EVALUATION OF MORPHOLOGICAL PARAMETERS OFSIX UPLAND NIGERIA COTTON(*GOSSYPIUM HIRSUTUM*L.)GENOTYPES

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Abstract
This study was carried out to access the variation in morphological and yield parameters among six Nigeria cotton genotypes. A total of six genotypes of cotton; Samcot 8, Samcot 9, Samcot 10 Samcot 11, Samcot 12, and Samcot 13 were evaluated for plant height, number of branches, number of bolls per plant and boll size. Seeds of the six genotypes were raised to maturity in a Complete Randomized Design (CRD) with five replicates and data were collected following standard procedures. Data collected were subjected to one-way analysis of variance (ANOVA) and results were considered significant at a significance level of 5 %. Results obtained showed significant variations in plant height with Samcot 13 having the highest plant height (106.10 ± 3.83cm) followed by Samcot 9 (103.00± 2.39 cm). The highest monopodialbranch was observed inSamcot 8 (21.40 ± 0.87) while the highest sympodialbranch was observed in Samcot 11 (16.40 ± 0.86). Significant variations were observed in the number of bolls per plant and boll size with Samcot 9 having the highest number of bolls (31.30 ± 3.23) while the least was recorded in Samcot 12 (19.30 ± 3.03). Samcot 8 had the highest boll size (11.25 ± 0.25 cm) while Samcot 11 had the least boll size (9.60 ± 0.28 cm). Yield and yield attributes varied significantly, with different traits been favored by different genotypes. Samcot 9 had the highest weight of bolls (32.17 ± 5.49 g) while the least was observed in Samcot 8 (11.90 ± 1.27 g). Samcot 11 recorded the highest number of seeds per boll (30.68 ± 1.50 g) while the least was recorded in Samcot 9 (26.82 ± 2.49). Samcot 8 has the highest weight of lint per plant (13.66 ± 1.10 g) while the least was recorded in Samcot 13 (6.34 ± 0.89 g). The distinct features of some genotypes in plant height, number of sympodial branches, boll size and weight of lint compared to other genotypes is a good indication of existence of high genetic variability and genotypes with desired characteristicscould be selectedand incorporated into cotton improvement programmes.

Keywords: Cotton, Morphological, Monopodial, Lint, Sympodial.

Introduction
Cotton (family malvaceae) is knownto be anagricultural crop with high industrial fibrevalue grown in many countries of the world (Shakeel *et al*., 2011, Vitale, 2018). From time immemorial, man has utilized cotton for his benefits (Goyal *et al*., 2014). The word "cotton" has its source derived from the Arabic word "al-qutun" meaning 'finetextile' (Chaudhary and Guitchounts, 2003). Only four speciesof cotton are domesticated worldwide, two of which are tetraploid cultivars from America, *Gossypium hirsutum* and *G. barbadense*, while the other two are diploid cultivars from Africa and Asia, namely *G. arboreum* and *G. herbaceum,* respectively (Montes *et al.,* 2017).Amongthese four species, *G.hirsutum* (upland cotton) has dominated world cotton commerce, being responsible for about 95% of the annual cotton production (Sun*et al*., 2019). According to Townsend (2020), cotton is the primary natural fibre used by humans and accounts for 80 % of world's natural fibre production.

In Nigeria, cotton is locally called by different names; "Auduga" in Hausa (Okunola*et al.*, 2020), "Ela– Owu" in Yoruba (Oladele *et al.*, 2020), "Owu" in Igbo (Williamson, 2006), "Wunfu" in Gbagi (Roger and Musa, 1993) and "Lulu" in Nupe(Blench, 2009). The crop's production has been a major economic component and driver of economic growth (Food and Agricultural Organization (FAO), 2018). Cotton production has servedas a source of income for approximately 180 million people with the fibre industry producing about 30 billion dollars' worth of raw cotton and its economic impact estimated to be approximately 500 billion dollars per annumglobally (Chen *et al.*, 2007).

Salahu and Ilyasu (2018) opined that no part of cotton plant is considered a waste. Apart from its major usage in cloth production, the leaves are used as medicine for curing neonatal jaundice and related diseases and the seeds can be processed into oil and used in varieties of ways including as vegetable oil for feeds. Cottonseed oil is used in preparing salad, cooking oils and margarine and in some cases; it is used in the packing of fish and cured meat(Sekhar &Rao, 2011).

Over the years, Nigeria's cotton production has been on the downtrend (Adeoti *et al.*, 2020).In the year 2014, the average Nigeria yield was about 232 kg/ha which has dropped from the 2010 average yield of about 252 kg/ha (USDA, 2014). Lower average yields of 193 kg/ha and 182 kg/ha were reported in 2015 and 2016 respectively, while in 2019, the average yield was 190 kg/ha (USDA, 2019). The low production of local landraces of this crop by the farmers could be attributed to lack of improved cotton genotypes, insect and disease attack among others.

Genetic improvement of this high-valued multi-purpose crop would not only enhance the nutrition and livelihoods of millions of people in food challenged economies but also enhanced its competitive value with petroleum in the world market (Chen *et al.*, 2007). However, narrow genetic base has been reported as one of the major factors militating against the improvement of upland cotton (Tyagi *et al.*, 2014). In order to broaden the genetic base, studying the divergence among the available germplasm is prerequisite. In view of this, this study was undertaken to investigate the variation in morphological and yield attributes of six upland cotton genotypes cultivated in Nigeria.

Materials and Methods

Study Area

The study was carried out both on the field (Garden) and in the laboratory of theDepartment of Plant Biology, Federal University of Technology, Minna, Niger State.

Sample Collection

Cotton seed genotypes used for the study were collected from Institute of Agricultural Research(IAR),Ahmadu Bello University, Zaria. The genotypes are Samcot 8, Samcot 9, Samcot 10, Samcot 11, Samcot 12 and Samcot 13. The samples were packed in a brown envelope and labeled properly according to Daudu *et al.*(2015).

Experimental Design and Planting of Seeds

All the different genotypes collected were raised using a complete randomized design (CRD) with five replicates. Five seeds of each genotype were sown at the depth of 1-2cm in an experimental pot of about 20 litre size of bucket. At 2 weeks after sowing, the emerged (seedlings) were thinned to two seedlings per plant per pot. The planting buckets were spacedat 75cm between the rows and 40cm within row to minimize the environmental variation (Abdullahi, 2015).

Data Collection

Data on morphological and yield parameters were collected from fiverandomly tagged plants per genotype. All the agronomic and yield traits data were taken at weekly interval following the standard procedures of Dangana *et al*. (2017)as describe below.

i. Plant height (cm) – the height was measured as the distance from the base of the plant to the apex using a metre rule
ii. Number of monopodial branches per plant - the number of monopodial branches on main stem was determined by direct counting.
iii. Number of sympodial branches per plant - the number of branches which areextra-axillary in position and normally horizontal with zigzag pattern of fruiting points at maturity were recorded as the sympodial branches.
iv. Number of bolls per plant - number of bolls per plant wasdetermined by direct counting at maturity.
v. Boll size- fully matured bolls per plant were used to determined boll size using tape rule.
vi. Boll weight (g) - fully matured and well dried boll per plant obtainedand measure in grams using electrical sensitive balance. (Citizen electric balance, Model: MP 600)
vii. Seed index (g) –are recorded as the absolute weight of 100 seeds in grams usingelectrical sensitive balance (Citizen electric balance, Model: MP 600).
viii. Weight of Lint (g) –are measured and recorded as the absolute weight of lint obtained from 100 seeds ingrams. (Citizen electric balance, Model: MP 600

Data Analysis

Quantitative data collected were subjected to one-way Analysis of Variance (ANOVA) at 5% significance level and Duncan's Multiple Range Test (DMRT) was used to separate the means where there was significant difference.

Result and Discussion

The analysis of variance (ANOVA) showed significant differences and confirmed the existence of variations among genotypes for the traits studied.Significant variations were observed in plant height of the genotypes across all the weeks (week 2 – week 10) (Table 1).Samcot 13 was observed to have the significant highest plant height at maturity (106.00 ± 3.83 cm) while the significant least was observed in Samcot 8 (82.50 ± 2.85 cm) (Table 1). The range of plant height at maturity obtained in this study (82.50 ± 2.85 cm – 106.00 ± 3.83cm) were lower than that previouslyreported by Ashokkumar (2011) (112.63 cm to 122.47 cm) andCopeland (2017) (100.00– 200.00cm). The variability in plant height across all weeks in the six genotypes could be attributed to the differences in genetic makeup of the crop. This is in conformity with reports of Rehman *et al.* (2020) who has reported existence of variations among genotypes for traits like plant height. According to Sajjad *et al.* (2011),the variability in germplasm is vital for acceptable exploitation of the attributes for selection and breeding.

Thecotton genotype with the highest monopodial branch at Week 10 was Samcot 8 (21.40) and was significantly different from number of monopodial branches observed in other genotypes while the significant least number of monopodial branches at week 10 was observed in Samcot 12 (18.00 ± 0.81) (Table 2).In terms of sympodial branches (Plate 1), the significant highest at week 10 was observed in Samcot 11 (16.40 ± 0.86) while the significantly least was recorded in

Samcot 10 (13.70 ± 0.96) (Table 3).The significant differences observed in the number of branches (monopodial and sympodial) could be an indication of high genetic variability in the six genotypes evaluated. Similar variations have been reported in number of monopodial and sympodial branches by Basbag and Gencer (2007) and Yahaya *et al.* (2013) and were attributed to differences in the plants genetic makeup. Khan *et al.*(2011) opined that morphological traits like sympodial branching are very important in the cotton plant because they are positively correlated with yield and could increase the cotton seed yield. The high number of branches observed in some of the genotypes is an indication of the boll bearing ability of the plant which in turn contributed to the yield. Bozorov *et al*. (2018) had earlier reported that sympodial branches are the fruit bearing branches and are positively associated with plant yield. Therefore, selection based on number of sympodial branches will be helpful in increasing the crop's productivity.

Theleast number of bolls per plant was recorded in Samcot 12 (19.30 ± 3.03) and was significantly different ($p < 0.05$) from the number of bolls produced by other genotypes (Table 4). The highest number of bolls per plant was recorded in Samcot 9 (31.30 ± 3.23) but was not significantly different ($p > 0.05$) from Samcot 8 (31.00 ± 5.50) (Table 4). In terms of boll size, the highest was recorded in Samcot 8 (11.25 ± 0.25 cm) and was significantly different ($p < 0.05$) from the boll size produced by other genotypes (Table 4). The notable variations observed in number and size of bolls per plant is in conformity with the report of Gnanasekaran*et al.* (2020), who reported significant variations in number of bolls of sixty-seven genotypes of upland cotton. The variations among cotton genotypes for these traits could be attributed to genetic as well as environmental factors. Similar claims have been made by Riaz *et al*. (2019).The number of bolls produced by each plant determines the yield potential of the genotype and it is considered as major yield component.

Samcot 8 was observed to have the least weight of boll per plant (11.90 ± 1.27 g) and was significantly different ($p < 0.05$) from the weight of boll observed in other genotypes (Table 5). The highest weight of bolls was observed in Samcot 9 (32.17 ± 5.49 g). The range of boll weight obtained in this study (11.90 ± 1.27to 32.17 ± 5.49 g) were greater than boll weight previously reported by Nawaz *et al*. (2019) (17.28 – 19.33 g)in cotton genotypes. The variation in the results could be attributed to the differences in the genetic make-up of the genotypes, geographical location and the response of the different cotton cultivars to the photoperiod of the area (He *et al.*, 2013). Similar to the results obtained, variations among varieties of cotton for average boll weight had earlier been reported by Hofs *et al.* (2006). Khan *et al*. (2007) had attributed the differences in weight of boll to varietal characteristics and environmental conditions of that area. Ashokkumar *et al*. (2010) has attributed maximum seed cotton yieldwith number of bolls, boll weight, ginning outturn, lint index and seed index.

The variability for economic attributes such as seed index in the given genotypes is vital for exploitation following selection and breeding (Sajjad, *et al.,* 2011). The significant variation in seed index among all the genotypes, with the highest value of 10.29 ± 0.56g observed in Samcot 12 and the least value of 8.05± 0.66 grecorded in Samcot 11 reflects the heterogeneity of the cotton genotypes. These seed index ranged were within the mean of 9.85 earlier reported by Ashokkumar *et al.* (2010). However, these values were greater than the value of 0.17 to 1.44 reported by Khan *et al.* (2015). Similar variability has been reported in seed cotton weight and yield by Eldessouky *et al.* (2021) and was attributed to genetic variance of the genotypes.

Samcot 8 was observed to have the significant ($p < 0.05$) highest weight of lint (13.66 ± 1.10 g) while the least was observed in Samcot 13 (6.34 ± 0.89 g). The high significant differences recorded in weight of lint among the genotypes demonstrate that adequate variability exist in the germplasm and the heterogeneity nature of the collected cotton genotypes.Similar findings have been reported by Bourgou *et al.*(2018) and were attributed to many factors number of bolls produced, boll weight and seed cotton yield.

Table 1: Plant Height of Six Nigeria Cotton Genotypes

Genotypes	Week 2 (cm)	Week 4 (cm)	Week 6 (cm)	Week 8 (cm)	Week 10 (cm)
Samcot 8	11.50 ± 0.92^{c}	17.80 ± 0.53^{a}	49.00 ± 1.99^{a}	69.00 ± 2.50^{a}	82.50 ± 2.85^{a}
Samcot 9	10.55 ± 0.45^{bc}	36.70 ± 1.08^{c}	76.00 ± 2.50^{cd}	89.70 ± 3.50^{b}	103.00 ± 2.39^{bc}
Samcot 10	10.55 ± 0.22^{bc}	36.70 ± 1.08^{c}	62.05 ± 1.42^{b}	87.90 ± 3.03^{b}	97.00 ± 2.07^{b}
Samcot 11	9.30 ± 0.56^{ab}	36.70 ± 1.08^{c}	71.50 ± 2.17^{c}	89.90 ± 2.56^{b}	95.90 ± 2.71^{b}
Samcot 12	8.20 ± 0.92^{a}	27.20 ± 3.98^{b}	72.90 ± 2.99^{c}	76.90 ± 2.23^{a}	85.40 ± 2.45^{a}
Samcot 13	10.02 ± 0.57^{abc}	38.70 ± 0.72^{c}	81.10 ± 3.77^{d}	103.00 ± 3.42^{c}	106.00 ± 3.83^{c}

Values are mean ± stand error of mean. Values followed by the same superscript along the same column are not significantly different at $P > 0.05$.

Table 2: Monopodial Branches of Six Nigeria Cotton Genotypes

Genotypes	Week 8	Week 9	Week 10
Samcot 8	12.20 ± 0.86^{a}	18.30 ± 0.70^{b}	21.40 ± 0.87^{c}
Samcot 9	17.60 ± 0.88^{b}	20.70 ± 1.39^{b}	19.60 ± 1.05^{abc}
Samcot 10	12.10 ± 0.91^{a}	14.60 ± 0.73^{a}	18.70 ± 0.78^{ab}
Samcot 11	12.30 ± 0.36^{a}	15.70 ± 0.63^{a}	20.80 ± 0.57^{bc}
Samcot 12	11.80 ± 1.53^{a}	13.80 ± 0.77^{a}	18.00 ± 0.81^{a}
Samcot 13	11.60 ± 0.74^{a}	15.80 ± 0.77^{a}	20.20 ± 0.95^{abc}

Values are mean ± stand error of mean. Values followed by the same superscript along the same column are not significantly different at $P > 0.05$.

Table 3: Sympodial Branches of Six Nigeria Cotton Genotypes

Genotypes	Week 8	Week 9	Week 10
Samcot 8	11.10 ± 0.43^{ab}	13.30 ± 1.03^{a}	15.40 ± 0.45^{c}
Samcot 9	11.80 ± 0.68^{b}	13.70 ± 0.59^{ab}	15.50 ± 0.94^{c}
Samcot 10	10.80 ± 0.09^{a}	13.10 ± 0.98^{a}	13.70 ± 0.96^{a}
Samcot 11	12.30 ± 0.63^{bc}	15.20 ± 0.57^{b}	16.40 ± 0.86^{d}
Samcot 12	12.30 ± 0.34^{bc}	13.10 ± 0.60^{a}	14.50 ± 0.62^{b}
Samcot 13	12.20 ± 0.66^{b}	14.40 ± 1.01^{ab}	15.70 ± 1.11^{c}

Values are mean ± stand error of mean. Values followed by the same superscript along the same column are not significantly different at P > 0.05.

Table 4: Number of Bolls and Boll Size of **six Nigeria cotton Genotypes**

GENOTYPES	Number of Bolls Per Plant	Boll Size (cm)
Samcot 8	31.00 ± 5.50^{c}	11.25 ± 0.25^{c}
Samcot 9	31.30 ± 3.23^{c}	10.85 ± 0.30^{b}
Samcot 10	20.00 ± 2.27^{b}	10.90 ± 0.31^{b}
Samcot 11	26.40 ± 2.23^{bc}	9.60 ± 0.28^{a}
Samcot 12	19.30 ± 3.03^{a}	9.70 ± 0.45^{a}
Samcot 13	22.10 ± 3.40^{ab}	10.10 ± 0.35^{ab}

Values are mean ± stand error of mean. Values followed by the same superscript along the same column are not significantly different at P > 0.05.

Table 5: Yield Parameters of Six Nigeria Cotton Genotypes in Minna

Genotypes	Weight of Bolls Per Plant (g)	Number of Seeds Per Bolls	Hundred Seed Weight (g)	Weight of Lint Per Plant (g)
Samcot 8	11.90 ± 1.27^{a}	27.66 ± 2.41^{b}	9.74 ± 0.67^{c}	13.66 ± 1.10^{d}
Samcot 9	32.17 ± 5.49^{d}	26.82 ± 2.49^{a}	8.33 ± 0.47^{b}	10.23 ± 1.19^{c}
Samcot 10	26.08 ± 5.27^{cd}	30.35 ± 1.40^{c}	8.64 ± 0.45^{bc}	10.23 ± 1.27^{c}
Samcot 11	25.67 ± 4.15^{c}	30.68 ± 1.50^{d}	8.05 ± 0.66^{a}	9.40 ± 1.03^{b}
Samcot 12	23.15 ± 2.74^{bc}	28.06 ± 2.46^{bc}	10.29 ± 0.56^{c}	7.78 ± 1.07^{ab}
Samcot 13	21.07 ± 3.19^{b}	30.40 ± 1.37^{c}	9.93 ± 0.57^{c}	6.34 ± 0.89^{a}

Values are mean ± stand error of mean. Values followed by the same superscript along the same column are not significantly different at P > 0.05.

Plate 1: Branching pattern observed in the six cotton genotypes. Red arrow shows a monopodial branch while yellow arrow shows a sympodial branch.

Conclusion

Conclusively, this study has reflected the existence of high genetic diversity among the six cotton genotypes examined. Genotypes with desirable characteristics like Samcot 11 (with highest sympodial branches) and Samcot 8 and 9 (with highest number of bolls per plant) could be selected and incorporated into future breeding programmes of cotton.

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