



Genetic Variability, Heritability and Correlation Studies in Fifty Sorghum (*Sorghum bicolor* L. Moench) Accessions Collected from Southern Nigeria

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Sorghum [*Sorghum bicolor* (L.) Moench] is an important food crop in southern Nigeria with high genetic variability. However, this variability is not characterized. Fifty sorghum accessions collected from different states in southern Nigeria were evaluated for eleven agronomic characters to determine the extent of genetic variability and character association among the accessions. The experiments were laid in a randomized complete block design with three replications at the Teaching and Research Farm of the Federal University of Technology, Akure (FUTA) Ondo State and Federal College of Agriculture Ishiagu research farm during the rainy season of 2018 and 2019. Data were collected on eleven quantitative traits for genetic variability and character association. Panicle weight had the highest GCV (24.96%) and PCV (30.61%). Ten out of the eleven traits have heritability estimates above 50% which implies an opportunity for improvement among the traits with the number of days to 50% heading having the highest (98.84%). Correlation analysis showed significant and positive association among growth, flowering traits and head traits.

The strong positive correlation coefficients of plant height with all the traits implies that simultaneous selection for these traits is possible for improvement in sorghum genotypes for fodder and grain traits.

Keywords: Heritability; correlation studies; sorghum; accessions.

1. INTRODUCTION

Sorghum is an important crop of the tropics and sub-tropics. It is the fifth most important cereal crop in the world after wheat, rice, maize and barley in both total area and production [1, 2]. It is well adapted to hot, semi-arid tropical environments with 400-600 mm rainfall; as a result, it is a very stable source of nutrition [3]. It is grown worldwide for food, feed, fodder and fuel [4]. Its main breeding objectives include higher grain yield, early maturity, heat and drought resistance, disease resistance, insect pest resistance, quality and adaptability. In Nigeria, sorghum is the most widely cultivated staple cereal covering 8.5 million hectares in three agroecological zones [5]. According to the survey conducted by [5] Southern Nigeria produces only 1% of the overall total. However, the region is dominated with uncharacterized sorghum accessions which are planted by small scale farmers for use as stake, feed and food. Recently, the interest in sorghum production keeps increasing on a daily basis by the rural and urban dwellers of the southern states, as it is used as a replacement for maize in animal feed and also combined with cassava flour as food for man. This cannot be ignored but backed with concise research on the genetic variability studies of the available accessions in the region to prevent genetic erosion especially when desertification and insurgency is threatening crop production in agro ecologies with high sorghum production. Sorghum evaluation is important for selection, conservation, identification of superior genotypes, improvement, adaptation and eradication of genetic erosion [6, 7]. Availability of genetic variability for component features is of significant advantage when starting a crop improvement program. Plant breeding has been broadly described as the intentional manipulation of variability [8]. Because the entire breeding process revolves around the creation and maintenance of genetic variability, having adequate information on it is a must before beginning any breeding procedure. Sorghum has been found to have a wide range of genetic variability in terms of fodder output and grain yield components, according to a number of researchers [2, 9, 10]. Hence, the need to study

the genetic variability among sorghum accessions collected from southern Nigeria.

2. MATERIALS AND METHODS

The experiment was conducted at two different locations in southern Nigeria (Akure and Ishiagu) from July to December, 2018 and repeated in 2019. The fifty accessions used for the experiment were collected from different farmers field during the 2017 planting season in ten southern states. The experiment was laid in a randomized complete block design (RCBD) with three replications. The experimental area measured 24 m×37.5 m (900 m²) with a spacing of 0.75 m×0.25 m. Each block measured 7 m×37.5 m with an alley of 1 m between the ranges and 1.5 m among the blocks. Standard plant protection and agronomic practices/measures for sorghum were followed during the cropping season. Quantitative data were collected on eleven characters on five randomly selected plants according to IBPGR and ICRISAT descriptor of 1993.

2.1 Data Analysis

Genotypic and phenotypic variance were computed from ANOVA according to the procedure of [11]. Genotypic and phenotypic coefficients of variation, heritability, genetic advance and repeatability were computed according to the procedure of [12]. Character association (Phenotypic and genotypic correlation coefficient) was computed as suggested by [13]. Test of significance of correlation was done by comparing the values against the 'r' values given by [14].

3. RESULTS

Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance and repeatability are presented in Table 1. The results of the coefficient of variation showed that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the parameters. Panicle weight had the highest

GCV (24.96%) and PCV (30.61%) while days to 50% anthesis and 100 grain weight had the lowest PCV and GCV values of 11.17% and 8.76% respectively. Heritability estimates in the broad sense were found to be high for 10 out of the 11 traits, ranging from 69.36% (leaf width) to 94.86% (days to 50% heading). Moderate genetic advance and moderate high heritability estimates for 100 grain weight (11.52), leaf width (16.84), leaf length (21.26), days to 50% anthesis (21.76), days to 50% heading (23.23), number of leaves (23.94), number of nodes (26.78), plant height (31.73), panicle width (38.07) and panicle length (41.73). Panicle length had the highest genetic advance value of 44.94. The highest repeatability (2.95%) was recorded in days to 50% anthesis, while 100 grain weight recorded the lowest with a value of 0.10. The genotypic (r_g) and phenotypic correlation (r_p) for Ishiagu and Akure locations during the 2019 planting season is presented in Tables 2 and 3 respectively. The genotypic correlation coefficients (r_g) for 11 quantitative traits characterized for 50 sorghum accessions at Ishiagu in 2019 are shown in Table 2. 100 grain weight had a negative and significant r_g with days to 50% heading (-0.38), days to 50% anthesis (-0.30) and panicle width (-0.21) while plant height and number of leaves showed a positive and significant r_g with all the traits apart from 100 grain weight. The number of nodes were positively correlated with panicle length (0.21) and panicle width (0.23). Panicle weight had a positive significant r_g with plant height (0.53), leaf length (0.57), leaf width (0.36) and number of leaves (0.21) while panicle length also had a positive significant r_g with plant height (0.57), leaf length (0.55), days to 50% heading (0.32), days to 50% anthesis (0.44), number of leaves (0.33), number of nodes (0.21) and panicle weight (0.50). Likewise, days to 50% heading and anthesis had positive r_g with plant height, leaf length, leaf width, number of leaves, number of nodes, panicle length and negative significant r_g with 100 grain weight. The phenotypic correlation coefficients (r_p) for the 50 sorghum accessions at Ishiagu in 2019 are presented in Table 2. Plant height and number of leaves had a positive significant r_p with all the traits except 100 grain weight, while 100 grain weight had a negative significant r_p with days to 50% heading (-0.30) and days to 50% anthesis (-0.31). Apart from leaf width, 100 grain weight and the number of nodes that were not significant, panicle length shows a positive significant phenotypic correlation with all the traits. The number of days to 50% heading and the number

of days to 50% anthesis were positively correlated with plant height (0.29 and 0.29), leaf length (0.29 and 0.29), leaf width (0.64 and 0.69), number of leaves (0.39 and 0.39), panicle length (0.29 and 0.35) and negatively correlated with 100 grain weight (-0.30 and 0.31). Also, leaf width had a positive significant r_p with plant height, leaf length, leaf width, days to 50% heading, days to 50% anthesis, number of leaves, panicle weight and panicle width. The genotypic correlation coefficients for 50 sorghum accessions at Akure in 2019 using 11 quantitative traits are depicted in Table 3. There was a significant and positive r_g between plant height and other traits except days to 50% heading. Apart from 100 grain weight, which was not significant with panicle length, all other traits had a positive significant r_g with panicle length. Panicle weight had a positive significant r_g with plant height (0.34), leaf width (0.30), number of leaves (0.37), number of nodes (0.35), panicle length (0.19) and panicle width (0.53). Also, days to 50% heading had a positive r_g with leaf length (0.19), number of nodes (0.99), panicle weight (0.37), panicle length (0.48), panicle width (0.63) and a negative significant r_g with leaf width (-0.22). However, leaf width showed a significant r_g correlation with plant height, leaf length, days to 50% heading, days to 50% anthesis, number of leaves, number of nodes, panicle weight, and panicle length, while it was not significant with panicle width and 100 grain weight. The phenotypic correlation coefficient for the 50 sorghum accessions at Akure are presented in Table 3. Panicle width (0.40), panicle length (0.32), number of nodes (0.84), number of leaves (0.81), leaf width (0.30) and leaf length (0.56) had a positive significant correlation with plant height. The highest significant r_p of 0.99 was observed between days to 50% heading and days to 50% anthesis, followed by 0.98 for number of leaves and number of nodes. There was a positive significant r_p between plant height, leaf length and leaf width.

4. DISCUSSION

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values are useful for making selection and comparison between the relative amount of phenotypic and genotypic variation among different traits. The study showed a higher PCV and GCV for all the characters which implies that greater potential could be expected in selection for these characters. This showed the influence of the environment on the expression of these

character. Higher magnitude of GCV: PCV recorded for panicle width, panicle weight, and panicle length indicated the presence of high magnitude of genetic variance. Moderate estimate of genotypic and phenotypic coefficient of variation were observed in plant height, days to 50% anthesis, number of leaves, number of nodes, leaf width, leaf length and days to 50% heading. Low magnitude for 100 grain weight and leaf width indicated limited genotypic variation for the two traits. These are in agreement with the findings of [15, 16, 17] for plant height, number of leaves, 100 grain weight, panicle weight and days to 50% flowering in sorghum. The most basic information required by a breeder in any crop improvement programme is the extent of inheritance for different characters. Such studies help in selection if the population under consideration is large due to additive genes. In the study, broad sense heritability was estimated, which involves additive as well as non-additive in order to draw conclusion on how to improve the characters. Hence, the need to interpret the estimate of heritability and genetic advance together. Estimate of broad sense heritability was found to be high for all the traits. This was similar to the findings of [2, 10, 18, 19] in the same crop. Improvement could be brought about by the phenotype selection of panicle length and weight because they are governed by additive gene action as high heritability value is accompanied by high genetic advance. This result is in agreement with the findings of [16] who reported

high heritability and high genetic advance for panicle length in sorghum. [20] reported low genetic advance for number of leaves per plant and 100 grain weight. Repeatability is a useful tool for quantifying the extent to which an individual performance or behavior remains consistent over time [21, 22]. The study is important for crop improvement since they represent the maximum value than the heritability of a trait in wide sense can reach [23]. High values of this coefficient for any trait shows that the genotypes are expressed with high stability [24]. In this study, two flowering trait (days to 50% heading and days to 50% anthesis) and one head trait (panicle length) with the highest and relative highest repeatability value are the most stable characters while 100 grain weight with the least value is the most unstable character of the studied sorghum accessions. Repeatability have been estimated in other crops species such as cowpea, fluted pumpkin and African yam bean by [25, 22, 26] respectively. Based on this, predicting performance and selection could be reliable if the choice of genotypes can be based on high GCV:PCV ratio, high broad sense heritability and high repeatability [24]. Effective characterization of sorghum genotypes and improvement could be successful if these criteria are employed. The correlation among various characters is an important part for initiating a breeding programme, as it provides an opportunity for the selection of genotypes having desirable traits simultaneously [27]. Positive or

Table 1. Estimates of genotypic and phenotypic coefficients of variation, broad sense heritability, genetic advance and repeatability of 50 sorghum accessions

| Character | Genotypic coefficient of variation (%) | Phenotypic coefficient of variation (%) | Broad sense heritability (%) | Genetic advance (%) | Repeatability (%) |
|----------------------|--|---|------------------------------|---------------------|-------------------|
| Plant Height (cm) | 16.26 | 17.16 | 89.76 | 31.73 | 1.50 |
| Panicle width (cm) | 21.64 | 25.33 | 72.95 | 38.07 | 0.42 |
| Panicle weight (g) | 24.96 | 30.61 | 66.50 | 41.93 | 0.33 |
| Panicle length (cm) | 22.68 | 23.57 | 92.56 | 44.94 | 2.15 |
| Days to 50% Anthesis | 10.86 | 11.17 | 94.52 | 21.76 | 2.95 |
| Number of leaves | 12.88 | 14.28 | 81.38 | 23.94 | 0.749 |
| Number of nodes | 14.81 | 16.87 | 77.05 | 26.78 | 0.58 |
| Leaf width (cm) | 9.82 | 11.79 | 69.36 | 16.84 | 0.36 |
| Leaf length (cm) | 11.19 | 12.13 | 85.09 | 21.26 | 0.93 |
| Days to 50% heading | 11.58 | 11.88 | 94.89 | 23.23 | 3.21 |
| Grain weight (g) | 8.76 | 13.69 | 40.86 | 11.52 | 0.10 |

Table 2. Genotypic and Phenotypic Correlations for 50 sorghum accessions in 2018

| Character | Correlation | PH | LL | LW | HEADIN | ANTH | NOL | NOD | PWEI | PLEN | PWID | GWEI |
|-----------|-------------|----|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|
| PH | GC | 1 | 0.73** | 0.38** | 0.31** | 0.31** | 0.76** | 0.45** | 0.53** | 0.57** | 0.36** | 0.10 |
| | PC | 1 | 0.66** | 0.35** | 0.29** | 0.29** | 0.67** | 0.41** | 0.39** | 0.48** | 0.27** | 0.12 |
| LL | GC | | 1 | 0.71** | 0.64** | 0.69** | 0.52** | 0.16 | 0.57** | 0.55** | 0.49** | -0.09 |
| | PC | | 1 | 0.64** | 0.56** | 0.58** | 0.43** | 0.10 | 0.52** | 0.43** | 0.43** | 0.09 |
| LW | GC | | | 1 | 0.50** | 0.54** | 0.24* | -0.19 | 0.36** | 0.11 | 0.22* | -0.12 |
| | PC | | | 1 | 0.45** | 0.47** | 0.23* | -0.14 | 0.38** | 0.13 | 0.19* | -0.11 |
| HEADIN | GC | | | | 1 | 1 | 0.50** | 0.25** | -0.08 | 0.32** | -0.01 | -0.38** |
| | PC | | | | 1 | 0.96** | 0.39** | 0.17 | 0.04 | 0.29** | 0.06 | -0.30** |
| ANTH | GC | | | | | 1 | 0.52** | 0.26** | 0.01 | 0.44** | 0.03 | -0.39** |
| | PC | | | | | 1 | 0.39** | 0.18 | 0.09 | 0.35** | 0.09 | -0.31** |
| NOL | GC | | | | | | 1 | 0.67** | 0.21* | 0.33** | 0.20* | 0.05 |
| | PC | | | | | | 1 | 0.65** | 0.13 | 0.29** | 0.14 | 0.08 |
| NOD | GC | | | | | | | 1 | -0.11 | 0.21* | 0.23* | 0.01 |
| | PC | | | | | | | 1 | -0.09 | 0.18 | 0.16 | 0.02 |
| PWEI | GC | | | | | | | | 1 | 0.50** | 0.26** | -0.15 |
| | PC | | | | | | | | 1 | 0.35** | 0.36** | -0.11 |
| PLEN | GC | | | | | | | | | 1 | 0.40** | 0.12 |
| | PC | | | | | | | | | 1 | 0.40** | -0.07 |
| PWID | GC | | | | | | | | | | 1 | -0.21* |
| | PC | | | | | | | | | | 1 | -0.18 |
| GWEI | GC | | | | | | | | | | | 1 |
| | PC | | | | | | | | | | | 1 |

** Significant at $P=0.05$ and $P=0.01$ respectively. Values without any asterisk are not significant. PH= plant height, LL= leaf length, LW= leaf width, HEADIN= days to 50% heading, ANTH= days to 50% anthesis, NOL=number of leaves, NOD= number of nodes, PWEI= panicle weight, PLEN= panicle length, PWID= panicle width, GWEI= 100 grain weight

Table 3. Genotypic and Phenotypic Correlations for 50 sorghum accessions in 2019

| Character | Correlation | PH | LL | LW | HEADIN | ANTH | NOL | NOD | PWEI | PLEN | PWID | GWEI |
|-----------|-------------|----|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| PH | GC | 1 | 0.53** | 0.28** | 0.18 | 0.20* | 0.88** | 0.89** | 0.34** | 0.41** | 0.45** | 0.37** |
| | PC | 1 | 0.56** | 0.30** | 0.12 | 0.13 | 0.81** | 0.84** | 0.32** | 0.37** | 0.40** | 0.17 |
| LL | GC | | 1 | 0.46** | 0.19* | 0.22* | 0.50** | 0.52** | 0.18 | 0.62** | 0.42** | 0.42 |
| | PC | | 1 | 0.43** | 0.16 | 0.17 | 0.47** | 0.49** | 0.20* | 0.52** | 0.36** | 0.18 |
| LW | GC | | | 1 | -0.22* | -0.21* | 0.50** | 0.54** | 0.30** | 0.27** | 0.17 | 0.14 |
| | PC | | | 1 | -0.22* | -0.22* | 0.48** | 0.52** | 0.26** | 0.26** | 0.18 | 0.15 |
| HEADIN | GC | | | | 1.00 | 1.00 | -0.03 | -0.08 | -0.13 | 0.24* | 0.08 | 0.11 |
| | PC | | | | 1 | 0.99** | -0.05 | -0.09 | -0.12 | 0.20* | 0.03 | 0.05 |
| ANTH | GC | | | | | 1 | -0.02 | -0.06 | -0.12 | 0.22* | 0.10 | 0.16 |
| | PC | | | | | 1 | -0.05 | -0.09 | -0.11 | 0.18 | 0.05 | 0.07 |
| NOL | GC | | | | | | 1 | 0.99** | 0.37** | 0.48** | 0.63** | 0.12 |
| | PC | | | | | | 1 | 0.98** | 0.33** | 0.42** | 0.49** | 0.09 |
| NOD | GC | | | | | | | 1 | 0.39** | 0.45** | 0.59** | 0.14 |
| | PC | | | | | | | 1 | 0.34** | 0.40** | 0.46** | 0.09 |
| PWEI | GC | | | | | | | | 1 | 0.19* | 0.53** | -0.01 |
| | PC | | | | | | | | 1 | 0.20* | 0.49** | -0.10 |
| PLEN | GC | | | | | | | | | 1 | 0.68** | 0.16 |
| | PC | | | | | | | | | 1 | 0.58** | 0.01 |
| PWID | GC | | | | | | | | | | 1 | 0.04 |
| | PC | | | | | | | | | | 1 | -0.01 |
| GWEI | GC | | | | | | | | | | | 1 |
| | PC | | | | | | | | | | | 1 |

** Significant at $P=0.05$ and $P=0.01$ respectively. The values without any asterisk are not significant. PH= plant height, LL= leaf length, LW= leaf width, HEADIN= days to 50% heading, ANTH= days to 50% anthesis, NOL=number of leaves, NOD= number of nodes, PWEI= panicle weight, PLEN= panicle length, PWID= panicle width, GWEI= 100 grain weight.

negative correlation between important traits is favourable to a plant breeder as it helps when making selection. Although a negative correlation hinders the recovery of the recombinants in two characters. In such case, any improvement applied to a character also brings about change in the other character. Generally, in all the environment, genotypic correlation coefficient values were higher than the corresponding phenotypic correlation coefficient for most of the traits suggesting that there was an inherent relationship between these traits. Furthermore, it shows that most of the traits are controlled by genetic influence than the environmental factors. This is similar to the findings of [8, 28]. Likewise, both phenotypic and genotypic correlation coefficient were significant in most of the character association which can be attributed to less influence of the environment on the traits. Therefore, phenotypic correlation coefficients will be a good indicator of genotypic correlation coefficients. However, the non-significant phenotypic correlation between any two characters relative to its significant genotypic counterparts suggest appreciable environmental effects. The positive and significant correlations observed in plant height with leaf length, leaf width, days to 50% heading, days to 50% anthesis, number of leaves, number of nodes, panicle weight, panicle length and panicle width across the locations suggests that simultaneous selection for these traits is possible for improvement in sorghum genotypes for fodder and grain traits. These findings are in concordance with the results of [2, 9, 28].

5. CONCLUSION

In conclusion, the character associations and genetic variability evaluated revealed that variation exist among the southern Nigeria accessions for the traits analyzed, suggesting the possibility for further improvement of these characters. The effect of environment was little on some of the characters because of the high heritability values observed for all the traits. The positive correlation between the growth, flowering and maturation traits could be used as selection criteria for high grain weight in sorghum.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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