



VARIABLE GENETIC EXPRESSIONS AND INTERRELATIONSHIP BETWEEN GRAIN YIELD AND SOME QUALITY TRAITS OF ACHA (*DIGITARIA SPP.*) ACCESSIONS IN JOS PLATEAU

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ABSTRACT

Acha (*Digitaria exillis* kippis. Stapf and *D. iburua* Stapf L) is one of the oldest West African cereal and of great value to the natives. It belongs to the Poaceae (Grass) family. Despite its potentials, Acha has remained a marginal crop. The present study focused on the evaluation of the variable genetic expressions and interrelationship between grain yield and some morphological traits of some Acha accessions. These accessions were collected from farmers in five villages of Bokkos Local Government Area of Plateau State. This work was conducted at the end of the 2019 rainy season at the Federal College of Forestry Jos. Grains were harvested from the experimental field and proximate analysis was conducted for the Ash content, crude fat, crude fibre, protein content, carbohydrate content, moisture content, dry matter content and energy values. Analysis of variance revealed variability among the different accessions and the variability spanned the nutritional composition of Acha. Grain yield was positive and significantly correlated with crude fibre content, while dry matter content, crude ash, crude fat content and carbohydrate content even though were positively correlated, the correlation was not significant. The phenotypic variance was slightly higher than the genotypic variance indicating the influence of environment on these traits. Phenotypic Coefficient of Variance (PCV) was equally higher than the corresponding Genotypic Coefficient of Variance (GCV) for all characters evaluated showing that they all interact to some extent. Broad sense heritability estimate coupled with genetic advance as percent mean was high, for most characters studied indicating that these traits are under the influence of additive gene effect and therefore, can be improved by selection except for grain yield which was low, indicating that selection will not be an appropriate method for improving this trait. Other methods of breeding such as mutagenesis can be used.

Keywords: *Digitaria spp.* (Acha), Proximate Analysis, Genotypic and Phenotypic Variance, Genotypic and Phenotypic Coefficient of Variance

INTRODUCTION

Acha crop (*Digitaria exilis* Kippis Stapf. and *Digitaria iburua* Stapf. L) is grown mainly in West and Central African regions. Acha is known with English names such as fonio and hungry rice, it is also known with other names such as findi, fundi, pom, kabuga, and so forth, in different West African countries (Saine, 2012). The crop has been described as the oldest West African cereal and of great value to the natives. Acha species belong to the family Poaceae, sub-family of Panicoideae, tribe of Paniceae and the genus Digitaria. This genus comprises 230-325 annual and perennial grass species with a wide geographic distribution in the tropics and subtropics (Henrard 1950; Clayton and Renvoize 1986; Adoukonou-Sagbadja, 2010).

In Benin, unlike other cereals such as maize, sorghum, millet and rice, that are cultivated everywhere throughout the country, Acha appears as an essentially local or endemic crop to the Atacora Mountain in the northwest of Benin (Vodouhe *et al.*, 2003). This crop has a socio-cultural importance for the Otamari ethnic group in Boukoubé, the main producer community providing 74% of the national production (Dramé and Cruz, 2002; Ballogoun, 2013; Paraïso *et al.*, 2013). It also plays an important role in food security in the population especially during the lean season when early varieties are used to curb famine.

Acha is mainly a plant of the savannas and is poorly adapted to lowland humid zones because it probably will succumb to different fungal and bacterial diseases. However, *D. exilis* are reportedly grown in South Eastern Sierra Leone around the Gola Forest. Similarly, *D. iburua* is reportedly grown in Zaire (now Democratic Republic of Congo) and some other equatorial locations (NRC 1996). Production statistics in Nigeria shows that about 70,000 metric tons of the crops is produced annually and the economic returns of which when computed showed that it is profitable to grow the crop compared to other crops like rice, sorghum and cowpea (Dauda and Luka, 2003).

It is sometimes considered as a small seed with a big promise and provides food early in the season when other crops are yet to mature for harvest (National Research Council, 1996). The grains have been reported to be the tastiest and most nutritious of all the grains. Temple and Bassa, (1991) documented that, it contains 7% crude protein, which is high in leucine (19.8%), methionine and cysteine of about (7%) and valine (5%). It has also been reported to form the staple food in some of the producing areas in Nigeria where it is processed into various kinds of menus (Kwon-Ndung, *et al.*, 2001).

Grain quality characteristics are very important in cereal crops breeding as it is predominantly consumed as a whole grain. The milling percentage,

grain appearance, cooking quality and nutritional components constitute the quality traits

This investigation focuses on assessing the variable genetic expressions and interrelationship between grain yield and some quality characters of some Acha accessions grown in Jos.

MATERIALS AND METHOD

This study was carried out in Jos North Local Government Area of Plateau State. The state is located in Nigeria's middle belt region with an area of 26,899 square kilometers. The state has semi temperate climate with average daily temperature ranging from 18°C (64.4°F) to 25°C (77.00°F) and an annual average rainfall of 1775.1mm. Plateau State is located between latitude 09°55'N, Longitude 08°53'E and altitude 1,217m above sea level.

The ten (10) Acha accessions used for this investigation were collected from farmers in five villages (Mwel, Toff, Kuba, Mbar and Kulere Richa) in Bokkos Local Government Area of Plateau state. These accessions were sown in Randomized Complete Block Design (RCBD) with three replications. Experimental plot measured (3×2) m². 30g of seed was weighed using a digital weighing balance. These were uniformly broadcast in each of the plots. All cultural practices were carried out throughout the growing season. The Data collected both at vegetative and productive stage were subjected to the analysis of variance and Duncan Multiple Range Test was used to separate the treatment means. Grains were harvested from the experimental field and proximate analysis was carried out for crude fat, crude ash, moisture content, crude fibre, crude protein, carbohydrate content, dry matter content and energy value (AOAC 1980).

The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were calculated using the formula according to Chaudhary and Prasad, (1968). Broad sense heritability was calculated using the formula according to Falconer (1996) and expected genetic advance was computed by the formula described by (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

Variability existed among the yield expressions of the ten Acha accessions studied. These results agrees with the report of the work by Kwon-Ndung and Ochigbo, (2014) that grain yield have shown high levels of variability in experimental studies. Martins, (1992) also reported high level of variability among some randomly collected Acha accessions assessed at Samaru, Zaria

Table 1: Proximate Composition of the Ten (10) Different Acha Accessions Grow in Jos.

Accessions	Crude Ash (%)	Crude protein (%)	Moisture (%)	Crude fibre (%)	CHO (%)	Crude fat (%)	Dry Matter (%)	Energy value Kcal/g
A	1.7035 c	10.66 bc	7.36300 c	0.61100 c	76.3185 cd	3.34300 e	92.6370 d	378.005 cd
B	1.48450 cd	9.41300 de	8.14350 b	0.98000 bc	74.9685 d	5.01050 bc	91.8565 e	382.622 b
C	1.07200 d	10.5515 bc	5.05950 f	0.708000 c	76.5610 cd	4.71250 c	94.9405 a	390.861 a
D	2.40850 ab	11.8425 a	6.77800 cde	1.58950 ab	75.3555 d	3.46550 e	93.2220 bcd	379.983 bc
E	0.96850 d	11.0770 ab	7.08150 cd	0.639000 c	75.4250 d	3.29400 e	92.9185 cd	375.653 d
F	2.48350 a	8.62500 e	9.28150 a	1.63900 a	73.1190 e	5.60650 a	90.7185 f	377.434 cd
G	1.72900 c	10.0695 cd	7.17550 cd	1.14100 abc	76.3695 cd	3.43300 e	92.8245 cd	376.654 cd
H	1.81100 c	8.95350 e	5.27100 f	1.19500 abc	77.5495 bc	5.14300 b	94.7290 a	392.297 a
J	1.888 bc	8.8435 e	6.60900 de	1.2460 abc	78.4505 ab	3.40450 e	93.3910 bc	379.818 bcd
I	1.4460 cd	9.15050 de	6.1060 e	0.9545 bc	79.8425 a	3.94700 d	93.8940 b	391.493 a
CV (%)	13.6	4.3	4.4	26.8	1.1	4.6	0.3	0.5

** = significant at 1% probability level, * = significant at 5% probability level

Any two means having a common letter within the same column are not significantly different at the 1% and 5% level of significance according to Duncan Multiple Range Test (DMRT).

Table 2: Correlation Matrix Between the Grain Yield and Some Quality Characters.

	Matter	Moisture	Ash	Crude Fat	Crude Protein	Crude Fibre	Cho (%)	Energy Value Kcal/G	Grain Yield Kg/Ha
Matter									
Moisture content	-0.99								
Crude Ash	-0.447	0.447							
Crude Fat	-0.160	0.160	0.187						
Crude Protein	0.164	-0.164	-0.185	-0.572					
Crude Fibre	-0.342	0.342	0.895	0.307	-0.273				
Carbohydrate	0.707	-0.707	-0.326	-0.354	-0.221	-0.286			
Energy Value Kcal/G	0.729	-0.729	-0.271	0.433	-0.291	-0.136	0.576		
Grain Yield Kg/Ha	0.267	-0.267	0.329	0.323	-0.326	0.604	0.263	0.482	

The present study also revealed that a significant correlation existed between grain yield and some quality traits. Positive and significant correlation existed between grain yield and fibre content (table 2). However, dry matter, ash content, crude fat and carbohydrate content were also positively correlated to yield, but the correlation was not significant (table 2). The significant and negative correlations between grain yield and protein content was reported by Pleijel *et al.* (1999) in bread wheat, and Garcia del Moral *et al.* (1995) in triticale. The present study also revealed negative and non-significant correlation between grain yield and protein content. Therefore, Selection for protein content in Acha is complicated by the negative relationship with grain yield, and the influence of environmental conditions on protein content. This agrees with those reported by Clarke *et al.* (2000).

Table 3: Estimation of the Genotypic Coefficient of Variance, Phenotypic Coefficient of Variance, Heritability, Genetic Advance and Genetic Advance as Percentage Mean.

Parameters	Genotypic variance (δ^2_g)	Phenotypic Variance (δ^2_p)	GCV %	PCV %	H ² b %	Genetic Advance GA	GAM %
Grain yield	0.0037	0.1177	0.003	0.017	3.20	0.023	0.001
Dry matter	1.529	1.651	12.8	13.3	92.6	0.254	0.27
Moisture content	1.529	1.651	47.1	48.9	92.6	2.455	35.6
Ash content	0.199	0.289	34.2	41.2	68.9	0.764	44.9
Crude fat content	0.758	0.826	42.8	44.7	91.7	1.719	41.6
Crude protein content	1.036	1.325	32.3	36.6	78.1	1.856	18.6
Crude fibre content	0.132	0.133	35.1	35.3	99.3	0.747	67.8
Carbohydrate content	2.546	4.624	18.3	24.6	55.1	2.443	3.2
Energy	42.238	43.815	33.2	33.8	96.4	13.164	3.44

GCV=genotypic coefficient of variance, PCV= phenotypic coefficient of variance, H²b = broad sense heritability, GAM =genetic advance as per percentage mean.

Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. This indicates that they all interacted with the environment to some extent Sivasubramanian and Madhavamenon, (1973). The higher estimate of phenotypic coefficient of variation (PCV) was obtained for almost all the characters corresponding to GCV and these characters could be used as selection indices for crop improvement. A comparison of estimates of GCV (%) with their corresponding PCV (%) for different traits revealed that in general, the GCV (%) were close to the estimates of PCV (%) for all the characters indicating that they have been influenced by the environment.

Heritability estimate was high for all characters studied except for grain yield which recorded low and carbohydrate content which recorded moderate. High values of heritability in broad sense indicate that the character is less influenced by environmental effects. Similar result was reported by Ojo *et al.*, (2006) and Kundu *et al.* (2008) recorded high heritability for grain yield per plant in rice contrary to low heritability recorded in the present study.

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. High heritability should be accompanied with high genetic advance to arrive at a more reliable conclusion. High heritability with high genetic advance as percentage mean was recorded for moisture content, crude ash content, crude fat content and crude fibre content indicating that the high heritability observed

is due to additive gene effects. Mass selection and progeny selection may be effective for the improvement of these characters.

However, high heritability coupled with moderate genetic advance in percentage of mean was observed for protein content indicating the role of both additive and non-additive gene effects for control of protein content. Energy value and dry matter content recorded high heritability coupled with low genetic advance in percentage of mean in the present investigation. This is similar to the findings of Singh *et al.* (2012). High heritability and low genetic advance as percentage mean indicates that these characters were controlled by non-additive gene effects. Therefore, these characters could be improved through heterosis breeding program.

CONCLUSION

The observed High heritability with high genetic advance as percentage mean recorded for moisture content, crude ash content, crude fat content and crude fibre content, indicated that it was due to additive gene effects and so, Mass selection and progeny selection may be effective for the improvement of these characters.

Again, the observed high heritability coupled with moderate genetic advance in percentage of mean for protein content, indicated the role of both additive and non-additive gene effects for control of protein content. This suggests that these characters were controlled by non-additive gene effects and therefore, the characters could be improved through heterosis breeding program

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