

## GENETIC VARIABILITY AND HERITABILITY STUDIES OF SOME REPRODUCTIVE TRAITS IN CUCUMBER (*Cucumis sativus* L.)

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### Abstract

The purpose of most crop improvement programs largely depends upon the genetic variability and the heritability of desirable traits. The magnitude and type of genetic variability help the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. A field experiment was carried out at the Teaching and Research Farm of Federal University of Technology, Owerri, Nigeria in 2018 planting season to estimate the genotypic variability of some reproductive traits and their heritability in selected cucumber genotypes. The experimental design was a randomized complete block design (RCBD) with three replications. Collected data were subjected to ANOVA for RCBD and significant means separated using least significant difference (LSD) at 5% probability level while means were used to calculate genetic parameters to show variability among genotypes. Results of the study showed that there was considerable variation among genotypes for reproductive traits studied. Genotypic coefficients of variation were high for number of fruits per plant (53.89), fruit weight per plant (52.70), total fruit yield per hectare (51.45). Broad-sense heritability estimate ( $h^2$ ) was 88.29% for fruit length, 88.00% for fruit weight per plant, 86.31% for fruit yield, 83.36% for number of fruits per plant, 80.43% for fruit girth, and 79.89 for plant height.

**Key words:** Cucumber, reproductive traits, variability, heritability.

### Introduction

To improve fruit yield potentials of any crop using planned breeding approaches, it is essential to obtain substantial information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability measures the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. Briggs and Knowles (1967) put forward the view that if environmental variability is negligible compared to genetic variability, selection will be effective in improving the character if such character with high genotypic variability and also easily measurable happened to be highly correlated with yield. For example, molecular markers have been used to

estimate genetic differences in germplasm accession of soybean and other crops (Thompson *et al.*, 1997). Autrique *et al.* (1996) reported that phenotypic differences show genetic differences while Van Beuningen and Bush (1997) used morphological, developmental, and physiological traits to create distance measures for use in examining the genetic diversity in large collection of crop genotypes. Grafius *et al.* (1976) and Grafius (1978) applied this concept to practical breeding by employing cultivar differences in morphological traits to select genetically diverse breeding pairs. The reproductive phase of cucumber represents the combined effects of genetic and environmental factors. Veena *et al.* (2012) reported high heritability estimate for characters like days to first female flower opening (83.72%), days to first male flower opening (92.63%), days to first harvest (83.04%), number of fruits per plant(85.78%), fruit length(88.92%), fruit breadth(86.91%), seed cavity length, seed cavity breadth, number of seeds per fruit and 100 seed weight. Similarly, high heritability for the above traits by Veena *et al.* (2012) was also reported by Dhiman and Chander (2005), Reshmi (2006) and Arunkumar *et al.*, (2011). Similar result was reported by Prasad and Singh (1994). Ene *et al.*(2016) recorded high estimate of heritability in the early and late planting season of cucumber for all the traits studied except for mean fruit weight (23.08%) in the early planting while mean fruit weight (46.88%) and total fruit yield ha<sup>-1</sup>(47.89%) had relatively low  $h^2$ s in the late planting season. Thus, a greater understanding is needed not only of the environmental factors that interact with the genotype to influence crop reproductive development and yield but also of the genetic factors that control these characters. The knowledge of genetic variability and correlations among genotypes will aid breeders in improving appropriate breeding strategies to solve problems of low yield in cucumber. Limited information is available on the nature of variability and magnitude of heritability of reproductive phase of cucumber in Owerri area of southeastern Nigeria. Therefore, the objective of this study was to investigate the genetic variability and heritability of some reproductive and quantitative traits in some selected cucumber genotypes.

Table 1. Qualitative traits of the cucumber cultivars evaluated.

Genotypes	Seed colour	seed shape	Leaf description	Vine description	Fruit colour at maturity	Fruit shape
'Songhai local'	Cream	Flat/short	Ovate-shaped/hairy texture	-Coarse vine -forms canopy -climbing vine	Light green with yellow stripe markings	cylindrical
'Marketer'	Light blue	Flat/short	-Ovate-shaped -Non-hairy	-Spreading vine. -Non-climbing vine	green with yellow stripe marking	cylindrical
'AOA/Cu'	Cream	Flat/long	Non-broad leaf -ovate shape -hairy texture -rigid -Broad leaf	-Forms canopy -Coarse vine -forms canopy -climbing vine	green with yellow stripe marking	cylindrical
'Beit alpha'	Cream	Flat/long	-ovate shaped -hairy texture	-Spreading vine. -Non-climbing vine -Forms canopy	green with yellow stripe marking	cylindrical
'Israelic Cu'	Pink	Flat/long	-Ovate shaped -Non-hairy	-Coarse vine -Forms canopy -Climbing vine	green with yellow stripe marking.	cylindrical
'Holland POP'	Orange	Flat/short	-Ovate-shaped -Non-hairy	-Spreading vine. -Non-climbing vine -Forms canopy	Light green with yellow stripe marking.	cylindrical
'Apulia'	Orange	Flat/short	Non-broad leaf -Ovate-shaped -Non-hairy	-Spreading vine. -Non-climbing vine -Forms canopy	Light green with yellow stripe markings	cylindrical
'Nagano F <sub>1</sub> '	Deep blue	Flat/long	Non-broad leaf -Ovate shaped -Broad leaves	- coarse -Forms canopy	-deep green. -presence of dotted spots. -Lacks stripes	cylindrical
'Cu 102'	Pink	Flat/short	-Hairy Ovate-shaped/hairy texture Non-broad leaves	-Non-branching -Coarse vine -forms canopy -climbing vine	Light green with white stripe markings	cylindrical
'Cu 986'	Pink	Flat/long	-Ovate shaped -broad leaves -Hairy	-Coarse vine -forms canopy -climbing vine	green with faint white stripe marking	cylindrical
'Super marketer'	White	Flat/long	-Ovate shaped -broad leaves	-Coarse vine -forms canopy	green with faint white stripe marking	cylindrical
'OHE/Cu'	Lightly cream	Flat/long	-Ovate shaped -broad leaves -Hairy	-Coarse vine -forms canopy -climbing vine	-dark-green with faint white stripe markings.	cylindrical
'Pov varietyADP'	Cream	Flat/long	-ovate shape -hairy texture	-Coarse vine -forms canopy -climbing vine	green with faint yellow stripe marking	cylindrical
'Cu 100'	Pink	Flat/short	-Ovate shaped -Non-broad leaves -Hairy	-Climbing vine -Coarse vine -Forms canopy	Light green with faint white stripe markings	cylindrical
'Cu 971'	Pink	Flat/short	-Ovate shaped	-Coarse vine	green with	cylindrical

'Cu 999'	Pink	Flat/long	-broad leaves -Hairy -Ovate shaped -Broad leaves -Hairy	-forms canopy -climbing vine -Coarse vine -Forms canopy -Climbing vine	faint yellow stripe marking -Dark-green with faint white stripe markings.	cylindrical
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### Materials and Methods

The experiment was conducted at the Teaching and Research Farm, Federal University of Technology, Owerri in 2018. The study was carried out between October – December, 2018. The study area is located at latitude 5° 29' N of the equator and longitude 7° 2' E of the Greenwich meridian, and at an altitude of 17 meters above sea level. Sixteen cultivars of cucumber (*Cucumis sativus* L.) sourced from different geographical regions of the country were investigated in an experimental field size measuring 22.1m by 11.7m (258.57m<sup>2</sup>). The experimental design was a randomized complete block design (RCBD) with three replications. Sixteen cucumber seed cultivars (treatments) were sown on the plots at three seeds per hill at a depth of 2.5cm, using spacing of 0.5m x 0.5m. A total of 18 seeds were sown in each plot which was later thinned down to six after two weeks of planting.

Weeds were controlled by hand pulling as and when necessary throughout the growing period of the crop. Two middle stands from each plot were tagged and used as sample plants upon which data collection was made. Observation was recorded on the following parameters; days to male flower initiation, days to first female flower initiation, number of pistillate flowers plant<sup>-1</sup>, days to fruit maturity, plant height 8WAP, number of fruits plant<sup>-1</sup>, fruit length, fruit girth, fruit weight plant<sup>-1</sup>, total fruit yield hectare<sup>-1</sup>.

### Statistical analysis

Collected data were subjected to ANOVA for RCBD using GenStat Release Software 10.3 Discovery Edition (2011), significant means separated using least significant difference (LSD) at 5% probability level as described by Obi (2002). Means were used to calculate genetic parameters such as coefficient of variation (CV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), genotypic variance, phenotypic variance, environmental variances and genetic advance to show variability among genotypes. The phenotypic variation for each trait was separated into genetic and non-genetic factors and estimated according to Burton (1952) and Sharma (1988):

$$\sigma^2_e = \text{MSe}; \sigma^2_g = (\text{MSg} - \text{MSe}) / r; \sigma^2_p = \sigma^2_g + \sigma^2_e.$$

Where  $\sigma^2_p$ ,  $\sigma^2_g$ , and  $\sigma^2_e$  are phenotypic variance, genotypic variance, and environmental variance, respectively, and MSg, MSe, and r are the mean

squares of genotypes, mean squares of error, and number of blocks, respectively.

$$\% CV = \frac{\sqrt{MSg}}{\bar{X}} \times 100$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

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

$$ECV = \frac{\sqrt{\sigma_e^2}}{\bar{X}} \times 100$$

Where  $\bar{X}$  is the grand mean for each measured trait.

Broadsense heritability ( $h^2_{bs}$ ) is expressed as the percentage of the ratio between the genotypic variance ( $\sigma^2_g$ ) and phenotypic variance ( $\sigma^2_p$ ) that was estimated according to Burton (1952). Genetic advance (GA) was estimated by the methods described by Fehr (1987) as  $GA = K(Sp) h^2_{bs}$  where  $K$  is a constant (2.06) at 5% selection pressure,  $Sp$  is the phenotypic standard deviation ( $\sqrt{\sigma^2_p}$ ) and  $h^2_{bs}$  is the heritability ratio. GA was also calculated as percentage of the mean.

### Results and Discussion

The results of the primary data of the various plant characters (Table 2) showed that the coefficient of variation, a measure of the relative levels for reproductive traits obtained in the study showed that moderate values were obtained in almost all the cases. Number of fruits had the highest coefficient of variability value of 96.36%. Days to male flower initiation and days to maturity showed low coefficient of variability values of 25.38 and 10.55 respectively. Mean squares for genotype were significant for all the characters studied. The phenotypic variance of the traits under study was grouped into heritable (genotypic variance) and non-heritable (environmental variance) components (Table 3). The magnitude of genotypic variances was higher than their corresponding environmental variances for all the traits. This result shows that the genotypic component of variation was the major contributor to total variation in the studied reproductive traits. The highest phenotypic coefficient of variation (PCV) was obtained for the number of fruits (59.02), fruit weight per plant

(56.18) and fruit yield per hectare (55.38). While the least PCV was recorded for days to maturity (7.32). High phenotypic coefficient of variation

(PCV) indicates the existence of a greater scope of selection for the trait being considered, which depends on the amount of variability present (Khan *et al.*, 2009). Thus, a greater potential is expected in selecting for the number of fruits, fruit weight per plant and fruit yield per hectare. Moreover, there is a narrow scope of selection for days to maturity because of low variability.

The wide ranges in the data observed for most of the traits and the significant mean square values obtained have shown the presence of genetic variability for the traits studied. This indicates that

these traits can be improved through breeding. Secondary traits are very valuable in selection for improved fruit yield (Omoigiu *et al.*, 2006). The significant genotypic effect observed for days to female flower initiation confirmed that genetic variability exist among the genotypes even though the day length was relatively shorter than the critical value needed for the photoperiodic responses. Most of the genotypes that flowered early had shorter reproductive phases than the late flowering ones, especially when the temperatures were cooler. Also, the long seeded genotypes like the NaganoF1 had longer reproductive periods but exhibited no yield advantage over the short seed size genotype. This suggests that seed size is not influenced by the duration of reproductive phase; rather it is governed by other genetic factors.

**Table 2. Primary data of the various plant characters evaluated**

Traits	Mean	Minimum	Maximum	Range	%CV	LSD <sub>(0.05)</sub>
Days to male flower initiation	33.65	22.00	42.00	20.00	25.38	4.68
Days to female flower initiation	39.27	27.00	48.00	21.00	26.11	5.52
Number of pistillate flower per plant	6.20	3.50	10.50	7.00	34.71	1.78
Days to maturity	55.98	50.00	64.00	13.00	10.55	4.65
Plant height at 8WAP(cm)	118.87	45.54	250.10	204.60	76.56	42.22
Number of fruits per plant	4.07	1.30	11.00	9.70	96.36	1.64
Fruit length(cm)	20.71	10.33	38.50	28.17	50.23	3.57
Fruit girth(cm)	5.35	2.76	11.50	8.74	64.72	1.58
Fruit weight per plant	0.89	0.24	2.29	2.05	92.65	0.31
Total fruit yield per hectare tha-1	5.39	1.44	13.74	12.30	91.44	1.84

%CV= Percentage Coefficient of Variation.

LSD<sub>(0.05)</sub> = Least Significant Difference at 5% probability level.

Table 3: Estimate of variance for 10 reproductive characters of some *Cucumis sativus* L. genotypes.

Traits	Mean	$\sigma_p^2$	$\sigma_g^2$	$\sigma_e^2$	PCV	GCV	ECV	H <sup>2</sup> bs(%)	GA	MSg
Days to male flower initiation	33.65	29.56	21.67	7.89	16.16	13.83	8.35	73.31	8.20	72.91**
Days to female flower initiation	39.27	42.34	31.39	10.95	16.57	14.27	8.43	74.13	9.94	105.12**
Number of pistillate flower per plant	6.20	2.30	1.16	1.14	24.46	17.37	17.22	50.43	1.58	4.63**
Maturity	55.98	16.80	9.03	7.77	7.32	5.37	4.98	53.75	4.54	34.87**
Plant height at 8WAP(cm)	118.87	3188.00	2547.00	641.10	47.50	21.30	5.80	79.89	92.92	8281.90**
Number of fruits per plant	4.07	5.77	4.81	0.96	59.02	53.89	24.07	83.36	4.12	15.38**
Fruit length(cm)	20.71	39.12	34.54	4.58	30.20	28.38	10.33	88.29	11.37	108.21**
Fruit girth(cm)	5.35	4.60	3.70	0.90	40.09	35.95	17.73	80.43	3.55	11.99**
Fruit weight per plant	0.89	0.25	0.22	0.03	56.18	52.70	19.46	88.00	0.91	0.68**
Total fruit yield per hectare tha-1	5.39	8.91	7.69	1.22	55.38	51.45	20.49	86.31	5.31	24.29**

$\sigma_p^2$ = phenotypic variance;  $\sigma_g^2$ = genotypic variance;  $\sigma_e^2$ = environmental variance; PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; ECV = environmental coefficient of variation; H<sup>2</sup>bs = broad-sense heritability; GA= genetic advance; MSg = mean square of genotypes.

Therefore, it could be suggested that the longer reproductive period observed for short seeded cucumber types was probably due to poor fruits establishment and photosynthate partitioning. This observation is in agreement with the earlier reports showing that the poor ability of some genotypes to assimilate carbon and nitrogen during reproductive

period and to partition large gains of these into pods limit cowpea yield (Jacquinot *et al.*, 1967). However, these results indicate that there is sufficient genetic variability within the genotype to warrant selection. This finding also provided some insight into the possible sources of large GCVs associated with some traits in the evaluation.

Generally, large GCVs may be caused by small means relative to large error terms, or vice versa. In this study, proportion of total variation attributable to the error variance was relatively small. High heritability estimates ( $h^2$ ) was obtained for fruit length (88.29%), fruit weight per plant (88.00%), total fruit yield (86.31%) and number of fruits (83.36%). The results of the present study corroborate those of Ene *et al.* (2016) and Veena *et al.* (2012) These authors reported high heritability for some of these traits.

The genotypic coefficient of variation (GCV) measures genetic variability that exists in different quantitative traits. The highest GCV was recorded in number of fruits (53.89), fruit weight per plant (52.70) and fruit yield per hectare (51.45); the lowest GCV was recorded for days to maturity (5.37). This indicates that though, the character is highly heritable, its improvement through early generation selection may not give the desired results. Yadav *et al.*, 2009 reported that high GCV shows the presence of exploitable genetic variability for the traits which can facilitate selection. Number of fruits (24.07) recorded the highest environmental coefficient of variation (ECV) of whereas; Plant height at 8WAP recorded the lowest environmental coefficient of variation (ECV) of 5.80. The estimate of PCV which was higher than those of GCV shows that genotype contributed more than environment in the expression of these characters and selection based on phenotypic values is therefore achievable. This is in line with Iwo and Ekaette (2010), who reported that a combination of both genotypic and phenotypic coefficient could be a considerable means for improvement on ginger and sesame respectively. Broad sense heritability for number of pistillate flower per plant was the least (50.43%) while fruit length had the highest (88.29%). This suggests that selection for these characters would be effective for further selection and improvement. Similarly, significant variations observed in the traits could be as a result of the genotypic differences existing among the genotypes which indicates that the characters are genetically controlled Precheur *et al.* (2007). Within the range of materials used in this study, there exist substantial genetic coefficient of variation and heritability in the characters studied to warrant selection in the genotypes for further improvement. The level of genetic variability observed for different characters would be useful for breeding varieties of cucumber for high yield. The high heritability estimates obtained for fruit length, fruit weight per plant, total fruit yield and number of fruits suggests that these characters are highly heritable and therefore the traits can be easily transferred from parent to offspring.

Secondary traits are very valuable in selection for improved cucumber fruit yield. The result of the present study revealed that longer duration of reproductive phase would not necessary

translate to high yield advantage but that genotypes with moderate period for this trait and combined with high efficiency of assimilate partitioning would result in higher fruit yield.

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