Genetic Variations, Heritability and Genetic Advance Studies among Okra Accessions grown in different Agro-ecological Zones in Nigeria

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Abstract

Some level of variation within crop varieties is highly important for its improvement with the aids of good plant breeding methods. A field research experiment was carried out with the aim to estimate genetic variation and heritability in the okra accessions grown in different agro-ecological zones in Nigeria. Twenty okra accessions were obtained from various locations in different agro-ecological zones of Nigeria. Twenty okra accessions were evaluated between April to August 2018 at Ekiti State University Teaching and Research Farm, Ekiti State. These twenty okra accessions constituted the treatment, which was lied out in a RCBD in a three replicates. The result were highly significant (p<0.01) for all the traits studied. Magnitude of the phenotypic coefficient of variances were slightly higher than genotypic coefficient of variances in this study which showed that environment did not much influence the estimates of genetic performance. The coefficient of phenotypic and genotypic variances were high in the traits studied. Heritability estimates ranges from 75.04% for days to 50% flowering to 98.85% for weight of 100 seeds. High heritability with high genetic advance were observed for all the studied traits indicating that they are governed by additive gene action and this could be improved through simple selection except days to 50% flowering with the lowest heritability value coupled with the lowest genetic advance value lesser than 10%.

Keywords

Heritability, Genetic advance, Improvement, Genetic variability, Okra.

1. Introduction

Okra [*Abelmoschus esculentus* (L) Moench] belongs to family of Malvaceae and genus *Abelmoschus* [1]. According to [2], okra is proposed to originate from the Tropical Africa from where it extensively spread to Asia, America, Southern Europe and other countries. It is self-pollinated, although 4 to 19 per cent out crossing by insects has been reported which brings about considerable level of genetic [3].Okra fresh fruit contains 175.2 mg minerals, 2.1 g protein, 0.2 g fat, 1.7 g fiber, 8 g carbohydrate, 36 calories, and 88 ml of water per 100 g of edible [4].Okra is a high yielding crop under a good cropping system, with yield varying from 4,480 to 5,500 kg ha^{-1} of green pods [5].The unripe green finger-like seed capsule of okra, usually called "pod" are processed and consumed as stews and salads, soups, sliced, boiled and fried vegetables [6].

The level of genetic variation present in crop germplasm is proportional to its improvement [7]. Genetic variability cannot be underestimated as a component of plant breeding tool being used to cope with world increasing population on food production [8].Variation in genetic composition of any given crop population is highly important to successfully select and manage its

improvement programs [9]. A good understanding of the components of variances and their effects, heritability and genetic advance of the trait(s) of interest help plant breeders in deciding the appropriate breeding method in improving the plant genetic makeup.

To determine the relative environmental influence on expression of genotypes, heritability is highly important. It became very difficult to judge how much of variability is heritable and much of variability is non-heritable. Partition of overall variability into its heritable and non-heritable components with the help of genetic parameters is essentials [10]. who reported that, the higher heritability percentage, the more the heritable variance that may offer the possibility of improvement through selection programme. Estimate of heritability alone is insufficient enough measure of the level of possible genetic progress that might arise in a breeding programme. Genetic advance is also used to enhanced heritability estimates for better improvement in crop [11]. Therefore, this study is to evaluate genetic variation, heritability and genetic advance in various traits in okra accessions grown in some agro-ecological zones in Nigeria, for high yielding okra accession(s) development.

2. Materials and Methods

2.1 Study Area Description

Field experiment was conducted on okra accessions during the early cropping season in year 2018 in Ekiti State University Teaching and Research Farm, Ekiti State. It lies between latitude 7° 31' and 7° 94' N. The land has been used continuously for the production of crops like yam, melon, cowpea and sweet potato for more than three years.

2.2. Treatments and Experimental Design

Twenty okra accessions were obtained from different agro-ecological zones in Nigeria. The twenty accessions used for the experiment and their sources were presented in Table 1. The accessions constituted the treatment, which was lied out in a RCBD in three replicates. Each of the accession were sown in single-row plot to minimise environmental effects associated with large plots. Two seeds were sown per hill by hand and later thinned to one after three weeks of planting. The length of each row was 7.5m and plants were sown at the distance of 1m x 50 cm. Good crop were raised in the field by adopting excellent agronomic practices. Ten plants were selected randomly for record observations.

2.3. Data Collection

Data were collected on final plant height (cm), days to 80% maturity, fresh fruit length (cm), fresh fruit diameter (cm), days to 50% flowering, number of fruits per plant, weight of 100 seeds (g), number of seeds per fruit, number of ridges per fruit and fresh fruit yield per plant (g).

2.4. Statistical Analysis

2.4.1. Analysis of variance

Analysis of variance (ANOVA) was carried out for the traits as per the procedure outlined by [12-13] was used to analyse. The analysis of variance (ANOVA) showing expected means squares is presented in table 2.

2.4.2. Estimation of genetic parameters

The components of phenotypic and genotypic variance were calculated according to [14]. Coefficient of variation for phenotypic and genotypic estimate were computed according to by [15] formula. The phenotypic and genotypic coefficient of variation values were categorized by [16] as follows: Low: 0-10 %, Moderate: 10-20%, High: >20%. The Heritability in the broad sense and genetic advance was estimated by adopting [17] method. Genetic advances under selection (GA) expected genetic advances for each trait at five percent selection intensity was calculated by the formula suggested by [17]. The genetic advances as per cent of mean was described by [17] as follows; Low: 0-10 %, Moderate: 10-20%, High: 20% and above.

3. Results and Discussion

3.1. Analysis of variance

The mean squares due to genotype were highly significantly different (p < 0.01) in all the traits studied. This indicates a wide range of variation and the existence of sufficient genetic variability (Table 2). This is in agreement with the research findings of [18-19].

3.2. Phenotypic and genotypic variations

Developing a superior varieties and selecting a good breeding program for any genotype depend on the magnitude of genotypic and phenotypic variability that exist among the genotype. The variability in a given population were measured by genotypic and phenotypic coefficients of variation [14]. In general, whenever phenotypic coefficient value(s) were higher than genotypic coefficient value(s) for any trait, this shows that environmental factors had play a cogent role in influencing the

trait expression. In this present study, almost similar trend and similar magnitude of phenotypic and genotypic coefficient of variances showed that environment had little influence on the estimates of genetic performance. Highest phenotypic coefficient of variances and genotypic coefficient of variances in all the traits considered were recorded in days to 50% flowering (46.09% and 39.09%) respectively. Moreover, high phenotypic and genotypic coefficient of variances were observed in weight of 100 seeds (36.65% and 36.39%) and final plant height (33.75% and 32.66%) while fresh fruit length had the least phenotypic and genotypic coefficient of variances (16.16% and 14.14.87) respectively. Final plant height, number of branches per plant, fresh fruit diameter, days to 50% flowering, days to 80% maturity, and weight of 100 seeds had phenotypic and genotypic coefficient of variance values greater than 20% while other studied traits had a phenotypic and genotypic coefficient of variance values greater than 10% which is moderate. Hence, these traits are responsive to selection for onward improvement. This result substantiates with the findings of [20]. Some researchers have noticed that high magnitude of phenotypic and genotypic coefficient of variance inferred a low environmental manifestation effects on the characters, which probably increase greater improvepment prospects through selection scheme [21-23].

3.3. Heritability estimates

Broad sense heritability is an estimate of the total contribution of the genotypic variance to the total phenotypic variance. The relative amount of heritable proportion of variability which is an important biometrical tool for selecting appropriate breeding procedure is determine by heritability. Therefore, it assist the plant breeders to select a particular trait when heritability is high. For this study, heritability in the broad-sense estimates ranged from (75.04%) for days to 50% flowering and (98.85%) for weight of 100 seeds. Agronomic traits seemed to respond effectively to the pressure of selection whenever heritability is up to 60 % or more of a character, selection would be easy for such traits. Broad sense heritability greater than 60 % was obtained for all the traits studied. This result with high broad sense heritability shows that the additive genetic variation was the key component of genetic variation in the inheritance of all these traits. However, improvement can be achieve through direct selection for these traits.

3.4. Estimates of expected genetic advance

The genetic advances as percent of the mean (GAM) at 5% selection intensity is presented in Table 4. It ranged from 7.11% for days to 50% flowering to 74.62% for plant height at first fruiting.

In all the studied traits, genetic advance expressed as percentage of mean observed was high. From weight of 100 seeds (74.62%), final plant height (65.12%), number of fruit per plant (48.21%), fresh fruit diameter (48.14%), days to 80% maturity (45.19%), number of ridges per plant (39.24), fresh yield per plant (32.80%), fresh fruit weight per plant (30.94%) and fresh fruit length (28.17%) except days to 50% flowering (7.11%). The high estimate for genetic advance expressed as percentage of mean indicated that these traits were control by additive gene actions which depict that improvement can be made selection for all these traits except days to 50% flowering (7.11%).

Table 1. List of okra accessions and their sources

ACCESSIONS	Place of Collection	Ecological Zone
ACCESSION 1	Iwo, Osun State	Forest zone
ACCESSION 2	Ado-Ota, Ogun State	Forest zone
ACCESSION 3	Ogbomoso, Oyo State	Forest zone
ACCESSION 4	Ibadan, Oyo State	Forest zone
ACCESSION 5	Odigbo, Ondo State	Forest zone
ACCESSION 6	Orin-Odo-Ekiti, Ekiti State	Forest zone
ACCESSION 7	Oke-Ako- Ekiti, Ekiti State	Forest zone
ACCESSION 8	Irun-Akoko, Ondo State	Forest zone
ACCESSION 9	Uromi, Edo State	Forest zone
ACCESSION 10	Egbe, Kogi State	Derived Savanna
ACCESSION 11	Ilorin, Kwara State	Derived Savanna
ACCESSION 12	Okenne, Kogi State	Derived Savanna
ACCESSION 13	Offa, Kwara State	Derived Savanna
ACCESSION 14	Odo-Owa, kwara State	Derived Savanna
ACCESSION 15	Suleja, Niger State	Southern Guinea Savanna
ACCESSION 16	Mokwa, Niger State	Southern Guinea Savanna
ACCESSION 17	Lafia, Nasarawa State	Southern Guinea Savanna
ACCESSION 18	Kaduna, Kaduna State	Northern Guinea Savanna
ACCESSION 19	Zaria, Kaduna State	Northern Guinea Savanna
ACCESSION 20	Samaru, Kaduna State	Northern Guinea Savanna

Table 2. The analysis of variance showing expected means squares

S/V	DF	EMS
Rep.	r - 1	
Accession	g - 1	$\delta^2 e + r\delta^2 g$
Error	$(r - 1)(g - 1)$	δ^2

Where: $\delta^2 e$: Environmental variance, $\delta^2 g$: Genotypic variance, S/V: Source of variation

DF: Degree of Freedom, EMS: Expected Means Squares

4. Conclusion

The result showed the existence of genetic variability in the okra accessions studied and this can be exploited in the future breeding program. The mean squares due to genotype were highly significantly different ($p < 0.01$) for all the studied traits, almost similar trend and similar magnitude of phenotypic and genotypic coefficient of variances were also observed in the result. Heritability in the broad-sense values were higher than 60% in all the studied traits, likewise the estimate for genetic advance expressed as percentage of mean indicated that these traits were greater than 20% except days to 50% flowering. Considering the result in this study, there is an indication of preponderance of additive gene actions and improvement can be made through selection except days to 50% flowering.

Table 3. Combined ANOVA for 10 okra traits studied, the values are mean square.

S. of V	DF	FPH (cm)	D80%M	FFL (cm)	FFD (cm)	D50%TF	NOF/P	W100S (g)	NOS/F	NOR/F	FFY/P(g)
Rep.	2	102.73*	22.68**	13.75**	12.58**	124.17**	60.07**	11.45*	84.63**	11.46**	0.22*
Acc.	19	2139.09**	6.41**	3.71**	15.55**	12.94**	115.56**	1672.21**	134.79**	7.27**	1.07**
Error	38	0.12	0.21	1.47	1..47	1.29	1.49	7.95	4.64	0.12	0.03

*, ** significant at 5% and 1% levels respectively

Rep.: replication, Acc.: Accession, FPH: final plant height, D80%M: days to 80% maturity, FFL: Fresh fruit length

FFD: Fresh fruit diameter, D50%TF: 50% days to fruiting, NOF/P: Number of fruits per plant,

W100S (g): weight of 100 seeds (g), NOS/F: Number of seeds per fruit, NOR/F: Number of ridges per fruit, FFY/P: fresh fruit yield per plant (g).

Table 4. Mean, Standard Error, Range, Phenotypic and Genotypic Variances

Character	Means ± S.E	Range Min-Max	Genotypic variances	Phenotypic variances
FPH (cm)	80.83 ± 3.97	38.60 - 125.60	697.30	744.49
D80%M	6.24 ± 0.19	2.50 - 10.50	2.0	2.12
FFL (cm)	7.24 ± 0.26	4.80 - 7.24	1.16	1.37
FFD (cm)	8.08 ± 0.70	3.80 – 19.2	4.69	6.16
DTF	49.33 ± 0.65	44.0 – 57.4	3.88	5.17
NOF/P	25.82 ± 0.7	17.4 – 38.80	38.02	39.51
W100S (g)	64.72 ± 1.63	26.2 – 100.1	554.75	562.70
NOS/F	41.72 ± 1.24	20.4 – 53.20	43.38	48.02
NOR/F	7.90 ± 0.20	6.00 – 12.00	2.38	2.50
FFY/P(g)	3.14 ± 0.10	2.00 – 4.10	0.34	0.37

*, ** significant at 5% and 1% levels respectively

FPH: final plant height, D80%M: days to 80% maturity, FFL: Fresh fruit length

FFD: Fresh fruit diameter, D50%TF: 50% days to fruiting, NOF/P: Number of fruits per plant,

W100S (g): weight of 100 seeds (g), NOS/F: Number of seeds per fruit, NOR/F: Number of ridges per fruit, FFY/P: fresh fruit yield per plant (g).

Table 5: Phenotypic and Genotypic Coefficients of Variation, Heritability and Genetic Advance

Character	Heritability (Broad sense) %	Genotypic Coefficients of Variation (%)	Phenotypic Coefficients of Variation (%)	Genetic dvance (%)	G.Amean (%)
FPH (cm)	93.66	32.66	33.75	52.64	65.12
D80%M	94.33	22.6	23.33	2.82	45.19
FFL (cm)	84.67	14.87	16.16	2.04	28.17
FFD (cm)	76.13	26.80	30.71	3.89	48.14
50%DTF	75.04	39.93	46.09	3.51	7.11
NOF/P	96.22	23.88	24.34	12.45	48.21
W100S(g)	98.85	36.39	36.65	48.30	74.62
NOS/F	90.33	15.78	16.60	12.91	30.94
NOR/F	95.20	19.52	20.01	3.10	39.24
FFY/P(g)	91.89	18.56	19.37	1.03	32.80

*, ** significant at 5% and 1% levels respectively

FPH: final plant height, D80%M: days to 80% maturity, FFL: Fresh fruit length

FFD: Fresh fruit diameter, D50%TF: 50% days to fruiting, NOF/P: Number of fruits per plant,

W100S (g): weight of 100 seeds (g), NOS/F: Number of seeds per fruit, NOR/F: Number of ridges per fruit, FFY/P: fresh fruit yield per plant (g).

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