



RESEARCH ARTICLE

VARIANCE IN YIELD AND AGRONOMIC PERFORMANCE OF EGUSI MELON
(*Citrullus lanatus* Thunb) GENOTYPES

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ARTICLE INFO

Article History:

Received 25th July, 2011
Received in revised form
28th August, 2011
Accepted 27th September, 2011
Published online 15th October, 2011

Key words:

Heritability,
Accessions,
Egusi melon and
Genetic advance

ABSTRACT

An experiment was carried out in 2006 and 2007 at the Teaching and Research Farm, University of Agriculture, in two Abeokuta environments to estimate the variability among 18 *egusi* melon accessions. The experiment was laid out in a randomized complete block design with three replicates. The phenotypic coefficient of variability (PCV) ranged from 2.15 % (days to 50 % flowering) to 51.20 % (pod weight) and 2.18 % (days to 50 % flowering) to 63.65 % (seed yield per plant), respectively in the two environments. Similar trend was observed in the genotypic coefficient of variability. Number of seeds per pod had the highest phenotypic variance (3,347.00 and 4884.42) and the least was pod weight (0.12 and 0.22), respectively in Abeokuta 1 and Abeokuta 2 study environments. Averaged over the two environments, seed yield per plant had the highest genotypic variance (531.60) while pod weight was the lowest (0.16). Number of pods per plant, pod weight per plant, seed weight per pod and seed yield per plant had a combined high heritability and genetic advance, which revealed limited influence of environment on them.

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INTRODUCTION

Egusi melon (*Citrullus lanatus* Thunb) is a member of the family Cucurbitaceae. The crop is cultivated for its seeds, which are prepared into condiments used especially in preparing soup. It is a veritable source of oil and protein; about 53.1 % and 33.8 %, respectively (Ogbonna and Obi, 2010). The use of the oil in the cosmetic and pharmaceutical industries is ever increasing (Badifu and Ogunsu, 1991). Increased seed yield with improved seed qualities are criteria for meeting the demand for melon, which has been on increase since the last decade. Unavailability of improved varieties has been identified as one of the major constraints. The gene introgression or recombination through hybridization is almost impossible. This shows a narrow genetic variability. Oseni and Khidir (1994) reported that improvement of any crop depends on the magnitude of genetic variability and yield related traits that can easily be exploited for efficient crop management and enhancement of yield. The situation encourages poverty alleviation and economic growth. Martin *et al.* (1991) confirmed that the degree of success in breeding of genetic improvement of crop is dependent to a large extent on the

understanding of the amount and distribution of the genetic variation existing among advanced and primitive cultivars. Hence, selection of good quality seed is of great importance to a plant breeder. This work is aimed at understanding the genetic variability in *egusi* melon genotypes and traits that are more genetically influenced for selection.

MATERIALS AND METHODS

Eighteen accessions of *egusi* melon seeds (Table I) were grown at the Teaching and Research Farm, University of Agriculture, Abeokuta in 2006 (Abeokuta 1) and 2007 (Abeokuta 2) environment. The experimental design was randomized complete block replicated three times. The total plot size was 425m². Seeds were sown at 1 m x 1 m giving a population of 10,000 plants per hectare. The plots were hoe weeded at 3 weeks and NPK fertilizer at the rate of 400 kg/ha was applied after weeding. From the inner rows, data were collected on days to germination, days to first flowering, days to 50 % flowering, vine length (cm), number of branches per plant, days to maturity, number of pods per plant, fresh pod weight per plant (kg), pod circumference (cm), number of seeds per pod, seed weight per pod (g), 100 seed weight (g), seed yield per plant (kg). Vine length was measured with a meter rule from the base of the longest vine to the tip of the

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canopy, while the number of branches per plant was determined by counting. Number of days to 50 % flowering was determined as the period between date of planting to date when 50 % of the plants had flowered while days to maturity was determined as the period from the date of planting to the date when 95 % of the plants had become dry. The number of pods per plant was determined by counting. At maturity, the collected fresh pods were beaten with strong, heavy sticks to break the hard shells. They were left for about a week to allow the pulp to soften. The seeds were extracted from the pulp, washed in clean water and dried. The seeds were weighed using a sensitive balance (Satories Master Series). Seed yield was obtained as the weight of clean, dry seeds. Quantitative data from each character were subjected to Analysis of Variance (ANOVA) procedures using Genstat computer package (Genstat, 2003). Means were compared using the least significant difference (LSD) at 5 % level of probability as outlined by Obi (1986). The phenotypic and genotypic Coefficient of correlations was calculated from the mean values of the genotypes using the procedure detailed by Miller *et al.* (1958). Broad sense heritability (h^2 %) was calculated according to the methods outlined by Burton (1952) and Allard (1960).

Table 1: The eighteen 'egusi' melon accessions and their Sources

Accession No.	Accession	Source
1	V2	NIHORT
2	131DA	NIHORT
3	DL99/71	NIHORT
4	DL99/75	NIHORT
5	DL99/76	NIHORT
6	DD95/549	NIHORT
7	DD98/3	NIHORT
8	DD98/4	NIHORT
9	DD98/7	NIHORT
10	DD98/506	NIHORT
11	DD98/11	NIHORT
12	DD98/533	NIHORT
13	DD98/550	NIHORT
14	L ₁	Okene, Kogi State
15	L ₂	Minna, Niger State
16	L ₃	Benin, Benin City
17	L ₄	Saki, Oyo State
18	L ₆	Abeokuta, Ogun state

RESULTS

The estimate of phenotypic and genotypic coefficient of variability, phenotypic and genotypic variances, broad sense heritability and genetic advance expressed as percentage of mean are presented in Table 2. The *egusi* melon accessions showed considerable variation for pod circumference, vine length, number of seeds per pod, seed weight per pod and seed yield per plant. Variances for the other traits in respect to the two environments were quite close. The phenotypic coefficient of variation (PCV) ranged from 2.15 % (days to 50 % flowering) to 51.20 % (fruit weight) and 2.18 (days to 50 % flowering) – 63 % (seed yield/plant) in the two environments, respectively. Similar trend was observed in the genotypic coefficient of variation (GCV) in both environments. Number of seeds/pod gave the highest phenotypic variance (PV) (3,347.00 and 4,884.42) while the least was pod weight (0.12 and 0.22), respectively in Abeokuta 1 and 2 study environments. Averaged over the two environments, vine length had the highest genotypic variance (GV) (572.28) followed by yield /plant (531.6) and the fruit weight (0.16). Considering heritability estimates and genetic advance together, number of branches per plant, , pod weight per plant, seed weigh per pod and seed yield per plant showed combined high heritability and genetic advance in all the environments. Days to 50 % flowering had moderate heritability and very low genetic advance. However, days to germination, days to first flowering, and days to maturity expressed high heritability with low genetic advance in the two environments. Vine length had very low heritability and genetic advance in the first environment and high genetic advance in the second environment. The dendrogram from Single Linkage Clusters Analysis (SLCA) explains the relationship between the accessions in Abeokuta one environment (Figure 1). At a minimum distance of 0.000 level of similarity, all the accessions were distinct from each other apart from DD99/71 and DD98/4 with a high level of similarity. At 1.5 level of similarity, single cluster was formed indicating that the accessions had at least one neighbour with more than 1.5 similarity level.

Table 2: Estimate of phenotypic and genotypic coefficient of variability, phenotypic and genotypic variance, heritability in broad sense and genetic advance in the two environment (Abeokuta 1 and 2)

Characters	Seasons	PCV (%)	GCV (%)	PV	GV	h^2	GA as % of the mean
Days to 50% flowering	1	2.15	1.36	1.11	0.45	40.01	1.77
	2	2.18	1.30	1.15	0.41	35.29	1.59
100 seed weight	1	18.73	18.68	5.00	4.97	99.54	38.40
	2	20.09	20.03	5.64	5.61	99.45	41.15
Pod circumference	1	11.34	10.61	19.05	16.65	87.40	20.3
	2	18.10	17.86	46.09	44.88	97.37	36.30
Days to 1 st flowering	1	4.44	4.16	2.91	20.56	87.83	8.04
	2	11.93	11.86	21.35	21.09	98.77	24.28
Days to germination	1	10.78	10.08	0.46	0.39	86.15	19.30
	2	15.48	13.21	1.01	0.74	72.86	23.24
Days to maturity	1	4.77	4.72	18.07	17.72	98.05	9.64
	2	5.18	5.08	20.32	19.54	96.17	10.26
Fruit weight	1	51.20	50.13	0.12	0.11	97.40	78.72
	2	56.22	55.18	0.22	0.21	96.32	68.55
Length of vine	1	15.15	6.71	624.34	122.37	19.60	6.12
	2	34.85	33.85	1587.90	102.19	96.54	69.31
No of branches per plant	1	20.83	17.96	0.62	0.46	74.35	31.90
	2	26.23	25.87	1.23	1.20	97.21	52.54
No of fruit per plant	1	29.45	28.44	0.21	0.19	93.27	56.58
	2	31.54	30.36	0.23	0.21	92.67	60.21
No of seed per fruit	1	39.43	25.04	3347.00	312.74	93.44	49.86
	2	44.20	30.33	4844.42	473.08	97.65	61.74
Seed weight per fruit	1	39.43	38.88	115.16	111.95	97.22	78.97
	2	44.20	43.89	149.57	147.46	98.59	89.76
Seed yield per plant	1	45.12	44.14	334.65	320.32	95.72	88.96
	2	63.65	62.61	767.81	742.88	96.75	74.87

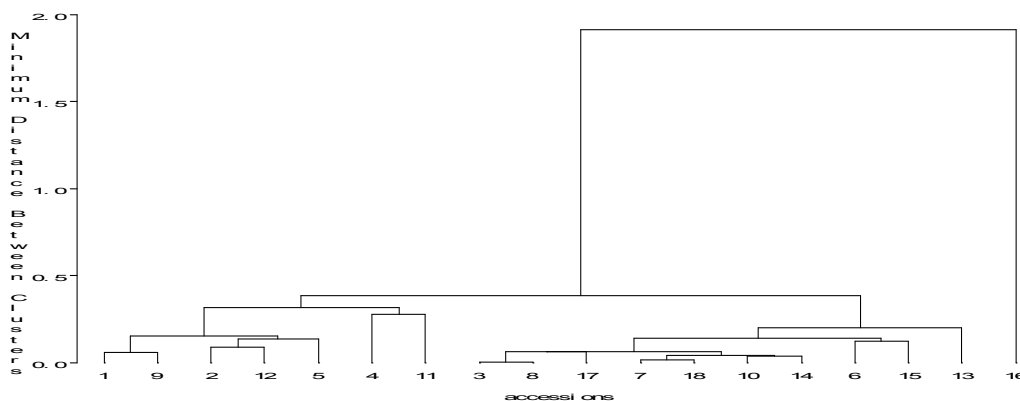


Fig. 1: Dendrogram from Single Linkage Cluster Analysis (SCLA) of eighteen accessions of 'egusi' melon in 2006 (Abeokuta) late season

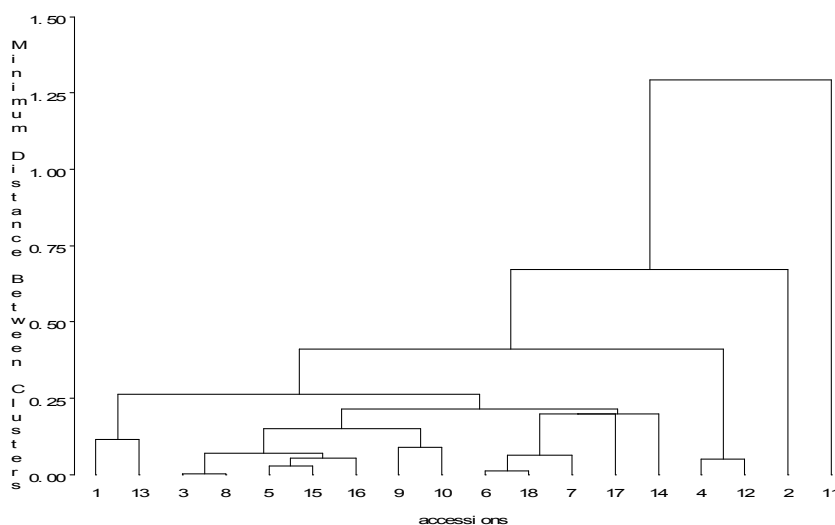


Fig. 2: Dendrogram from Single Linkage Cluster Analysis (SCLA) of eighteen accessions of 'egusi' melon in 2007 (Abeokuta) early season

But at a minimum level of 0.04, accessions DD98/506 and L1 were not similar. Seventeen accessions formed a single cluster at a minimum of 0.4 while at a distance of 1.5, only accession L3 was distinct from the rest of the population. The SCLA for the accessions in Abeokuta two environment is shown in Figure 2. At 0.00 level of similarity, the accessions were distinct from each other except for DL99/71 and DD98/4. At a measure of 0.8, the accessions formed a single cluster, which indicates that accessions had at least one neighbour with more than 0.8 similarity levels. Accessions DL99/75 and DD98/533 had a single cluster at 0.04 with V2 and DD98/11 being distinguished from the rest population. The phenotypic coefficient of variation was generally higher than the genotypic coefficient of variation for all the characters across the two environments, though the two values differed slightly. The same trend was reported by Osanyinjobi (2002). This suggests that environmental influence constitutes a major portion of the total phenotypic variation in some characters. The higher heritability estimates for first day to flowering, pod circumference, number of seeds per pod, seed weight per pod, and 100-seed weight indicated that environmental factors did not greatly affect phenotypic variation of such characters and can be depended upon for genetic improvement in *egusi*

melon. The relatively low heritability estimates for day to 50 % flowering in the two environments and vine length in the first environment establishes the ineffectiveness of direct selection for these characters. High genetic advance observed for seed weight per pod and seed yield per plant in both environments as well as moderate genetic advance for number of pods per plant, number of seeds per pod and seed yield per plant could be due to additive gene action. Hence, simple selection for these characters can be made. Mustadha *et al.*, (2000) suggested that traits with high GCV, heritability and genetic advance could serve as good predictors for seed yield in crops. Also, Ariyo (1990) reported the need to breed for specific environments because the response of most characters to the environment was non-linear. Moreso, duration of flowering and life span are often affected by the length of the growing season, which is correlated with the environment.

Conclusion

The mean value of the six similarity clusters of grouping of accessions confirmed the contribution of days to first flowering, seed weight per pod, 100-seed weight and seed yield per plant among the eighteen accessions. This implies

that if selection is to be made between cluster groups for future breeding programme, these form traits should be given high priorities.

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