Genetic Performance of Some Watermelon [*Citrullus lanatus* (Thumb.) Mastum and Nakai] Genotypes in Humid Tropical Agro-ecology

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Authors' contributions

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

Original Research Article

ABSTRACT

Six varieties of watermelon (Sugar baby, Sugar dragon, Kaolack, Crimson sweet, Koloss and baby doll) were evaluated in the field to assess the genetic parameters associated with morphological traits in the watermelon genotypes. The experiment was laid out in Randomized Complete Block Design (RCBD) in three replications. There were variations in number of branches per plant, vine length, number of days to 50% flowering, number of male flowers, number of fruits per plant and fruit weight per plant. Low response to selection and genetic variation was observed in most traits. The number of days to 50% flowering had the highest heritability estimates (97%), genetic gain of 15.84% and genetic advance of 5.33. Fruit weight per plant had high heritability estimates of 89%, moderate genetic gain of 46.20% and genetic advance of 2.31. Moderate broad sense heritability estimates ranging from 55% for number of male flowers per plant to 63% for number of fruits per plant. Mean branch number had the highest genetic gain of 49.33% but moderate heritability estimates of 58.91% signifying moderate response of selection. Koloss and Kaolack had the highest genetic performance for fruits yield than Baby doll and other varieties plant in the humid environment. Therefore, Koloss and Kaolack is recommended in the humid ecology and should be cultivated in the ecological zone.

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1. INTRODUCTION

Watermelon [*Citrullus lanatus* (Thumb.) Mastum and Nakai] is a member of the plant family Cucurbitaceae; it is grown in both temperate and tropical regions of the world. World production is about 77.5 MT of fruit from 3.1 million hectares of cultivated land [1]. According to FAO [1] and Horticultural Statistics [2], the major watermelon producing countries are China (70.3%), Turkey (4.7%), Iran (2.3%), United States of America (2.2%) and Egypt (1.7%). It is one of the most widely grown vegetable crops in the world after tomato, onions and cabbage [3,4,5]. Watermelon is an economically important fruit crop which provides important source of minerals and water for human consumption and use in the pharmaceutical industries for heavy syrup making in Europe [6,7].

However, despite the high nutritional value of watermelon and its importance, production level hardly meets the demand requirement due to lack of genetic information about local and exotic lines cultivated at varies agro ecological zones. The genetic information and literature on watermelon is scanty and farmers rely on landraces with little or no genetic information. These contribute to low productivity of watermelon yield grown in Nigeria. The humid tropic has about two – third population of Nigeria and it is an important market for watermelon. Morphological traits contribute significantly to yield improvement and each of these components adds its own value to the genetic system and is useful in the improvement of yield trait [8]. The genetic potentials of the traits need to be exploited and improve upon before selection and recommendation. Fruit yield in watermelon is quantitatively inherited, thus improvement in yield trait requires an indirect approach of selecting yield characteristics that have high heritability. Ndukauba et al. [9] noted variability in morphological traits among genotypes study in Egusi melon. Afangideh and Uyoh [10]' Afangideh et al. [11]; *have* earlier affirmed the existence of genetic variation in cucumber in respect to number of branches per plant, vine length per plant, number of pod per plant and seed yield per plant. Agah et al. [12], Kumar and Wehner [13,14] and Ogbonna and Obi [15] have also reported variation in morphological traits among watermelon genotypes.

Several workers have studied the heritability of certain traits in the Cucurbitacae family. Adjoumani et al. [16] studied genetic variability and heritability of fruit characters in watermelon and observed the high heritability and genetic advance in number of fruits per plant, number of days to fruit maturity and weight of fruit per plant. The above result agrees with the results of Afangideh et al. [11] on cucumber, Johnson et al. [17] and Wehner [4] on watermelon, Ndukauba et al. [9], Ogbonna and Obi [18] on Egusi melon and landrace of culinary melon.

Genetic variability is an essential step to realize response to selection. This could be attributed to high proportion of genetic variation for yield. High PCV and GCV were reported in watermelon seed yield by Ogbonna and Obi [15]. Thus high genetic variability coupled with high heritability estimates offer a most suitable condition for selection [19].

Several breeding programme have been conducted and studied in temperate region on the genetic components in watermelon and in countries like Japan, U.S.A, Patiskan, Bangladesh, India and China. While there has been an extensive breeding programme in Nigeria on genetic components in crops like Cowpea, Pumpkin, Rice, Maize, Sorghum, Soybean, Snake gourd and Tomato there is little or no research on genetic components of watermelon for the humid tropical agro – ecology [19,20,21,22].

A large number of local lines and exotic varieties of watermelon are cultivated in Nigeria yet there is no genetic information that the breeders will rely on for crop improvement. Thus, knowledge of genetic information guides a plant breeder to predict behaviour of succeeding generation, progeny testing; prediction of selection response and formulation of breeding plan. This poses a challenge for watermelon breeding in the humid ecology as the plant breeders rely heavily on genetic information of watermelon for effective selection and recommendation among genotypes. The choice of breeding programme for watermelon improvement of traits reliable on the exploitation of its genetic components such as heritability, coefficient of variability, genetic gain and genetic advance [20]. The breeders rely on the genetic information as a mean of identifying and obtaining germplasm for

improvement and selection of morphological traits. This study is therefore designed to bridge the gap of providing adequate genetic information by evaluating the genetic potentials of existing genotypes in the country and developing materials for farmers in the region. The objective of the study was to assess the genetic parameters associated with morphological traits in the watermelon genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Site

The experiment was conducted in Akpabuyo Local Government Area, Cross River State, Nigeria. Akpabuyo is a humid environment and rainforest vegetation; it is characterized by high rainfall with distinct wet and dry seasons. The wet season start from March to early November and the dry season commenced in early November to late February (Meteological data report 2018). The rainfall requirement for the growing season range from 400 mm to 600 mm, daily temperature of 27^0C and relative humidity is 82 % (FAO [23] and Meteorological data report 2019). The soil type in the experimental area is coastal plain soil [24]. Soil is predominantly coarse in texture, derived cretaceous sandstone and is low in productivity, pH is between 4.0 and 6.0 and high buffering capacity of about 2 to 10 cm/100 g soil, low base saturation, high exchangeable aluminium, low in organic matter and severe leaching causes losses of nutrient in the soil [24].

2.2 Planting Materials and Experimentation

Six varieties of watermelon seeds were obtained from Agritropic Nigerian Limited, Calabar. The varieties were Sugar baby, Kaolack, Sugar dragon, Crimson sweet, Koloss and Baby doll. Two seeds were sown per hole at a spacing of 120 cm X 120 cm and seedlings were thinned to one seedling per stand at two weeks after sowing. The experiment was laid in a Randomized Complete Block Design (RCBD) with three replications; the six watermelon varieties formed the six treatments. A plot of land, 42.8 m x 18.8 m (804.64 m^2) was manually cleared, prepared and planted in September 2015. Cured poultry manure was incorporated into the soil two weeks before sowing at the rate of 5 t/ha. The spacing of 120 cm X 120 cm and a

plant population of 558.77 plant/ha, seedling rate of 66,168.38 kg/ha and a net plot size of 2.40 m x 1.20 m (2.88 m^2) were maintained and set aside for data collection.

Data, based on six tagged plants were collected on number of leaves per plant at two, four and six weeks after planting (WAP), number of branches per plants at four and six (WAP) and at harvest, Vine length at 4 and 6 (WAP) and at harvest, number of days to 50 % flowering, number of male and female flowers per plant, fruit Weight per pod (kg), number of fruit per plant, weight of 100 seeds per fruit and number of days to fruit maturity.

Data collected were analyzed using GENSTAT statistical package [25] for randomized complete block design while means that were significantly different were compared with Duncan's Multiple Range Test (DMRT). Components of variance for morphological data were divided into genotypic variance, environmental variance and phenotypic variance using the method described by Sharma [26].

Genotypic variance: $\sigma_g^2 = \frac{VMS - EMS}{R}$

Environmental variance: i.e. $\sigma_e^2 = EMS$

Phenotypic variance: i.e. $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Broad sense heritability (h_b^2) estimates: i.e. $h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$

Genotypic coefficients of variation $(GCV) = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$

Phenotypic coefficient of variation $(PCV) = \frac{\sqrt{\sigma_p^2}}{\overline{X}} \times 100$

Environmental coefficient of variation (ECV) = $\frac{\sqrt{\sigma_e^2}}{\overline{X}} \times 100$

Genetic advance $(GA) = k. psd. h_b^2$

Genetic gain (GG) = $\frac{GA}{\overline{X}} \times 100$

Where σ_g^2 = genotypic variance, σ_e^2 = environmental variance, σ_p^2 = phenotypic variance, EMS = error variance mean square, VMS = variety mean square, R = number of

replications, h_b^2 = broad sense heritability estimates, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, $\bar{X}$ = grand population mean of the traits, √ = square root of variance, ECV = environmental coefficient of variation, GA = genetic advance, Where k = selection differential of 5% plant selected, psd = phenotypic standard deviation, h_b^2 = Broad sense heritability estimate of the trait under selection.

3. RESULTS AND DISCUSSION

3.1 Heritability Estimates, Genetic Advance and Coefficient of Variation in Six Cultivars of Watermelon Planted in Humid Environment

The result of broad sense heritability estimates and other genetic parameters on the watermelon varieties planted in the humid environment are presented in Table 1. Characters assessed included the number of leaves per plant, number of branches per plant, vine length, number of days to 50 % flowering, number of male and female flowers, number of fruits per plant, weight of 100 seeds per fruit, weight of fruits per plant and number of days to fruit maturity.

Low broad sense heritability estimates was observed for number of leaves per plant (12.89 %), vine length (24 %), number of female flowers per plant (10 %), weight of 100 seeds per fruit (16 %) and number of days from planting to fruit maturity (1 %), the environmental variance of (13.74. for number of leaves per plant, 3883.02 for vine length, 3.43 for number of female flowers per plant, 5864 for weight of 100 seeds per fruit and 9.60 for number of days from planting to fruit maturity greatly influenced the expression of these phenotypes. For all these characters examined, environmental variance (σ_e^2) were highly superior to genotypic variance (σ_g^2). The result of components of variability presented in Table 1 had further revealed higher percentage of environmental coefficient of variation (ECV) of 45.42 %, 51.41 %, 15.21 %, 15.69 % and 3.94 % against genotypic coefficient of variation (GCV) of 17.54 %, 29.38 %, 4.86 %, 2.01 % and 3.94 % for number of leaves per plant, vine length, number of female flowers per plant, weight of 100 seeds per fruit and number of days from planting to fruit maturity. This could be an indication for low response for selection of these traits and further improvement of watermelon for morphological traits with low response to

selection is necessary. Similar reports were presented by Wehner [18], and Gabriele and Todd [27], in respect of number of leaves, vine length per plant in watermelon. Moderate broad sense heritability estimates was observed in number of branches per plant (58.9 %), number of male flowers per plant (55 %) and number of fruits per plant (63 %), the genotype contributed about half of the phenotypic expression of these traits. This could be an existence of genetic variation that were moderately superior to environmental variance for number of branches per plant, number of male flowers per plant and number of fruits per plant. Ogbonna and Obi [15] also observed a moderate heritability for number of fruits per plant, number of days to 50 % flowering, weight of fruits per plant and fruit yield in Egusi melon. Afangideh et al. [28] observed similar genetic variation in cucumber.

High broad sense heritability estimates of 97 % were observed for number of days to 50 % flowering and 89 % for weight of fruits per plant, the environment contributed very little to the phenotypic expression of these characters. Selection for earliness in flowering and fruit yield would be very effective because of the very high influence of the genotype. High genetic variation existed for weight of fruits per plant in broad sense heritability and genetic gain among all characters studied. The genotypic variance is also greater than environmental variance. This could be an indication that the higher broad sense heritability estimate, higher genetic again could led to higher morphological trait to derived expected benefit and gain for effective selection response by the farmers. This report confirmed studies of Ndubauka et al. (2015), Ogbonna and Obi [15] and Gabriele and Todd [27] on high heritability estimate and genetic gain for fruit weight in Equsi melon and watermelon.

The genetic advance and genetic gain for six cultivars of watermelon planted in the humid environment ranged from 3.11 GA: 40.62% for number of male flowers, 2.31 G A : 46.20% for fruit weight per plant and 3.83 GA : 49.33% for number of branches per plant. This is an indication that the characters measured are fixed in a homozygous state in the cultivars tested and selection response is possible. Additive gene action could be an indication of moderate selection response pressure. This could also be an indication that number of female flowers, mean fruits weight per plant and number of branches per plant is helpful in exploiting the expected benefit and gain by farmers for

watermelon grown in the humid environment. The higher the morphological traits, the more expected benefit and grain derived for selection. Hence, watermelon improvement will rely on higher morphological traits to derived higher benefit and gain by farmers for effective selection response and to avoid further improvement. This result confirmed Khan et al. [6] which observed high genetic advance and gain for number of fruit per plant and fruit weight per plant.

Table 1. Heritability estimates, genetic advance and coefficient of variation in six cultivars of watermelon planted in humid environment

Trait	σ_g^2	σ_e^2	σ_p^2	GCV%	ECV%	PCV%	h_b^2	GA	GG%
MLN	2.05	13.74	15.79	17.54	45.42	48.69	12.98	1.06	13.02
MBN	5.85	4.08	9.93	31.16	26.02	40.60	58.91	3.83	49.33
MVLN	1268.68	3883.02	5151.70	29.38	51.41	59.22	24.00	35.48	29.27
D50%F	6.90	0.23	7.13	7.80	1.42	7.93	97.00	5.33	15.84
NMF	4.15	3.43	7.58	26.56	24.14	35.89	55.00	3.11	40.62
NFF	0.35	3.43	3.78	4.86	15.21	15.95	10.00	0.39	3.24
MFN	0.20	0.12	0.32	18.71	14.49	23.66	63.00	0.74	30.95
SW100	98.00	5864	5962	2.01	15.56	15.69	16.00	25.44	5.17
MFWP	1.14	0.18	1.59	23.74	8.48	25.21	89.00	2.31	46.20
DFM	0.10	9.60	9.70	0.40	3.94	3.96	1.00	6.41	8.15

MFN= mean fruit number per plant, MBN= Mean branch number, MLN= Mean leaves number, MVLN= Mean vine length number, D50%F= Number of days to 50% flowering, NMF = Number of male flowers, NFF = Number of female flowers, MFN= mean fruit number per plant, Wt00S = Weight of 100 Seed per plant, MFWP = Mean fruit weight per plant, σ_g^2= Genotypic variance, σ_e^2 = Environmental variance, σ_p^2= Phenotypic variance, h_b^2 = Broad sense heritability, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation. GA= Genetic advance, GG%= Genetic advance as percentage of gain.
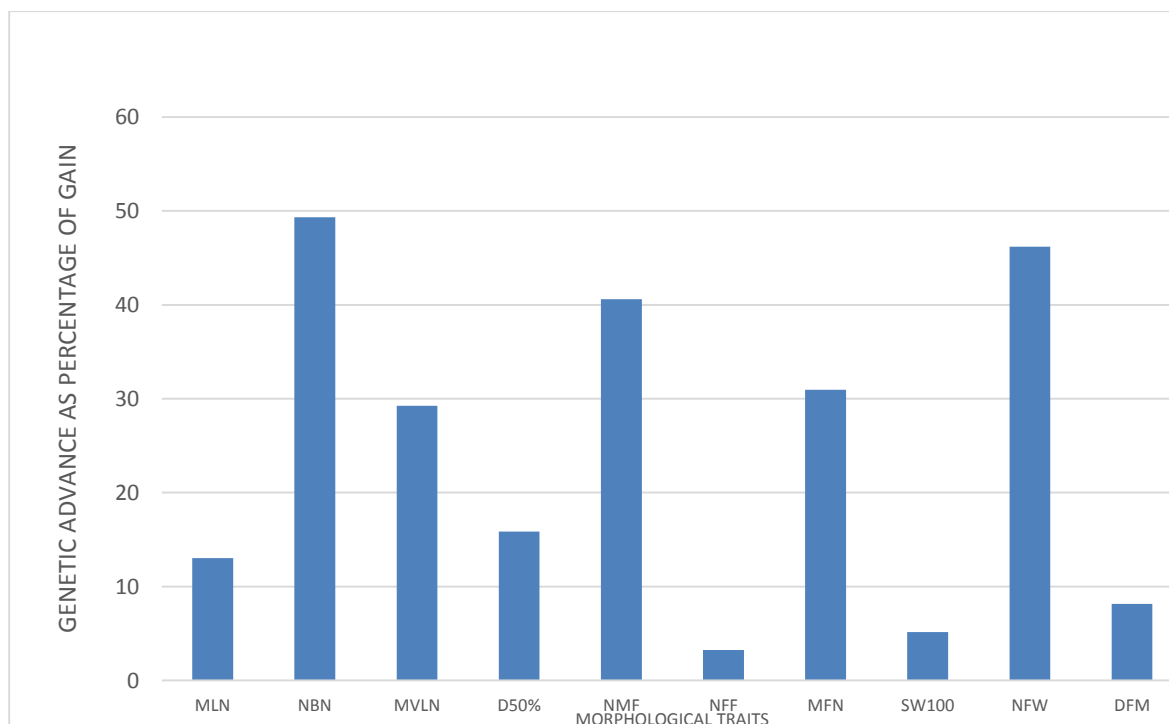

Fig. 1. Genetic gain of some morphological traits in watermelon grown in humid environment

This result confirmed Singh et al. [29] which observed high heritability estimates and genetic advance for number of flower appearance in cucumber. However, number of female flowers (3.24 %), weight of 100 seeds per plant (5.17 %) and number of days to fruit maturity (8.15%) had low genetic gain. Hence, low selection response is expected for the traits.

Phenotypic coefficient of variation (PCV) was higher in magnitude than genotypic coefficient of variation (GCV) for all characters measured in the humid environment. The close resemblance between the corresponding estimate of both PCV and GCV in characters tested could be an indication of little environment influence in phenotypic expression of traits. High GCV ranged from 31.16% for number of branches per plant, 26.56% for number of male flower per plant and 25.21% for weight of fruits per plant. This high GCV could be an indication of the genetic variation present in the expression of the characters. This result confirmed Ogbonna and Obi [15] which observed high proportion of genotypic coefficient of variation for number of branches per plant and number of flower per plant in Equsi melon.

Low proportion of phenotypic coefficient of variation (PCV) of 3.96 % was observed for number of days to fruit maturity. This is an indication that the character measured is strongly influence by environment in their phenotypic expression of this trait.

4. SUMMARY

Low response to selection and genetic variation was observed in the number of days to fruit maturity, vine length implying that there was a strong environmental influenced on these morphological traits. There was also high response to selection for number of branches, number of days to 50 % flowering, number of fruits per plant and weight of fruits per plant.

5. CONCLUSION AND RECOMMENDA-TIONS

Further breeding work is recommended for morphological traits with low response to selection among genotypes of watermelon grown in humid ecology while selection is effective for morphological traits with high response.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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