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Multivariate analysis and the choice of parents for hybridization in Okra (*Abelmoschus esculentus* (L.) Moench)

O. J. Ariyo *

Department of Agronomy, University of Ibadan, Ibadan, Nigeria

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Summary. Thirty okra genotypes of diverse eco-geographical origin were grown in single-row plots in a randomised complete block design. The data collected on 14 characters were subjected to analysis of variance. By multivariate analysis (Mahalanobis D^2 technique), the genetic divergence among the genotypes were quantitatively measured. The genotypes were grouped into five clusters by this technique. There was no relationship between clustering pattern and eco-geographic distribution. The effects of genetic divergence on the choice of parental stock in hybridization was discussed.

Key words: Okra – Mahalanobis D^2 technique – Clusters – Parents – Hybridization

Introduction

Progress in breeding for economic characters often depends on the availability of a large germplasm representing a diverse genetic variation. In self-pollinated crops such as okra, germplasm is available in the form of a multitude of homozygous lines which can be released as improved cultivars in specific ecological areas. However, for a long-term improvement programme, a large and diverse germplasm collection is an invaluable source of supply of parental strains for hybridization and subsequent development of improved varieties. The limitations resulting from normal pollination concerning biparental heredity, makes a critical choice of parents in breeding programmes necessary, especially when polygenic characters are involved.

* Current address: Crop Production Department, Ogun State University, Ago-Iwoye, Nigeria

Various methods have been employed in the analysis of variation in many crop species. The value of multivariate analysis (Mahalanobis' D^2 statistic, Mahalanobis 1936) has been demonstrated in choosing parental stocks for hybridization (Malhotra and Singh 1971; Bhatt 1970; Katiyar and Singh 1979; Dasgupta and Das 1984). The D^2 statistic groups a set of potential parents on the basis of genetic divergence with the assumption that the best parents may be those showing the maximum genetic divergence (Bhatt 1970).

The objective of this paper is to group a set of potential parents on the basis of genetic divergence so that a crossing programme between genotypes of divergent groups will produce a desirable variation.

Materials and methods

The 30 genotypes of okra used in this study comprised 25 accessions collected from different ecogeographical areas of Nigeria, and one each from Ghana, Turkey, Zambia, Japan and Zaire. Following land preparation, they were grown in single-row plots to minimize environmental variations affecting accessions and to obtain a reliable measure of the existing genetic variability. Planting was done during the rainy season (April) of 1982 and each entry was replicated 3 times in a randomised complete block design. Each row was 3.15 m long with 90 cm between rows and plants were spaced 45 cm apart within the row to give eight plants in a row.

From five competitive plants in each row, data were collected on the following characters: pod yield per plant, number of branches per plant, number of leaves per plant, number of days to flowering, height at the commencement of flowering, number of pods per plant, edible pod length, edible pod width, duration of flowering, final plant height, lifespan, number of seeds per plant, weight of 100 seeds and length of matured pods.

An analysis of variance was carried out for each of the 14 characters. The genetic divergence among the genotypes was studied by means of Mahalanobis' D^2 technique. Uncor-

Table 1. Analysis of variance, mean, and range of plot means

Source of variation	D.F.	Mean square												
		Edible pod yield/ plant (g)	No. of days to flowering	Height at flowering (cm)	Length of edible pod (cm)	Width of edible pod (cm)	No. of branches/ plant	Final plant height (cm)	No. of seeds/ plant	Weight of 100 seeds (g)	Length of matured pod (cm)	No. of leaves/ plant	Lifespan (days)	Duration of flowering (days)	No. pods/ plant
Block	2	1,586.27	74.45	87.24	0.74	0.20	0.55	270.72	328.28	0.08	112.66	35.51	22.64	176.04	58.78
Genotype	29	7,381.41*	63.63**	315.5**	4.88**	0.41**	7.11	2,222.61**	774.42**	2.48**	104.13*	861.32**	248.66**	191.76**	96.96**
Mean		114.19	55.05	60.75	5.98	2.60	5.01	92.43	71.61	4.48	8.86	46.27	105.10	50.13	6.0
Range		31.42–241.34	46.67–65.45	19.59–107.44	4.08–11.12	1.88–3.35	3.22–8.89	51.22–142.56	28.75–95.83	2.62–6.24	4.98–16.17	17.33–85.5	87.58–118.33	34.39–63.31	2.00–11.4

* $P < 0.05$; ** $P < 0.01$

Table 2. Clustering pattern of 30 okra genotypes on the basis of genetic divergence

Cluster	Genotype	Origin
1	UI 45, UI 13, UI 211, UI 72, UI 58, UI 209, UI 38, UI 10, UI 208, UI 143, UI 86, UI 104, UI 21, UI 9	S.W. Nigeria
	NHAe 301, UI 117	S.E. Nigeria
	NHAe 47-4, NHAe 10,	N.W. Nigeria
	UI 313	Ghana
	UI 72-209	Turkey
	NHAe 626	Zambia
2	UI 72-11	Japan
3	UI 92	S.E. Nigeria
4	NHAe 81	S.W. Nigeria
	NHAe 251	S.E. Nigeria
5	UI 123	S.E. Nigeria
	NHAe 65, NHAe 101	S.W. Nigeria
	NHAe 398	N.W. Nigeria
	NHae 70	Zaire

related linear functions of the original values were obtained by transforming the original correlated unstandardised character means by the pivotal condensation method as outlined by Rao (1952). The differences between the variates for the set of characters taken together, were tested according to the procedure of Wilks (1932).

The genotypes were grouped into a number of clusters, D^2 being treated as the square of generalised distance, according to the method described by Tocher (Rao 1952).

The relative contribution of each character to the total D^2 value between each pair of genotypes was determined following the procedures outlined by Bhatt (1970).

Results and discussion

The analysis of variance for the 14 characters evaluated revealed significant differences among the genotypes (Table 1). Using 'V' statistic, the analysis of dispersion for the test of significance of differences in the mean values based on Wilks' criterion revealed highly significant differences between the genotypes for the aggregate of 14 characters ($X^2 = 826.6$: for 406 df).

By using D^2 values between the 435 possible combinations of the genotypes, the 30 genotypes were clustered into 5 groups. The clustering pattern and the geographical distribution of the genotypes are presented in Table 2. A large majority of genotypes from Nigeria were found in cluster 1, which, in addition, contained the largest number of genotypes. Clusters 2 and 3 contained one entry each from Japan and South East Nigeria, respectively. The assumption of this technique is that the best parental materials may be those showing the maximum genetic divergence (Bhatt

Table 3. Inter-Cluster D^2 and D values among five clusters of okra genotypes (D values are in parenthesis)

	2	3	4	5
1	8.99 (3.00)	6.53 (2.56)	6.98 (2.64)	7.35 (2.71)
2		10.77 (3.28)	12.23 (3.50)	12.19 (3.49)
3			4.28 (2.07)	5.97 (2.44)
4				5.9 (2.43)

1970). The clustering pattern of the okra genotypes did not indicate any relationship between genetic divergence and eco-geographical distribution. Cluster 1 contained the most geographically diverse genotypes by including those from Nigeria, Ghana, Turkey and Zambia. Cluster 5 also contained entries from Nigeria and Zaire. Duddley and Davies (1966), Bhatt (1970), Chedda and Fatokun (1982) and Dasgupta and Das (1984), working with cultivars of alfalfa, wheat, okra and black gram respectively also noted that cultivars clustered in different groups, irrespective of their countries of origin.

Inter-cluster divergence values (D^2) between the five clusters and their statistical distances are presented in Table 3. The highest genetic divergence occured between clusters 2 and 4 ($D^2 = 12.23$), followed closely by that between clusters 2 and 5 ($D^2 = 12.19$). The lowest divergence was between clusters 3 and 4 ($D^2 = 4.28$). It is expected therefore that any cross between UI 72–11 in cluster 2, and any genotype from either cluster 4 or 5 will produce transgressive variation within a segregation population. However, in selecting parental materials, important characteristics such as pest and disease resistance, quality of produce and stability of performance should be considered.

The analysis of D^2 values showed that edible pod yield per plant accounted for a significant portion (38.01%). Number of days to flowering contributed 19.82%, while height at the commencement of flowering, edible pod length, number of branches per plant and final plant height contributed 11.57%, 7.89%, 6.13%, 4.53% and 3.8%, respectively. The least contributions to the D^2 values came from the number of pods per plant, duration of flowering, lifespan and number of leaves per plant with 0.18%, 0.50%, 0.54% and 0.94%, respectively. The fact that edible pod yield per plant and number of days to flowering accounted for 57.83% of total divergence indicates that the two characters would be reliable in distinguishing among okra varieties.

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