



## GENETIC DIVERSITY STUDIES, HERITABILITY, CORRELATION AND PROXIMATE ANALYSIS AMONG ACHA (*Digitaria exilis*) ACCESSIONS

<sup>1</sup>Buba, U. M., <sup>2</sup>Abdul, S. Dangana and <sup>3</sup>Ibrahim, H.

<sup>1</sup>Department of crop Production, Abubakar Tafawa Balewa University, Bauchi.

<sup>2</sup>Department of Biological Science, Abubakar Tafawa Balewa University, Bauchi.

<sup>3</sup>Department of Agronomy, Bayero University, Kano.

**Corresponding Author's E-mail:** umbuba@atbu.edu.ng **Tel.:** 08069466566

### ABSTRACT

The study assessed variability, heritability and genetic relationships in the proximate composition among 14 Acha (*Digitaria exilis* Staph) accessions collected from Tafawa Balewa and Bogoro Local Government Areas of Bauchi State in North Eastern Nigeria. Entries were pretested in the screen house in plastic pots in 2017 and later evaluated in the field under rain-fed conditions in 2017 and 2018 using a randomized complete block design with three replications. Three (3) samples of harvested grain, for each entry, were subjected to proximate analysis in the laboratory to determine their percent proximate composition in: Crude protein (% CP), Crude fiber (% CF), Ether extract (% EE), Ash content (% Ash) and Nitrogen free extract (%NFE) using standard Analytical methods. Analysis of variance was done using Genstat version 16th). Results obtained in this study revealed that all biochemical parameters differed significantly ( $P \leq 0.001$ ) among these accessions. Mean percent in crude protein (CP) was 7.5 %, Crude Fiber was 0.85 %, while that of ether extract (%EE) and ash content (% Ash) were 1.94% and 1.87%, respectively. Except for Ether Extract, other biochemical variables under investigation recorded negative correlation with grain yield. Phylogenetic studies revealed two cluster groups among acha accessions. High percent heritability values, in broad sense of (between 77% and 99 %), couple with high genetic advance as percent of mean (GAM) were recorded for most of characters under investigation, indicating a good scope for improvement through selection.

**Keywords:** Proximate analysis, Correlation, variability, heritability and genetic advance and phylogenetic relationship

### INTRODUCTION

Fonio or Acha (*Digitaria* spp) as they are popularly known in Nigeria, are minor cereals, indigenous to and widely cultivated in West Africa. Although the genus *Digitaria* comprises several wild species, only four cultivated species are of economic importance (Buba *et al.*, 2016). All cultivated species belong to the grass (*Poaceae*) family: genus *Digitaria* Haller (Clayton, 2014). Of the four cultivated species namely *D. iburua*, *D. exilis*, *D. cruciata* and *D. sanguinalis*; two species: *Digitaria exilis* (white fonio) and *D. iburua* (Stapf or black fonio) are predominantly found in West Africa. The other two species are found outside Africa, e.g., Raishan (*Digitaria cruciata* var. *esculenta*) is grown in some parts of Khasi hills in North Eastern province of India, while crab grass (*D. sanguinalis*) is found in Eastern Europe. The crop has received little attention in terms of research and genetic development as said by Adoukonou (2007) and Balde *et al.* (2008). However, recent reports by Balougou *et al.* (2013) and Jideani (2012) shows that the crop is receiving greater attention because of its multiple uses and nutritional benefits: its amino acid profile is considered unique, comprising methionine and cysteine, two important amino acids that assist the liver in detoxifying food



and preventing colon cancers (Anonymous, 2015). Acha is utilized in many forms; in salads, stews, porridges, bread and many other recipes can be prepared from the grain.

Few numbers of workers have investigated the proximate composition of acha (Temple and Bassa, 1991; Chukwu and Abdulkadir, 2008; Adoukonou *et al.*, 2010; Balougou *et al.*, 2013). Temple and Bassa (1991) submitted that Acha contains about 7.0% crude protein whose composition is rich in leucine (9.8%), methionine (5.6%) and valine, while Glew *et al.* (2013) reported 6.53 % protein, and opined that its essential amino acid pattern compared favorably to World Health Organization (WHO) reference protein, except for lysine. Balougou *et al.* (2013) reviewed the proximate analysis in Acha and reported that crude fiber contents in Acha grains were in the range of 0.41-11.3%, with a mean value of 5.85%, while crude fiber contents reported for Acha grains were in the range of 0.41-11.3% with a mean value of 5.85%. They also indicated that Ash contents of Acha grains varied from 1 to 6% with an average value of 3.5%.

Hundreds of Acha landraces, belonging almost exclusively to *D. exilis*, the most widespread cultivated Acha species, are recognized and maintained for generations through traditional *in situ* on-farm conservation practices by farmers in the West African region. (Buba *et al.*, 2016). Extensive studies on adaptability and variability have been conducted in West Africa and several land races identified (Aliero and Morakinyo, 2000; Adoukonou, 2010; Buba *et al.*, 2016). The special richness of Acha grains need to be assessed for future breeding program by investigating heritability, genetic advance and correlations among yield and biochemical characters, Hence, the objective of the current study was to assemble and assess the level of genetic variability with the aim of identifying superior genotypes among them and the study also investigated broad sense heritability and genetic advance in proximate composition among fourteen acha accessions.

## MATERIALS AND METHODS

Fourteen (14) Acha accessions, were collected from Tafawa Balewa and Bogoro local Governments in Bauchi State, North Eastern Nigeria in 2008. They included; Aburu, Gege, Wondat-Baptist, Wondat- Dunga, Wondat-Coci, Kamana, Kanana, Rikwe, Riweh, Chit-Kusung (Baptist), Chit-fhyali (Dunga), Chit-fhyali (Kusung), Lhardzhjeli and Nakusni. These germplasm collections represent a sample of land races grown by local farmers in the study area.

Accessions were pre-tested, first in a preliminary trial, in the screen house, at the Teaching and Research Farm of the Abubakar Tafawa Balewa University, Bauchi at 10° 17' N, 9° 49' E, 609 m. a. s. l. in 2017. While, in 2018 rainy season they were evaluated in the field under rain-fed condition. Entries were sown on field plots measuring 1m x 1.5 m (1.5 m<sup>2</sup>) and fitted into a randomized complete block design in three replicates. Uniform quantity of seeds, at the rate of 8g were broadcasted evenly over the plots surface in all the three replications as per the experimental design. Seeds were then covered lightly with soil. All recommended agronomic practices were appropriately followed. At physiological maturity Acha grain were harvested separately and stored in a cool and dry place.

### Data collection

Data were collected on grain yield on per plot basis by weighing harvested seed per each entry, while proximate analysis was carried out in the Plant and Soil Analytical Laboratory of the Abubakar Tafawa Balewa University Bauchi, to assess their proximate grain composition which included; Dry matter content (DM) percent crude protein (%CP), percent crude fiber (% CF), percent ether extract (% EE), ash content (% ASH) and nitrogen free extract (%NFE) as follows:



1. Dry Matter Content: Percent dry matter content among entries was determined by oven drying the test material in oven so as to estimate its water content as follows: Percent dry matter (%DM) = Dried sample weight/ original sample weight x 100.
2. , 2000). The Kjeldahl method was used to determine the nitrogen content in the acha Determination of Crude Protein (%): The proximate composition of the samples was determined according to the International Analysis of Official Chemist methods (AOAC samples, following three basic steps: digestion of the sample in sulfuric acid with a catalyst: distillation of the ammonia, and the finally, estimating nitrogen, and hence the crude protein. Percent nitrogen (%N) was used to estimate the fraction of crude protein (% CP) using the relationship: % CP = % N x 6.25.
3. Determination of Ether Extract (EE): The determination of crude fat followed the recommendation of official methods of analysis of the association of analytical chemists (AOAC, 2000), using petroleum ether in Soxhler extractor. 2.0g was used per each sample. All analyses were done in triplicates.
4. Determination of Crude Fiber (CF): Crude fiber was estimated as described by Sadiq *et al.* (2015), first by treating sample with petroleum ether, which render the sample fat-free. Subsequently, the defatted sample is treated with boiling H<sub>2</sub>SO<sub>4</sub> and later with boiling NaOH,
5. Determination of Ash content (Ash): Percent ash content was determined by burning 2.5 g per each sample in a crucible at 550 °C for 12 hours. It was then left to cool before transferring it to a dryer. The ash content was calculated as the difference between weight of the crucible with sample and weight of crucible with ash divided by weight of sample expressed as percent (Ilodibia *et al.*, 2014).

### Statistical Analysis

Data generated on characters under investigation were subjected to analysis of variance using GLM and analysis of variance procedures of Statistical Analysis Software (Genstat 16th). These data were also used to construct a dendrogram via the un-weighted pair group method of arithmetic averages (UPGMA). All other computations were carried out using Genstat 16th version (Genstat, 2012).

Components of variance:  $\delta^2_g$  (genotypic variance),  $\delta^2_p$  (phenotypic variance) and error variance ( $\delta^2_e$ ) were estimated using the procedure provided by Wricke and Weber, (1986):

$$\text{Genotypic variance } (\delta_g^2) = (M_{sg} - M_{se}) / r \quad \dots(1)$$

$$\text{Phenotypic variance } (\delta_p^2) = (M_{sg} / r) \quad \dots(2)$$

$$\text{Error variance } (\delta_e^2) = (M_{se} / r) \quad \dots(3)$$

where;  $M_{sg}$ ,  $M_{sp}$ , and  $M_{se}$  are the mean squares for genotypes, phenotype and error mean squares respectively, while  $r$  is the number of replications. Mean and variances of the traits were used in estimating; Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of variation (PCV), and Environmental variance (ECV) were as suggested by Singh and Chaudhary (1985) as follows:

$$GCV = \frac{\sqrt{\delta_g^2}}{\bar{x}} \times 100 \quad ECV = \frac{\sqrt{\delta_e^2}}{\bar{x}} \times 100 \quad \dots(4)$$

$$\text{and } PCV = \frac{\sqrt{\delta_{ph}^2}}{\bar{x}} \times 100 \quad \dots(5)$$



Broad sense heritability (%) and Genetic Advance (GA) values were estimated according to Singh and Chaudhary (1985) as follows:

$$H_b^2 = \left( \frac{\delta_g^2}{\delta_p^2} \right) \times 100 \quad \dots(6)$$

where;  $h_b^2$ ,  $\delta_g$  and  $\delta_{ph}$  = broad sense heritability, genotypic and phenotypic variance, respectively. While genetic advance was based on the formula provided by Fehr (1987) as:

$$GA = (K)(\delta_{ph})(h_b^2) \quad \dots(7)$$

where; K = selection differential at 5% selection pressure = 2.063

$\delta_{ph}$  = phenotypic variance,  $h_b^2$  = heritability

$$\text{Genetic advance as percent of mean (GAM) was estimated as: } = \frac{GA}{X} \times 100 \quad \dots(8)$$

## RESULTS AND DISCUSSION

### Descriptive Statistics

Result of the analysis of variance investigating proximate composition for year 2017 and 2018 were statistically similar, therefore data were pooled across the two seasons (Table 1). It revealed that mean square error were significant for all characters under investigation, suggesting the existence of substantial variability in the chemical composition among the acha accessions under study and the possibility for further improvement. However, the combined ANOVA revealed that, except for yield per hectare, year as a factor had no significant effect on the result. However, this is not unexpected from a bio-chemical laboratory experiment, in which there is negligible environmental impact.

In our previous work (Buba *et al.*, 2016) these accessions exhibited similar genotypic differences in their morphological and phenological features. Results obtained in the current study (Table 2 and Table 3) also revealed that these germplasm collections vary significantly ( $P < 0.01$ ) in their proximate composition for all the characters under investigation in both seasons 2017 and 2018, indicating a good scope for future selection and genetic improvement of the characters under study. Similar results were reported by: Irving and Jideani (1997); Chukwu and Abdulkadir (2008) who also submitted that acha exhibit both inter and intra-generic variability. On the hand, result obtained in this study revealed that percent coefficient of variability (%CV), for yield (YLHA) and percent nitrogen free extract (PCEE) in 2017 were comparatively higher than those observed in 2018, suggesting error in laboratory estimates between the two seasons.



**Table 1: Combined Analysis of variance for six characters among 14 acha accessions evaluated in 2017 and 2018**

SOV	DF	YLHA	PCNFE	PCCP	PCCF	PCASH	PCEE
Genotype (G)	13	423.06**	27.930**	0.7670**	0.1826**	0.0759**	0.1495**
Year (Y)	1	28.39*	0.0138	0.0030	0.0002	0.0004	0.0315
G x Y	13	11.67	0.0224	0.0050	0.0002	0.0003	0.0046
Pooled Error	27	50.57	0.0056	0.013	0.0016	0.0005	0.0228
LSD		10.31	0.1092	0.171	0.0589	0.0344	0.2193
SE		3.556	0.0376	0.022	0.0203	0.0118	0.0756
CV		8.9	1.8	2.2	1.0	1.4	15.3



**Table 2: Table of means showing: Percent crude protein, Percent Ash content and percent ether extract among 14 Acha accessions recorded in 2017, 2018 and combined analysis**

Cultivar		Percent Ash			Percent Crude Protein			Percent Ether extract		
No.	Name	2017	2018	Combine Analysis	2017	2018	Combine Analysis	2017	2018	Combine Analysis
01	Wondat Coci	0.885	0.837	0.861 <sup>h</sup>	7.620	7.610	7.615 <sup>b</sup>	0.830	0.820	0.825 <sup>cdef</sup>
02	Gege	0.850	0.845	0.848 <sup>i</sup>	7.170	7.175	7.172 <sup>f</sup>	1.100	1.095	1.097 <sup>ab</sup>
03	Wondat Baptist	0.920	0.925	0.923 <sup>g</sup>	6.875	6.883	6.879 <sup>g</sup>	0.915	1.912	0.914 <sup>bcd</sup>
04	Riweh	1.105	1.117	1.111 <sup>c</sup>	7.170	7.200	7.185 <sup>ef</sup>	0.670	0.675	0.672 <sup>ef</sup>
05	Chitfyeli Dunga	1.240	1.240	1.240 <sup>a</sup>	7.430	7.430	7.430 <sup>cd</sup>	0.580	0.575	0.577 <sup>f</sup>
06	Wondat Baptist	1.095	1.092	1.094 <sup>cd</sup>	7.510	7.500	7.505 <sup>bc</sup>	0.825	0.812	0.819 <sup>cdef</sup>
07	Aburu	1.005	1.012	1.009 <sup>cd</sup>	8.100	8.105	8.102 <sup>a</sup>	1.010	1.020	1.015 <sup>abcd</sup>
08	Rikwe	0.990	0.995	0.993 <sup>ef</sup>	8.150	8.190	8.170 <sup>a</sup>	1.180	1.190	<b>1.185<sup>a</sup></b>
09	Lhardzhjeli	1.215	1.097	1.096 <sup>cd</sup>	7.615	7.628	7.621 <sup>b</sup>	1.205	0.857	1.097 <sup>ab</sup>
10	Chitkusung	0.960	0.960	0.960 <sup>e</sup>	8.205	8.187	8.201 <sup>a</sup>	0.620	0.635	0.627 <sup>ef</sup>
11	Chitfyeli Baptist	1.215	1.222	1.219 <sup>a</sup>	7.405	7.418	7.411 <sup>cd</sup>	0.760	0.780	0.777 <sup>cdef</sup>
12	Nakusni	0.800	0.800	0.800 <sup>i</sup>	7.425	7.302	7.364 <sup>cde</sup>	1.015	1.027	1.021 <sup>abc</sup>
13	Kanana	1.185	1.145	1.164 <sup>b</sup>	7.275	7.328	7.301 <sup>def</sup>	0.790	0.765	0.770 <sup>def</sup>
14	Kamana	1.080	1.055	1.068 <sup>d</sup>	8.390	8.170	8.280 <sup>a</sup>	0.660	0.685	0.627 <sup>f</sup>
	Mean	1.03	1.02	1.025	7.596	7.581	7.588	0.869	0.854	0.861
	SE	0.021	0.026	0.011	0.133	0.101	0.058	0.188	0.096	0.107
	CV	2.1	2.6	2.3	1.7	1.3	1.5	21.7	11.3	16.5





**Table 3: Estimated mean yield per hectare, percent dry matter and percent crude fiber across 2017, 2018 and combined analysis**

Character Accession	Percent crude fiber			Percent Dry matter			Yield per hectare		
	2017	2018	Combine Analysis	2017	2018	Combine Analysis	2017	2018	Combine Analysis
Wondat Coci	1.620	1.595	1.607 <sup>g</sup>	94.64	94.665	94.65 <sup>cd</sup>	75.35	77.17	76.26 <sup>abcd</sup>
Gege	1.170	1.710	1.707 <sup>f</sup>	94.815	94.762	94.79 <sup>ab</sup>	67.10	71.20	69.15 <sup>cde</sup>
Wondat Baptist	1.815	1.822	1.819 <sup>d</sup>	94.810	94.805	94.81 <sup>a</sup>	65.95	66.27	66.11 <sup>de</sup>
Riweh	2.020	2.020	2.022 <sup>bc</sup>	89.530	89.545	89.54 <sup>j</sup>	81.55	83.82	82.69 <sup>a</sup>
Chitfyeli	2.080	2.075	2.077 <sup>bc</sup>	94.440	94.525	94.48 <sup>e</sup>	67.67	70.64	69.16 <sup>cde</sup>
Dunga									
Wondat Baptist	1.805	1.777	1.791 <sup>d</sup>	94.745	94.767	94.75 <sup>abc</sup>	56.55	60.22	58.77 <sup>ef</sup>
Aburu	1.725	1.732	1.729 <sup>ef</sup>	91.885	91.857	91.87 <sup>f</sup>	83.45	85.32	84.39 <sup>a</sup>
Rikwe	2.195	2.212	2.204 <sup>a</sup>	85.690	85.790	85.74 <sup>k</sup>	58.80	58.75	58.77 <sup>ef</sup>
Lhardzhjeli	1.530	1.545	1.537 <sup>h</sup>	94.670	94.705	94.79 <sup>ab</sup>	51.65	50.87	51.26 <sup>f</sup>
Chitkusung	2.105	2.117	2.111 <sup>b</sup>	94.655	94.692	94.67 <sup>bcd</sup>	71.70	72.65	72.17 <sup>bcd</sup>
Chitfyeli Baptist	2.080	2.095	2.087 <sup>b</sup>	93.405	93.542	93.47 <sup>f</sup>	72.95	66.37	69.66 <sup>cde</sup>
Nakusni	2.070	2.070	2.070 <sup>bc</sup>	92.580	92.595	92.59 <sup>g</sup>	74.55	81.27	77.91 <sup>abc</sup>
Kanana	1.690	1.715	1.702 <sup>f</sup>	94.580	94.625	94.60 <sup>d</sup>	84.00	81.109	82.55 <sup>ab</sup>
Kamana	1.775	1.787	1.781 <sup>de</sup>	91.685	91.692	91.87 <sup>h</sup>	79.25	84.77	82.01 <sup>ab</sup>
Mean	1.873	1.876	1.875	93.01	93.04	93.02	70.8	72.18	71.46
SE	0.054	0.021	0.036	0.072	0.070	0.053	9.03	4.83	3.55
CV	2.9	1.2	2.05	0.1	0.1	0.1	12.8	6.7	7.45
CV	2.9	1.2	2.05	0.1	0.1	0.1	12.8	6.7	7.45



Percent Ash content: Acha is a veritable source of plant minerals like potassium, and magnesium (Temple and Bassa, (1991). Although the current study did not investigate mineral ash content among accessions PCASH varied between 0.800 (Nakusni) and a maximum of 1.24 % in Chitfyeli-Dunga with a mean value of 1.04 %. In a similar study, Irving and Jideani (1997) reported that percent ash was  $1.40 \pm 0.01$  in acha. However, Sadiq *et al.* (2015) recorded 2.13 % in *D. exilis*.

Acha is a valuable food among diabetic patients, owing to its low glycemic index (rate of glucose absorption) being 66 in acha compared 95 in rice, reducing risk of hyperglycemia among diabetic patients. Result obtained in this study indicated that percent Nitrogen free extract which comprise carbohydrates varied between 85.75% in Rikwie and 94.87% in Aburu. This could suggest that variation for sugar is very low among the accessions under investigation.

### **Estimates of Variances, Coefficient of Variation, Heritability and Genetic Advance**

Estimates of phenotypic, genetic and environmental variances were statistically similar across 2017 and 2018 (Table 1). Therefore, a combined analysis was run to calculate other genetic parameters: genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV), broad sense heritability ( $h^2_b$ ), genetic advance (GA) and genetic advance as percent of mean (GAM) (Table 4). It reveals that in general, phenotypic variances ( $\delta_p^2$ ) were statistically similar to their corresponding genotypic variances ( $\delta_g^2$ ), indicating negligible impact of the environment in the expression of this trait. Result on Table 4 also shows that although estimates of PCV were higher than their respective GCV values implying that the environment had little impact on the expression of these characters.

In the combined ANOVA estimate of genotypic coefficient of variability (GCV) for yield per hectare was comparatively higher (19.35) than environmental coefficient of variability (ECV) which was 6.30. The wide gap between the two genetic parameters may an indication that plant genotype played a more significant role compared to the environment in the expression of this quantitative character. However, Allard (1960) opined that yield is a polygenic trait whose expression is affected by many genes and highly influenced by the environment.

Crude Fiber: Estimates of genotypic coefficient of variation (GCV) provides a measure of genetic variability that exist among quantitative traits in the test material (Ene *et al.*, 2016). A significant difference in crude was observed between PCV value (4.08) compared to (ECV) value of 0.05 for this trait, indicating environment had little effect in the expression of this character.

The highest Shiringani, 2010). Ample estimates of genetic advance (GA) among these traits. This indicate that these traits can be improved through direct phenotypic selection in early generation.

Despite the fact that these accessions were collected from a relatively small area; Bogoro and Tafawa Balewa local areas, the performances of these acha accessions in the current study suggest that the area holds substantial genetic diversity that can provide a base line study for future selection. Apart from its traditional value acha is generally favored because of its nutritional quality (Adoukonou, 2010). In order to improve its amino acid and mineral profile there is need to exploit existing genetic diversity through intensive genetic studies that should involve a larger germplasm collection by evaluating a larger collection. Future studies should also investigate the mode of inheritance of these characters to facilitate to provide effective breeding procedures for this crop.





GCV value (20.90) was recorded for the character nitrogen free extract, followed by ether extract (0.195). Estimates of phenotypic coefficient of variation (PCV) were higher than their corresponding genotypic coefficient of variation (GCV). High PCV and GCV as observed in the current study, could suggest a scope of selection for all the characters and even greater potential for genetic improvement. Thus, selection based on phenotypic values is very feasible.

Literature on the heritability in acha are scanty to provide valid comparison. However, estimates of broad sense heritability values (BSH) were high for all traits under investigation, ranging from 77% for ether extract to 98% for crude protein and crude fiber were recorded. High heritability values as seen in this study could be ascribed to the greater contribution due to genotypic variance compared to error variance among the tested lines (Shimelis and



**Table 4: Variance components, coefficient of variability, heritability in broad sense genetic advance and genetic advance, expressed as percent of mean among Acha accessions evaluated in Bauchi**

Trait	$\delta^2g$	$\delta^2e$	$\delta^2p$	GCV	PCV	ECV	BSH	GA	GAM
% Crude Protein	0.038	0.000	0.038	18.910	19.036	1.550	98.674	0.398	38.694
% Dry matter	0.091	0.001	0.092	16.066	16.168	1.286	98.734	0.617	32.885
% Ash	0.378	0.005	0.389	8.106	8.220	0.966	97.237	1.249	16.465
% Ether extract	0.066	0.008	0.083	29.934	33.476	10.597	79.958	0.475	55.139
% Crude fiber	13.963	0.002	13.967	4.017	4.018	0.052	99.966	7.696	8.273
YLHA	191.245	20.285	231.815	19.352	21.306	6.303	82.499	25.875	36.210

Where,  $\delta^2g$  = genetic variance,  $\delta^2e$  = Error variance,  $\delta^2p$  = Phenotypic variance, GCV, PCV and ECV = Genotypic, Phenotypic and environmental variance, respectively; while BSH = Broad sense heritability, GA = genetic advance GAM = Genetic advance expressed as percent of mean.



## Results of Correlation Studies

Result on Table 5 provides pair-wise spearman correlation matrix among five grain composition in Acha. It indicated that crude fiber content (%CF) in Acha grain had a significant, negative correlation ( $P < 0.01$ ) with yield (-0.392\*\*). Crude fiber also recorded negative association with crude protein (-0.239\*\*); and also, a highly significant negative correlation with carbohydrates (NFE) (-0.407\*\*\*). A significant negative association ( $P < 0.01$ ) was also seen between percent crude protein (%CP) and lipid content (-0.563\*\*). Negative but non-significant correlations was also seen between grain yield and EE, NFE and CP.

Before selecting genotypes for nutritional quality characters like protein content, oil and micronutrients content, it is important to know how much selection is likely to affect yield (Govindaraj *et al.*, 2009). The authors of this work could not access literature on the correlation among nutritional traits in acha. At present, grain yield and protein /amino acid content are probably the two most important breeding objectives in acha. Results obtained in the current study revealed negative correlations between grain yield and biochemical components (CP, CF, EE and NFE). The implication in this study is that selection for direct increase in yield may result in the attendant decrease in crude protein, crude fiber, ether extract and nitrogen free extract. However, Govindaraj *et al.* (2009) working on pearl millet, a closely related crop specie, reported significant positive correlation between grain yield and crude protein, crude fiber.

**Table 5:** Spearman correlation matrix of the relationship among six biochemical traits

Trait	Yield/ha	% CP	% DM	%EE	%CF
Yield/ha	1.00				
% CP	-0.045	1.000			
%DM	-0.064	0.117	1.00		
%EE	0.0160	-0.563	-0.162	1.00	
%CF	-0.392**	-0.239**	-0.407***	0.028	1.00

Where, \*, \*\* and \*\*\* = significant at 0.05, 0.01 and 0.001 level of probability

## Phylogenetic Studies

Acha is an allogamous specie in which cross fertilization generates natural variability within the genome and its genetic diversity seems not threatened by genetic erosion (Adoukonou, 2010). Results in this experiment indicated that even though the number (14) of accessions evaluated in this study was relatively small, they exhibited significant genetic variability that can be exploited in future breeding programs. This result is similar to previous works reported by Adoukonou (2010) as well as Kwon-Ndung and Ndachi (2007) who also observed substantial genetic variability among acha accessions.

Figure 1 is a Dendrogram showing phylogenetic relationships among the fourteen acha accessions under investigation. The calculated values of dissimilarity were obtained using hierarchical clustering with weighted pair group (WPGMA) method. The Dendrogram clustered fonio accessions into two main clusters. The first cluster is made up of only one cultivar, Lhadzjeli. The second cluster is made up of two main sub- groups and three sub-sub clusters with the first group comprising: Aburu, Wondat-Baptist, Chitfyli- Kusung, while the second sub-cluster Group 1 is was made of three local cultivars: Gege, Kamana and Rikwe, occurring at almost 9.8, while in the third sub –sub cluster had seven closely related accessions; Wodat-Bonga, Wondat-Coci, Chitfyeli-Dunga a more distant relative, Nakusni, appearing

more of a single outlier (Nakusni) others. Assessment of genetic diversity is major pre-requisite in plant breeding as it help in identifying potential parents that can use to create s more prospective breeding populations The present study, especially, the Dendrogram was useful in revealing genetic diversity in the proximate composition of acha among these germplasm collection.

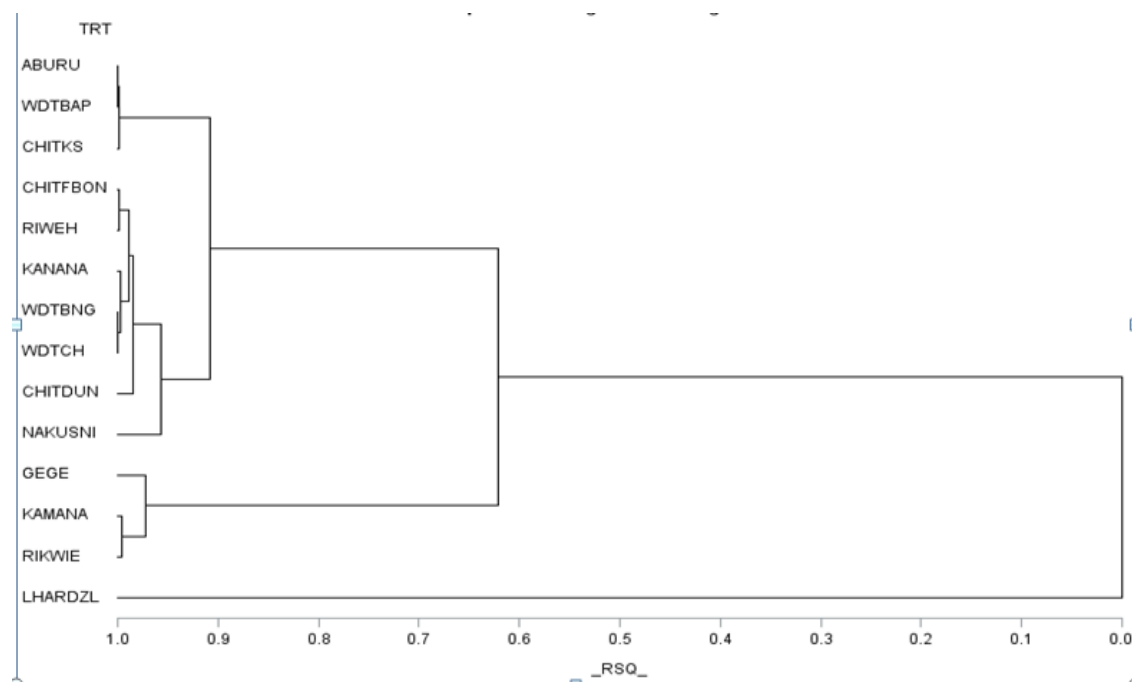


Figure 1: *Dendrogram showing the phylogenetic relationships among the fourteen Acha genotypes evaluated in this study.*

## CONCLUSION AND RECOMMENDATIONS

The result of the current study revealed that acha accessions exhibited ample genetic variability for all the traits under investigation which can be exploited for future breeding programs. In addition, high broad sense heritability (77% to 98%) couple with ample genetic advance for all the characters under investigation offer a good scope for further selection and genetic improvement. However further investigation is required to collect a larger germplasm collection to explore genetic diversity, examine the phylogeny of local land races in Nigeria and ways of improving the crop. Support for research using modern technologies is needed. Team breeding involving inter-disciplinary approaches could speed up breeding. In particular, the employment of Next generation technologies would assist in identifying candidate genes and quantitative trait loci (QTL) that affect important traits like grain yield and quality.

## ACKNOWLEDGEMENTS

The authors wish to thank farmers in Tafawa Balewa and Bogoro local government areas, who provided acha accession used in this study.



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