

Genetic Variability, Heritability and Genetic Advance for Yield and some Agronomic Traits in *Digitaria exilis* Accessions

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ABSTRACT

The study was to evaluate the genetic variability, broad sense heritability and genetic advance in the *D. exilis*. The experiment was conducted in 2018 raining season using twelve (12) accessions of *D. exilis*, laid out in a Randomised Complete Block Design with three replications. The plot size was of 4 x 5 m², observations were made on eight traits, and data were subjected to statistical analysis. Days to 50% flowering, number of tillers per plant, panicle length, days to maturity and grain yield showed significant difference at 5% probability. Higher GCV (20.28%) for days to 50% flowering as compared to PCV (6.06%) indicates that the trait is under genetic control. The higher extent of PCV for number of spikes/panicle, length of spike and plant height as compared to GCV indicates greater contribution of environmental influence in the expression of these traits. The close magnitude of GCV and PCV observed for number of tillers per plant, panicle length, days to maturity and grain yield indicates the effectiveness of selection for these traits. High heritability in broad sense was recorded for number of tillers per plant (74.56%), days to maturity (99.81%) and grain yield (76.57%). High heritability coupled with high to moderate genetic advance over mean was observed for number of tillers per plant, days to maturity and grain yield, this indicates the presence of additive gene action, and selection could be effective for these traits. However, low heritability coupled with low genetic advance recorded for number of spike per panicle, length of spike and plant height indicates the action of non-additive gene.

Keywords: Acha, *D. exilis*, Heritability

INTRODUCTION

Acha (*Digitaria exilis*) is one of the oldest West African cereal crops with cultivation dating back to 7000 B.C (Dachi et al., 2016). While it is commonly known as ‘acha’ in Nigeria, it is called ‘fundì’, ‘fonio’, ‘pom’ and

‘kabug’ in other West African Countries (Kalat, 2014).

Acha is considered as an orphan crop, the grains have been reported to be the tastiest and most nutritious of all the grains (Kwon-Dung et al., 2017).

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It is reported to contain 7% crude protein, which is high in leucine (19.8%), methionine and cystine of about (7%) and valine (5%) (Temple & Bassa, 1991). It has a lower glycemic index as compared to maize and wheat making it safe for diabetic patients (Igomo, 2016). Acha production in Nigeria is hampered by many problems such as low yield, weed, pest, diseases, small seeds size and post-harvest processes (Dachi, 2014). The crop can grow on poor and marginal soil that is not suitable for other cereals (Adolfina et al., 2013).

In Senegal, annual production was estimated at 1,068 tonnes with grain yields ranging from 200 to 700 kg/ha (Ghislain, 2013) while in Nigeria, annual production was 85,000 tonnes with grain yield of 500Kg/ha (Dachi, 2016). Like any other important crop, Acha is used for making porridges, flour, alcohol and non-alcoholic beverages, couscous, and in traditional medicine (Adolfina et al., 2013). Genetic variability among Acha traits is important for breeding and in selecting promising accessions so as to know if the variations are heritable or non-heritable. However, little effort has been devoted to study the genetic variability of this important health benefit crop. Heritability alone cannot provide the prediction of gain under effective selection, there is need to study along with genetic advance. In view of this, the study was designed to study the genetic variability, broad sense heritability and genetic advance of some traits in *D. exilis* accessions.

MATERIALS AND METHODS

The experiment was conducted at National Cereals Research Institute, Badeggi in 2018 (Lat. 9° 45'N and Long. 6° 07'E) located in the Southern Guinea Savannah of Nigeria. Twelve accessions of *D. exilis* were used. The experiment was laid out in a Randomised Complete Block Design (RCBD). Each accession was broadcasted in a plot of 4 x 5 m² with three replications at seed rate of 30 kg/ha. Fertilizer (NPK 15:15:15) was applied in two split doses 30kg N/ha, 30 kg P₂O₅ and 30 kg/ha K₂O at 4 and 8 weeks after sowing

(WAS). Weeding was done by manual hand pulling at 4 and 8 WAS.

Data were collected on days to 50% flowering, number of tiller per plant, panicle length, plant height, number of spikes per panicle, spike length, days to maturity and grain yield. Data collected were subjected to analysis of variance using Statistical Analysis System (SAS) versions 9.0 (2002). Variability parameters were estimated following the method of Panse, (1957). Both genotypic and phenotypic coefficients of variation were estimated using the formula below:

$$GCV (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

$$PCV (\%) = \frac{\sqrt{\sigma_{ph}^2}}{\bar{X}} \times 100$$

Where:

GCV= Genotypic coefficient of variation

σ_g^2 = genotypic variance

\bar{X} = grand mean of the respective trait

PCV= phenotypic coefficient of variation

σ_{ph}^2 = phenotypic variance

\bar{X} = grand mean of the respective trait

The PCV and GCV values were categorised as low, moderate and high according to Sivasubramanian and Menon, 1973. Broad sense heritability values were estimated by formula as suggested by Hanson et al. (1956). The broad sense heritability estimates were categorized as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966). Genetic advance was estimated as;

$$K \times Hb \sqrt{\sigma_p^2}$$

Where:

K= the standardize selection differential at 5% selection intensity

(K=2.063).

Hg= heritability in broad sense

σ_p^2 = phenotypic variance

RESULTS AND DISCUSSION

Analysis of variance

The result from the analysis of variance revealed significant difference for days to 50% flowering, number of tillers per plant, panicle length, days to maturity and grain yield ($P < 0.05$) (Table 1.). This result indicates the existence of genetic variability for these traits. The existence of this genetic variability recorded for these traits gives an opportunity for Acha breeders to improve these traits through selection and hybridization.

Range of 8 Traits under Observation

Days to 50% flowering ranged from 83 for accessions Napas and Tishi to 102 for accessions Loma and Namuruk, number of tillers /plant ranged from 4.0 to 18.5 for accessions Shen and Kureep respectively. Accession kureep recorded the highest value for length of spike (16.5 cm), panicle length varied from 28.8 cm to 43.5 cm for accessions Nding and Kureep respectively, Namuruk recorded the highest value for plant height (107.6 cm) while Nding recorded the lowest value for this trait (42.4 cm). Days to maturity ranged from 99 in accessions Tishi and Napas to 141 for accession shen. Napiya recorded the lowest value of 550.0 Kg/ha for grain yield while kureep recorded the highest value for this trait (950 Kg/ha). The wide range observed for most traits indicates the existence of genetic variability among the accessions; this implies the possibility of selection in acha breeding programme.

Estimate of Genetic Parameters

The results of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are shown in Table 2. Genotypic coefficient of variation ranged from 3.68 cm for plant height to 27.25 for number of tillers/plant whereas phenotypic coefficient of variation ranged from 6.06 for days to 50% flowering to 31.56 for number of tillers/plant.

The high magnitude of genotypic coefficient of variation recorded for days to 50% flowering (20.28) as compared to phenotypic coefficient of variation indicates the possibility of improving this trait through selection.

The higher extent of phenotypic coefficient of variation recorded for number of spikes per panicle, length of spike and plant height as compared to genotypic coefficient of variation indicates greater contribution of environmental influence in the expression of these traits, therefore selection for these traits need to be done carefully as this result can mislead. This agrees with the findings of Karnwal and Singh (2009). The close magnitude of genotypic coefficient of variation and phenotypic coefficient of variation observed for number of tillers/plant, panicle length, days to maturity and grain yield indicates the effectiveness of selection for these traits as it may likely to have a considerable improvement at early generations. This agrees with the findings of Mahbub et al. (2015).

The result of heritability in broad sense estimate revealed a high heritability for number of tillers/plant (74.56%), days to maturity (99.81%) and grain yield (76.57%), moderate heritability estimate was recorded for days to 50% flowering (58.54%) while low heritability was recorded for number of spikes/panicle (20.0%), length of spike (25.0%), panicle length (39.13%), and plant height (12.23%). Heritability alone cannot provide a reliable result on selection value; hence it must be coupled with genetic advance for effectiveness of selection in breeding programme (Johnson, et al., 1955). Genetic advance over mean expected ranged from 2.65 to 48.56% for plant height and number of tillers/plant respectively. Genetic advance as per cent of mean expected was classified as low (<10%), moderate (10-20%) and high (>20%) according to Johnson et al. (1955). High heritability coupled with high to moderate genetic advance over mean observed for number of tillers/plant, days to maturity and grain yield indicates the preponderance of additive gene action and selection could be effective for these traits. Similar result has been reported by Reza et al. (2015) on wheat.

Low estimate of heritability coupled with low genetic advance over mean expected recorded for number of spike/panicle, length of spike and plant height indicates the action

Table 1: Mean square of 8 traits for 12 accessions of *D. exilis*

Source	DF	Days to 50% flowering	Number of tillers/plant	Number of spikes/panicle	Length of spikes (cm)	Panicle length(cm)	Plant height(cm)	Days to maturity	Grain yield (Kg)
Rep	2	33.08	7.59	0.03	0.354	19.53	806.93	0.03	13121.47
Genotype	11	77.70*	28.19*	0.27	4.52	25.93*	131.67	327.57*	47806.14*
Error	22	20.33	4.12	0.19	2.69	11.33	103.98	0.33	6344.27

Table 2: Mean, Range, Genotypic (σ_g^2) and phenotypic variance (σ_p^2), genotypic coefficient (GCV) and phenotypic coefficient of variance (PCV), broad sense heritability (Hb), genetic advance (GA) and genetic advance as per cent of mean (GAM) for 8 traits

Characters	Mean	Range	Phenotypic variance	Genotypic variance	Genotypic coefficient of variation	Phenotypic coefficient of variation	Broad sense heritability (Hb %)	Genetic advance	Genetic advance over mean (%)
Days to 50% flowering	94.33	83.0-102.0	32.68	19.13	20.28	6.06	58.54	6.90	7.31
Number of tillers/plant	10.40	4.0-18.5	10.77	8.03	27.25	31.56	74.56	5.05	48.56
Number of spikes/panicle	3.78	3.0-5.0	0.15	0.03	4.58	10.25	20.00	0.16	4.23
length of spike (cm)	13.09	8.5-16.5	2.40	0.60	5.92	11.83	25.00	0.80	6.12
Panicle length (cm)	35.74	28.8-43.5	12.42	4.86	6.17	9.86	39.13	8.10	22.66
Plant height (cm)	84.11	42.4-107.6	78.22	9.57	3.68	10.52	12.23	2.23	2.65
Days to maturity	115.39	99.0-141.0	109.30	109.09	9.05	9.06	99.81	21.53	18.66
Grain yield (kg/ha)	796.40	550.0-1050.0	18050.14	13820.63	14.76	12.59	76.57	212.22	26.65

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