%) = Percentage magnesium, Fe = Iron, Cu = Copper.

of 62.43% was recorded in genotype BL/SM/16. The energy level of the genotypes ranged from 34.4% to 35.58%. Genotype BL/SM/16 recorded the highest energy level of 35.58% and genotype KA/035 had the least (34.40%).

3.1.2. Mineral Composition. Table 3 shows the mineral composition of the taro genotypes that were studied. There were significant differences ($P < 0.05$) among the genotypes that were studied.

The phosphorus content was between 0.12% and 0.23%. Genotype KA/019 recorded the highest value (0.23%). Genotype BL/SM/80, however, recorded the least (0.12%). The potassium content ranged between 0.34% and 0.83%. Genotype CE/MAL/14 had the highest value of 0.83% and genotype CE/IND/16 had the least (0.34%). The calcium content ranged from 0.29% to 0.72%. Genotype SAO/006 had the highest value of 0.72% while, genotype ELO/002 had the least with 0.29%. The magnesium content of the genotypes ranged

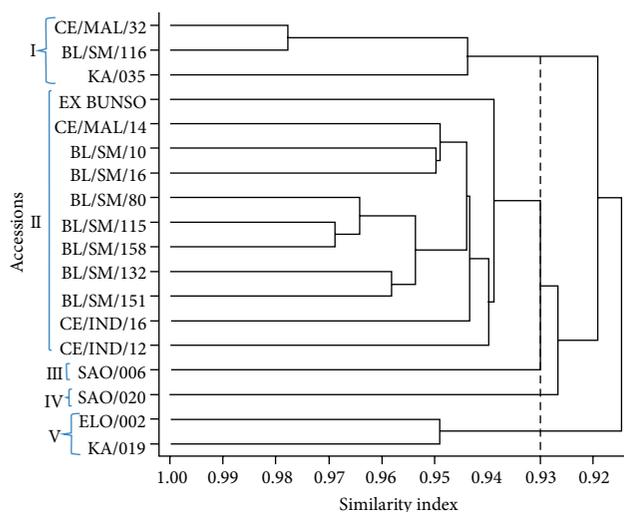


FIGURE 1: Cluster analysis based on biochemical traits.

from 0.28% to 0.53% with genotype SAO/006 recording the highest value of 0.53%. Genotype ELO/002 recorded the lowest value of 0.28%. The copper content of the genotypes ranged from 0.15 mg/100 g to 0.87 mg/100 g with genotype CE/IND/12 recording the highest value of 0.87 mg/100 g and genotype BL/SM/151 had the least value (0.15 mg/100 g). The iron content ranged from 0.18 mg/100 g to 1.18 mg/100 g. Genotype KA/035 had the highest value of 1.18 mg/100 g and genotype BL/SM/16 had the least value (0.18 mg/100 g).

3.2. Diversity among the Genotypes. Figure 1 shows the dendrogram summarizing the existing diversity and similarity among the taro genotypes for their biochemical traits. At similarity index of 0.93 (93.0%), five major clusters were identified and the number of genotypes belonging to each cluster varied from 1 to 11. Cluster I consisted of three genotypes (CE/MAL/32, BL/SM/116, and KA/035). Cluster II was made up of eleven genotypes (EX-BUNSO, CE/MAL/14, BL/SM10, BL/SM/16, BL/SM/80, BL/SM/115, BL/SM/158, BL/SM/132, BL/SM/151, CE/IND16, and CE/IND/12). Clusters III and IV had one genotype each; SAO/006 and SAO/020, respectively. Cluster V consisted of two genotypes (ELO/002 and KA/019). At similarity index of 0.98 (98.0%) all the genotypes were totally distinct from each other.

3.3. Principal Component Analysis. Table 4 shows the principal component analysis based on biochemical characters. Ordination among the genotypes showed that the first five principal components (PCs) cumulatively accounted for over 98% of variation (Table 4). The first component (PC1) alone explained 96.72% of the total variation and was mainly associated with protein content. The second component explained 2.43% of variation and was mainly characterized by fat and energy content.

3.4. Association among the Traits. There were correlations between pairs of variables for biochemical traits (Table 5). The minerals did not show any significant correlation with

carbohydrate and this result does not agree with [16] who reported a significant positive correlation between minerals and starch. There was also significant ($P < 0.05$) positive correlation between magnesium and iron (0.46*); between protein and energy (0.57**); between magnesium and calcium (0.93***); between Potassium and ash (0.59**). Percentage moisture also had a significant and positive ($P < 0.05$) correlation with calcium (0.48*). There was also a significant and positive correlation ($P < 0.05$) between fat and copper (0.55*) and again significant and positive correlation ($P < 0.001$) with energy (0.90***). Some of the traits had positive correlations although not significant (calcium and ash, iron and carbohydrate, iron and calcium, phosphorous and crude fibre). There were significant but negative correlations between some traits, such as fat and carbohydrate (-0.56**), phosphorous and calcium (-0.48*), crude protein and carbohydrate (-0.98***), and between iron and fat (-0.59**).

4. Discussion

4.1. Analysis of Variance. The analysis of variance showed significant differences among the genotypes that were studied. The crude protein content among the genotypes was moderately high (13.06–25.70%). These values were higher than protein content reported by [17, 18]. However, the study supports the findings of [8] who reported that taro can be an excellent source of protein to children who are sensitive to milk. Moisture contents (5.73%–6.39%) of the genotypes were below 11%, thereby giving the corms a better shelf life. This biological parameter is important in the storage of the corms, moisture content greater than 12% allows for microbial growth. Low levels are favourable and give a relatively long shelf life [19]. The lower moisture content of the corms also gives efficiency of drying because much of the water contained in the corm will be removed during drying [20]. The moisture contents of the corms in this study are lower than those reported by [21] (6.92%) in taro and much lower than those reported by [22] (65–79.8%) and [18] (69.1%). The study also showed that total carbohydrate (62.43–76.08%) is the most important component in the corms. Although the carbohydrate contents were lower than those reported by [21] in taro, it collaborated with the findings of [23] for taro corms in Cameroon. Taro is therefore said to be a good source of carbohydrate for diabetics and for those with gastrointestinal disorders [24]. This suggests that taro corms may have very good digestibility [25]. These findings however, improve the competitiveness of taro with other root and tuber crops and therefore enhance its inclusion in food system. The results in this study indicated that taro corms has a higher content of ash (1.06–1.84%) than that reported in taro (0.71%) by [26] in India and [18] (0.87%), but lower than those reported by [21] in Cote d'Ivoire in taro. The findings of this study also showed that the taro corms had a higher crude fibre content (1.02%–2.12%) than that from [21] in taro corms and corresponds to the findings of [18] (1.46%). The findings are important as crude fibre provides roughages that aid digestion [27]. The fat contents of the study were higher than those reported by [17, 18]. It is reported that taro is an excellent

TABLE 4: Principal component analysis of the biochemical traits of the 18 taro genotypes.

Characters	PC1	PC2	PC3	PC4	PC5
Ash	-0.01259	0.10252	-0.21361	-0.59813	-0.30401
Carbohydrate	-0.7298	-0.4231	0.29514	0.12024	-0.04112
Ca	-0.00004	-0.02081	-0.03371	-0.22475	0.23701
Cu	0.01006	0.1039	-0.03500	-0.23555	0.05148
Energy	0.03721	0.20458	0.49191	0.03351	0.14858
Fat	0.06055	0.64478	0.44460	0.05456	0.09063
Fibre	-0.00723	0.23408	-0.55669	0.58033	0.00898
Fe	-0.01452	-0.11194	-0.10452	-0.09979	0.79014
K	-0.00429	0.02118	-0.02469	-0.24281	-0.26709
Moisture	0.00946	-0.03618	-0.21210	-0.27807	0.29597
Mg	0.00023	-0.01048	0.00420	-0.13447	0.17412
P	-0.00022	-0.0018	-0.02077	0.04319	-0.0041
Protein	0.67949	-0.52199	0.24163	0.12127	-0.05564
Variation (%)	96.72	2.43	0.38	0.21	0.12

TABLE 5: Correlation matrix among biochemical characters at 5% and 1% probability.

Characters	%ASH	%C	%Ca	%Cu	EL	%FAT	%CF	%Fe	%K	%M	%Mg	%P	%CP
%ASH	1												
%C	0.26	1											
%Ca	0.27	0.005	1										
%Cu	0.25	-0.36	-0.22	1									
EL	-0.20	-0.67**	-0.14	0.53	1								
%FAT	0.10	-0.56**	-0.16	0.55*	0.90***	1							
%CF	0.16	0.05	-0.30	0.18	-0.02	0.35	1						
%Fe	-0.06	0.41	0.38	-0.26	-0.54*	-0.59**	-0.19	1					
%K	0.59**	0.19	-0.07	0.31	-0.12	-0.001	-0.07	-0.17	1				
%M	0.06	-0.33	0.48*	0.29	-0.10	-0.11	-0.11	0.22	0.04	1			
%Mg	0.21	-0.007	0.93***	-0.15	-0.03	-0.10	-0.37	0.46*	-0.09	0.40	1		
%P	-0.19	0.05	-0.48*	0.05	-0.20	-0.10	0.38	0.12	0.12	-0.27	-0.44	1	
%CP	-0.37	-0.98***	0.01	0.24	0.57**	0.40	-0.21	-0.33	-0.23	0.33	0.03	-0.04	1

* = Significant at $P < 0.05$, ** = Significant at $P < 0.01$, *** = Significant at $P < 0.001$. %ASH = Percentage ash, %C = Percentage carbohydrate, %Ca = Percentage calcium, %Cu = Percentage copper, EL = Energy level, %FAT = Percentage fat, %CF = Percentage crude fibre, %Fe = Percentage iron, %K = Percentage potassium, %M = Percentage moisture, %Mg = Percentage magnesium, %P = Percentage phosphorus, %CP = Percentage protein.

energy supplier [28], but the results of this finding indicated a moderate content of energy (34.40–35.58%). The range in value for the minerals is probably due to the potential of each genotype to obtain nutrients from the soil [29]. The mineral content in the taro corms were found to be relatively high. The most abundant mineral was potassium with values ranging between 0.34% and 0.83%. These results are similar to those reported by [18, 30], but lower than those reported by [22] (1.59–2.90%). The contents of calcium (0.29–0.72%) and phosphorus (0.12–0.23%) were comparable to the findings of [22] but were higher than the reports from [18, 30]. The magnesium contents ranged between 0.28% and 0.53% and these values are similar to the findings of [30], but lower than those from [18] and [22], respectively. The results also show that, the genotypes were good sources of copper and iron with values ranging between 0.45 mg/100 g–0.87 mg/100 g, and 0.18 mg/100 g–1.18 mg/100 g, respectively. These values are similar to the findings of [18, 22].

4.2. Diversity among the Genotypes. The study indicated that the traits were clustered based on geographic affinity. Genotypes BL/SM/80, BL/SM/115, BL/SM/158, BL/SM/132, and BL/SM/151 all appear to have come from Samoa. Genotypes CE/MAL/32, BL/SM/116, ELO/002, CE/MAL/32, BL/SM116, and SAO/006 which were more distinct and diverse can serve as a source of variability for the improvement in the traits of taro. The dendrogram suggests that genotypes in the same cluster may not produce any significant improvement when crossed since the genotypes are expected to have similarities and may therefore produce no reasonable variation. Ref. [31, 32] in South Africa and Ethiopia, respectively, have reported similar results in the study of taro.

4.3. Principal Component Analysis. The results of the study showed that PC1 contributed highest (96.72%) to the total variation. The second component explained only 2.43% of variation. This means that higher amounts of protein could restrict the contents of ash,

carbohydrates, potassium, phosphorus, and fibre. Therefore, for improvement in the biochemical components of taro, attention should be on protein and fat alongside with traits that correlated positively and significantly with them. The findings of this study corroborate with those of [16] who also reported higher contribution of PC1 to total variation in taro in India.

4.4. Association among the Traits. There were correlations between pairs of variables for the traits studied. The minerals did not show any significant correlation with carbohydrate and this result does not agree with [16] who reported a significant positive correlation between minerals and starch in taro. There was also significant ($P < 0.05$) positive correlation between magnesium and iron; between protein and energy; between magnesium and calcium; between Potassium and ash, and this suggests the improvement of these traits simultaneously. These relationships indicate that improving mineral nutrition could accompany improvement of taro quality. These findings also support those made earlier by [21] and [16] in taro. The absence of a significant positive correlation between protein and calcium; carbohydrate and ash; protein and copper; and moisture and copper are indications that selections for high protein, carbohydrate, and moisture contents are without concern of having high values of calcium, ash, and copper, respectively. The negative and insignificant correlation between energy and most minerals is in agreement with [16] in taro. The results in this study indicated that most of the minerals did not significantly correlate with protein and these findings do not support the findings of [33] who earlier reported that most minerals had positive correlation with protein.

5. Conclusion

The study shows that there were significant ($P < 0.05$) variations among the genotypes studied for their biochemical traits. The corm of taro (*Colocasia esculenta* L. Schott.) is a good source of carbohydrate, iron, protein, fibre, potassium, and total ash going by the biochemical score and therefore, should be appreciated as a food security crop for the people living in Ghana (West Africa) and also the germplasm of the genotypes should be conserved for further improvement of the crop in Ghana.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest regarding the publication of this article.

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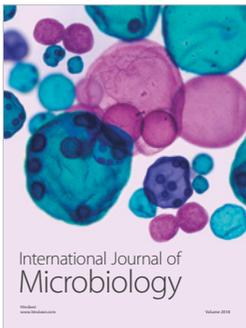
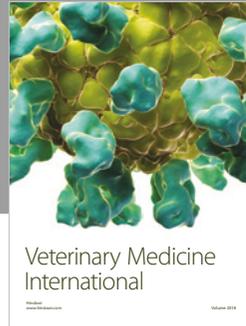
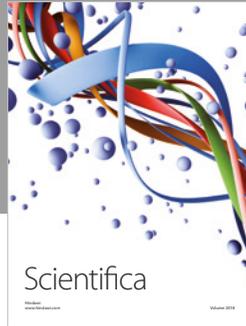
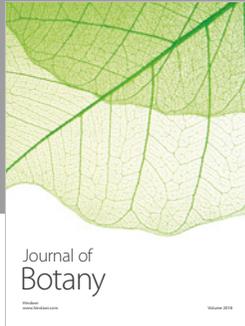
Acknowledgments

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