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Analysis of Genotypic Diversity in Sesame Based on Morphological and Agronomic Traits

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Introduction

Sesame is known to be the most ancient oil seed crop dating back to 3050-3500 B.C (Bedigian and Harlan, 1986). It is grown in tropical and subtropical areas of the world. It can set seed and yield well under fairly high temperature it can grow in stored soil moisture without rainfall and irrigation. But continuous flooding or severe drought adversely affect sesame plants and resulted in low yield (Mensah et al., 2009). Another major cause of poor yield of sesame is due to low yielding cultivars. Development of improved plant cultivars is restricted by mainly limited genetic variability. Due to narrow genetic pool it is not possible to restructure the sesame crop. It has been suggested that sesame cultivation under such degradable condition has caused serious genetic erosion for yield, where selections within the local varieties fails to respond favorably to high input managements.

The characterization and conservation of sesame germplasm are essential for both safe guarding and the future use of existing genetic resources of sesame. Wide genetic diversity is very important in selecting the parents for hybridization programmes for identifying herterotic crosses and obtaining desirable recombination in the segregating generations. (Banerjee and Kole, 2009).Hence, the systemic management of plant genetic resources is very important to augment productivity of sesame.

This study aims to analyze genetic diversity of sesame germplasm from India and Ethiopia to find the parents for improvement of hybridization programme and important yield component for higher yield based on 36 sesame genotypes.

Material and Methods

A total of 36 sesame germplasm were collected from the sesame growing areas from India and Ethiopia, were grown in a randomized complete block design during (March 2011- June 2011)on experimental farm of Calcutta University, Baruipur (latitude 22°20'58"N, longitude 88°26'21"E), located near Kolkata city, India. The soil of the experimental plot was alluvial in texture (with medium to low fertility status (N: 235.4 kg/ha, P: 20.4 kg/ha, K: 172.3 kg/ha, and organic C: 0.5%) and acidic (pH: 6.5) in nature. Each genotype was grown in 10 row plots of 4 m long, with a spacing of 45 cm between rows and 15 cm between plants. Standard agronomic package and practices were followed to raise a healthy crop. The analysis is based on the determination of the following 11 physiological parameters: Days to flowering, Days to 50% flowering, Flower duration, Days to maturity, Plant height (cm), No. of branches/plant, No. of capsules/plant,

Capsules length(cm), No. of seeds/capsules, 1000 seed weight (gm), Seed yield/plant (gm). Single plant selection was made from these population based on different agromorphic traits and yield potential. Considerable care was taken while the seed was harvesting, due to non- uniform maturity and shattering habit of sesame. Data on all the flowering characters, flower colours, hairiness and leaf shapes were recorded on the basis of observations of the whole plot for each treatment.

Statistical Analysis

Differences between genotypes for different characters were tested for significance using analysis of variance. GCV, PCV, heritability (broad sence) and GA was measured by Burton (1968) and Hanson (1963) method.

Multivariate statistics

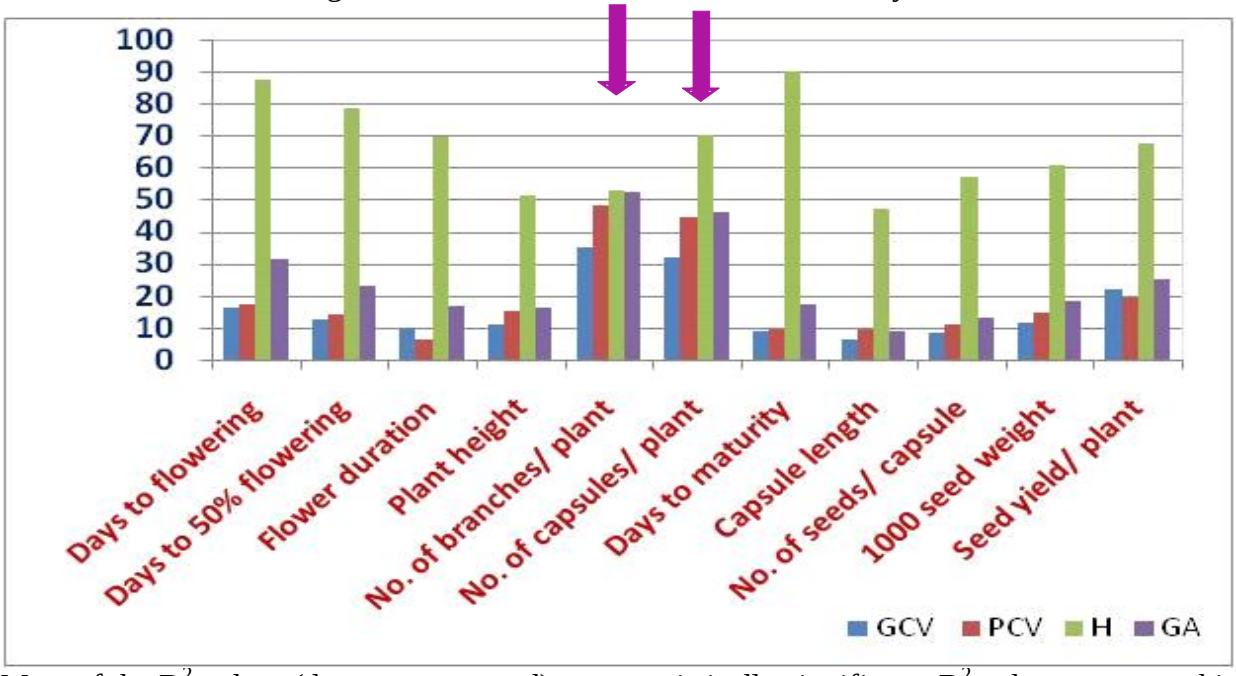
Genetic divergence among 30 genotypes was estimated using the Mahalanobis D^2 statistics. Character means were transformed into sets of uncorrelated variables using the pivotal condensation of common dispersion matrix according to Rao (1952). Although the D^2 statistics can handle a multidimensional situation, higher order interactions do not contribute very much in any experiment. In all the D^2 combinations, the characters were ranked 1 to 11 on the basis of their contribution to D^2. Grouping of genotypes into different clusters was done according to Tocher's method (Rao 1952). The data were subjected to principal component analysis (PCA). PCs with Eigen-values > 1.0 were selected. Correlations between the traits and the respective PCs were obtained.

Results and Discussion

Genetic diversity and characterization:

The analysis of variance revealed statistically significant differences among the 36 sesame genotypes for all 11 characters studied. GCV and heritability were high for no. of branches/plant and no. of capsules/plant which indicated the effectiveness of selection on these traits(fig 1). Such a high estimates of PCV, GCV and h^2 were mainly due to additive gene action (Panse, 1957).

Fig 1. Effect of GCV, PCV, GA, H% on seed yield



Most of the D^2 values (data not presented) were statistically significant. D^2 values represent high value. D^2 values exhibited a high range. It was possible to group the examined sesame genotypes

into seven different clusters (Fig 2). Cluster 1(15 genotypes) contained genotypes from Orissa, Rajasthan, West Bengal, Karnataka, and Gujarat. Cluster II (15 genotypes) contained accessions coming from Orissa Madhya Pradesh, Haryana, Rajasthan, Ethiopia, Tamil Nadu, West Bengal. Cluster III, IV, V, VI and VII consisted of only one genotype originating from Madhya Pradesh, Gujarat, Tamil Nadu, Ethiopia, respectively. Maximum inter-cluster distance (table 4) existed between cluster 6 and cluster 3. However, lower inter-cluster divergence was noticed between clusters 4 and 6 (5.09) and also clusters 2 and 7 (5.98). Clustering by Tocher method (Fig. 2) also revealed that the seven distinct clusters.

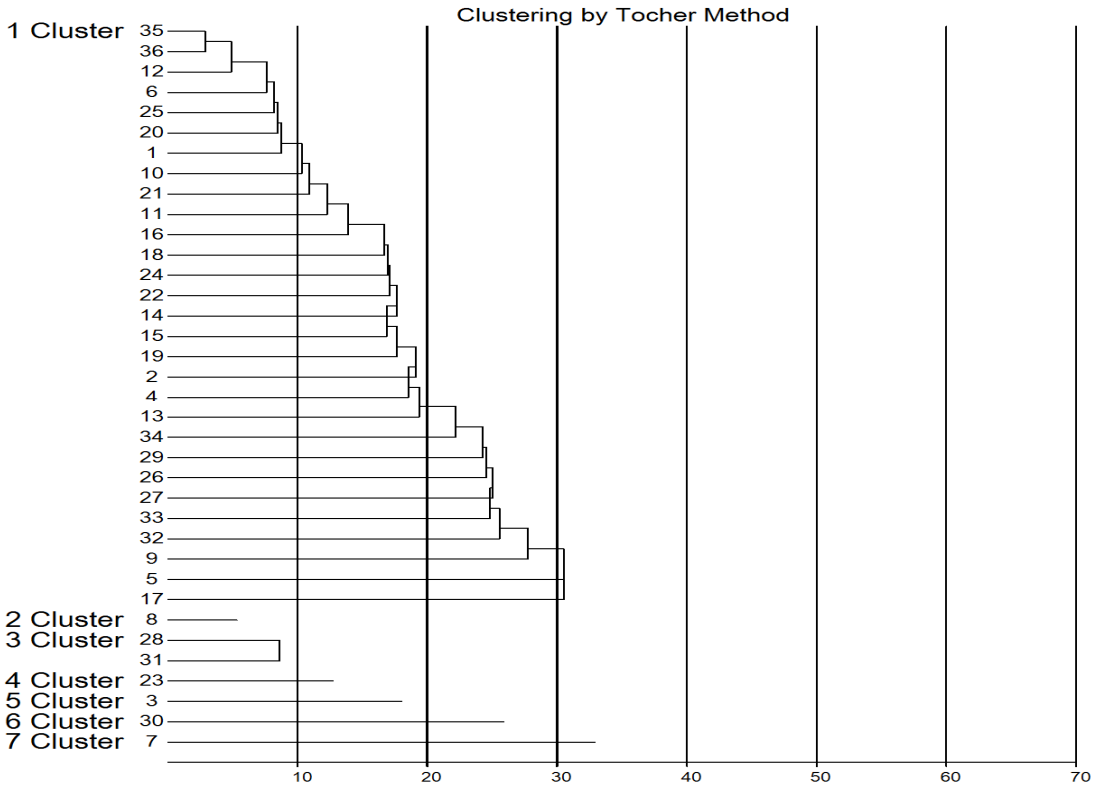
The clustering pattern of the varieties revealed that varieties from the same state did not form the single cluster. Furat et. al (2010) reported that the regional isolation was not the sole factor contributing to diversity in a natural population.

D^2 analysis and clustering patterns indicated no strict and narrow relationship between the observed genetic diversity and geographical differentiation. It shows that geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity.

To initiate a crossing programme it is desirable that the putative parents will be chosen for those clusters which will have high magnitude of genetic distance. Crossing between genotypes belonging to the same cluster could not be expected to yield desirable segregates. This approach is however based on the assumption that suitable parents for crossing may be showing greater amount of genetic divergence.

From the study presented here, it was observed that crossing between Humera and Utawadia (D^2 = 576.64), or between DSS and Utawadia (D^2 = 479.34), or between S. *malabaricum* and Utawadia (D^2 = 472.72) are most likely to express a considerable amount of heterosis in F_1 generation and to provide a wide spectrum of recombinants in segregating generations.

Fig 2. Clustering pattern by Tocher method of 36 sesame genotypes



Correlation and inter-relationships of the characters with seed yield in sesame were examined through the study of genotypic and phenotypic coefficient (table not presented). The character,

capsules/plant that was positively associated with seed yield also exhibited significant positive correlation coefficient with plant height, branches/ plant, and no. of seeds/ capsules.

A plant breeder is interested for selection with minimum number of traits in the field to accelerate the selection procedure. Under this situation; instead of selection for more capsules, branches/ plant, more seeds/ capsule and taller plant; only selection for more capsules/ plant would result in higher yield. Similarly selection for longer capsule would engender more 1000 seed weight along with higher seed yield, as capsule length was significantly and positively associated not only with seed yield/ plant but also with 1000 seed weight.

Principle component analysis showed (table not presented) association in PC1 with days to flowering, days to maturity, plant height, no. of branches/plant, PC2 with no. of capsules/plant, seed yield/plant, PC3 with no. of seeds/cap, 1000 seed wt .Thus, re-structuring plant type with more capsules/ plant and capsules length would obviously generate plants with high seed yield.

Conclusions and Outlook

The results showed that there was high genetic diversity with regard to morphologic and agronomic characters in the sesame collection. The diversity could mainly be attributed to diverse agro-climatic conditions in the different country. Accessions from different regions were sometimes closely related and accessions from the same region had different genetic background. The intraregional diversity could be as a valuable source as interregional diversity for sesame improvement. The germplasm represents a valuable source of genetic diversity that is expected to be highly useful for future breeding programs. The success in genetic improvement of the crop, however, depends on the availability of genetic resources and their diversity. Future study will be needed to determine the genetic diversity at molecular level.

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