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Genetic relationship within accessions of beniseed (Sesamum indicum. L)

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ABSTRACT: A study of the genetic relationship within some accessions of Beniseed (*Sesanum indicum* L.) was carried out with the aid of multivariate analysis of Eucilidean Distance of nearest and further neighbour as well as group average.

Data on agronomic traits showed significant differences both in the vegetative and reproductive phases of the genotypes. The resulting dendrograms from the numerical analysis delineated the accessions into groups and subgroups which can be assessed to serve as base lines for parental selection in respect of future genetic breeding programmes.

Key Words: Genetic relationship; Agronomic traits; Beniseed; Sesanum indicum L.; Eucilidean Distance.

Introduction

Beniseed (*Sesanum indicum* L) is one of the most ancient oil producing crops known to man. Ethiopia is generally accepted as the origin of cultivated sesame with considerable argument in favour of the Afgan-Persian region.

Nigeria is classified among the major producers of sesame for export in Africa (Weiss, 1979). The four major areas of beniseed production in Nigeria are Tiv, Idoma area of Benue State, Igbira area of Kogi State and Kwali area of Niger State with more than 90% of the Nigerian export from Benue State alone.

Cultivated sesame has 13 pairs of chromosomes (2n = 26). Interspecific hybridization has been widely studied and some crosses have produced viable seeds (Nayar and Mehra, 1970). Sesame is considered as having a very great range of variation (Hildebrandt, 1931; Vavilov, 1949), realizing that material from each locality is frequently represented by a distinct ecotype.

Quantitative studies in population and ecological genetics reveal that both natural and domestic species of plants contain large amounts of genetic variants (Awopetu, 1982) such variants extensive geographical as well as inter- and intra-population variability such that when practicalities of plant exploration and exploitation are considered, it is obvious that any collection can only be a fraction of the total variabilities of the crop species.

However, geographical distribution as well as centres of origin and deliberate human interference by way of breeding preferences and crop introductions is heavily implicated in variability patterns in crop species and genetic resources (Awopetu, 2000).

Studies in genetic variability could be greatly enhanced by adopting the more efficient biometric techniques on evaluating the similarity and/or dissimilarity among crop genotypes. Such established numerical clustering procedures include the cetroid sorting, the group average as well as Euclidean distance nearest and furthest neighbours (Clifford and Stephenson, 1975; Awopetu, 1982; Ezeakwu and Awopetu, 1992; Awopetu and Aliyu, 2000; Awopetu, 2000). Such long established and reliable biometric principles have been adopted in estimating the amount of genetic diversity among the beniseed accessions in this study. This is the first time a study of this nature has been carried out in Kwara State – a typical Southern Guinea agro-ecosystem.

Materials and Methods

The experimental material consisted of seventeen cultivars of beniseed collected from the National Cereals Research Institute of Nigeria (N.C.R.I.), Badeggi, Niger State, Nigeria (see Table 1). Pot and field investigations were conducted on the samples at the premises of the Faculty of Agriculture, University of Ilorin (Lat. 08° 26'N; Long. 04° 29'E at about344.7m above sea level) in the Southern guinea Savanna agro-ecosystem.

S/N	ACCESSIONS	COUNTRY OF ORIGIN	
1	Yandev	Nigeria	
2	Panshin – 98	Nigeria	
3	Kano – 98	Nigeria	
4	530-3	-	
5	859-3-1	-	
6	Wamba	Nigeria	
7	Chimkwallu – 98	Nigeria	
8	S – 530	-	
9	Ciano – 27	-	
10	Eva – 98		
11	Domu 98	Nigeria	
12	SM – 11	-	
13	$73^{\mathrm{A}} - 82^{\mathrm{B}}$	-	
14	Potiskum	Nigeria	
15	Jigawa	Nigeria	
16	T-4	-	
17	Cameroon	Cameroon	

Table 1: A list of Sesame with their countries of origin.

Pot Experiment: Seeds from the seventeen cultivars of beniseed were sown in 16" diameter polythene bags filled with sterilized top soil. The experimental layout was a randomized complete block design (RCBD) with three replicated. The pots were watered by 8.00a.m. and 6.00p.m. daily. Seedlings were thinned down to three plants per stand at three weeks after planting. Three manual seedlings were carried out during the experimental period.

Field Experiment: The layout consisted of three replicates in a randomized complete block design. Fifteen cultivars were sown in each plot of 20cm spacing. The seedlings were thinned to three plants per stand at three weeks after planting. The plots were weeded manually three times during the experimental period.

The following data were collected from both the pot and field plantings:

- (a) Days to germination from sowing
- (b) Days to 50% flowering from sowing
- (c) Number of leaves at flowering
- (d) Length of flowers (average)
- (e) Days to maturity from sowing (senescence of 75% of plants)
- (f) Plant height at maturity
- (g) Number of primary branches per plant
- (h) Total number of branches per plant
- (i) Number of pods on primary branch
- (j) Total number of pods per plant
- (k) Seed yield per plant (average weight of seeds collected from ten plants).

Collected data were subjected to analysis of variance. Six separate dendrograms were produced by the computer from the data based of Euclidean distance of nearest neighbour further neighbour and group average cluster analysis. (Clifford and Stephenson, 1975; Awopetu, 1982; Ezeakwu and Awopetu, 1992; Olisa and Awopetu, 1995; Awopetu and gana, 1997; Awopetu and Aliyu, 2000; Awopetu, 2000).

Results and Discussion

Tables 2and 3 show the brief statistical summaries of the analysis of variance respectively of the genetic traits in the pot experiment and field studies of the beniseed accessions. Values with asterisks in the tables indicate statistically significant traits among the accessions.

Figures 1, 2 and 3 refer to the pot experiment while Figures 5, 6 and 7 refer to the field investigation dendrograms respectively for nearest neighbour, furthest neighbour and group average multivariate analysis of the data collected from the beniseed accessions. As a result of the clustering pattern of the accessions in the dendrograms (Figs 1 - 6), Table 4 represents possible grouping of the accessions into genetic and agronomic proximity categories. The rationale for such grouping arises from the overall affinity of the individual accessions to identify itself with closely related biotypes in respect of the character states studied (Awopetu, 2000). On the other hand, the ability of the individual accession to discriminate among the groups is based on the clustering principle of dissimilarity matrix which is the essence of the biometric systems adopted for the exercise.

The distinguishing traits of the respective groups are discussed as follows:

Group I: Members of this group are the early flowering biotypes with fewer number of leaves and pods at flowering and physiological maturity respectively.

Group II: In contrast to group I members, these are the late flowering and maturing genotypes with characteristically tall phenotypes. They are compatively the high yield cultivars.

Group III: Majority of the accessions fall into this group. They are the medium maturing biotypes possibly combining the qualities of groups I and Ii members. It is suspected that they have undergone more breeding and selection pressures compared with other group members (Gana, pers comm.).

Group I	Group II	Group III	Group IV
Wamba	Yandev	Potiskum	
Domu – 98	Kano – 98	Cameroon	Chimkwallu
T-4	S - 530	530 - 3	Eva
Ciano - 27		Pankshin	73A – 82B
		Sm - II	
		Jigawa	
		859-3-1	

Table 4: Summary of the cluster analysis showing group affinities among beniseed cultivars derived from nearest neighbour, furthest neighbour and group average methods of biometric analysis.

Group IV: These are irregularly classified material that probably have no genetic relationship. The distinguishing characteristic attributes of the numerical methodology may have influenced their common classification (El-Gazar *et al.*, 1968; Mumm and Dudley, 1994; Awopetu, 2000). The genetic gains from such identification is that crosses obtained within each group would not generate as much gene recombinants compared with crosses between the groups. This will assist in selection of parents for breeding strategies (Thompson *et al.*, 1998).

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