

**GENETIC DIVERGENCE STUDIES IN
FOXTAIL MILLET (*Setaria italica* Beauv.)**

RIAZ AHMED SHREIFF, M.Sc. (Agri.)

**DEPARTMENT OF AGRICULTURAL BOTANY
UNIVERSITY OF AGRICULTURAL SCIENCES
BANGALORE**

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By
RIAZ AHMED SHERIFF, M.Sc(Agri.)

THESIS
SUBMITTED TO THE
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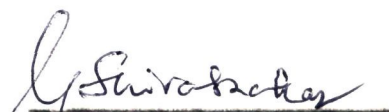
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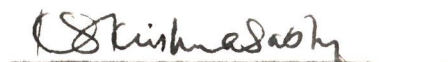
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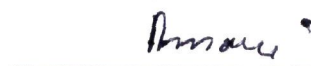
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INTRODUCTION

CHAPTER I

INTRODUCTION

The world's millet crop is grown largely in China, India, Russia and several African countries (Anderson, 1948). India and China contribute about 50 per cent of the world's crop (Leonard and Martin, 1963). The term minor millet refers to the group of small grained cereals viz., Foxtail millet (Setaria italica Beauv), Kodomillet (Paspalum scrobiculatum L.), little millet (Panicum milliare Lam.), proso or common millet (Panicum milliaecum L.) and Barnyard millet (Echinochloa frumentacea (Roxb) Link.). Minor millets besides serving as staple food for large section of economically poor people in general, have utility in animal feed industry, in antibiotic production and as forage to cattle (Gautam, 1977; Guruswamy Raja, 1977; Rachis, 1975). Minor millets are consumed like cooked rice, baked as bread, pudding, gruel and other delicacies (Rachis, 1975). Minor millets play a significant role in dryland agriculture as they are capable of producing fairly high yields in short duration. They have ability to thrive under scanty, erratic rainfall in poor soils, even at high temperate and hot climate. They are capable of growing at a higher altitudes of about 6000 feet and form an important food grain grown in the foot hills of Himalayas (Ayer, 1980). Minor millets are grown on an area of 4.74 million hectares with an annual

production of 2.12 million tons in India. The important States are Madhya Pradesh, Andhra Pradesh, Uttar Pradesh, Tamil Nadu and Karnataka. Karnataka ranks fifth with an area of 4.28 lakh hectares with a production of 1.58 lakh tonnes (Anon, 1974).

Fox tail or Italian millet (Setaria italica Beauv) is one of the world's oldest cultivated crops. The grain of Italian millet is prized as a food, considered as a holy food for religious ceremonies, festivals and is frequently prescribed in the diet of invalids and expectant women (Wright and Finch, 1962). In Karnataka, this is the second important minor millet with an area of 2.2 lakh hectares with a production of 0.5 lakh tonnes (Seetaram, 1982).

The collection and assessment of divergent germplasm in a uniform environment is an absolute pre-requisite in any crop improvement programme. The genetic architecture of a population is the result of prolonged selection by nature. The population from areas with heterogeneous environments could be expected to accumulate enormous genetic variability as compared to population occupying ecologically marginal habitats.' In foxtail millet, considerable diversity for maturity, plant height and yield component is prevalent (Viswanatha, 1977; Nagarajan and Prasad, 1980). Hybridization in this crop is relatively difficult as the

florets are very small for emasculation and pollination. Thus, the improvement^{Kal} has been brought about, is mostly through selection. The hereditary component of the available variability in the germplasm is a valuable attribute in view of its relevance to the selection programme. Selection of superior genotypes would be effective only in a population with high genetic variability. But the variability of any character is the result of interaction of heredity and environment. Yield being a complex character is collectively influenced by various component characters which are polygenically inherited and highly subjected to environmental variations. In selection for yield, more emphasis should be placed on the attributes that show less variability due to environment. Besides partitioning the variance into genotypic and phenotypic components, a study of correlations among yield and its components and their relative contribution to the yield is of great value in planning and evaluating breeding programmes. The usefulness of the naturally occurring diversity in genetic improvement of any crop plant can hardly be over-emphasized. Exploitation of genetic variability either through introduction or hybridization is a common approach in crop improvement. Since the natural variations cannot be everlasting and sooner there may not be response to selection, synthesised variability is the ultimate resort. The prime aim of the plant breeder

is to improve yield and quality by evolving superior varieties. The knowledge about the source of genetic diversity for the different character is thus of paramount importance. An investigation into the nature and degree of divergence is useful for an understanding of the course of evolution and for classifying the populations into groups on the basis of diversity particularly when they are overlapping for one or more characters. Such a study, utilising multivariate analysis has been successfully adopted in several biological populations like plankton, locusts and in crop plants (Blackith, 1957; Cassie, 1963; Murty et al., 1967). Besides its use in taxonomic problems, multivariate analysis also helps in choosing parents for specific breeding objectives, since now it is established that exploitation of heterosis and success in getting desirable segregates in breeding programme depends to greater extent on the degree of genetic divergence between the parents chosen (Harrington, 1940; Weinhaus, 1960; Murty and Pavate, 1962; Ram and Panwar, 1970; Bhatt, 1973; Ramanujam et al., 1974; Chaudhary and Singh, 1975; Joshi and Singh, 1979; Arunachalam et al., 1980). Therefore, an evaluation of the germplasm is of greater significance to examine the trends of genetic changes prevailing in the genotypes of diverse geographical origin.

The genetic studies in foxtail millet have been limited to a few selected material. The present study is envisaged by multivariate analysis to assess the magnitude of genetic diversity prevalent in the germplasm, to classify them under different groups based on the genetic distance and to identify the superior divergent parents to be considered in the hybridization programme.

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Setaria italica Beauv., commonly known as Foxtail millet or Italian millet is one of the world's oldest cultivated crops. In different States of India, it is known as (1) Kangni in Hindi, (2) Tennai in Tamil (3) Korralu in Telgu, (4) Rale in Marathi, (5) Ral, Kang in Gujarati and (6) Navane in Kannada. It belongs to the family Graminae, sub family panicealdae and tribe paniceae (Hitchcock, 1950). Hector (1936) presented the following Key to the principal types of foxtail millets (Setaria italica).

- A. Heads small, uniform, compact, seeds yellowish to black with usually a large percentage very dark; beards brown or purple. Hungarian Millet.
- AA. Heads large, more or less open; seeds more or less bunched.
- B. Heads long, slender, very open, lax drooping; seed groups very distinct. Aino millet.
- BB. Heads shorter and plumper, bushy, erect or slightly drooping; seed groups indistinct.
- C. Seeds yellow
- D. Profusely bearded; Medium large heads.

- E. Heads large, seeds small, seed groups more distinct,
German millet.
- EE. Heads small, seeds large, seed groups less distinct.
Common millet.
- DD. Sparingly bearded; head very large. Golden wonder millet.
- CC. Seeds red or pink. Siberian millet.

Classification of sub species

Scholz(1960) believed it was justified to split the S.italica group into convar. maxima and convar. moharia, the reason being that the maxima group has papillae on the epidermal cells of the glumes and the moharia group has no papillae. He cited S.viridis as the ancestral type of convar. maxima.

Gritsenko (1957; 1960) presented a general description of the sub species with diagnostic characters, their range of variation and key for identification of botanical varieties which are arranged in three groups: manchuria, Chinese - Korajensis and australe - mongolica.

The Manchurian (north eastern China) was characterized by a relative earliness, thin stems, short and delicate leaves,

chiefly short panicles, small and poorly hulled grain, average drought resistance and low grain productivity.

The Chinese-Korean group (north and central-east China and North Korea) included middle and late forms with high growth, rough stems, long and narrow leaves, low drought resistance and high yield of grain and fodder.

The South-Mongolian group (north west China and Manchuria-Mongolia) was very early, exhibited superior drought resistance, broad and rough leaves, low grass stand, rather poor leafage, mostly compact panicles, large grain with thick hulls, difficult threshing and good yielding.

Musil (1950) grouped seeds of foxtail millets into two general types : German millet including white wonder, and common millet and such varieties as Siberian, Hungarian, Kursk and Goldmine.

China is considered as the place of origin of foxtail millet (Vavilov, 1935) and the species seems to occur in wild form in Japan (Williams, 1898). In Russia, it was grown as early as 1,500 years ago (Mousisyants, 1950). Seeds of this species has been found in abundance in the remains of the lake dwellings of Switzerland (Williams, 1898).

There is evidence that *Setaria* was used as a plant food by early Mexican Indians at a number of sites (Callen, 1965). An analysis of the plant remains from a cave in New Mexico revealed fragments of *Setaria* sp. (Smith, 1965).

Portail millet is still a chief source of food in China, Korea, Japan, the East Indies and Trans-caucasia (Malm and Rachie, 1971). It was one of the five sacred plants of China in about 2,700 B.C. (Krishnaswamy, 1951).

The somatic chromosome number is $2n = 18$ (Kishimoto, 1941) and one pair of chromosome was observed to be larger (Krishnaswamy and Ayyangar, 1935).

The knowledge of the breeding systems and the inheritance of yield and associated characters are necessary in planning a successful breeding programme in any crop. *Setaria* being a self pollinated crop, much improvement in this crop is mainly through selection of superior types. Wide variation for most of the attributes are observed in this crop which contribute to the yield (Vishwanatha, 1977). The improvement in this crop can be resorted through hybridization and it is essential to identify the superior genotypes to be considered as parents of distant origin from different groups possessing greater diversity assessed through the technique of genetic distance. Very little

information is available on the quantitative inheritance of yield attributes through genetic distance in setaria. An attempt has been made to summarize relevant work on multivariate analysis adopted by several workers in Setaria, paddy, sorghum, finger millet, tobacco, sesame, cotton, maize etc.

2.2 Multivariate analysis in biological diversity

Multivariate analysis is extremely useful in giving more convincing evidence of phenetic relationships and is also said to have a capacity of detecting unsuspected relationships between populations (Sneath and Sokal, 1973).

The multivariate studies help in isolating the varieties that are distinctly related and in bringing together of closely related varieties. The distinction of strains will be made use of in selecting the parents for hybridization (Bhatt, 1973, Ramanujam et al., 1974). The multivariate analysis is also a powerful tool in finding out the relative contribution of individual characters to total divergence.

2.2.1. Genetic diversity and heterosis

The precise information about the extent of genetic divergence is crucial for a productive heterosis breeding programme. This information is frequently sought for

picking the well nicking heterotic crosses. The extent of heterosis has been related to genetic diversity of parents in a number of species (Hagberg, 1952; Sriwatanpongse and Wilek, 1968; Canje and Carlson, 1973). The choice of diverse parents with good general combining ability for components of yield has helped in substantial genetic advance in self as well as in cross pollinated crops such as green gram, wheat, rice, barley, maize, Nicotiana, alfalfa, linseed and pearl millet (Gupta and Singh, 1970; Bhatt, 1970; Ram and Panwar, 1970; Whitehouse, 1971; Griffing, 1956; Matsinger and Wensinger, 1967; Carnahan and Carlson, 1963; Anand and Murty, 1968 and Upadhyaya and Murty, 1971).

In wheat itself the pedigrees of fifty of the World's most successful varieties and some valuable German wheats (Weinhues, 1960) provide convincing illustrations of the value of genetic diversity.

Harrington (1940) concluded that the magnitude of heterosis in wheat depended on the degree of genetic divergence between parental stocks and consequently may be used as an indicator of the inherent yielding capacity of a cross.

The more diverse the parents, with an overall limits of fitness, the greater are the chances of obtaining higher amount of heterotic expression in F_1 's and broad spectrum of

variability in segregating generations (Harrington, 1940; Joshi and Dhawan, 1966; Murty, 1965; Anand and Murty, 1968).

The relationship between genetic diversity and consistency of performance in different environments by using three distinct levels of genetic diversity was described by Allard (1961). He concluded that genetic diversity and stability appeared more simply related, as genetic diversity consistently conferred populations with stability irrespective of number of characters of the components involved.

Timothy (1963) studied genetic diversity and heterosis and the use of exotic stocks of maize. His observation has revealed that with the exception of F_2 of Eto x long ear synthetic cross, all the yields equalled or exceeded that of local race and that certain varieties were excellent source with great deal of heterosis. He also observed considerable phenotypic divergence between Mexican, Brazilian and Andean maize collection but little genetic diversity between them as measured by the performance of crosses between them.

Moll et al. (1965) observed that the yields in maize tended to increase divergence of parents. Crosses of more distantly related parents showed greater heterosis than crosses of more closely related parents. ✓

Matzinger and Wensmen (1967) studied genetic diversity and heterosis in Nicotiana which resulted in the conclusive evidence that the phenomenon of maximum heterosis was associated with an optimal level of genetic diversity.

Singh and Bains (1968) reported that American varieties exhibited greater diversity and hence appeared desirable parents in improving ginning-out-turn in upland cotton.

Singh and Murty (1971) observed that the magnitude of heterosis in varietal crosses is strongly influenced by the degree of genetic relationship between parents in upland cotton.

Ramanujam et al. (1974) in Mungbean observed that divergence in the parents was associated with heterosis in F_1 s.

Srivastava and Arunachalam (1977) in Triticale, considered the range of divergence in order to realise a large number of fruitful heterotic crosses.

Singh and Ramanujam (1981) in Cicer arietinum L. observed that greater the differences between the parents then greater would be the differences between the hybrids.

2.2.2 Use of numerical methods in the assessment of genetic divergence

The earliest attempt to apply numerical method to measure resemblance or divergence between populations for a set of characters date back from the development of biometrics in 19th century. Heinke (1898) used a measure of phenetic distance to distinguish between races of the hering. Czekonowski (1909) employed a distance coefficient in physical anthropology.

In the present century, the foundation of modern biological theory was laid by Tshetverikov, Fisher, Wright and Haldane, who leaned heavily on numerical deductions from few fundamental postulates, especially those of Mendelian inheritance (Dobzhansky, 1970).

Pearson (1926) suggested the 'Coefficients of Racial likeness' (CRL) as a numerical measure of the system of differences between two races with limited number of individuals. Rao (1948) pointed out that in CRL, the characters were treated as independent, which were not true in biological populations. Moreover, the magnitude of CRL increased rapidly with the increase in number of characters.

Galton (1889) developed the concept of 'correlation and regression'. Hotelling (1936) derived T^2 as a method of

testing the significance of sets of means of regression coefficients and of differences of means. Fisher (1936) developed the concept of discriminant function for achieving the best discrimination between populations through certain linear functions. A review on the methods that are being employed in the present investigation is presented below.

2.2.3. Mahalanobis' D^2 - Statistics and Canonical analysis

For the purpose of discriminating any two populations having unknown origin, the anthropologists adopted Karl Pearson's coefficient of Racial likeness (CRL) (Morant, 1923). But Mahalanobis (1936) after identifying that CRL was a test of divergence between two samples rather than a measure of actual magnitude of divergence between them, developed D^2 -statistics which provides a measure of actual magnitude of divergence between the two groups under comparison. This technique in the form of generalised distance was first used by Mahalanobis et al. (1930, 1936) in an anthropometric survey of the United Provinces of India. The generalised distance was adopted for examining the cases of two sets of measurements of anthropological characters of individuals belonging to two classes of human beings, he introduced the notion of 'group distance'. He also pointed out that D^2 would remain reasonably constant when samples were drawn from two different populations irrespective of the size of

representative samples which indicated that D^2 supplied a measure of the actual magnitude of divergence between the two groups under comparison. Fisher (1938) also believed that for the discrimination between populations when the number of groups was more than two, then Mahalanobis's D^2 (1936) would be more useful. An exact distribution and moments for D^2 statistic was given by Bose (1936). Rao (1948) indicated that D^2 satisfied some mathematical and logical requirements such as (1) distance between two groups was not less than zero (2) sum of distances of a group from two other groups was not less than the distance between the two other groups similar to that of differential geometry; (3) the distance should not decrease when additional characters were considered (4) the increase in distance by the addition of some characters to a suitably chosen set, must be relatively small. Rao (1960) opined that the D^2 concept lies at the heart of morphometrics which has led to many useful developments and thus became an indispensable tool.

Mahalanobis et al. (1949) used D^2 statistic for the analysis of anthropological data of United Provinces and formulated three major clusters of Brahmins, Artisans and Tribal groups.

Mukherji (1951) examined the differences in physical development among different socio-economic status using D^2 -statistic, and found that economic status of families had

a significant bearing on the physique of family members.

Nair (1952) applied discriminant function and D^2 analysis to discriminate the sexes among the gregarious and solitary locusts. However, for a long time the application of D^2 statistics was limited to anthropometric and physiological studies (Majumdar and Rao, 1958) and ecological investigations (Hughes and Lindley, 1955).

Nair and Mukherji (1960) were the first to apply the D^2 statistics in biological populations. They applied this method in classifying the natural and plantation teak tree types, based on four important characters such as specific gravity, nodules structure, nodules of elasticity and maximum crushing stress.

Subsequently, its application was extended to plant breeding and Murty and Pavate (1962) felt that these techniques can be extended to the situations where overlapping species are to be discriminated and also to the discrimination at sub-species level. They used it for testing the genetic divergence among flue-cured tobacco varieties. They studied thirteen varieties considering four characters together and could classify them into four clusters. Since then, the technique of Mahalanobis' D^2 -statistics has been employed widely to resolve genetic divergence at

inter-varietal, sub-specific and species levels in several crops.

The application of D^2 -analysis for such problems of classification is almost invariably associated with the use of canonical variate analysis. In the canonical variate analysis the entries are plotted on two or three dimensional graph so that all the characters are expressed as a linear combination in each dimension, accounting the variability produced by these characters in a descending order of magnitude i.e., the first axis absorbs the greater variation than the second axis and third will absorb lesser than first two etc. Such a graphical representation helps in locating the genotype with its other closely related genotypes and also in isolating two groups which are distantly related. Thus its associated easy methodology in forming clusters has resulted in its use with D^2 -analysis. However, through canonical analysis we cannot easily derive the measure of divergence between the two groups, which is possible by the D^2 -analysis.

The canonical analysis was used by Mahalanobis et al. (1949) while analysing the Anthropometric survey and they observed a close agreement between D^2 -statistic analysis and canonical analysis with respect to the cluster formation.

Nair and Mukherji (1960) also used this technique in comparing the natural and plantation grown teak. Murty and

Pavate (1962) employed this technique along with D^2 analysis and observed a striking similarity between clusters formed through D^2 - analysis and congregates formed on the canonical variate graph.

The canonical analysis was subsequently used by several others in different crops.^{vi} In Nicotiana rustica (Murty et al., 1965), in sorghum (Arumachalam and Ram, 1967), in rice (Ram and Panwar, 1970), in groundnut and soybean (Shwe et al., 1972) in mungbean (Ramanujam et al., 1974) and in Chickpea (Narayan and Maccofield, 1976). A brief review in this aspect in different crops is given below.

In foxtail millet, Nagarajan and Prasad (1980) studied the genetic diversity using Mahalanobis' D^2 -statistic and grouped 50 genotypes into fifteen clusters. They observed that geographic distribution was not related to genetic diversity. Genotypes chosen from the same ecographic regions were found scattered in different clusters. This points to the availability of wide genetic variability in types from the same eco-graphic region. The rank total analysis disclosed that number of branches, grain yield, panicle length and grain per branch contributed maximum to the genetic divergence.

In finger millet, Hussaini et al. (1977) studied the genetic divergence among 640 entries of cultivated strains

using 'principle component analysis' and 'canonical variate analysis'. They observed that congregations were more clearly separated in canonical variate than in principle component analysis. The entries were grouped into 12 clusters.

In paddy, Ram and Panwar (1970) used the Mahalanobis' D^2 -statistic and canonical analysis to assess the nature of divergence and its relationship with the components of genetic variation in rice. The D^2 and canonical analysis were potent enough to distinctly discriminate the indica and Japonica races viz. the early, medium and late maturity groups. A brief scheme of the Indica x Japonica hybridization programme based on genetic divergence for the maximum exploitation of heterotic effect was also put forth.

Vairavan et al. (1973) studied the nature of genetic divergence in 190 strains of rice collected from Assam and North East Himalayas along with four standard cultivars. They employed canonical analysis so as to minimise the amount of labour and time required to group the 190 entries. By this preliminary grouping they obtained 42 groups which are finally clustered into 9 major clusters.

Das and Brothakur (1973) applied D^2 -statistic technique to study the genetic divergence in 26 photoperiod insensitive

varieties of rice. A very high degree of divergence was noticed in a number of cases. Tall varieties were distinctly separated from the semidwarf types. Flowering time, thousand grain weight and plant height were found to be important contributors to genetic divergence.

Maurya and Singh (1977) assessed the nature and magnitude of genetic divergence in 43 varieties of rice using D^2 statistic. The population was grouped into 16 clusters. Maturity time, plant height and tillers contributed most to divergence.

In wheat, Somayajulu et al. (1970) studied the genetic divergence among 67 strains of wheat using D^2 statistics. The material comprised of Indian and exotic origin selected to represent a wide range of the characters influencing yield and ecological diversity. The divergence was quantified for three different environments representing soil fertility. Their observations revealed that widely divergent groups remained distinct for all the environments. The genetic diversity was of low magnitude amongst the 49 strains of Indian origin, inspite of using widely diverse exotic germ plasm in evolving them. They also concluded that selection towards uniformity in various characters have a great depleting effect on genetic diversity.

Bhatt (1970) measured the genetic divergence on several characters in 40 populations of wheat. The genotypes were grouped into 12 gene constellations using D^2 -statistics.

Lee and Kaltsikes (1973) used Mahalanobis' generalised distance to measure genetic divergence in ten cultivars of Triticum turgidum L. durum wheat. The results revealed the association between genetic divergence and geographic origin. The analysis, however, succeeded in differentiating between these cultivars of tropical origin adopted to short day length and those of temperate origin requiring larger days. The influence of the characters studied assigning cultivars to particular groups varied from cultivar to cultivar.

Ziauddin Ahmed et al. (1980) measured the genetic divergence by Mahalanobis's D^2 technique in 40 strains of Triticales obtained from different parts of India. The strains were grouped into 9 different clusters. The clustering pattern did not follow the geographic origin. Test weight and spike length were the potent variables which could be used as parameters in selecting genetically diverse parents for hybridization programme.

Yadav and Murty (1981) subjected sixty four F_1 's and F_2 of wheat to D^2 analysis to measure the genetic diversity and components of genetic variation involving different height group parents and their F_2 populations. These were grouped

into 10 clusters. Considerable divergence was present both within and between height groups. Culm length and 100 grain weight were the major components of divergence at both intra and intercluster levels.

In sorghum, Arunachalam and Jawahar Ram (1967) studied the geographical diversity in relation to genetic divergence in eighty stocks in cultivated sorghum and ten characters were studied. The importance of flowering time in the differentiation of this genus was confirmed by the divergence in three different physiological groups of sorghum of early (75 days), medium (76-99 days) and late (100 days) in the cultivated varieties of sorghum. This was supported by canonical analysis also.

Murty et al. (1967) extended the D^2 analysis to a large world collection of sorghum comprising both cultivated and wild species. About 70 working taxonomic groups were recognised. Each of them were based on an amplification of 'Snowden' with sub-groups having varying degrees of the combinations of two or more major groups.

Chandrasekharaiah et al. (1969) made an attempt to classify populations belonging to 22 'Snowdenian species' of the section *Eu-sorghum* using D^2 analysis. Both the grain and fodder types were included in their study.

Using intra and intercluster D^2 , the population were formed into 15 clusters. The groupings obtained were also confirmed by the canonical analysis. On the basis of D^2 and canonical analysis, these two 22 'Snowdean species' of *Eusorghum* were divided into 9 major groups.

Govil and Murty (1973) studied genetic divergence and nature of heterosis in 24 varieties of grain sorghum representing different geographical areas and taxonomical groups following D^2 -statistic the varieties were grouped into eleven clusters. Grain size, protein content, lysine, endosperm texture and leucine accounted for most of the divergence between the varieties studied.

In Barley, Whitehouse (1971) has used multivariate method to predict the parents most likely to yield desirable hybrids in Barley.

Singh et al. (1980) in 26 varieties of barley assessed the genetic divergence for seven characters related to yield using D^2 -statistic. The population was grouped into 7 clusters. Cluster III, II and I were large consisting more than two thirds of the total population. The geographical diversity was not related to genetic diversity. 1000 grain weight, plant height and tillers per plant were mainly responsible for genetic divergence. Clusters with small

statistical distances were considered less than those with large distances. They considered that only genetically diverse lines with specific characters of interest and having high yield potential should be intercrossed.

Chaudhary and Singh (1975) studied the genetic divergence in Barley as measured by Mahalanobis' D^2 statistic. The 64 population consisting of 4 exotic and 4 indigenous barley varieties and their 56 F_1 hybrids, including reciprocals. The 64 varieties were grouped into ten clusters including one single variety cluster. The clustering pattern of the hybrids was somewhat influenced by their parents. An exotic strain E.B.1556 was uniquely divergent from the remaining varieties, also heterozygotes appeared to cause more divergence as compared to homozygotes.

In Pearl millet, Murty and Tiwari (1967) studied the effect of dwarfening on the genetic divergence and showed that presence of single gene like D_2 and D_4 can evolve the greater diversity.

Upadhya and Murty (1970) studied the pattern of grouping in pearl millet with respect to different environments (stress and non-stress and found that clustering pattern may change in different environments.

In Maize, Goodman (1968) used the Mahalanobis D^2 -statistics to measure morphological similarities among 15 races of maize. Based on the distances, a phenogram of corn from South-eastern south America was constructed. Essentially the same relative distances were obtained when only a single plant from each race was used per block. In all the cases, the distances obtained were relatively very similar to the distance obtained from the Mahalanobis' Generalised Distance(D^2) technique.

In cotton, Singh and Bains (1968) studied genetic divergence for ginning out turn and its components in upland cotton. Twenty six varieties of upland cotton from different countries viz. U.S.S.R., U.S.A., Pakistan and India were studied. The D^2 -statistic revealed highly significant differences between the varieties for the aggregate of the six characters. Seed surface area and lint index contributed maximum towards the total divergence. The varieties were grouped in five clusters. The clustering pattern did not follow the pattern of their geographical distribution. The intra-cluster divergence was parallel in almost all the groups and the American varieties exhibited greatest diversity in ginning outturn.

Singh and Gupta (1968) studied the genetic divergence in thirty two advanced generation strains derived from diverse upland crosses of cotton varieties in respect of eight

important quantitative characters. Among the yield components the boll weight contributed the maximum towards the total divergence. The clustering pattern of varieties was somewhat influenced by their parentage and the thirty three strains could be grouped in nine clusters.

Singh et al. (1971) used D^2 -statistics to study the nature of divergence among 25 varieties of upland cotton representing a wide collection of genetic stocks belonging to five different countries. The varieties could be grouped into six clusters on the basis of D^2 values. The investigation revealed that geographic diversity is not necessarily related to genetic diversity as found by the grouping pattern. The pattern of divergence at the inter-cluster level is slightly different from the intracluster level and the major forces for differentiation being yield and yield component characters.

Siddiqui and Swaminathan (1971) studied various races of Gossypium arboreum and hybrids among them for divergence using Mahalanobis' D^2 -Statistic. Based on the divergence data, the genetic relationship between races was inferred. It was concluded that the race Sudanese might have arisen directly or simultaneously from race acrifolium of G. herbaceum from which race indicum is believed to have emerged.

Siddiqui et al. (1976) used Mahalanobis' D^2 -statistics to study the performance of fourteen cotton hybrids in relation

to genetic divergence with ten parents. Plant height and sympodia number were two main components which contributed substantially by two of the main components of yield, namely sympodia number and bell number per plant. Further, whenever one of these components showed heterosis in F_1 , this invariably leads to heterosis for yield also. ✓

In green gram, Gupta and Singh(1970) studied the genetic divergence for yield and its component in thirty six strains of green gram using D^2 -statistics. Highly significant differences between the strains for the aggregate of the nine characters was observed. The result revealed that weight of fifty seeds and pod length together contributed 61.93 per cent of the divergence in the material. The thirty six strains were grouped into ten clusters. The clustering pattern indicated that the strains usually did not cluster according to their geographic distribution.

Malhotra et al.(1974) studied the magnitude of genetic diversity, using D^2 -analysis in sixty indigenous and exotic strains of green gram. Analysing seven quantitative characters, they could group all the 60 strains into fourteen clusters. They observed that days to flowering, seed size, and primary branches contributed maximum towards the genetic divergence. The clustering pattern indicated that the geographic diversity had no any association with genetic diversity.

Ramanujam et al. (1974) used D^2 -statistic to study thirty five populations of Mungbean which included ten parents and 25 F_1 's for testing the genetic divergence. These 35 populations could be grouped into 19 clusters with distances ranging from 20.5 (D^2) to 1231.96 (D^2). The ten parents included in the study were clustered into 8 separate groups, indicating a substantial genetic divergence among groups. Flowering time, maturity, seed density and 100 seed weight showed the higher contribution in discriminating the entries. The canonical analysis also proved the similar pattern of divergence among the entries and there was a close agreement between results of D^2 -analysis and canonical analysis. A study on the relation between heterosis and genetic divergence of parents showed that the divergence in the parents was associated with heterosis in F_1 s.

In cowpea, Mehindritta and Singh (1971) studied 40 promising lines using D^2 statistics to measure the genetic diversity in respect of grain yield and its components. The varieties were grouped into 8 clusters based on the D^2 -values. Seed size was found to be most important character contributing towards genetic divergence while the remaining traits made little contribution. It was also observed that wide genetic diversity was present in the material selected from the same geographic regions.

Jayaprakash et al. (1974) studied 60 strains of cowpea from twelve different countries and observed that these sixty strains could be grouped into twenty one clusters. Days to flower and days to maturity showed more differences indicating their substantial contribution in discriminating the groups. They also observed a wide genetic diversity in the material collected from same geographical region and the diversity was not related to geographical distribution.

Angadi et al. (1979) used Mahalanobis' D^2 -statistic to study the divergence in 50 types of cowpea. Types studied had no apparent parallelism between genetic and geographical divergence. Maximum divergence was contributed by 100 seed weight. Based on D^2 values they were grouped into fifteen clusters.

In Chickpea, Narayan and Macfield (1976) studied the adaptive responses and genetic divergences in a world germ plasma collection of 5477 lines evaluated for 8 characters related to fitness and yield at two locations. The D^2 analysis was helpful in grouping the collection into six clusters with substantial divergence between them. Despite the overall parallelism between genetic diversity and geographic distance stringent natural and human selection or geographical barriers preventing gene flow were found to have played a significant role in the genetic divergence. Plant height was reflected

as the most important character operating in the genetic divergence between geographical groups, followed by seed colour and flower colour. Significant negative correlations were found between 100 seed weight and number of seeds per pod and seed colour. Further, independent classification using canonical analysis confirmed the results obtained from the D^2 analysis.

Katiyar (1978) applied D^2 -statistic to 30 indigenous and exotic strains of Chickpea to study the genetic divergence for morphological and quality determinant of yield on the basis of relative magnitude of D^2 values, the varieties were grouped into seven clusters. Salimath (1980) in 80 collections of chickpea, studied the D^2 analysis. In all they were grouped into 23 groups. Desi cultivars distinctly formed a different group when compared to kabuli cultivars.

In Soybean, Shwe et al. (1972) subjected 16 varieties for 11 characters for measuring the divergence which could be grouped into 5 clusters. The clustering pattern did not follow their geographic origin. The groupings were confirmed by canonical analysis.

Verma et al. (1973) studied the nature of genetic divergence and its relation to adaptability in seventy eight varieties of soybean from different countries. The D^2 -analysis showed that these varieties formed eleven clusters which were

heterogenous with respect to place of origin of the varieties. This was attributed to frequent exchange of breeding materials and also to the pattern of introduction of soybean in the past to the United States and from there to other European and Asiatic countries. However, they observed a regular clustering pattern with respect to the early and late varieties. The canonical analysis applied for the same data showed that days to flowering followed by 100 grain weight, days to maturity and plant height contributed more towards discriminating the groups. The congregates formed on canonical graph supported the clusters formed through D^2 - analysis.

In Vicia faba, Cubero (1973) used D^2 analysis as a measure of genetic distance between 30 natural populations of Vicia faba. He was able to detect the existence of a nucleus from which different trends of evolution have arisen in the species.

In Field bean, Nayar (1980) subjected 81 genotypes of D^2 analysis for twenty characters. Sixteen clusters were formed based on D^2 values. There was close agreement between the canonical groupings and D^2 clusters. The discrimination was marked for days to flowering, days to maturity and seed protein.

In Horsegram, Ganeshaiah (1979) studied the magnitude of genetic diversity and the pattern of association among yield

and other characters in a collection of one hundred entries of horsegram by grouping them into 23 clusters and observed a perfect agreement between the canonical variate and D^2 analysis. The character that contributed for the diversity are mainly associated with plant maturity. No perfect association was evident between geographic and genetic diversity. Greater diversity was found to occur for the crop in India itself.

Ramakrishna et al. (1979) studied genetic divergence in eleven varieties of horsegram from diverse indigenous collections representing different geographic areas. They were grouped into 6 clusters. The D^2 -statistic is in conformity with the canonical analysis.

In groundnut, Shwe et al. (1972) studied the nature of divergence among 24 elite groundnut varieties consisting of bunch, spreading and semi-spreading types, using 17 characters. The 24 varieties were grouped into three clusters with 7, 13 and 4 varieties respectively. Based on the variation in the cluster means, the characters important for grouping were plant height, days to first flowering, days to peak flowering, growth habit, leaf colour and resistance to cercospora. The clustering pattern of the varieties did not follow their geographic origin. Canonical analysis confirmed the groupings done by Mahalanobis D^2 -statistics.

Sandhu and Sangha (1974) examined a collection of 27 bunch groundnut varieties for genetic divergence among them using Mahalanobis' D^2 -statistic. Number of pods was the only character which was found to be a potential force of divergence at the inter and intra-cluster levels of differentiation. The 27 varieties were clustered into seven groups. The divergence between the populations could not be related to their geographical origins.

Sigamani (1981) studied 144 genotypes of groundnut of diverse origins to classify and estimate the diversity existing using Mahalanobis' D^2 statistic and classified them in 16 clusters, with inter-cluster distance (D) ranging from 10.80 to 45.82. The characters days to maturity and days to flowering were important in differentiating the genotypes in all the studies.

In sesame, Trehan et al. (1974) studied the genetic divergence in 52 varieties of sesame adopting Mahalanobis' D^2 -statistic. They observed that plant height and days to flowering contributed to the divergence. They were grouped into 17 clusters based on D^2 values with a range of 114.85 - 3.59. It was observed that geographic diversity was not related to genetic diversity.

Anand and Murty (1968) studied the genetic divergence, as measured by D^2 -statistic in fifty five populations

in linseed consisting of ten parents and all possible F_1 hybrid combinations. There was considerable diversity amongst the parents which is not necessarily related to their geographical diversity. One of the parent M.10 was uniquely diverse from the rest of the types. The fifty five populations could be grouped into ten clusters. The analysis has revealed that the diversity amongst the parents is mostly reflected in the corresponding F_1 s also.

Jeswani et al. (1970) adopted the D^2 -statistic to analyse the genetic divergence of one hundred types of linseed representing different geographical regions. The varieties were grouped into seven clusters. It was observed that Indian group is distinctly different from rest of the seven groups. The diversity of Indian material from rest of the world collection confirms that Indian linseed is of polyphyletic origin which thought to have been introduced in India by Aryans from Central Asia, Egypt and Abyssinian sources. An examination of the combination of individual characters to the divergence between pairs of varieties showed that the number of primary branches has contributed the maximum to divergence followed by the level at which fruiting branches start within European and Russian groups. The level of first fruiting branches made the maximum contribution. These two are also potent for differentiation of oil seeds from the flax types.

In Brassica, Murty et al. (1965) studied for two years the divergence in forty self compatible forms of Brassica campestris var. Brown sarson. They observed considerable variability among the self compatible types for all the characters except the number of primary branches. On the basis of D^2 -analysis the forty varieties were grouped into nine clusters. The divergence between the populations could not be related to their geographical distribution.

Dubey (1976) utilised Mahalanobis' D^2 -statistic to study the genetic divergence in 70 genotypes of Indian Rai from different states. Based on D^2 -value the genotypes were grouped into 16 clusters. The divergence was not related with geographical diversity. The flowering time at inter-cluster level and yield itself followed by height at intra-cluster level were important factors for differentiation. The genetically distant genotypes could be effectively used in hybridization programme.

In Castor, Singh and Srivastava (1978) studied the divergence in 17 castor varieties belonging to India and other countries. The varieties were grouped into 7 clusters based on the relative D^2 values. The clustering pattern revealed that geographic diversity was largely related to genetic diversity. The findings have brought out two important facts. First, the indigenous 'Tarai' was genetically more divergent not only from the other exotic stock

but also from the other indigenous stocks. Secondly, there was no parallelism between genetic diversity and geographic diversity as collections under cluster 1 and cluster 3 were possessing the genotypes of heterogeneous geographic origin. Number of effective branches, length of the main raceme, days to flower, number of capsules per plant and yield in secondary axis were the characters attributed for genetic diversity.

In Safflower, Ranga Rao et al. (1980) involving 30 genotypes representing broad spectrum of variability available in the traditional areas of its cultivation in India and 10 introductions from U.S.A. subjected to multivariate analysis for assessing the nature and degree of intra-specific divergence in two diverse environments. Based on 14 characters by using D^2 - technique, the entire collections formed 14 clusters in stress and 13 in non-stress environments. The indigenous collections showed relatively greater homogeneity and formed closely related groups. The different constellation did not follow any consistent pattern in relation to geographic diversity. The composition of clusters and their mutual association in general, remained more or less stable in both stress and non-stress conditions. Various characters such as height of branching from ground level, size and number of capitula, seed number and weight, yield per plant and hull per cent exerted marked influence on genetic diversity both at inter and intra-cluster levels. The relative

importance of these characters for genetic divergence, however, varied depending on growth conditions. The degree of spineness showed negligible role in influencing intra-specific divergence in crop.

In Tobacco, Murty et al. (1965) analysed the sub-specific genetic divergence as measured by D^2 -statistic, in fifteen varieties of Nicotiana rustica. The study revealed the use of leaf size and proportion of panicle height as classification criteria. The canonical analysis confirmed the grouping done by D^2 -statistic. They concluded that the classification by Howard and Howard (1910) could be revised by assigning appropriate roles to leaf size and relative proportion of panicle to height.

Narasimhayya and Venkat Rao (1974) adopted D^2 -statistics to study the genetic divergence in 20 varieties of cigarette tobacco. The varieties were separated into 4 groups on the basis of 4 morphological characters (plant height, curable leaf number, leaf length and leaf width) and 2 yield characters (cured leaf yield and total bright-leaf equivalent). The variation did not follow the definite pattern of distribution in a particular group on the basis of the country of origin.

Earlier workers relied on geographic or ecological diversity as an index of genetic diversity (Vavilov, 1926;

Wienhues, 1960; Singh, 1979; Joshi and Dhawan, 1966). But geographic diversity need not be related to genetic diversity as is evident from the studies in different crops (Timothy, 1963 in maize; Arunachalam and Ram, 1967 in sorghum, Gupta and Singh, 1970 in green gram; Bhatt, 1970, 1973 in wheat; Sangha, 1971, 1973 in groundnut, Verma et al., 1973 in soybean; Jayaprakash et al., 1974 and Angadi et al., 1979 in cowpea; Siddiqui et al., 1976 in cotton, Chandra, 1977 in linseed).

Besides, the importance of the D^2 -analysis in taxonomic problems in biological populations at intervarietal, sub-specific and species levels, D^2 -statistic is also important in the selection of the parents for hybridization programme.

The germ plasm in a self pollinated crop can be considered as a heterogenous set of groups, each group being homozygous within itself. Selecting the parents for a breeding programme in such crop is critical event because the success of the programme particularly when the aim is to improve the complex quantitative characters like yield, depends upon the segregants of the cross. With the exception of those crosses specifically designed to incorporate particular characteristics (agronomic, pathological or morphological), generally maximum improvement can be obtained from crosses which releases the maximum amount of variation.

To aid the plant breeder in the process of selection, different methods have been evolved to identify the parents, that nick better (Allard, 1960). The following are the three types by which such selection can be made (Bhatt, 1970).

1. Testing of the hybrid performance.
2. Methods tend to identify crosses which give rise to superior transgressive segregates
3. Methods to study the performance of homozygous lines from which the parents are to be selected.

In the first method the parents are selected using the technique like (a) combining ability (b) Diallel analysis etc. (Whitehouse et al., 1958). But these methods have been criticised for (a) it puts a limit on the number of lines that could be tested at a time and (b) F_1 and F_2 performance on which the method concludes are not necessarily the true indicator and for the performance of the segregants in the later generations.

The second method is also criticised because, it involves the study of F_4 and further generations, which when number of entries increase could be difficult to employ.

The third method involves the assessment of genetic diversity (Murty and Arunachalam, 1966), and analysis for

yield and yield components. The use of methods involving diversity analysis through multivariate technique has been favoured recently (Bhatt, 1973). These methods involve less labour and less time.

The usefulness of the naturally occurring diversity in genetic improvement of any crop plant can hardly be over-emphasized. Exploitation of genetic variability either through introduction or hybridization is a common approach in crop improvement. Knowledge about the source of genetic diversity for the different character is thus of paramount importance. The multivariate analysis helps in isolating the varieties that are distinctly related and in bringing together the closely related varieties. The more diverse the parents, within overall limits of fitness, the better are the chances of obtaining higher amount of heterotic expression in F_1 's and a broad spectrum of variability in segregating generations (Harrington, 1940; Murty et al., 1962; Joshi and Dhawan, 1966; Murty, 1965; Anand and Murty, 1968).

Thus, inspite of the recognition by breeders of the crucial importance of genetic diversity among the breeding populations in self pollinated crops, the difficulty was one of obtaining defendable estimate of such diversity without actually making the crosses. In recent works, Mahalanobis' D^2 -statistic has been found to be a powerful tool for estimating

the genetic divergence and for selecting diverse parents for hybridization (Harrington (1940); Weinhuess (1960), Singh and Gupta (1968), Pathak and Bindlish (1976) ^{in wheat} and Siddiqui et al. (1976) in cotton; Moch zuki (1968) in maize, Endang et al. (1971) and Ram and Panwar (1970) in rice, Jeswani et al. (1970) and Chandra (1977) in linseed, Gupta and Singh (1970) in green gram, Ramanujam et al. (1974) in mungbean, Shwe et al. (1972) and Arumachalam et al. (1980) in groundnut; Bhat (1973) Joshi and Singh (1979) in wheat, Lal and Srivastava (1978) in Brinjal; Singh and Singh (1977) in ohilli, Peter and Rai (1977) and Khanna and Misra (1976) in Tomato; Mehindri-tta et al. (1971); Govil and Murthy (1973) and Rena and Murty (1971) in Sorghum; Murty and Pavate (1982) and Lakehminarayan et al. (1970) in Tobacco; Trehan et al. (1974) in sesame; Murty et al. (1965) and Murty and Quadri (1966) in brassica; Narsinghani et al. (1978) in pea).

Bhatt (1973) conducted a study with the objective of rationalising the method of choosing parents for hybridization in a wheat breeding programme aimed at yield improvement. The various systems of selecting parents included:

- a) conventional method
- b) random method
- c) multivariate analysis method using Mahalanobis' D^2 - statistic and
- d) according to geographic diversity.

The relative merits of these systems was measured by:

- i) F_2 hybrid bulk yield.
- ii) Means and Variances of yield of F_5 -lines and
- iii) the number of useful transgressive segregates for yield detected in F_5 .

He observed that the application of multivariate analysis using Mahalanobis' D^2 -statistic method of selecting parents representing high inter-genotypic divergence appeared to be more efficient than the method of selecting parents according to ecogeographic diversity. The conventional and random methods were found relatively less efficient.

MATERIALS AND METHODS

CHAPTER III

MATERIAL AND METHODS

3.1.1. Experimental material

The material used for the present investigations comprised of 225 genotypes of foxtail millet, randomly chosen from the germplasm maintained at Millets Germplasm mobilization scheme, University of Agricultural Sciences, Bangalore-560065. The material comprised of diverse sources representing collections from Africa, China, Ethiopia, Kenya, Turkey and U.S.A. besides the collections from several States of India. The list of these genotypes and their sources is presented in Appendix I.

3.2. Methods

3.2.1. Layout of the experiment

The experiment was laid out in the Experimental fields of the department of Agricultural Botany, U.A.S. Hebbal, Bangalore-560024, during the summer of 1978.

The 225 genotypes were planted in a 15 x 15 simple lattice design with two replications, following the procedure given by Cochran and Cox (1957). Each genotype was sown in two rows of 1.5 m length and 22 cm between the rows with a spacing of 10 cm between the plants in a row. There were 30 plants per replication out of which 5 plants were chosen

at random avoiding the border plants for recording observations. Fertilizer application and other cultural practices were carried out as per the recommendations in the Package of Practices (Anon., 1978) of the University of Agricultural Sciences, Bangalore.

3.2.2. Recording the observations

The following observations were recorded on all the five randomly chosen plants of each genotype, in each replication. The pre and post harvest studies of various characters were recorded on these random plants. The average values were computed for analysis.

3.2.3. Character studied and symbols adopted

<u>Character</u>	<u>Symbol</u>
1. Grain yield/plant (g)	X ₁
2. Plant height (cm)	X ₂
3. Days to 50% of the plants to bloom	X ₃
4. Days to maturity	X ₄
5. No.of productive tillers	X ₅
6. Panicle length (cm)	X ₆
7. Panicle breadth(cm)	X ₇
8. Panicle weight (g)	X ₈
9. Number of seeds	X ₉

10. Straw weight (g)	X ₁₀
11. Harvest Index(%)	X ₁₁
12. 1000 seed weight (g)	X ₁₂
13. Leaf angle	X ₁₃
14. Internodal length(cm)	X ₁₄
15. Panicle exertion (cm)	X ₁₅
16. Peduncle length(cm)	X ₁₆

Grain yield per plant (g)

The grain weight of each of the selected plants was recorded for each of the genotype.

Plant height(cm)

The height of the main tiller from the ground level to the tip of the panicle excluding the bristles in the bristled genotypes was measured.

Days to 50% of the plants to bloom

The number of days taken from the date of sowing to the day on which anthesis occurred in 50 per cent of the plants in the main panicle and recorded as the days to 50 per cent of the plants to bloom.

Days to maturity

The number of days taken from the date of sowing to the

day on which the panicles of the plants turn yellowish prior to drying up which coincided with the free separation of seeds from panicles. The duration for this from the date of sowing was computed for analysis as days to maturity.

Number of productive tillers per plant

The number of productive tillers was recorded at the time of harvest. The number of tillers bearing the earheads were counted for each of the selected plants and then averaged per plant.

Panicle length (cm)

The length of all the panicles in the selected random plants was measured from the base of the panicle to the tip excluding the bristles in bristled genotypes and the average was computed.

Panicle breadth(cm)

The breadth of all the panicles in the selected random plants was measured in the middle region using slide calipers and the average was computed.

Panicle weight (g)

The total weight of all panicles of each of the five selected plants was recorded and the average panicle weight per plant was computed.

Number of seeds

The number of seeds was counted in the central 2 cm portion of the main earhead of the selected plants. The average number of seeds thus counted was computed as an index of density of seeds in the earhead.

Straw weight (g)

The harvest index was recorded as the ratio of grain weight to the total dry weight constituted by straw weight and panicle weight per plant. It is expressed in percentage.

1000 grain weight (g)

1000 grains of each of the genotypes of the selected plants was counted and the average weight was recorded.

Leaf angle

The leaf angle on the third leaf from the top at 30 days was measured using protractor.

Internodal length (cm)

The length of all the internodes of the random plants was measured and the average was computed as the internodal length per plant.

panicle insertion (cm)
of the panicle ^{the total length between the leaf leaf collar to the base} was measured to indicate the extent of panicle insertion
peduncle length (cm)

The length between the top most internode to the base

of the panicle was measured as the peduncle length.

In addition to the above the observations on other characters like pigmentation, panicle orientation, fertility of the panicle tip, bristle length, leaf length and breadth, number of nodes and seed colour was also recorded but not analysed statistically.

3.2.4. Statistical analysis:

The statistical analysis of the data on individual character was done on the mean values of five plants over two replications. The statistical method followed are given below:

Multivariate Analysis of Variance (MANOVA):

A simultaneous test of significance was conducted for all the 16 characters taken together. The data on the means of the individual plant character was subjected for computing the variance and covariance as per the table given below.

Source of variation	Mean sum of squares(X)	Mean sum of squares (Y)	Mean sum of products (XY)
Treatment	$(M.SS.X)^{n \times m}$	$(M.SS.Y)^{n \times m}$	$M.S.P(XY)^{n \times n}$
Error	$(M.SS.X)^{n \times n}$	$(M.SS.Y)^{n \times n}$	$E.S.P(XY)^{n \times n}$

Wilk's lambda criterion

After testing for the differences between populations for each of the 16 characters, a simultaneous test of significance of differences in the mean values of a number of correlated variables with regard to pooled effect was carried out, using Wilk's lambda criterion (λ) (Wilks, 1932). For this purpose, sums of squares and sums of products of the experimental error were used. The Wilks' λ (lambda) test criterion was used for testing the significance of the genotypes. The Wilks' lambda criterion was estimated using the following relationship.

$$\lambda = \frac{|E|}{|T|} \text{ where,}$$

$$|E| = \begin{array}{l} \text{determinant of the error dispersion} \\ \text{(error sum of squares and sum of product)} \\ \text{matrix.} \end{array}$$

$$|T| = \begin{array}{l} E + B = \text{determinant of the error dispersion} \\ \text{matrix plus treatment dispersion (population} \\ \text{sum of squares and sum of product) matrix.} \end{array}$$

The significance of λ was tested by
V - Stat (X^2).

$$\text{where V-Stat} = -m \ln \lambda$$

$$= -m \log_e \lambda$$

$$m = t - \frac{1}{2} (p + q + 1)$$

$$t = \begin{array}{l} \text{Total degrees of freedom} \\ \text{(degrees of freedom for error plus varieties)} \end{array}$$

$$p = \text{number of characters}$$

$$q = \text{number of treatments or genotypes}$$

V - Stat was compared with table X^2 values at pq degrees of freedom (Rao, 1952). Thus MANOVA was done for the 225 entries.

Analysis of Variance

After the MANOVA test showed significance, the analysis of variance for each character was performed separately for the 225 genotypes as per analysis of lattice design (Cochran and Cox, 1957). While constructing the ANOVA, the error variations due to intrablock and interblock were pooled and treated as in randomised block design. Whenever the error variation due to interblock was more than intra-block variation, the treatment means were adjusted for block effect. The adjusted treatment means were computed by applying the correction factor to the uncorrected treatment total as suggested by Cochran and Cox (1957), the adjusted treatment means were tested for significance according to the standard procedure.

If the 'F' test was significant then the significance of difference between any two varietal means was tested by the standard method of using the critical difference.

Mahalanobis's D^2 analysis

A measure for group distance based on multiple characters was given by Mahalanobis (1928). The square of the Mahalanobis Generalised Distance (D^2) between any two populations is given by the formula:

$$\Delta^2 = \sum_i \sum_j \lambda^{ij} d_i d_j$$

where Δ^2 = square of generalised distance

λ^{ij} = $(ij)^{\text{th}}$ element in the inverse of the common covariance matrix.

$$d_i = (\mu_{i1} - \mu_{i2})$$

$$d_j = (\mu_{j1} - \mu_{j2})$$

μ_{ij} = the mean values for i^{th} character in the j^{th} population ($i = 1, 2 \dots p, j = 1, 2$)

The formula for the estimation of distance D for a sample is given by:

$$D^2_p = d' S^{-1} d$$

Where D^2_p = estimate of square of the distance considering p variables

d = vector of observed differences of the mean values of all the characters = $(\bar{X}_{11} - \bar{X}_{12})$

S^{-1} = Inverse of variance co-variance matrix.

Since inverting the matrix is complicated especially when the number of variables under study is large, the original correlated variables (x_i) were transformed to non-correlated variables (Y_i); so that the computation of D^2 values reduce to simple summation of the squares of the differences between

values of transformed variables the two populations i.e.

The transformation was effected by Dwyer's square root method (Majumdar and Rao, 1958) as follows:

Let $X_1, X_2, \dots, X_p$ to be correlated unstandardised values, and $Y_1, Y_2, \dots, Y_p$ to be the uncorrelated standardised variables.

$A = a_{ij}$, be the dispersion matrix of $X_1, X_2, \dots, X_p$ and

$B = b_{ij}$ be the matrix obtained from A.

Then the relationship between matrices A and B after reduction of matrix A would be that the triangular matrix (b_{ij}) is the square root of (a_{ij}) . Then the transformed would be:

$$\begin{bmatrix} X_1 \\ X_2 \\ \vdots \\ X_p \end{bmatrix} \begin{bmatrix} b_{11} & & & \\ & b_{22} & & \\ & & \ddots & \\ & & & b_{pp} \end{bmatrix} \begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_p \end{bmatrix}$$

and hence $Y_1, Y_2, \dots, Y_p$ could be successfully calculated from the formula

$$Y_1 = (1/b_{11}) x_1$$

$$Y_2 = (1/b_{22}) x_2 - (b_{21}/b_{22}) Y_1$$

$$\begin{matrix} \vdots \\ \vdots \\ \vdots \end{matrix} \quad \begin{matrix} \vdots \\ \vdots \\ \vdots \end{matrix} \quad \begin{matrix} \vdots \\ \vdots \\ \vdots \end{matrix} \quad \begin{matrix} \vdots \\ \vdots \\ \vdots \end{matrix}$$

$$Y_p = \left(\frac{1}{b_{pp}} \right) X_p \left(b_{pp} - \frac{1}{b_{pp}} \right) Y_{p-1} - \left(b_{pp} - \frac{2}{b_{pp}} \right) Y_{p-2} \\ - \left(b_{pp} - \frac{3}{b_{pp}} \right) Y_{p-3} - \left(b_{pp} - \frac{4}{b_{pp}} \right) Y_{p-4} \dots \\ - \left(\frac{a_{p1}}{b_{pp}} \right) Y_1$$

The coefficients b_{ij} and b_{ij} were calculated as:

$$b_{11} = \frac{1}{a_{11}}$$

$$b_{21} = (a_{21}/b_{11})$$

$$b_{31} = (a_{31}/b_{11})$$

$$\dots$$

$$b_{10,1} = (a_{10,1}/b_{11})$$

$$b_{20,1} = (a_{20,1}/b_{11})$$

$$b_{22} = (a_{22} - b_{21})^{\frac{1}{2}}$$

$$b_{32} = (a_{32} - b_{31} b_{21}) / b_{22}$$

$$\dots$$

$$b_{20,2} = (a_{20,2} - b_{20,1} b_{21}) / b_{22}$$

$$b_{33} = (a_{33} - b_{31}^2 - b_{32}^2)^{\frac{1}{2}}$$

$$b_{43} = (a_{43} - b_{41} b_{31} - b_{42} b_{32}) / b_{33}$$

$$\dots$$

$$b_{10,10} = (a_{10,10} - b_{10,1}^2 - b_{10,2}^2 - b_{10,3}^2 - b_{10,4}^2 \\ - b_{10,5}^2 - b_{10,6}^2 - b_{10,7}^2 - b_{10,8}^2 - b_{10,9}^2)^{\frac{1}{2}}$$

$$\dots$$

$$b_{20,20} = (a_{20,20} - b_{20,1}^2 - b_{20,2}^2 - b_{20,3}^2 - b_{20,4}^2 - b_{20,5}^2 - b_{20,6}^2 - b_{20,7}^2 - b_{20,8}^2 - b_{20,9}^2)^{\frac{1}{2}}$$

Thus the transformation would be of the form:

$$X_1 = b_{11} Y_1$$

$$X_2 = b_{21} Y_1 + b_{22} Y_2 \text{ etc.}$$

Therefore, the transformed uncorrelated variables with unit variance would be:

$$Y_1 = \frac{X_1}{b_{11}}$$

$$Y_2 = \frac{X_2 - b_{21} Y_1}{b_{22}}$$

$$Y_3 = \frac{X_3 - (b_{31} Y_1 + b_{32} Y_2)}{b_{33}}$$

$$Y_4 = \frac{X_4 - (b_{41} Y_1 + b_{42} Y_2 + b_{43} Y_3)}{b_{44}}$$

$$Y_5 = \frac{X_5 - (b_{51} Y_1 + b_{52} Y_2 + b_{53} Y_3 + b_{54} Y_4)}{b_{55}}$$

.....

$$Y_{20} = \frac{X_{20} - (b_{20,1} Y_1 + b_{20,2} Y_2 + b_{20,3} Y_3 + \dots + b_{20,19} Y_{19})}{b_{20,20}}$$

From the newly transformed uncorrelated variables, the square of the distance was computed using the formula

$$D^2 = \sum (\bar{Y}_{11} - \bar{Y}_{12})^2$$

where $\bar{Y}_{1j}$ = vector of transformed mean values.

The square root of the D^2 values gives the general distance between the two populations (Rao, 1952). The D^2 values were arranged in a matrix form. The significance of the D^2 values between any two populations was tested using the formula:

$$F = \frac{(n_1 + n_2 - P - 1)}{(n_1 + n_2 - 2)P} \times \frac{(n_1 n_2) D^2}{(n_1 + n_2)}$$

This computed 'F' was compared with the Table 'F' value at 5 per cent and 1 per cent levels of significance with P and $(n_1 + n_2 - p - 1)$ degrees of freedom.

Clustering of the D^2 values

All the $\frac{n(n-1)}{2}$ i.e. 25,200 values were clustered as per Rao (1952). The criterion used in clustering by this method is that any two varieties belonging to the same cluster should at least on the average show a smaller D^2 value than those belonging to different clusters. The device suggested by

Tocher (Rao, 1952) was to start with two closely associated populations and find a third population which had the smallest average D^2 from the first two. Similarly the fourth was chosen to have a smallest average D^2 from the first three and so on. The permissible increase in D^2 values for clustering in to the same group was fixed approximately near to the maximum D^2 value shown by a population to the nearest population. If at any stage increase in average D^2 value because of the addition of a new genotype exceeded the average of those already included, then that genotype was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those that are already included in the former cluster and grouping them to different clusters, followed by calculation of intra and inter cluster distances

Population added to a cluster	D^2	No. of terms (n)	$\frac{\text{Increase in } D^2}{\text{Increase in } n}$	Average D^2 i.e. D^2/n	Cluster
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Intra-cluster distances

The average intra-cluster distances were computed following the method of Singh and Chaudhary (1977).

$$\text{Square of intra-cluster distance} = \sum_i D_i^2 / n,$$

Where, $\sum_i D_i^2$ is the sum of distance between all possible combinations (n) of the entries included in a cluster.

Inter-cluster distances

The average intercluster distances were calculated by the method outlined by Singh and Chaudhary (1977).

$$\text{Square of inter-cluster distance} = \frac{\sum_i D_i^2}{n_i n_j}$$

Where $\sum_i D_i^2$ is the sum of distances between all possible combinations ($n_i n_j$) of the entries included in the two clusters under study (i and j) and

n_i = number of entries in cluster i

n_j = number of entries in cluster j.

Normalised Mean values

For each character, the mean values for all clusters is adopted as the base or origin and is subtracted from the mean value of the same character for each cluster. This differences is then divided by the pooled estimates of standard deviation of the mean. These normalised deviations of the mean values for all characters of two distantly related groups are plotted in a chart.

The significance of these normalised mean values is that the original inequalities in magnitude between the various clusters measurements have been eliminated and therefore, comparable in size (the cluster mean being reduced to the same scale).

Canonical variate analysis

Besides the clustering by Mahalanobis' D^2 statistics, the preliminary grouping was done by Canonical variate analysis. In this method vectors or canonical roots are calculated to represent the varieties in graphical form (Rao, 1952). The analysis was followed to represent the number of uncorrelated variables by lesser number of canonical variates. These are obtained as a linear combinations of a number of uncorrelated variables. The coefficients $(\lambda_1, \lambda_2, \lambda_3, \dots, \lambda_p)$ are obtained by solving the equation

$$|A - \lambda I| = 0$$

Where I = Identity matrix

= eigen values of matrix 'A'.

The method follows the construction of a matrix of sums of squares and sums of product for the transformed mean values. The suitable power of the original matrix was obtained, and canonical vectors were obtained by iteration, starting from a trial vector (1, 1, 1.....1).

The canonical roots were also obtained by subtracting the product of (λ_I) (i^{th} element $\times j^{\text{th}}$ element) of the first vector, from the power matrix. Then the process of iteration was repeated to get subsequent roots (λ_2) and vectors (I_2). The roots were obtained in the decreasing order of magnitude. The Z values were calculated for each genotype from the mean values of (Y_1) transformed variables through the formula $Z = (I) (Y)$

where (I) = Canonical vector

(Y) = Transformed variables in a vector.

Two or three 'Z' values were computed for each genotype corresponding to $\lambda_1, \lambda_2, \lambda_3 \dots$ respectively using their corresponding vectors. These Z values were plotted on a two or three dimensional graph taking λ_1 and λ_2 , λ_1 and λ_3 or λ_2 and λ_3 . The group constellations were marked arbitrarily. The percentage contribution from each of the canonical root was calculated by the formula.

$$\begin{array}{l} \text{Percentage contribution} \\ \text{from each of the} \\ \text{canonical root} \end{array} = \frac{\lambda}{(\text{Total of trace of} \\ \text{the dispersion} \\ \text{matrix})} \times 100$$

EXPERIMENTAL RESULTS

CHAPTER IV

EXPERIMENTAL RESULTS

The experimental results of the present investigation are presented below.

4.1. Studies on genetic divergence

4.1.1 Multivariate analysis of variance

The list of 225 genotypes with their accession number and source are given in Appendix I. The mean values of each entry for all the characters is presented in Table 1.

Multivariate analysis of variance was used to test the significance of the mean values of 16 characters. The simultaneous test of significance was employed for the mean vectors of 16 characters, using Wilk's Λ (lambda) criteria. From this Λ (lambda) value V-Stat was calculated.

The value of V-Stat was 8863.39, which when compared with table χ^2 -value at 5 per cent for 3584 degrees of freedom was found to be highly significant.

4.1.2. Analysis of variance

The analysis of variance was done separately for each character. The range mean and mean sum of squares for all the 16 characters are presented in Table 2. The analysis

Table 1. The Mean values of the 16 characters in the 225 genotypes of *Sotaria italica* Beauv.

Sl. No.	I. Sc. No.	Grain yield/plant (g)	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of tillers/plant	Panicle length (cm)	Panicle breadth (cm)	Panicle weight (g)	No. of seeds	Straw weight (g)	Harvest index (%)	1000 grain weight (g)	Leaf angle	Inter-nodal length (cm)	Panicle exertion length (cm)	Panicle peduncle length (cm)
		X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
1	214	7.39	123.10	57.00	73.50	2.95	12.30	1.38	8.90	170.20	9.72	39.64	2.80	17.10	10.09	12.60	44.00
2	274	11.83	116.10	56.00	78.50	4.20	12.80	1.27	13.92	270.80	17.06	35.96	2.90	25.10	9.42	12.20	32.10
3	24	6.09	117.60	56.50	77.50	3.70	9.65	1.31	9.34	182.32	10.21	30.83	3.35	19.05	9.57	11.90	16.40
4	145	6.03	66.10	48.00	66.00	3.70	12.70	1.00	7.28	130.30	7.72	40.16	2.95	19.40	8.44	9.40	30.90
5	324	5.51	97.90	45.00	64.50	2.70	11.40	1.08	6.04	236.02	9.40	35.18	2.85	19.30	8.88	8.90	43.80
6	158	9.01	103.32	54.50	71.00	3.00	12.35	1.12	11.70	151.78	11.12	38.84	2.35	23.50	9.50	10.90	37.30
7	137.A	14.12	133.10	48.50	64.50	3.23	15.20	1.56	16.19	191.60	18.63	40.49	3.65	22.85	9.33	13.00	41.90
8	509	12.45	108.80	54.00	72.00	4.80	11.27	1.02	14.07	306.49	13.23	41.96	3.70	20.80	8.63	12.60	19.80
9	978	4.15	109.30	49.50	69.00	3.50	11.20	1.11	5.74	181.39	10.70	25.21	3.35	20.70	8.36	7.25	47.80
10	108	3.34	117.90	51.00	74.50	2.55	14.00	1.39	6.29	215.68	19.08	14.93	3.80	19.30	10.27	12.45	36.65
11	89	8.08	109.70	52.00	73.50	2.90	15.75	1.34	9.72	242.86	10.03	41.61	4.55	22.30	10.68	10.90	41.85
12	459	9.39	111.00	46.50	71.50	3.40	13.60	1.36	10.52	149.60	11.54	42.55	2.90	30.25	9.93	11.80	42.80
13	253	11.36	116.25	49.50	73.50	4.30	12.40	1.11	13.33	148.74	15.74	38.29	2.95	28.00	10.01	11.80	36.55
14	222.A	6.23	122.00	53.00	80.50	2.50	15.75	1.34	8.98	234.50	8.05	36.53	3.85	25.90	10.88	10.90	41.85
15	223.B	9.47	101.50	56.00	76.50	4.30	10.60	1.17	11.39	173.00	11.76	40.34	2.60	20.60	9.75	9.60	34.00
16	359	18.77	111.90	56.00	79.50	2.80	10.76	1.04	21.70	126.20	14.15	52.52	2.80	29.05	9.88	11.15	36.20
17	172	6.90	104.20	51.00	73.00	2.60	11.66	1.34	9.45	257.48	7.55	40.46	3.15	21.85	10.21	11.00	39.50
18	68	6.80	115.90	55.00	81.50	2.60	14.20	1.48	7.47	292.46	11.09	40.29	2.95	26.20	9.92	12.80	44.65
19	234	5.99	126.20	49.00	75.50	3.10	11.70	1.06	6.82	193.20	9.00	37.90	3.25	22.50	9.00	11.95	36.90
20	265	6.70	111.77	51.00	116.50	6.40	10.45	1.13	7.97	189.08	11.02	35.65	3.90	21.70	9.55	12.67	37.40
21	323	10.40	104.80	59.50	75.50	3.00	12.50	1.20	11.65	153.40	11.51	45.52	3.55	27.60	10.00	14.45	41.30
22	591	8.92	107.60	54.50	74.50	4.90	11.10	1.26	11.10	238.68	10.29	41.69	3.15	22.35	9.72	11.20	10.40
23	183	10.12	106.60	58.00	78.50	5.20	11.40	1.23	13.81	216.28	13.53	38.23	3.00	24.80	9.39	11.60	38.20
24	386	11.23	57.80	55.50	80.50	4.10	15.00	1.18	12.48	151.12	10.08	49.89	3.40	21.90	10.20	13.70	40.50
25	60	7.22	106.50	70.50	77.50	5.60	12.87	1.28	8.47	348.46	12.93	35.61	3.50	29.20	10.18	10.80	38.80

Table 1 (continued)

		X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
26	345	5.06	70.35	44.00	66.50	2.95	11.75	1.10	6.30	235.48	7.83	35.31	1.00	26.10	6.54	6.10	24.00
27	146	14.69	91.55	55.00	83.00	3.90	12.60	1.03	15.86	267.76	11.34	54.26	1.35	28.70	8.83	10.90	38.10
28	RS.118	9.82	102.00	50.50	75.50	4.80	15.30	1.18	11.41	353.08	12.19	41.61	1.65	29.60	9.56	12.65	40.00
29	519	10.81	145.25	54.00	77.00	3.70	12.90	1.35	14.20	202.08	13.87	39.94	2.80	30.90	10.57	13.14	41.70
30	160	11.83	119.60	55.00	77.50	5.00	13.90	1.17	13.52	194.54	13.63	40.09	3.15	29.20	9.82	13.00	41.70
31	103	10.28	121.50	72.00	103.00	3.20	12.00	1.30	14.01	362.00	13.42	38.17	2.55	24.80	11.54	11.50	35.10
32	164	12.55	108.15	61.50	84.50	4.00	13.90	1.27	14.93	338.00	14.23	42.89	3.85	23.20	11.44	11.20	37.70
33	363	5.61	35.20	47.50	61.50	5.10	13.20	1.04	6.91	179.85	5.84	42.91	2.65	26.40	10.10	14.20	31.30
34	131	7.36	88.10	50.00	57.50	2.60	11.50	1.29	9.53	116.76	10.55	36.52	2.50	27.50	7.67	10.00	30.28
35	518	9.67	116.50	48.00	69.00	0.90	15.50	1.32	11.38	232.00	11.64	42.03	3.25	24.60	10.55	12.90	47.17
36	186.8	7.92	103.20	49.50	70.00	1.80	9.40	2.20	10.52	145.90	15.57	31.28	3.05	32.00	11.67	9.50	25.40
37	150	6.95	114.80	52.00	77.00	3.60	14.70	1.38	9.02	183.94	11.23	34.02	2.85	26.50	9.68	16.40	40.40
38	342	6.27	81.90	50.50	74.00	4.80	10.95	1.17	6.86	216.51	10.60	35.37	3.00	28.10	11.29	11.30	35.30
39	176	11.26	106.00	74.00	92.50	4.80	13.50	1.23	8.34	245.50	12.70	41.11	5.10	27.20	10.04	11.40	31.60
40	154	6.09	79.00	47.00	74.00	3.90	7.60	1.06	5.67	237.52	9.58	40.03	3.05	24.60	11.95	9.60	26.10
41	369	12.59	124.40	56.00	79.50	3.80	11.85	1.25	15.62	117.80	14.88	41.31	3.35	27.60	9.81	13.70	30.95
42	4108	8.57	104.70	53.00	76.50	5.60	11.05	1.16	7.84	161.75	10.19	43.35	3.15	30.40	10.88	10.55	36.50
43	531	7.08	115.30	53.50	72.50	4.60	11.40	1.22	9.52	110.54	15.63	28.05	2.39	22.70	10.74	10.50	35.90
44	483	7.35	115.25	44.50	61.00	4.55	10.70	1.14	9.62	259.67	10.18	37.05	3.15	24.00	9.14	11.00	39.80
45	63	13.98	93.28	51.00	76.00	2.05	11.80	1.12	14.74	179.46	13.14	50.09	2.70	20.40	10.83	12.50	39.80
46	135	5.27	153.60	55.50	75.50	2.40	13.90	1.22	6.74	307.50	14.79	24.90	3.00	24.50	9.30	16.90	34.30
47	62	8.96	120.50	54.50	84.00	3.00	14.30	1.33	10.10	146.75	11.99	39.47	3.10	22.20	10.50	12.80	37.10
48	231	11.79	106.30	71.50	92.50	7.00	14.20	1.22	13.60	240.50	18.84	36.57	4.15	14.50	10.73	19.92	35.50
49	352	12.71	106.30	73.00	95.50	5.30	13.75	1.38	13.71	157.40	14.03	38.97	3.50	13.20	10.89	10.70	34.90
50	329	17.60	120.50	71.50	94.00	4.30	15.80	1.45	20.22	198.20	20.67	44.65	2.85	15.30	9.53	15.40	41.90

Table 1 (continued)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	x_{11}	x_{12}	x_{13}	x_{14}	x_{15}	x_{16}
276	18.47	120.20	51.50	70.00	3.60	14.80	1.52	20.87	251.05	22.03	43.16	4.55	30.10	9.94	10.10	15.50
388	12.56	84.00	53.50	75.50	4.70	10.20	1.20	15.53	190.45	15.53	40.80	2.60	20.00	10.39	10.10	15.80
99.3	13.32	107.30	51.51	71.00	5.00	13.90	1.39	15.38	156.83	23.58	36.90	3.50	16.50	10.00	12.90	11.00
133	13.49	83.95	54.00	80.50	2.80	13.85	1.09	16.14	243.65	15.86	40.13	3.25	24.55	10.40	12.55	11.80
60	16.90	139.25	41.50	61.00	2.80	13.25	1.65	21.12	241.70	26.50	35.49	4.60	21.75	9.80	14.25	10.25
390	12.99	108.16	47.00	67.00	4.70	10.90	1.04	14.72	280.70	14.11	44.76	3.75	23.70	9.22	17.65	16.30
184	6.07	105.60	54.00	80.00	2.50	12.60	1.17	7.40	260.50	10.13	34.76	2.55	25.30	10.93	9.70	19.20
392	9.16	97.50	47.00	62.50	4.10	11.90	1.13	11.73	227.75	12.15	37.94	2.40	24.50	9.82	12.20	16.60
236	11.98	125.50	51.50	73.00	3.50	12.20	1.45	14.54	368.00	13.90	42.13	2.60	18.30	11.07	11.40	17.00
203	14.97	157.85	49.50	71.50	2.10	14.70	1.36	17.46	278.25	17.17	43.23	2.85	18.60	11.44	15.50	44.20
263	13.27	103.60	48.50	66.50	5.20	12.10	1.17	15.55	236.50	13.28	45.93	3.55	17.30	10.47	12.20	16.50
373	8.27	97.70	47.00	66.00	3.90	12.80	1.07	9.10	300.80	10.73	41.03	2.50	23.90	10.36	10.50	22.60
256	9.75	83.20	47.50	69.00	3.80	12.80	1.18	10.79	186.25	11.94	42.72	3.25	16.30	9.49	11.20	22.15
155.4	13.31	116.00	56.00	78.00	3.90	15.80	1.45	17.67	260.60	14.40	41.35	3.75	20.20	11.82	15.55	42.40
173	11.61	113.40	54.00	76.00	3.70	15.00	0.99	13.73	235.60	17.85	36.73	3.70	13.80	10.61	10.10	17.00
59	12.08	87.20	49.00	70.50	1.90	15.12	1.20	14.34	302.25	12.12	50.90	3.35	12.30	10.32	11.20	11.90
162	13.17	98.25	48.00	70.50	4.75	15.60	1.16	11.98	316.15	17.27	42.85	4.30	24.40	11.42	15.60	37.70
303	9.60	81.30	53.50	75.50	3.70	14.20	1.38	10.22	216.40	10.43	45.95	2.75	19.50	8.93	10.42	13.50
165	12.17	104.80	56.00	77.50	3.70	11.70	1.17	13.02	169.65	13.83	45.92	3.25	18.80	10.37	11.00	15.30
370	10.84	99.60	56.00	77.00	4.20	11.90	1.28	13.42	178.38	18.59	33.96	3.86	18.50	11.38	9.95	14.40
460	13.19	117.00	51.50	72.50	4.90	12.90	1.25	14.22	216.20	20.57	38.07	2.90	20.70	11.52	12.80	32.50
193	10.47	101.60	50.00	71.00	4.80	13.40	1.33	13.80	224.48	12.45	39.48	3.15	23.00	10.42	12.00	40.70
582	11.56	104.20	49.50	65.00	3.30	12.70	1.21	15.27	505.25	15.42	33.07	2.45	22.70	11.15	12.70	11.10
153	5.47	101.20	54.00	86.00	3.90	11.90	1.18	7.09	216.70	10.01	31.73	2.95	24.20	9.01	11.20	27.60
148	11.68	106.95	52.00	73.00	1.40	13.00	1.11	14.70	177.50	16.69	37.20	3.35	14.40	10.42	13.20	38.80

Table 1 (continued)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	x_{11}	x_{12}	x_{13}	x_{14}	x_{15}	x_{16}	
76	573	7.83	105.90	47.50	70.50	5.90	13.20	1.20	10.98	194.84	14.61	30.62	3.10	19.70	9.36	12.45	36.45
77	456	14.60	114.00	50.50	98.50	1.30	14.20	1.24	16.92	277.00	11.31	51.69	3.00	17.60	9.98	12.70	37.20
78	482	9.77	98.20	53.50	75.50	2.40	12.10	1.04	14.63	137.60	11.21	37.76	3.10	20.20	11.04	11.10	36.90
79	471	12.96	99.90	49.50	70.50	2.50	9.50	1.20	17.15	130.00	18.35	38.04	3.55	26.40	11.13	12.50	36.70
80	455	11.38	93.55	46.50	68.50	1.35	12.90	1.22	13.46	113.50	14.64	42.18	3.00	15.30	10.27	10.65	35.30
81	406.A	7.64	125.40	51.00	72.00	4.75	12.85	1.32	7.72	149.25	9.21	44.61	3.55	17.70	9.21	11.90	38.00
82	K.222A	11.31	105.00	50.50	71.50	5.50	13.90	1.20	13.03	245.53	13.30	40.25	3.15	24.50	12.38	10.80	38.30
83	226	7.80	78.00	48.00	69.00	3.10	12.66	0.85	7.69	367.73	10.50	43.74	2.80	16.80	10.49	10.90	24.10
84	643.A	16.03	111.80	48.00	68.50	4.90	14.60	1.77	18.99	269.26	14.20	48.15	3.70	16.50	9.60	12.10	35.30
85	405.A	16.28	101.90	55.50	80.00	2.40	15.40	1.17	17.22	126.60	20.71	43.35	3.75	20.30	10.97	13.00	34.02
86	217	13.93	103.10	58.50	79.00	2.82	12.30	1.16	15.12	182.42	21.72	39.91	3.25	19.80	11.91	11.50	32.80
87	251	12.30	95.10	51.50	73.00	6.10	11.00	1.10	14.07	122.95	18.57	39.94	3.20	19.00	10.53	11.75	34.45
88	389	22.79	121.00	52.50	74.00	3.40	14.40	1.41	31.17	169.60	28.65	41.59	3.40	23.00	9.57	16.20	35.20
89	507	22.27	104.45	51.50	73.50	5.00	12.80	1.30	24.32	137.48	27.92	42.62	1.90	16.40	9.88	11.70	39.60
90	106	13.37	97.25	51.50	77.00	4.20	14.50	2.60	14.76	154.64	19.08	39.54	2.80	16.00	11.86	13.20	41.20
91	406	9.64	112.50	51.00	73.00	3.80	18.30	1.33	14.75	290.20	15.02	32.67	2.80	21.40	10.53	14.65	33.15
92	264	15.75	115.40	51.00	76.00	4.20	14.75	1.30	17.30	158.45	17.57	47.55	3.20	27.20	10.63	14.50	39.10
93	270	16.43	99.90	49.00	71.00	2.60	16.05	1.22	17.76	212.63	18.20	48.27	3.75	19.80	11.35	13.15	40.25
94	432	7.55	90.40	57.00	79.00	3.90	12.40	1.28	10.30	236.50	8.81	41.17	3.60	17.90	11.11	10.50	34.85
95	326	9.37	116.30	50.50	72.50	2.30	11.50	1.19	11.36	176.85	12.62	38.75	3.00	13.20	14.99	9.40	36.60
96	448	12.32	90.75	47.30	67.00	4.80	12.20	1.07	13.96	273.25	15.97	41.11	4.25	17.90	10.13	11.50	33.40
97	505	13.56	112.40	49.00	69.00	4.70	18.25	1.52	15.58	122.26	19.47	38.73	3.65	19.80	10.40	13.90	42.80
98	331	17.15	107.90	53.00	75.00	2.20	16.50	1.37	20.29	256.80	15.82	47.45	2.80	13.90	10.67	13.10	43.50
99	521	18.37	97.05	57.50	79.50	5.60	12.95	1.14	20.74	439.00	17.41	48.27	3.25	17.30	11.00	12.50	44.40
100	325	10.85	115.60	61.00	83.00	2.70	10.15	1.05	11.96	165.50	17.59	34.80	3.55	19.40	11.04	13.20	41.70

Table 1 (continued)

	x_1	x_2	x_3	x_4	x_5	$\bar{x}$	x_7	x_8	x_9	x_{10}	x_{11}	x_{12}	x_{13}	x_{14}	x_{15}	x_{16}
101 360	9.75	112.20	76.00	100.50	4.20	14.30	1.09	12.23	178.05	12.62	39.06	2.70	15.20	10.02	12.75	38.70
102 267	12.97	120.14	53.00	73.50	4.30	11.05	1.44	15.23	259.00	16.36	41.08	3.60	18.30	11.06	10.30	34.70
103 508.A	7.31	100.20	68.00	87.00	4.85	11.40		10.35	157.90	17.97	25.68	3.25	24.20	10.02	12.05	45.80
104 168	14.32	115.20	74.50	94.50	3.70	11.00	0.37	17.72	150.80	16.26	41.35	2.95	16.60	10.73	10.40	41.25
105 340	13.81	163.70	50.50	71.50	1.40	11.60	0.95	15.82	347.50	18.26	40.51	2.70	20.10	10.68	11.60	33.20
106 192	13.43	126.70	83.50	103.50	3.75	13.35	1.40	15.97	182.65	18.78	40.20	3.40	21.40	9.17	11.30	30.70
107 169	5.03	122.80	55.00	76.50	4.70	14.69	1.61	7.15	186.05	8.22	32.68	2.55	14.70	11.31	13.15	42.20
108 253	9.73	110.60	71.50	96.50	5.10	10.70	1.50	10.04	254.00	10.26	39.28	3.40	15.50	10.72	11.90	36.00
109 259	17.25	114.40	54.00	76.50	3.80	13.50	1.15	19.35	142.50	18.55	45.28	3.75	18.50	11.46	11.50	30.40
110 39.B	15.22	118.30	52.50	73.00	2.65	13.90	1.12	19.02	251.10	19.60	38.75	3.40	17.11	11.29	12.20	35.45
111 268	12.26	122.60	52.00	73.50	3.40	12.15	1.15	13.71	158.12	17.22	39.84	3.40	22.00	10.29	12.70	38.95
112 504	18.87	118.00	64.50	81.50	3.70	14.70	1.24	21.05	246.05	19.31	46.72	3.55	16.10	11.40	12.15	40.60
113 140	10.92	119.00	49.00	69.50	2.20	12.57	1.23	13.30	204.00	13.35	41.13	3.55	20.10	9.72	14.70	35.50
114 371	9.89	103.60	71.00	98.00	4.10	15.00	1.24	12.08	150.53	12.60	40.62	2.60	19.60	4.44	11.30	35.50
115 469	9.26	110.90	75.50	102.00	3.90	13.00	1.22	10.09	176.30	12.66	41.41	3.15	17.03	11.61	11.60	35.60
116 46	6.23	98.20	50.50	68.50	3.40	13.00	1.07	7.92	176.10	7.52	39.55	2.80	25.30	9.99	10.90	31.90
117 211.B	3.05	90.50	33.00	104.00	3.20	13.60	1.22	9.20	204.00	13.90	34.71	3.75	23.20	10.81	13.60	33.60
118 458	6.63	89.60	47.50	68.00	2.10	11.30	1.20	8.55	117.00	11.24	33.18	2.85	14.40	9.52	11.93	39.60
119 255	10.88	100.90	48.00	68.50	4.40	12.45	0.94	12.54	129.80	15.33	39.00	2.95	20.70	9.25	10.75	39.60
120 156	5.09	105.55	44.00	65.00	2.60	11.20	1.08	6.41	261.30	8.56	33.23	3.55	24.70	8.91	12.20	30.20
121 354	13.92	103.90	50.50	68.00	3.45	11.15	1.09	16.29	165.00	16.09	43.63	2.55	17.40	11.21	13.30	40.55
122 138	11.10	107.40	44.60	68.00	2.10	11.90	1.10	12.37	231.20	16.73	38.91	3.15	30.25	11.97	20.60	25.20
123 417.B	7.98	126.30	51.50	72.00	3.50	13.40	0.99	11.42	192.70	11.50	34.94	3.10	21.70	12.25	12.40	33.80
124 210	7.84	112.70	53.50	73.50	3.60	12.70	1.13	9.56	153.00	11.96	37.16	2.95	24.30	12.18	11.75	29.80
125 398	11.36	116.50	49.50	70.50	4.10	14.80	1.21	13.20	161.40	12.69	43.81	2.90	25.50	12.40	14.00	38.50

Table 1 (continued)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	x_{11}	x_{12}	x_{13}	x_{14}	x_{15}	x_{16}
126	320	8.26	115.20	60.00	3.10	14.25	1.24	9.16	179.10	12.76	35.75	3.65	16.20	10.45	11.30	36.80
127	410.A	4.35	65.50	44.00	2.20	12.00	1.06	5.11	169.68	7.04	35.70	3.20	21.10	8.62	9.60	33.30
128	165	12.93	87.90	45.00	4.60	12.40	1.03	12.93	300.60	12.47	39.47	3.35	30.50	10.02	9.40	
129	350	7.52	101.40	70.50	4.00	13.50	1.88	9.28	262.50	14.13	32.11	2.84	21.80	10.80	12.60	27.70
130	197	6.76	102.50	52.50	2.30	12.60	1.09	8.72	167.95	17.22	26.19	1.55	17.10	11.45	9.80	31.90
131	34	12.69	116.50	50.00	3.40	11.50	1.16	17.06	76.00	18.25	35.97	2.65	16.30	10.70	13.90	36.50
132	101.A	6.39	85.20	44.50	1.70	11.10	1.03	8.58	149.85	11.62	31.91	2.30	14.80	12.21	10.70	30.30
133	232	8.00	484.90	54.00	2.80	13.95	1.21	10.21	116.95	11.20	37.38	2.55	21.80	10.10	9.60	28.40
134	202	10.86	120.65	46.50	2.70	15.70	1.40	14.00	180.90	14.37	38.13	3.10	23.80	11.06	12.10	36.55
135	377	6.41	114.20	53.50	2.10	12.20	1.27	9.14	170.05	11.54	30.46	3.05	27.50	11.60	14.80	39.20
136	508.A	10.17	89.50	54.00	3.40	12.40	1.01	10.58	173.10	15.87	29.41	2.25	18.70	9.54	11.30	31.30
137	472	4.16	80.80	72.00	2.40	13.80	1.32	5.98	303.70	4.60	32.12	2.40	20.30	8.68	9.30	31.70
138	234	8.47	101.00	53.00	5.35	12.70	1.14	12.15	171.50	11.51	35.67	2.65	17.50	12.17	13.00	44.20
139	525	6.42	84.50	44.00	4.80	10.00	1.15	8.09	211.33	7.30	42.44	2.35	18.10	9.90	10.70	30.20
140	235	9.23	108.50	50.00	2.63	15.10	1.47	21.42	271.00	13.60	38.80	2.45	15.50	11.28	12.30	34.10
141	343	2.83	89.60	44.00	1.40	14.20	1.54	5.54	225.00	5.69	33.21	3.35	16.10	10.26	14.00	34.50
142	335	15.94	105.10	54.00	5.40	13.40	1.15	18.26	215.25	17.71	44.28	3.20	25.10	10.14	11.00	32.80
143	137	6.34	110.00	50.00	1.10	18.00	1.18	8.14	268.76	8.43	38.50	3.05	19.60	9.20	10.70	38.10
144	142	3.80	92.65	48.00	4.80	18.80	1.12	5.18	245.40	6.60	31.06	2.40	18.30	8.99.	10.20	34.30
145	385	5.51	140.00	52.50	4.45	14.20	1.32	9.17	182.00	11.01	32.40	2.45	21.90	11.07	15.50	25.80
146	465.B	6.36	101.30	48.50	3.40	11.60	1.17	7.34	137.50	9.09	40.03	2.90	21.40	10.17	12.70	36.70
147	238	12.09	104.90	53.00	4.60	13.60	1.11	14.89	127.60	14.38	41.32	3.00	20.50	11.47	11.40	40.10
148	155	5.37	98.80	44.50	1.40	13.70	1.17	6.35	201.15	7.48	38.64	2.50	17.60	11.31	11.70	34.60
149	376	5.80	109.80	53.00	3.00	13.30	1.74	7.06	244.60	9.2.	30.75	3.00	16.10	10.87	15.00	43.10
150	101	4.63	104.10	52.50	3.20	12.10	1.40	5.64	155.00	9.11	31.36	3.40	14.40	10.87	13.90	38.50

Table 1 (continued)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	x_{11}	x_{12}	x_{13}	x_{14}	x_{15}	x_{16}
151 107	6.85	128.90	55.00	81.50	2.75	12.30	1.17	8.34	269.00	11.69	33.53	3.20	19.30	11.65	11.90	36.10
152 180	9.49	116.70	54.00	79.00	3.45	14.15	1.09	11.74	229.30	11.11	41.50	3.95	21.20	10.73	10.15	35.25
153 90	7.57	201.60	52.00	80.50	1.80	13.90	1.26	8.75	192.75	11.47	38.01	1.80	20.00	9.94	11.00	37.00
154 58	16.12	112.60	46.00	69.50	5.20	14.90	0.98	16.95	146.62	18.38	41.45	3.00	21.30	9.60	14.00	43.60
155 1	8.21	104.35	47.50	66.00	4.50	16.00	1.20	9.58	220.62	14.38	34.44	3.05	19.40	10.10	13.75	39.90
156 102	6.76	105.90	61.00	97.00	2.20	10.20	1.62	12.00	215.60	9.99	37.65	2.80	18.40	10.37	11.20	34.50
157 178	14.55	109.90	51.00	71.00	3.80	13.80	1.46	18.18	122.50	17.76	40.66	2.95	19.10	10.57	16.85	32.00
158 397	7.78	128.40	46.50	62.50	2.60	15.75	1.48	10.10	117.50	12.75	33.69	3.10	17.50	10.12	13.50	41.50
159 260	9.36	93.30	54.00	67.00	5.70	9.60	1.17	10.26	215.15	11.73	42.62	3.25	18.20	10.77	11.80	33.60
160 136	11.23	129.30	46.00	70.00	5.10	12.80	1.42	13.51	215.70	11.96	35.95	2.65	20.40	10.67	11.10	33.00
161 99.C	12.15	104.75	49.50	78.50	4.10	13.20	1.15	13.80	148.60	17.40	38.79	2.90	20.20	13.02	15.70	39.20
162 80	9.88	131.00	49.00	65.00	4.30	13.60	1.18	11.26	169.50	13.23	42.92	3.00	27.50	11.54	12.40	40.60
163 245	6.49	94.40	48.00	67.50	4.90	13.30	1.21	7.67	171.20	10.02	35.39	3.45	16.40	10.99	11.50	38.30
164 190	7.56	106.50	51.00	70.00	3.50	11.70	1.30	8.79	220.96	13.77	33.40	3.15	18.50	11.68	11.80	37.70
165 200	5.07	129.45	69.00	98.50	2.00	12.15	1.24	7.72	122.60	8.92	36.57	3.75	21.90	10.47	10.50	40.10
166 52	17.85	120.00	50.50	75.00	5.20	17.70	1.36	21.30	185.60	20.72	42.39	3.20	23.20	9.87	16.00	43.40
167 177	7.61	115.50	48.00	70.00	2.62	17.40	1.62	8.32	200.50	11.38	38.44	2.75	24.20	9.73	13.15	39.06
168 257	9.77	101.10	51.00	76.00	4.10	12.10	1.41	1.3	138.59	12.33	40.13	2.90	21.30	9.61	13.20	40.60
169 35.B	10.96	108.40	49.00	71.00	3.90	13.95	1.12	10.22	225.70	19.75	38.71	3.45	20.50	11.35	13.70	34.50
170 40	11.76	112.90	54.00	82.00	2.10	11.95	1.27	13.56	262.02	19.73	34.62	2.90	27.10	11.17	11.40	37.50
171 198.A	10.43	109.80	54.50	79.00	2.31	12.80	1.03	13.46	212.59	13.43	39.78	2.90	18.90	10.75	11.45	35.80
172 45	9.30	114.70	45.00	71.00	4.70	16.40	1.48	12.25	216.92	19.03	29.54	2.85	19.42	11.39	10.95	35.20
173 159.A	10.55	128.65	51.50	76.50	3.35	15.70	1.33	13.75	262.80	17.84	39.10	3.20	18.90	10.80	17.55	43.90
174 73	8.20	106.20	50.00	76.50	4.93	14.90	1.13	9.76	317.50	16.69	30.94	3.25	23.50	11.67	13.10	38.10
175 221	15.03	111.80	49.40	73.50	4.83	14.30	1.41	9.60	224.30	19.87	37.76	3.60	21.40	9.63	14.20	38.30

Table 1 (continued)

	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	x_{11}	x_{12}	x_{13}	x_{14}	x_{15}	x_{16}
176 141	13.83	118.20	51.00	72.00	6.10	14.40	1.31	16.59	218.36	24.11	34.20	3.60	20.20	9.73	15.40	41.10
177 405.B	2.21	111.50	50.00	70.00	3.30	13.60	1.26	3.94	357.76	4.17	26.68	3.30	19.40	9.16	14.60	35.30
178 212.A	6.67	125.80	48.00	68.50	3.90	13.70	1.22	8.29	225.60	11.98	33.28	2.90	19.20	10.52	13.30	41.00
179 375	16.64	103.80	49.50	70.00	4.50	18.40	1.26	18.80	299.60	23.09	39.61	3.00	20.20	12.05	14.50	41.90
180 132	7.37	74.90	41.00	61.00	2.70	8.75	1.44	8.36	168.89	11.87	36.66	2.85	23.80	10.53	11.90	36.51
181 254	16.18	102.30	47.50	68.50	5.00	17.00	1.34	17.74	166.86	22.07	40.57	3.00	19.50	10.00	13.80	44.60
182 64	17.40	106.70	58.00	83.00	5.00	13.10	1.33	16.81	228.14	24.40	36.18	3.30	20.40	10.30	14.05	41.95
183 362	11.56	97.70	56.50	78.50	4.25	13.15	1.13	13.75	200.08	18.70	35.65	4.00	17.60	11.28	11.00	35.30
184 Arjuna	5.66	63.50	40.00	63.50	2.40	12.00	1.08	5.64	195.64	10.30	33.28	2.90	21.50	9.08	11.60	32.50
185 266	4.51	78.10	42.00	63.00	4.16	13.40	1.24	6.02	158.10	7.10	34.50	2.90	24.50	10.33	10.60	31.40
186 262	5.21	101.50	46.50	70.50	5.40	16.55	1.19	6.43	148.40	10.24	31.38	3.70	24.50	11.89	11.50	38.30
187 417.A	13.50	114.90	56.50	80.50	3.40	14.80	1.40	16.57	175.50	19.78	37.21	3.05	26.30	10.95	10.70	39.30
188 96	13.77	98.50	59.50	73.50	4.70	12.90	1.23	15.86	258.50	19.68	34.62	2.90	26.70	10.64	8.40	37.00
189 66	12.48	84.00	50.50	75.50	3.45	14.10	1.09	14.96	236.45	18.40	37.58	2.80	19.60	9.08	8.75	33.50
190 464	8.81	98.30	47.00	73.00	5.60	11.85	1.34	10.65	185.50	16.31	32.82	3.00	17.40	11.02	11.80	39.15
191 104	8.30	53.00	53.50	81.50	5.30	13.00	1.38	9.30	171.54	12.44	39.93	3.10	18.30	9.84	11.10	31.15
192 339	17.63	108.70	46.00	62.00	5.75	13.90	1.10	18.92	250.05	21.10	44.06	3.45	17.90	11.34	13.80	39.60
193 417.B	8.12	115.15	56.00	79.00	3.50	8.75	1.10	10.47	191.20	11.35	37.28	3.30	20.10	9.03	14.20	42.50
194 457	9.44	79.50	50.50	75.50	3.45	18.20	1.22	11.38	216.60	10.21	43.93	3.05	21.80	8.86	12.70	39.90
195 400	15.19	103.90	53.50	74.50	4.35	14.10	1.10	15.95	166.94	18.67	43.85	3.35	20.50	11.54	13.40	45.40
196 271	17.33	84.00	54.50	74.50	2.50	14.10	1.25	16.12	267.50	24.85	34.56	2.75	22.50	9.95	11.70	39.60
197 70	6.89	84.10	54.00	82.50	4.40	12.10	1.12	8.62	154.80	16.15	31.51	2.90	20.10	10.17	9.70	31.40
198 138	10.91	103.60	45.00	69.00	5.95	10.20	1.15	14.61	267.50	20.43	31.57	3.20	20.90	11.67	11.30	36.80
199 191	8.80	103.20	56.00	81.50	3.25	12.40	1.29	10.64	157.00	15.71	33.47	2.95	18.90	8.80	11.70	35.10
200 474	17.16	116.20	57.00	85.00	5.00	14.05	1.75	18.97	220.50	22.13	41.61	3.20	23.00	11.01	20.20	46.60

Table (continued)

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
201 95	13.21	117.30	49.00	71.00	5.30	14.10	1.54	15.23	259.60	17.87	37.81	3.55	20.40	10.85	12.75	42.63
202 334	10.54	72.14	40.00	62.00	5.73	13.50	1.39	13.55	166.90	14.89	38.44	2.90	24.60	9.64	14.10	42.80
203 97	11.07	115.80	49.00	73.00	5.30	11.90	1.18	12.93	211.50	15.00	39.56	3.15	21.30	8.77	11.10	34.80
204 143	13.31	121.30	56.50	82.00	5.60	14.70	1.63	15.56	220.20	24.40	33.13	2.65	22.70	10.03	12.90	33.40
205 248	8.87	99.85	42.00	60.50	6.00	11.00	0.99	11.01	158.70	12.96	36.98	2.90	21.00	11.61	13.90	37.35
206 101.2	12.03	109.80	44.50	71.50	4.20	13.65	1.12	13.15	194.50	16.32	37.68	3.85	21.70	10.13	12.85	
207 122	13.93	117.00	26.95	75.00	4.50	7.34	0.64	28.76	241.25	22.18	37.58	3.85			7.62	53.88
208 354	18.85	110.00	44.50	72.50	4.90	12.10	1.00	10.15	171.20	18.36	28.94	2.65	21.30	9.03	11.30	36.50
209 161	14.56	116.55	57.00	83.00	5.50	20.00	1.21	16.62	316.10	19.03	40.88	3.75	22.00	11.03	12.25	36.95
210 481	13.95	118.00	54.50	79.00	6.62	12.50	1.14	17.10	148.00	18.36	39.24	3.80	26.90	10.95	15.55	41.30
211 395	13.89	127.50	52.00	76.00	6.70	14.60	1.22	15.01	274.28	18.66	41.25	2.90	28.60	9.99	13.90	34.00
212 35.2	15.49	116.05	63.00	78.00	4.50	16.20	1.39	20.13	187.40	25.40	33.99	3.35	24.00	9.25	11.10	40.70
213 152	15.80	100.70	58.00	84.00	2.30	17.70	1.67	17.65	265.60	26.32	35.90	3.00	24.00	11.30	11.90	46.20
214 642.2	12.03	90.30	49.50	69.50	4.36	12.80	1.14	13.94	209.60	17.66	38.05	3.00	17.20	11.20	10.80	34.80
215 Co. 3	13.88	103.20	50.00	70.50	3.50	14.90	1.07	15.63	225.36	21.59	37.28	3.00	23.00	10.86	13.90	46.30
216 36	9.44	74.60	56.50	83.50	4.50	8.50	2.30	9.86	498.40	9.44	11.20	3.65	23.60	10.02	9.30	23.80
217 643	7.89	93.50	54.00	72.50	2.60	15.00	1.15	9.41	186.06	9.97	40.74	3.00	24.60	10.69	12.00	31.20
218 196	5.70	77.00	44.50	66.50	3.60	13.50	1.20	7.00	181.44	7.78	37.65	3.20	26.70	10.21	10.30	27.80
219 374	5.68	76.10	44.00	66.50	2.70	10.80	0.83	6.28	142.10	8.47	38.59	2.65	23.20	10.37	9.95	30.30
220 171	14.77	107.00	61.00	75.30	3.10	17.90	1.96	20.18	289.40	26.51	37.95	4.10	27.50	10.23	13.62	41.30
221 642	8.49	95.00	49.50	73.00	5.31	15.70	2.33	10.42	259.62	13.66	35.26	2.50	26.90	10.75	14.35	43.60
222 470	8.15	100.20	44.00	66.80	2.30	16.70	1.36	9.27	278.64	15.09	34.48	4.10	24.90	9.90	12.50	37.20
223 675	17.87	104.00	56.00	77.80	4.81	15.50	1.51	19.44	282.96	18.58	45.41	3.85	20.50	10.63	12.80	40.50
224 175	43.01	69.50	53.00	74.00	5.33	11.80	1.39	16.79	197.30	18.62	36.52	3.65	25.00	10.20	12.50	39.40
225 873	6.80	112.40	56.50	69.00	3.50	12.13	1.33	8.07	144.30	11.15	35.34	2.45	21.80	12.08	11.10	45.48
226	11.31	108.60	52.52	75.32	3.85	13.24	1.29	12.53	209.83	14.48	38.24	3.14	21.33	10.30	12.26	17.08
227	8.30	114.63	2.66	1.12	0.45	1.87	0.86	2.21	35.28	2.29	3.82	8.49	1.51	2.43	2.38	8.12

Table 2. The Range, Mean, Mean squares of the 16 characters for the 225 genotypes of Setaria italica, B.

Character	Range	Mean	Treatment Mean sum of squares	Error Mean sum of squares
Grain weight (g)	3.34 - 22.79	11.31	130.34**	18.87
Plant height(cm)	53.00 -157.85	108.68	2387.20	2149.37
Days to 50% of the plants to bloom	44.00 - 74.50	52.52	108.11**	7.11
Days to maturity	60.05 -116.50	75.32	27.71**	1.64
Number of produ- ctive tillers	1.10 - 6.70	3.85	3.30**	0.42
Panicle length(cm)	7.60 - 15.75	13.24	8.11**	2.47
Panicle breadth(cm)	0.14 - 2.66	1.29	52.18**	0.44
Panicle weight(g)	5.54 - 21.05	12.53	39.48**	4.90
Number of seeds	76.00 -505.25	209.83	8198.87**	1245.07
Straw weight (g)	4.10 - 28.65	14.48	44.04**	5.26
Harvest Index (%)	11.20 - 52.52	38.24	61.86**	14.61
1000 grain weight(g)	1.80 - 5.40	3.14	0.48**	0.24
Leaf angle	12.30 - 32.50	21.33	32.79**	2.28
Internodal length(cm)	7.67 - 12.25	10.38	2.19	2.06
Panicle exertion(cm)	8.40 - 20.20	12.26	9.15**	5.67
Peduncle length(cm)	19.80 - 47.80	37.09	51.36**	26.23

** Significant at 1% level

of variance revealed highly significant differences existing among 225 genotypes for the 14 of the 16 characters studied. The results of the two techniques employed in divergence studies viz. canonical variate analysis and D^2 analysis are presented below.

4.1.3. Canonical variate analysis

The canonical variate analysis was employed to obtain the spatial positioning of all the 225 genotypes on a graph. The mean values of the first two canonical vectors were plotted on the graph and preliminary grouping was done through canonical analysis.

Preliminary grouping by canonical analysis would be efficient only if the first two canonical roots account for most of the total variation.

The amount of variability extracted by each of the first three principle components or the canonical vectors and subsequent six vectors derived in the decreasing order of magnitude are presented in Table 3.

The first three canonical vectors supplying best linear functions of the variates accounting in all 55.99 per cent of variability are given in Table 4. It could be seen from the first vector that the variables like Days to 50 per cent of

Table 3. Canonical roots and total variability extracted

	Canonical roots								Total
	1	2	3	4	5	6	7	8	
Variability extracted	3727.07	1783.71	1673.36	1289.00	928.98	866.26	625.11	489.11	11382.60
Percentage of variability extracted	29.05	13.90	13.04	10.04	7.24	6.75	4.87	3.81	88.70
Cumulative percentage of variability extracted by canonical roots upto	29.05	42.95	55.99	66.03	73.27	80.02	84.89	88.70	

Table 4. The first three canonical vectors

Characters	Vector-1	Vector-2	Vector-3
X_1 = Grain weight (g)	0.049	0.172	0.053
X_2 = Plant height (cm)	0.018	0.064	0.005
X_3 = Days to 50% of plants to bloom	0.588	0.112	0.383
X_4 = Days to maturity	0.491	0.626	0.591
X_5 = Number of productive tillers	0.186	0.165	0.169
X_6 = Panicle length(cm)	0.158	0.019	0.135
X_7 = Panicle breadth(cm)	-0.080	0.110	0.022
X_8 = Panicle weight(g)	0.456	0.019	0.344
X_9 = Number of seeds	0.087	0.003	0.020
X_{10} = Straw weight (g)	0.189	0.099	0.055
X_{11} = Harvest Index (%)	0.031	0.050	0.051
X_{12} = 1000 grain weight (g)	0.097	0.070	0.058
X_{13} = Leaf angle	0.236	0.687	0.512
X_{14} = Internodal length(cm)	0.092	0.007	0.073
X_{15} = Panicle exertion(cm)	0.012	0.175	0.169
X_{16} = Peduncle length(cm)	0.134	0.027	0.154

the plants to bloom, Days to maturity, number of productive tillers, panicle length, panicle weight, straw weight, leaf angle and peduncle length were the most important variables that contributed more towards discriminating the entries. The variables that contributed through the second vector were grain weight, Days to 50 per cent of the plants to bloom, Days to maturity, Number of productive tillers, panicle breadth, leaf angle, and panicle exertion could be considered as the most contributing towards the divergence. The third vector that contributed for the variables were Days to 50 per cent of the plants to bloom, Days to maturity, Number of productive tillers, panicle length, panicle weight, leaf angle, panicle exertion and peduncle length could be considered as the most contributing towards the divergence. Thus the variables like 50 per cent of the plants to bloom, Days to maturity, Number of productive tillers and leaf angle could be considered as the most contributing towards the divergence.

The first canonical vector absorbed 28.05 per cent of the total variability and second and third vectors absorbed 13.90 and 13.04 per cent respectively. Thus, three vectors put together accounted for 55.99 per cent of the total variability produced by all the characters under study. The remaining five vectors absorbed only 32.71 per cent of the variability and so they were not considered further.

4.1.4. Canonical graph.

Two Dimensional graph

Using the first two principle components, the canonical variables for 225 genotypes were derived and plotted on the graph (Fig.1). The Z_1 -axis refers to the first vector and Z_2 to the second vector. Most of the genotypes aggregated over short range towards Z_1 on Z_1 scale and some genotypes spatially at the extreme right of the Z_1 axis. However, along the Z_2 axis the genotypes showed a spatial distribution, thus separating the crowded genotypes on Z_1 axis, into distinct clusters. In general the entries showed a wider distribution in the graph. Along the first vector, the entry 77 (Strain I.Sc.456 from U.S.A) was on top at the extreme right. In the second vector the entry 12 (Strain I.Sc.459 from U.S.A) was at the top of the Z_2 axis. The remaining entries distributed within the extremes.

4.1.5. Primary clustering using canonical graph

By visual observation arbitrarily 225 genotypes were grouped into 56 clusters as shown in Fig. 1 and the entries in them are given in Table 5. Z_1 is accounted for more variability hence for primary clustering using canonical graph, the weightage needs to be given to Z_1 . Subsequently a second type of clustering was followed in which the Z_1 was

**Fig. 1. The Primary clusters formed on
the Canonical graph**

- Two dimensional graph.

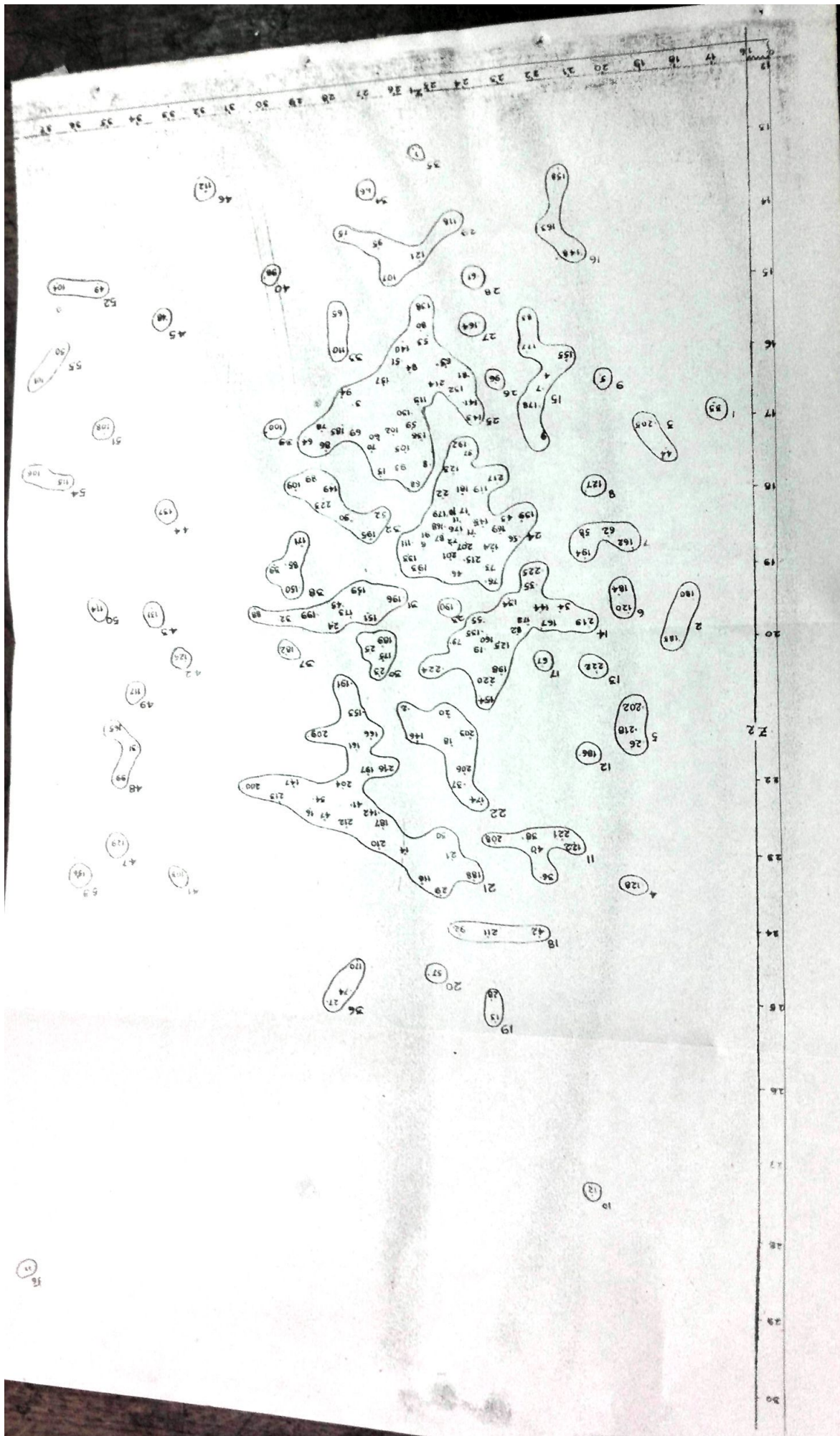


Table 5. Primary cluster formed on canonical graph

Cluster number	Number of strains	Accession number of entries (I.Sc.numbers)
1	1	33
2	2	180, 185
3	2	44, 205
4	1	128
5	3	26, 218, 202
6	2	120, 184
7	4	162, 62, 194, 58
8	1	127
9	1	5
10	1	12
11	6	122, 221, 36, 40, 38, 208
12	1	186
13	1	222
14	19	219, 34, 167, 144, 172, 35, 225, 82, 125, 198, 220, 19, 160, 135, 55, 79, 224, 134, 154
15	7	178, 7, 4, 155, 177, 83, 9
16	3	148, 163, 158
17	1	67

Table 5
(continued)

Cluster number	Number of strains	~~Accession number of entries~~ (I.Sc.numbers)
18	3	42, 211, 92
19	2	13, 28
20	1	57
21	25	188, 29, 21, 30, 116, 14, 210, 187, 142, 41, 212, 47, 16, 213, 200, 147, 54, 204, 216, 197, 161, 166, 153, 209, 191
22	8	174, 37, 206, 203, 18, 20, 146, 2
23	1	190
24	33	76, 73, 124, 56, 169, 43, 139, 215, 46, 201, 207, 71, 145, 72, 176, 10, 11, 17, 119, 181, 217, 193, 133, 111, 6, 91, 87, 168, 179, 22, 123, 97, 192
25	32	143, 141, 132, 81, 214, 68, 113, 130, 59, 136, 8, 15, 93, 105, 102, 70, 60, 69, 86, 183, 64, 78, 3, 94, 157, 84, 51, 140, 53, 80, 138, 63
26	1	96
27	1	1614
28	1	61
29	5	118, 121, 107, 95, 75
30	5	23, 175, 25, 189, 152

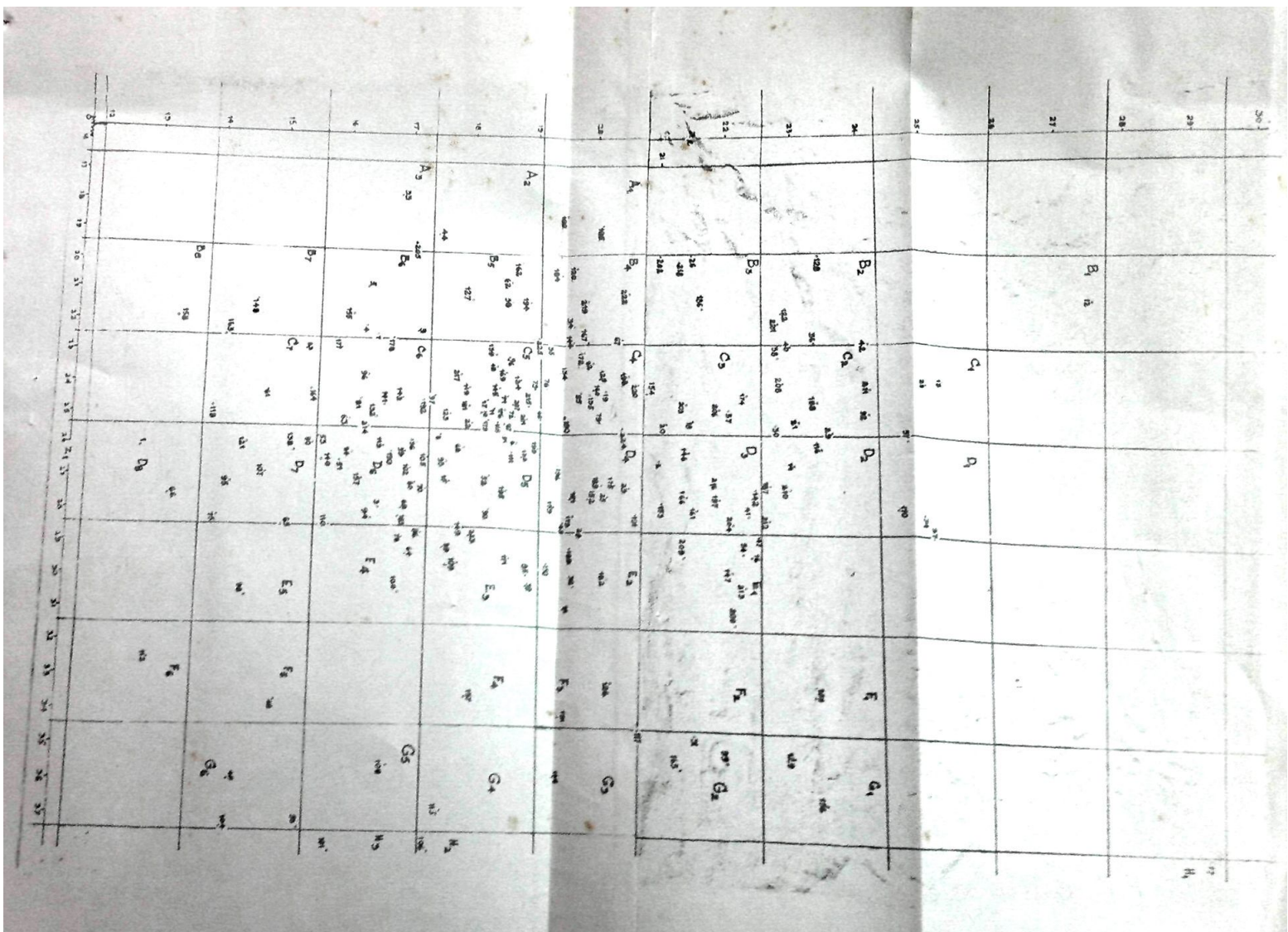
Table 5
(continued)

Cluster number	Number of strains	Accession number of entries (I.Sc.numbers)
31	9	196, 173, 24, 159, 45, 199, 32, 88, 151
32	7	52, 195, 90, 223, 149, 89, 109
33	2	110, 65
34	1	66
35	1	1
36	3	27, 74, 170
37	1	182
38	4	150, 85, 39, 171
39	1	100
40	1	98
41	1	103
42	1	126
43	1	131
44	1	137
45	1	48
46	1	112

Table 5
(continued)

Cluster number	Number of strains	Accession number of entries (I.Sc.numbers)
47	1	129
48	3	99, 31, 165
49	1	117
50	1	114
51	1	108
52	2	49, 104
53	1	156
54	2	115, 106
55	2	50, 101
56	1	77

Fig. 2. The Secondary clusters formed on the canonical graph and named as $A_1 - H_4$ are represented as a rectangular cell



divided into 8 equal parts and each part was considered as a main group. Again along the Z_2 axis each main group was subdivided into 10 equal parts as shown in Fig. 2.

Table 6 indicates the 46 groups formed with the entries included in them and the source of these entries.

The main group 'A' included 5 entries of which 4 are from India and one from China. In the main group 'B' there are 37 entries of which 28 are from India, 2 from Ethiopia and 7 from U.S.A. In the main group 'C' out of 72 entries, 58 are from India, 1 from Kenya, 12 from U.S.A. and 1 from Africa. In the main group 'D', 58 are from India, 1 from China, 1 from Kenya, 1 from Turkey, 5 from U.S.A. and 1 from Africa. In the main 'E' group, 19 were from India, 1 from China, 1 from Turkey, 1 from Africa. The main group 'F' included 6 entries, 4 are from India, 1 from Turkey and one from U.S.A. In the main 'G' group, there are 12 entries, 9 from India and 2 from USA and in the main 'H' group, there are 3 main group of which 2 are from India and 1 from U.S.A. Thus in this type of clustering thirty six of forty three exotic genotypes revealed random distribution along with the indigenous types. However, 13 (7 exotics and 6 indigenous) out of 46 clusters were solitary clusters in this grouping. Tables 7 and 8 indicate the entries included in the secondary clusters and their source.

Table 6. The Secondary clusters formed on the canonical graph

Main group	Sub group	Serial number	Accession number of the entry	Source of collection
1	2	3	4	5
A	A6	180	132	Jammu and Kashmir
		185	266	Karnataka
	A7	44	483	China
	A8	205	248	Karnataka
		33	363	Uttar Pradesh
	B	B2	12	459
B4		128	165	Madhya Pradesh
		42	410.B	Ethiopia
		122	138	Kerala
		36	186.B	Tamil Nadu
		221	642	U.S.A.
		40	154	Madhya Pradesh
B5		26	345	Uttar Pradesh
		218	196	Tamil Nadu
		202	334	Uttar Pradesh
		186	262	Karnataka
B6		222	470	U.S.A.
		67	162	Madhya Pradesh
		184	Arjuna	Andhra Pradesh
		35	518	U.S.A.
		120	156	Madhya Pradesh
		225	473	U.S.A.
		219	374	Assam

Table 6
(continued)

1	2	3	4	5
	34	131	Jammu and Kashmir	
	167	127	Jammu and Kashmir	
	144	142	Madhya Pradesh	
B7	162	80	Biher	
	139	525	U.S.A.	
	194	457	U.S.A.	
	62	373	Assam	
	58	392	Madhya Pradesh	
	127	410.A	Ethiopia	
B8	5	324	Uttar Pradesh	
	9	378	Assam	
	7	137.A	Jammu and Kashmir	
	178	212.A	Maharashtra	
	4	145	Maharashtra	
	177	405.B	Assam	
	155	1	Andhra Pradesh	
B9	148	155	Madhya Pradesh	
	163	245	Karnataka	
B10	158	397	Madhya Pradesh	
C3	13	253	Karnataka	
	57	184	Tamil Nadu	
	28	RS.118	Karnataka	
C4	211	395	Madhya Pradesh	
	92	264	Karnataka	
	188	96	Gujarat	
	29	519	U.S.A.	

Table 6
(continued)

1	2	3	4	5
		38	342	Uttar Pradesh
		208	354	Uttar Pradesh
		21	323	Uttar Pradesh
		30	160	Madhya Pradesh
05		174	73	Bihar
		37	150	Uttar Pradesh
		154	58	Bihar
		206	101.8	Himachal Pradesh
		203	97	Gujarat
		18	68	Bihar
		20	265	Karnataka
06		220	171	Madhya Pradesh
		224	175	Tamil Nadu
		198	358	Uttar Pradesh
		160	136	Karnataka
		125	398	Madhya Pradesh
		19	234	Karnataka
		190	464	U.S.A.
		135	377	Assam
		79	471	U.S.A.
		55	60	Bihar
		82	K.222-1	Karnataka
		172	45	Bihar
		134	202	Tamil Nadu
		76	573	U.S.A.
07		73	582	U.S.A.
		46	135	Jammu and Kashmir
		215	Co.3	Tamil Nadu
		201	96	Bihar

Table 6
(continued)

1	2	3	4	5
	72	193	Tamil Nadu	
	124	210	Maharashtra	
	207	182	Tamil Nadu	
	87	251	Karnataka	
	56	396	Madhya Pradesh	
	169	35.B	Bengal	
	43	531	U.S.A.	
	145	385	Assam	
	71	460	U.S.A.	
	176	141	Kerala	
	168	257	Karnataka	
	91	406.B	Assam	
	179	375	Assam	
	11	89	Bihar	
	17	172	Madhya Pradesh	
	10	108	Himachal Pradesh	
	22	581	U.S.A.	
	181	254	Karnataka	
	119	255	Karnataka	
	217	643	U.S.A.	
	123	417.B	Africa	
	97	505	Kenya	
08	192	339	Uttar Pradesh	
	143	137	Jammu and Kashmir	
	141	343	Uttar Pradesh	
	132	101.A	Himachal Pradesh	
	113	140	Kerala	
	96	448	U.S.A.	
	81	406.A	Assam	

Table 6
(continued)

1	2	3	4	5
		63	256	Karnataka
		214	642	U.S.A.
		65	173	Tamil Nadu
		164	190	Tamil Nadu
	C9	83	226	Maharashtra
		118	458	U.S.A.
		61	263	Karnataka
D	D3	27	146	Madhya Pradesh
		74	153	Madhya Pradesh
		170	40	Bihar
	D4	116	46	Bihar
		14	222.A	Maharashtra
		210	481	China
		187	417.A	Africa
	D5	142	335	Uttar Pradesh
		212	35.A	Bengal
		41	369	Uttar Pradesh
		204	143	Madhya Pradesh
		216	36	Bengal
		197	70	Karnataka
		161	99.C	Gujarat
		166	52	Bihar
		146	465.B	U.S.A.
		2	274	Karnataka
		153	90	Bihar
	D6	191	104	Himachal Pradesh
		23	183	Tamil Nadu
		175	221	Maharashtra
		25	69	Bihar
		189	66	Bihar

Table 6
(continued)

1	2	3	4	5
		152	180	Tamil Nadu
		24	386	Bihar
		196	271	Karnataka
		151	107	Himachal Pradesh
		173	159.A	Madhya Pradesh
		45	63	Bihar
		159	260	Karnataka
D7		193	417.B	Africa
		133	232	Uttar Pradesh
		16	359	Uttar Pradesh
		111	268	Karnataka
		195	400	Madhya Pradesh
		52	388	Bihar
		90	106	Himachal Pradesh
		15	223.B.	Maharashtra
		93	270	Karnataka
		68	380	Assam
		8	509	Turkey
		149	376	Assam
		223	475	U.S.A.
D8		105	340	Uttar Pradesh
		70	370	Uttar Pradesh
		136	508.A	Kenya
		59	236	Karnataka
		102	267	Karnataka
		60	203	Tamil Nadu
		69	189	Tamil Nadu
		183	362	Uttar Pradesh
		3	84	Bihar
		94	432	U.S.A.

Table 6
(continued)

1	2	3	4	5
		157	178	Tamil Nadu
		130	197	Tamil Nadu
		84	643.A	U.S.A.
		51	276	Karnataka
		53	99.B	Gujarat
		140	235	Karnataka
		110	39.B	Bengal
	D9	80	455	U.S.A.
		138	234	Uttar Pradesh
		107	169	Madhya Pradesh
		121	364	Uttar Pradesh
		95	326	Uttar Pradesh
		75	148	Madhya Pradesh
	D10	66	59	Bihar
		1	214	Maharashtra
B	E5	47	62	Bihar
		6	158	Madhya Pradesh
		54	133	Jammu and Kashmir
		213	152	Madhya Pradesh
		147	238	Karnataka
		200	474	U.S.A.
		209	161	Madhya Pradesh
	E6	182	64	Bihar
		199	181	Tamil Nadu
		32	164	Madhya Pradesh
		88	389	Bihar
		150	101	Himachal Pradesh

Table 6
(continued)

1	2	3	4	5
	E7	39	176	Tamil Nadu
		85	405.A	Assam
		171	198.A	Tamil Nadu
		89	507	Turkey
		109	259	Karnataka
	E8	86	217	Maharashtra
		64	215.A	Maharashtra
		78	482	China
		100	325	Uttar Pradesh
	E9	98	331	Uttar Pradesh
F	F4	103	508.A	Kenya
	F5	31	103	Himachal Pradesh
	F6	126	320	Uttar Pradesh
		131	34	Bengal
	F7	137	472	U.S.A.
	F9	48	231	Maharashtra
	F10	112	504	Turkey
G	G4	156	102	Himachal Pradesh
		129	350	Uttar Pradesh
	G5	99	521	U.S.A.
		165	200	Tamil Nadu

Table 6
(continued)

1	2	3	4	5
	G6	114	371	Uttar Pradesh
		117	211.B	Maharashtra
	G7	115	469	U.S.A.
	G8	108	253	Karnataka
	G9	50	329	Uttar Pradesh
		49	352	Uttar Pradesh
		104	168	Madhya Pradesh
H	H1	77	456	U.S.A.
	H7	106	192	Tamil Nadu
	H8	101	360	Uttar Pradesh

Table 7. Entries included in each of the 46 groups
formed on canonical graph

Main group	Sub group	Number and source of collection						
		India	Africa	China	Ethiopia	Kenya	Turkey	U.S.A.
A	A6	2	-	-	-	-	-	-
	A7	-	-	1	-	-	-	-
	A8	2	-	-	-	-	-	-
B	B2	-	-	-	-	-	-	1
	B4	4	-	-	1	-	-	1
	B5	4	-	-	-	-	-	-
	B6	7	-	-	-	-	-	3
	B7	3	-	-	1	-	-	2
	B8	7	-	-	-	-	-	-
	B9	2	-	-	-	-	-	-
	B10	1	-	-	-	-	-	-
C	C3	3	-	-	-	-	-	-
	C4	7	-	-	-	-	-	1
	C5	7	-	-	-	-	-	-
	C6	11	-	-	-	-	-	3
	C7	19	1	-	-	1	-	5
	C8	9	-	-	-	-	-	2
	C9	2	-	-	-	-	-	1
D	D3	3	-	-	-	-	-	-
	D4	2	1	1	-	-	-	-
	D5	10	-	-	-	-	-	1
	D6	12	-	-	-	-	-	-
	D7	10	1	-	-	-	1	1
	D8	14	-	-	-	1	-	2
	D9	5	-	-	-	-	-	1
	D10	2	-	-	-	-	-	-

continued

Table 7
(continued)

Main group	Sub group	Number and source of collection					
		India	Africa	China	Ethiopia	Kenya	Turkey U.S.A.
E	E5	6	-	-	-	-	1
	E6	5	-	-	-	-	-
	E7	4	-	-	-	-	1
	E8	3	-	1	-	-	-
	E9	1	-	-	-	-	-
F	F4	-	-	-	-	1	-
	F5	1	-	-	-	-	-
	F6	2	-	-	-	-	-
	F7	-	-	-	-	-	1
	F9	1	-	-	-	-	-
	F10	-	-	-	-	-	1
G	G4	2	-	-	-	-	-
	G5	1	-	-	-	-	1
	G6	2	-	-	-	-	-
	G7	-	-	-	-	-	1
	G8	1	-	-	-	-	-
	G9	3	-	-	-	-	-
H	H1	-	-	-	-	-	1
	H7	1	-	-	-	-	-
	H8	1	-	-	-	-	-
Total		182	3	3	2	3	3
							29

Table 8. Entries collected from Indian origin, included in each of the 46 groups formed on canonical graph

Main group	Sub group	Number and source of collection (Indian States)														
		Andhra Pradesh	Assam	Ben-gal	Bihar	Gud-jarat	Hima-chal Pradesh	Jammu and Kashmir	Karna-taka	Kerala	Maha-rashtra	Madhya Pradesh	Tamil Nadu	Uttar Pradesh		
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15		
A	A6	-	-	-	-	-	-	1	1	-	-	-	-	-		
	A8	-	-	-	-	-	-	-	1	-	-	-	-	1		
B	B4	-	-	-	-	-	-	-	-	1	-	2	1	-		
	B5	-	-	-	-	-	-	-	1	-	-	-	1	2		
	B6	1	1	-	-	-	-	2	-	-	-	3	-	-		
	B7	-	1	-	1	-	-	-	-	-	-	1	-	-		
	B8	1	2	-	-	-	-	1	-	-	2	-	-	1		
	B9	-	-	-	-	-	-	-	1	-	-	1	-	-		
	B10	-	-	-	-	-	-	-	-	-	-	1	-	-		
C	C3	-	-	-	-	-	-	-	2	-	-	-	1	-		
	C4	-	-	-	-	1	-	-	1	-	-	2	-	3		
	C5	-	-	-	3	1	1	-	1	-	-	-	-	1		
	C6	-	1	-	2	-	-	-	3	-	-	2	2	1		
	C7	-	3	1	2	-	1	1	4	1	1	2	3	-		
	C8	-	1	-	-	-	1	1	1	1	-	-	2	2		
			-	-	-	-	-	-	-	-	-	-	-	-		
			-	-	-	-	-	-	-	-	-	-	-	-		
			-	-	-	-	-	-	-	-	-	-	-	-		

Continued

Table 8
(continued)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
D	D3	-	-	-	-	1	-	-	-	-	-	-	2	-	-
	D4	-	-	-	-	1	-	-	-	-	-	1	-	-	-
	D5	-	-	-	2	2	1	-	-	2	-	-	1	-	2
	D6	-	-	-	-	4	-	2	-	2	-	1	1	2	-
	D7	-	-	2	-	1	-	1	-	2	-	1	1	-	2
	D8	-	-	-	1	1	1	-	-	4	-	-	-	4	3
	D9	-	-	-	-	-	-	-	-	-	-	-	2	-	3
	D10	-	-	-	-	1	-	-	-	-	-	1	-	-	-
E	E5	-	-	-	-	1	-	-	1	1	-	-	3	-	-
	E6	-	-	-	-	2	-	1	-	-	-	-	1	1	-
	E7	-	-	1	-	-	-	-	-	4	-	-	-	2	-
	E8	-	-	-	-	-	-	-	-	-	-	2	-	-	1
	E9	-	-	-	-	-	-	-	-	-	-	-	-	-	1
F	F5	-	-	-	-	-	-	1	-	-	-	-	-	-	-
	F6	-	-	-	1	-	-	-	-	-	-	-	-	-	1
	F9	-	-	-	-	-	-	-	-	-	-	1	-	-	-
G	G4	-	-	-	-	-	-	1	-	-	-	-	-	-	1
	G5	-	-	-	-	-	-	-	-	-	-	-	-	1	-
	G6	-	-	-	-	-	-	-	-	-	-	1	-	-	1
	G8	-	-	-	-	-	-	-	-	1	-	-	-	-	-
	G9	-	-	-	-	-	-	-	-	-	-	-	1	-	2
H	H7	-	-	-	-	-	-	-	-	-	-	-	-	1	-
	H8	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Total		2	12	4	5	22	4	9	7	30	3	12	26	21	29

4.1.6. D²- Analysis

The square of the distance (D²-values) between any two entries, calculated as the sum of squares of the differences between the mean values of all the 16 transformed variables were used for final grouping of the entries. Since each entry produced 224 combinations, 25200 D² values were obtained for 225 genotypes. The D² values were tested for the significance using Hotelling's T² analysis. It was found that all these combinations having a D² value more than 167.04 were significant. Accordingly about 63.22 per cent of the D² values were not significant. Following Tocher's method of clustering, 33 clusters were formed from the 225 genotypes.

Table 9 indicates the distribution of genotypes, the accession of the entries and the source in the 33 clusters. Cluster 1 was the largest cluster with 87 entries possessing entries of diverse origin viz. India, U.S.A., Kenya, Africa and Turkey.

Cluster 2 possessed 26 entries possessing genotypes from India, Ethiopia, U.S.A. and China.

Cluster 3 had 19 entries from India, Africa, China, U.S.A. and Ethiopia.

Cluster 4 had 8 entries from India and U.S.A.

Fig. 3. The 33 clusters formed through D^2 -analysis (super imposed on the Canonical graph). The entries encircled represent the inclusions of the respective D^2 clusters, while the canonical variate based clusters are named as $A_1 - H_4$ are represented as a rectangular cell



Table 9. The D² clusters and the entries included in them

Cluster Number	Number of entries	Serial number	I.Sc.number of the entry	Country (source)
1	87	70	370	Uttar Pradesh
		183	362	Uttar Pradesh
		102	267	Karnataka
		52	388	Bihar
		15	223B	Maharashtra
		69	189	Tamil Nadu
		168	257	Karnataka
		71	460	U.S.A.
		214	642	U.S.A.
		201	95	Bihar
		96	448	U.S.A.
		192	339	Uttar Pradesh
		176	141	Kerala
		181	254	Karnataka
		53	99.B	Gujarat
		154	58	Bihar
		119	255	Karnataka
		76	573	U.S.A.
		190	464	U.S.A.
		172	45	Bihar
		198	358	Uttar Pradesh
		203	97	Gujarat
		191	104	Himachal Pradesh
		97	505	Kenya
		169	35.B	Bengal
		65	173	Tamil Nadu
		160	136	Karnataka
		206	101.B	Himachal Pradesh
		20	265	Karnataka
		159	260	Karnataka
		111	268	Karnataka

Continued

Table 9
(continued)

Cluster number	Number of entries	Serial number	I. So. number of the entry	Country (source)
		110	39.B	Bengal
		140	235	Karnataka
		63	256	Karnataka
		94	432	U.S.A.
		6	158	Madhya Pradesh
		22	581	U.S.A.
		3	84	Bihar
		23	183	Tamil Nadu
		225	475	U.S.A.
		84	643.A	U.S.A.
		56	396	Madhya Pradesh
		179	375	Assam
		195	400	Madhya Pradesh
		145	385	Assam
		19	234	Karnataka
		146	465.B	U.S.A.
		86	217	Maharashtra
		90	106	Himachal Pradesh
		45	63	Bihar
		189	66	Bihar
		136	508.A	Kenya
		113	140	Kerala
		72	193	Tamil Nadu
		224	175	Tamil Nadu
		2	274	Karnataka
		81	406.A	Assam
		109	259	Karnataka
		60	203	Tamil Nadu
		59	236	Karnataka
		17	172	Madhya Pradesh
		152	180	Tamil Nadu
		130	197	Tamil Nadu

Continued

Table 9
(continued)

Cluster Number	Number of entries	Serial number	I.Se.number of the entry	Country (source)
		123	417.B	Africa
		157	178	Tamil Nadu
		124	210	Maharashtra
		175	221	Maharashtra
		223	475	U.S.A.
		215	Co.3	Tamil Nadu
		10	108	Himachal Pradesh
		68	380	Assam
		82	K.222-1	Karnataka
		173	159.A	Madhya Pradesh
		151	107	Himachal Pradesh
		93	270	Karnataka
		64	215.A	Maharashtra
		134	202	Tamil Nadu
		35	518	U.S.A.
		164	190	Tamil Nadu
		11	89	Bihar
		217	643	U.S.A.
		8	509	Turkey
		91	406.B	Assam
		196	271	Karnataka
		51	276	Karnataka
		43	531	U.S.A.
		105	340	Uttar Pradesh
2	26	26	345	Uttar Pradesh
		218	196	Tamil Nadu
		180	132	Jammu and Kashmir
		120	156	Madhya Pradesh
		185	266	Karnataka

Continued

Table 9
(continued)

Cluster Number	Number of entries	Serial number	I.Sc.number of the entry	Country (source)
		219	374	Assam
		184	Arjuna	Andhra Pradesh
		127	410.A	Ethiopia
		167	127	Jammu and Kashmir
		222	470	U.S.A.
		186	262	Karnataka
		58	392	Madhya Pradesh
		44	483	China
		5	324	Uttar Pradesh
		34	131	Jammu and Kashmir
		205	248	Karnataka
		62	373	Assam
		202	334	Uttar Pradesh
		162	80	Bihar
		33	363	Uttar Pradesh
		194	457	U.S.A.
		40	154	Madhya Pradesh
		67	162	Madhya Pradesh
		38	342	Uttar Pradesh
		221	642	U.S.A.
		125	398	Madhya Pradesh
3	19	29	519	U.S.A.
		30	160	Madhya Pradesh
		14	222.A	Maharashtra
		41	369	Uttar Pradesh
		42	410.B	Ethiopia
		188	96	Gujarat
		128	165	Madhya Pradesh
		187	417.A	Africa

Continued

Table 9
(continued)

100

Cluster number	Number of entries	Serial number	I,So.number of the entry	Country (source)
		210	481	China
		211	395	Madhya Pradesh
		212	35.A	Bengal
		28	RS.118	Karnataka
		21	323	Uttar Pradesh
		116	46	Bihar
		37	150	Uttar Pradesh
		174	73	Bihar
		142	335	Uttar Pradesh
		18	68	Bihar
		16	359	Uttar Pradesh
4	8	101	360	Uttar Pradesh
		115	469	U.S.A.
		49	352	Uttar Pradesh
		108	253	Karnataka
		50	329	Uttar Pradesh
		104	168	Madhya Pradesh
		106	192	Tamil Nadu
		48	231	Maharashtra
5	11	47	62	Bihar
		147	238	Karnataka
		54	133	Jammu and Kashmir
		213	152	Madhya Pradesh
		200	474	U.S.A.
		197	70	Karnataka
		209	161	Madhya Pradesh
		161	99.0	Gujarat
		166	52	Bihar
		153	90	Bihar
		204	143	Madhya Pradesh

Continued

Table 9
(continued)

Cluster Number	Number of entries	Serial number	I.So number of the entry	Country (source)
6	14	155	1	Andhra Pradesh
		163	245	Karnataka
		4	145	Maharashtra
		148	155	Madhya Pradesh
		158	397	Madhya Pradesh
		7	137.A	Jammu and Kashmir
		178	212.A	Maharashtra
		9	378	Assam
		139	525	U.S.A.
		144	142	Madhya Pradesh
		143	137	Jammu and Kashmir
		83	226	Maharashtra
		177	405.B	Assam
		141	343	Uttar Pradesh
7	12	80	455	U.S.A.
		118	458	U.S.A.
		95	326	Uttar Pradesh
		75	148	Madhya Pradesh
		138	234	Uttar Pradesh
		107	169	Madhya Pradesh
		61	263	Karnataka
		1	214	Maharashtra
		121	364	Uttar Pradesh
		98	331	Uttar Pradesh
		66	164	Madhya Pradesh
		132	101.A	Himachal Pradesh

Continued

Table 9
(continued)

Cluster Number	Number of entries	Serial number	I.So.number of the entry	Country
8	8	149	376	Assam
		150	101	Himachal Pradesh
		199	181	Tamil Nadu
		171	198.A	Tamil Nadu
		85	405.A	Assam
		24	386	Bihar
		182	64	Bihar
		32	164	Madhya Pradesh
9	5	129	350	Uttar Pradesh
		165	200	Tamil Nadu
		31	103	Himachal Pradesh
		117	211.B	Maharashtra
		114	371	Uttar Pradesh
10	3	99	521	U.S.A.
		126	320	Uttar Pradesh
		131	34	Bengal
11	3	27	146	Madhya Pradesh
		170	40	Bihar
		74	153	Madhya Pradesh
12	2	79	471	U.S.A.
		135	377	Assam
13	2	87	251	Karnataka
		193	417.B	Africa

Continued

Table 9
(continued)

Cluster number	Number of entries	Serial number	I.So.number of the entry	Country (source)
14	2	25	69	Bihar
		39	176	Tamil Nadu
15	2	78	482	China
		100	325	Uttar Pradesh
17	2	55	60	Bihar
		220	171	Madhya Pradesh
18	2	36	186.B	Tamil Nadu
		122	138	Kerala
19	1	73	582	U.S.A.
20	1	208	354	Uttar Pradesh
21	1	133	232	Uttar Pradesh
22	1	156	102	Himachal Pradesh
23	1	103	508.A	Kenya
24	1	89	507	Turkey
25	1	137	472	U.S.A.
26	1	112	504	Turkey
27	1	88	389	Bihar
28	1	46	135	Jammu and Kashmir
29	1	12	459	U.S.A.
30	1	207	182	Tamil Nadu
31	1	92	264	Karnataka
32	1	77	456	U.S.A.
33	1	216	36	Bengal

Cluster 5 had 11 entries originated from India and U.S.A.

Cluster 6 had 14 entries from India and U.S.A.

Cluster 7 had 12 entries from India and U.S.A.

Cluster 8 had 8 entries of Indian origin only.

Cluster 9 had 7 entries with no exotic entry.

Cluster 10 had 3 entries, 2 from India and 1 from U.S.A.

Cluster 11 had 3 entries of Indian origin only.

Cluster 12 had 2 entries, one each from India and U.S.A.

Cluster 13 had 2 entries, one each from India and Africa.

Cluster 14 had 2 entries from Indian origin.

Cluster 15 had 2 entries of Indian origin.

Cluster 16 had 2 entries, one from India and another from China.

Cluster 17 had 2 entries of Indian origin.

Cluster 18 had 2 entries of Indian origin

Cluster 19 had a solitary entry (I.Sc.582) from U.S.A.

Cluster 20 had a solitary entry (I.Sc.354) from India.

Cluster 21 had a solitary entry (I.Sc.232) from India.

Cluster 22 had a solitary entry (I.Sc.102) from India.

Cluster 23 had a solitary entry (I.Sc.508.A) from Kenya.

Cluster 24 had a solitary entry (I.So. 89) from Turkey.

Cluster 25 had a solitary entry (I.So.472) from U.S.A.

Cluster 26 had a solitary entry(I.So.504) from Turkey.

Cluster 27 had a solitary entry(I.So.389) from Bihar
(India).

Cluster 28 had a solitary entry (I.So.135) from
Jammu and Kashmir, India.

Cluster 29 had a solitary entry (I.So.459) from U.S.A.

Cluster 30 had a solitary entry (I.So.182) from
Tamil Nadu, India.

Cluster 31 had a solitary entry (I.So.264) from
Karnataka, India.

Cluster 32 had a solitary entry(I.So.436) from U.S.A.

Cluster 33 had a solitary entry(I.So.36) from
Bengal, India.

In general, there was no relation between the clustering pattern of the genotypes and their geographic origins but 16 were distinctly remained solitary of diverse geographic origin.

The clusters formed through D^2 analysis are superimposed on the canonical graph in Fig. 3.

The mean values of the 16 characters for the 33 clusters are presented in Table 10.

Table 10. The mean values of the 16 characters for the 33 clusters

Cluster Number	Grain yield per plant (g)	Plant height (cm)	50% of the plants to bloom (days)	50% of the plants to maturity (days)	Number of tillers/plant	Panicle length (cm)	Panicle breadth (cm)	Panicle weight (g)	No. of seeds	Straw weight (g)	Harvest index (%)	1000 grain weight (g)	Leaf angle	Inter-nodal length (cm)	Panicle exertion cle	Peduncle length (cm)
	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
1	11.38	118.80	50.48	73.12	4.11	13.28	1.19	13.32	213.63	15.54	38.88	3.20	19.85	10.55	12.28	36.61
2	7.37	91.29	45.88	66.59	3.84	12.94	1.21	8.64	206.38	10.76	37.94	3.03	24.43	10.17	11.17	35.16
3	11.40	112.51	54.16	76.66	4.29	13.56	1.23	8.50	206.46	15.34	39.19	3.14	27.36	10.25	12.31	38.31
4	12.32	113.59	74.63	97.38	4.66	13.26	1.27	14.21	191.00	15.52	41.46	3.26	16.09	10.45	11.87	36.82
5	12.75	107.67	54.18	81.50	4.02	15.00	1.33	14.76	202.12	18.16	38.47	2.98	22.16	10.80	13.30	39.60
6	6.35	101.82	47.46	66.82	3.31	14.19	1.21	7.58	222.38	9.73	35.35	2.79	18.66	9.98	11.96	36.74
7	10.27	103.59	51.00	71.16	4.93	12.86	1.28	12.62	185.29	12.72	39.92	2.69	15.19	11.23	12.17	38.73
8	10.95	100.15	55.81	82.87	3.40	13.50	1.30	12.28	199.00	14.61	32.22	3.31	19.22	10.52	13.00	38.58
9	8.34	110.95	71.10	101.00	3.30	13.25	1.37	10.45	221.32	12.59	36.43	3.09	22.22	9.60	11.50	34.40
10	13.10	108.91	58.50	82.50	4.03	12.90	1.18	12.32	131.36	12.60	39.99	3.18	16.60	10.71	12.56	39.26
11	10.64	101.88	54.35	83.66	3.30	12.15	1.16	12.30	249.49	13.69	40.20	3.06	26.66	10.22	11.16	34.53
12	9.68	107.55	53.52	72.45	2.30	10.85	1.23	13.32	150.02	14.98	34.25	3.30	26.95	11.36	13.65	38.95
13	10.21	105.12	53.75	71.00	7.30	9.87	1.10	12.77	157.07	14.96	38.56	3.45	19.55	9.76	12.97	38.47
14	9.24	107.75	72.25	85.00	5.20	13.19	1.25	8.40	295.48	12.81	38.38	4.45	38.20	10.11	11.10	35.20
15	8.71	110.92	72.25	76.75	3.60	12.50	1.14	10.36	204.67	13.27	36.52	2.75	26.50	10.48	10.25	37.87
16	10.41	106.90	57.25	74.25	2.35	11.30	1.04	13.29	181.41	14.40	36.28	3.32	19.80	11.04	12.15	38.80
17	15.83	123.12	51.25	67.00	2.95	15.52	1.80	20.65	215.55	26.50	36.74	4.35	24.62	10.01	13.98	44.78
18	9.51	105.30	46.75	69.00	1.95	10.15	1.15	11.49	188.55	16.15	35.09	3.10	21.12	11.87	15.05	25.30
19	11.56	104.20	49.50	65.00	3.30	12.70	1.21	15.27	505.25	15.42	33.07	2.45	22.70	11.75	12.70	32.10
20	8.85	110.00	44.50	72.50	4.90	12.10	1.00	10.50	171.20	18.36	28.94	2.65	21.38	9.03	11.30	36.50
21	8.00	484.90	54.00	55.00	2.80	13.95	1.21	10.21	116.95	11.20	37.38	2.55	21.80	10.10	9.60	28.40
22	5.76	105.70	51.00	97.00	2.20	10.20	1.62	12.00	215.60	9.99	37.85	2.80	18.40	10.37	11.20	34.50
23	7.31	110.20	68.00	87.00	4.85	11.40	1.44	10.35	157.90	17.97	25.68	3.25	24.20	10.02	12.05	45.80
24	22.27	104.45	51.50	73.50	5.00	12.80	1.30	24.32	137.48	27.92	42.62	1.80	16.40	9.88	11.70	39.60
25	6.16	80.80	72.00	96.00	2.40	13.80	1.32	5.98	303.70	4.60	32.12	2.40	20.30	8.68	9.30	31.70
26	18.87	118.00	64.50	81.50	3.70	14.70	1.24	21.05	246.05	19.31	46.72	3.55	16.10	11.40	12.15	40.60
27	22.79	121.00	52.50	74.00	3.40	14.40	1.41	31.17	169.60	26.65	41.59	3.40	23.00	9.57	16.20	25.30
28	5.27	155.60	55.50	75.50	2.40	13.80	1.22	6.74	307.50	14.79	24.90	3.00	24.50	9.30	26.20	34.30
29	9.39	111.00	46.50	71.50	3.80	13.60	1.36	10.58	149.60	11.54	42.75	2.90	30.25	9.93	11.80	42.80
30	13.33	117.00	26.95	75.00	4.60	7.34	0.64	20.76	241.25	22.18	37.58	3.65	13.10	4.66	7.62	53.88
31	15.75	115.40	51.00	76.00	4.20	14.75	1.30	17.30	156.45	17.58	47.55	3.20	27.20	10.63	14.50	39.10
32	14.60	111.00	50.50	98.50	1.30	14.20	1.24	16.92	277.00	11.31	51.69	3.00	17.06	9.98	12.70	32.20
33	9.44	74.60	56.60	83.50	4.50	8.50	2.30	9.66	496.40	9.44	11.20	3.65	23.60	10.02	9.40	23.80

The Intra-cluster and Inter-cluster D^2 values

The intra-cluster distances (D^2 values) and inter-cluster distances (D^2 values) are presented in Table 11. The intra-cluster D^2 values ranged from 15.50 (cluster number 4) to 57.00 (cluster number 18). The other intra-cluster distances lying between these values. There were 15 solitary clusters viz., 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 and 33 possessing single entries in them and had no intra-cluster distances.

The inter-cluster D^2 values varied from 53.78 to 981.70. The other inter-cluster D^2 values were lying between these values.

The Z values obtained for 16 characters means for 4 clusters viz., 12 and 18(nearest) and 29 and 32(distant) are presented in a profile graph (Fig. 4) to represent the pattern of differences existing among these clusters. It could be seen from this graph that the clusters 12 and 18 have similar trend for most of the characters while the distant clusters 29 and 32 indicated an opposite trend for all the characters.

Table 11. Inter-cluster and Intra-cluster D^2 values for 33 clusters in Setaria italica B.

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	37.57 (6.14)	9.14	8.72	13.80	8.59	8.74	8.35	8.14	12.58	11.53	10.17	6.02	9.72	12.84	14.05	8.73	9.59	11.06	10.74	9.12
2	83.58	37.82 (6.15)	9.44	18.08	11.24	9.04	10.93	11.32	16.32	15.66	11.51	9.09	11.22	14.23	14.36	12.00	11.09	9.22	10.89	9.61
3	76.05	89.17 (6.60)	46.24	15.29	9.86	11.21	11.87	9.69	12.38	12.67	8.33	8.32	10.91	11.96	13.19	10.66	10.42	9.67	10.58	9.49
4	190.47	326.90	234.02 (5.05)	25.50	13.29	16.37	13.67	11.72	9.08	10.96	14.90	15.26	15.13	12.73	19.34	11.22	17.05	19.52	17.15	17.35
5	70.48	126.56	97.29	176.75 (6.40)	40.96	11.64	10.61	7.62	11.18	9.47	8.36	9.79	11.15	13.88	13.75	9.61	10.14	11.80	11.46	8.64
6	76.44	81.86	125.79	268.14	135.62 (6.71)	45.02	9.04	10.72	15.71	14.81	12.85	10.31	11.48	14.58	15.45	11.04	11.90	12.27	13.37	10.62
7	69.81	119.59	141.00	186.94	112.71	81.85	38.44 (6.20)	8.96	13.06	12.03	12.35	10.08	11.73	14.63	16.29	8.78	12.00	13.56	12.08	11.64
8	66.31	128.29	93.94	137.39	58.14	114.99	80.35 (6.18)	35.19	10.71	9.84	9.41	9.80	10.92	13.61	14.57	8.02	12.32	12.81	12.25	9.88
9	161.01	266.45	153.36	82.59	128.02	246.95	170.78	114.72	44.48 (6.67)	8.66	10.85	13.29	14.31	11.53	17.17	10.40	15.96	16.63	15.68	14.93
10	132.99	245.36	160.54	120.66	89.76	219.45	144.91	61.72	75.09 (7.13)	50.83	10.89	13.56	12.90	16.36	25.28	10.18	14.98	16.57	16.26	12.00
11	103.58	132.50	69.41	222.18	69.98	165.23	152.64	88.69	117.92	116.62 (7.19)	51.69	10.34	12.67	13.52	13.77	11.04	11.85	11.19	12.10	9.55
12	74.46	88.04	69.38	233.05	95.99	106.48	101.67	96.08	176.73	184.07	107.09	28.94 (5.38)	11.87	12.13	13.56	7.71	9.20	7.33	11.92	10.75
13	94.50	125.91	119.13	230.64	124.50	131.97	137.67	119.44	205.03	167.69	160.74	140.92	35.88 (5.99)	13.09	15.62	12.57	13.89	14.44	12.92	9.91
14	165.08	202.57	143.26	162.17	192.75	212.62	214.30	185.47	133.10	267.81	182.83	147.85	171.36	36.60 (6.05)	17.14	12.70	14.67	15.30	13.20	16.81
15	197.65	206.27	174.15	374.51	189.19	238.92	265.49	212.34	295.95	639.49	189.04	184.05	244.22	294.09	39.18 (6.26)	15.11	15.05	14.29	15.55	13.72
16	76.33	144.12	113.68	125.89	92.47	122.05	77.26	64.42	108.36	103.76	122.00	59.50 (6.44)	158.19	161.47	228.47	41.47	13.33	12.13	13.20	12.91
17	93.90	123.19	108.58	290.88	103.01	141.78	144.20	151.98	254.99	224.41	140.60	84.00	193.08	215.36	226.72	128.40 (6.88)	47.53	10.30	10.52	11.32
18	122.36	90.47	93.64	381.30	139.28	150.78	184.10	164.19	276.60	274.84	125.37	53.78	208.76	234.23	204.40	147.16	106.24	57.00	12.65	10.97
19	101.00	118.80	111.97	294.40	131.54	178.97	146.05	150.11	246.05	261.47	166.44	142.28	166.96	174.33	242.06	174.21	110.88	160.50	-	12.43
20	84.03	92.03	90.22	301.27	74.77	112.92	135.53	97.72	223.01	144.16	91.33	115.67	98.39	282.66	188.47	151.71	128.32	120.52	154.71	-

Values in the diagonal = Intracluster D^2 Values in parenthesis = Intracluster D ($\sqrt{D^2}$)Values above the diagonal = Intercluster D^2 Values below the diagonal = Intercluster D ($\sqrt{D^2}$)

Table 11. (continued)

Cluster	21	22	23	24	25	26	27	28	29	30	31	32	33
1	10.72	14.66	12.41	9.80	12.88	11.26	11.97	10.42	22.12	13.00	12.37	23.20	13.22
2	11.91	18.07	15.41	13.54	15.25	15.45	15.68	11.23	21.66	15.01	12.58	25.98	14.22
3	11.42	14.77	11.41	12.01	13.48	13.87	12.53	11.75	21.18	15.46	11.33	22.81	13.12
4	15.68	13.09	12.87	13.47	7.47	8.85	14.13	16.13	26.10	20.18	18.44	23.47	16.73
5	11.74	12.43	10.50	9.33	13.27	12.37	10.73	11.87	21.99	13.17	12.35	21.08	13.64
6	11.69	17.48	15.84	12.14	14.23	13.80	15.64	13.13	23.02	14.55	14.55	25.63	14.75
7	11.66	15.19	14.48	10.44	13.09	10.59	13.26	11.32	23.68	13.72	14.83	23.92	15.28
8	11.38	11.32	10.15	10.10	10.39	11.02	11.89	11.51	22.92	13.79	13.07	20.01	13.44
9	14.19	9.21	7.76	14.20	7.62	12.07	14.02	14.71	25.52	19.44	15.95	19.66	13.98
10	13.81	7.68	9.60	10.70	12.31	12.69	12.47	15.64	24.68	14.84	15.77	16.53	16.05
11	12.48	11.16	10.37	12.87	11.59	14.97	13.30	13.20	22.05	15.25	11.95	18.65	12.60
12	10.87	16.05	11.82	11.49	13.81	12.68	11.39	9.59	1.33	15.61	11.84	25.43	13.94
13	13.13	16.71	12.10	11.15	15.15	13.87	15.20	13.51	1.29	14.43	14.00	25.72	14.66
14	14.95	18.16	12.04	16.60	10.92	12.05	16.01	13.16	24.69	21.54	16.05	27.77	13.30
15	15.77	18.75	16.05	15.31	17.84	17.88	16.60	16.60	10.00	18.41	15.80	25.06	16.02
16	11.19	12.66	10.70	10.23	10.62	9.05	10.72	10.67	23.83	15.38	14.11	22.81	14.38
17	13.59	18.05	14.97	11.12	17.05	13.13	10.17	11.42	22.18	12.81	12.91	24.90	14.92
18	12.64	18.20	15.31	14.29	17.36	17.10	13.99	11.51	21.37	16.93	11.67	25.06	15.18
19	14.31	17.88	16.06	14.01	14.22	13.57	14.81	10.18	23.27	14.59	14.71	25.25	9.27
20	12.15	14.46	12.38	11.07	16.39	17.08	14.82	12.83	21.70	11.34	12.62	21.32	13.99

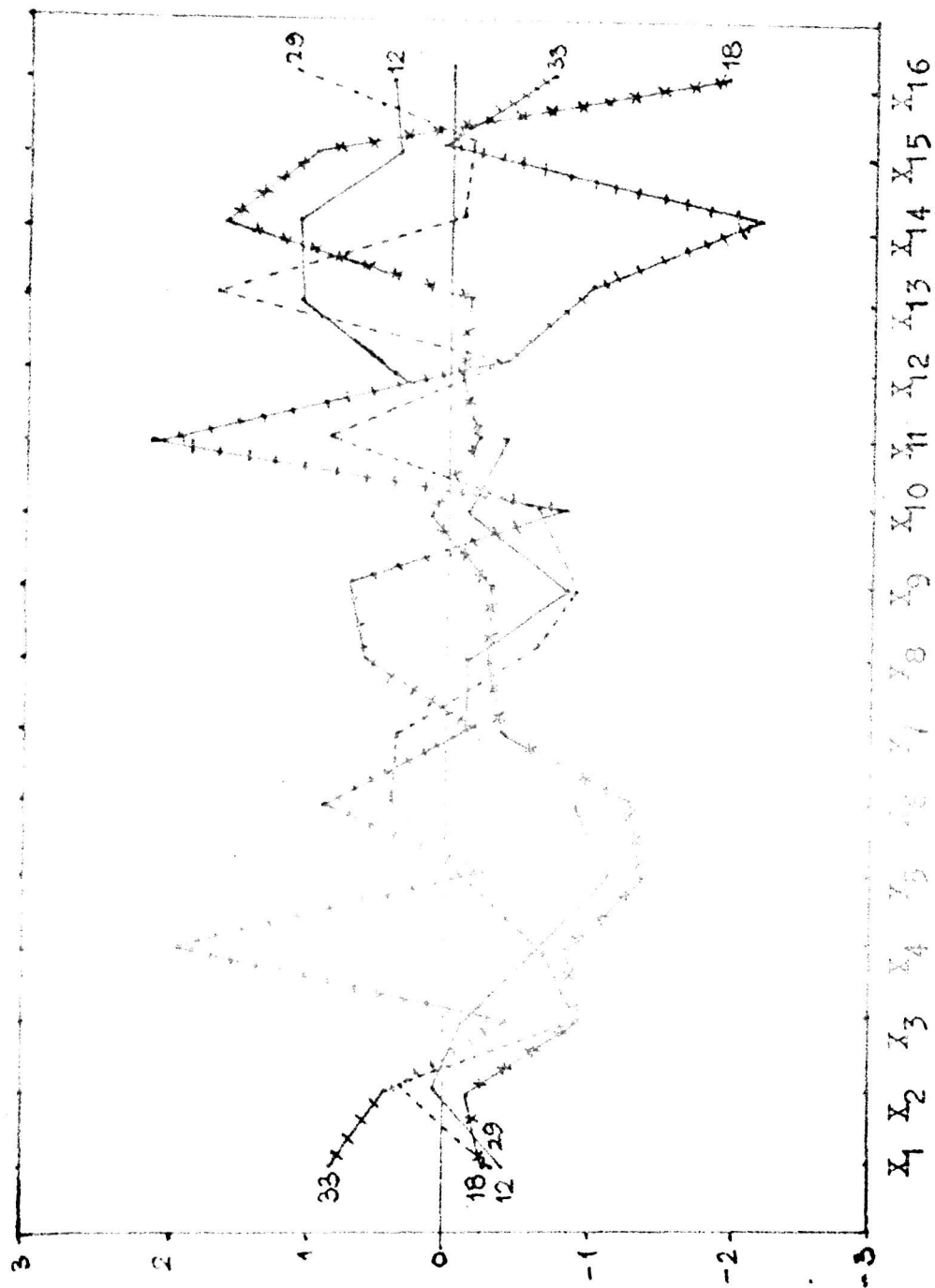
Table 11 (continued)

Class-	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
21	115.00	142.00	130.61	245.92	138.05	135.82	136.05	129.55	201.56	190.80	155.87	118.20	172.64	223.61	248.94	125.27	184.77	159.80	205.05	147.83
22	215.00	326.53	218.25	171.54	154.53	305.85	230.98	128.16	85.00	59.08	124.57	257.69	279.30	329.84	351.63	160.40	325.88	335.23	320.05	209.31
23	154.02	237.67	130.28	118.32	110.28	250.99	209.83	103.03	60.34	92.21	107.70	139.89	146.45	145.12	257.85	114.84	224.34	234.63	258.00	153.37
24	96.16	183.48	144.25	181.58	87.10	162.31	109.15	102.11	201.87	114.49	165.82	132.16	124.21	275.76	234.70	104.84	133.80	204.39	196.51	122.65
25	165.69	232.67	181.93	89.81	176.10	202.65	171.44	120.90	58.11	151.67	134.33	190.75	229.68	119.37	318.30	112.81	291.00	301.70	202.24	268.67
26	126.79	238.74	192.62	78.44	153.08	192.85	112.27	121.61	145.75	161.08	224.35	160.99	192.59	145.42	319.78	82.02	172.46	292.59	184.24	292.00
27	143.32	245.86	157.23	199.90	115.19	244.76	175.92	139.64	196.69	155.64	176.92	129.88	231.10	256.38	275.63	114.87	103.48	195.82	219.56	219.91
28	108.68	126.44	138.26	260.33	141.01	172.63	128.36	132.61	216.46	244.84	174.28	92.13	182.61	178.62	275.60	114.05	130.43	132.58	103.80	164.68
29	489.13	469.39	448.99	681.24	483.90	529.97	560.96	525.75	651.41	609.31	486.53	455.36	542.81	609.62	160.07	541.95	492.23	456.72	541.75	471.23
30	169.23	225.45	239.03	407.44	173.48	211.73	188.29	190.37	378.13	220.36	232.63	246.39	202.24	464.48	339.10	236.83	164.27	286.92	213.09	128.61
31	153.07	158.39	128.43	340.13	152.53	211.93	220.08	171.05	254.64	233.34	142.83	140.20	196.14	257.67	249.96	202.13	148.66	136.41	216.54	159.47
32	538.35	675.28	520.35	551.15	444.41	656.95	572.31	400.61	386.54	273.26	448.14	647.41	661.53	771.58	628.33	521.35	620.45	674.09	637.67	454.93
33	175.00	202.47	172.24	280.09	186.10	218.37	233.57	180.37	195.47	257.84	158.87	194.59	214.93	176.92	256.89	207.07	222.96	230.49	89.75	195.69

Table 11 (continued)

Cluster	21	22	23	24	25	26	27	28	29	30	31	32	33
21	-	16.17	14.51	13.24	14.27	14.25	14.44	12.96	23.23	17.16	14.20	24.55	16.33
22	261.49	-	10.57	15.42	11.78	17.23	16.03	17.53	26.95	17.72	17.10	12.27	15.77
23	210.64	111.80	-	13.12	10.92	14.03	13.39	14.44	24.49	18.28	14.96	21.19	13.62
24	175.43	237.78	172.15	-	15.23	10.61	8.14	14.59	22.85	11.95	13.75	23.28	17.69
25	203.64	138.85	119.44	263.53	-	11.55	14.40	13.45	26.15	20.78	17.55	22.42	12.30
26	203.20	263.46	197.00	112.75	133.50	-	10.30	13.69	25.34	17.29	16.79	25.34	16.52
27	208.54	258.70	195.89	66.30	269.19	106.12	-	14.47	23.56	14.73	14.04	23.42	17.56
28	168.19	307.34	208.55	213.09	180.86	187.53	209.60	-	24.13	17.10	15.20	26.49	12.30
29	539.99	726.37	600.06	522.43	683.65	642.55	555.18	582.27	-	25.04	25.40	31.33	23.96
30	294.56	314.06	334.32	142.95	432.22	302.49	217.13	292.62	677.10	-	17.00	22.18	17.78
31	201.92	292.64	223.89	182.95	308.88	282.19	197.32	231.05	677.10	289.27	-	23.90	16.65
32	602.76	150.79	449.31	542.19	502.74	642.55	558.91	702.22	931.70	492.79	571.40	-	24.22
33	266.77	248.78	185.57	313.17	151.30	272.98	308.67	151.52	574.36	316.26	277.47	596.95	-

Fig. 4. The pattern of Deviations of Mean values
of 4 clusters (Z values) for the
16 characters



—•— = CLUSTER 12 }
 -x-x- = CLUSTER 10 }
 ----- = CLUSTER 29 }
 -+--+ = CLUSTER 2 }

Variables that contribute towards the diversity

The variables that contribute more towards the divergence were identified by ranking the variance in the "between product matrix of transformed variables". Accordingly the variables Days to maturity, Panicle weight, Grain weight, number of seeds, leaf angle and peduncle length were the characters contributed towards the diversity.

DISCUSSION

CHAPTER V

DISCUSSION

The precise information about the extent of genetic divergence is crucial for an effective breeding programme. Multivariate analysis is utilised in quantifying the degree of divergence between populations to understand the trend of evolutionary pattern, to assess the relative contribution of different components to the total divergence and to determine the nature of forces operating at inter and intra-cluster levels (Mischner and Sokal, 1957; Sokal, 1958; Morishima and Oka, 1960; Nair and Mukherjee, 1960; Murty and Quadri, 1966). The application of multivariate analysis to measure divergence between biological population has been successfully established by many workers (Blackith, 1960; Nair and Mukherjee, 1960; Rao, 1960; Murty and Pavate, 1962; Cassie, 1963; Murty, 1965 and Murty et al., 1965).

The genetic architecture of a population is the result of prolonged selection by nature. Genetic variability which forms the basis for improvement by selection can be obtained by pooling genotypes from different geographical regions or by isolating transgressive segregates. The magnitude of variability and its quantitative estimation for each character would only indicate the potentiality of the collection and the scope for improving the studied character

through selection. In addition to estimation of variability a knowledge of the genetic diversity among different entries of the germplasm is necessary for the proper choice of parents in hybridization. Thoday (1953) and Daoumha and Dobzhansky (1954) have shown that the genetic heterogeneity of the population was positively associated with heterogeneity in space and time. This was particularly so within species (Beardmore and Shami, 1976). Thus it was thought that geographic diversity was positively associated with genetic diversity. This association was found to be not always true (Arunachalam and Jawahar Ram, 1967; Bhatt, 1970; 1973; Ram and Panwar, 1970; Gupta and Singh, 1970; Malhotra et al., 1974). . Hence, geographic diversity cannot be considered while selecting the parents, nor it can be used as a measure to judge the genetic diversity. Usually to assess the diversity in population of diverse origin, two important methods viz. canonical variate analysis and Mahalanobis' D^2 - statistics are employed. These techniques have recently been used for assessing the pattern of genetic diversity (Arunachalam and Jawahar Ram, 1967) and were proved to be very good techniques for selecting the best parents for hybridization (Bhatt, 1973).

In the present study, 225 genotypes of foxtail millet were included for the assessment of the nature of genetic diversity by multivariate analyses.

In the canonical variate analysis the number of variables is reduced to linear functions called canonical vectors which accounts for most of the variations produced by these characters. The second and succeeding vectors were also formed similarly which account for the residual variability. The first three canonical vectors accounted for 55.99 per cent of the total variability produced by all the sixteen characters under study (Table 3). Days to 50 per cent plants to bloom, days to maturity, panicle weight, panicle length, panicle breadth, number of productive tillers, leaf angle, panicle exertion and peduncle length are the variables which contributed to the genetic diversity.

Days to flowering was invariably an important character in differentiating genotypes (along with days to maturity) as observed by Shwe et al. (1972) in groundnut; Verma et al. (1973) in soybean, Das and Brothakur (1973) in rice; Trehan et al. (1974) in sesamum; Shoran (1975) in pigeon pea; Narayan and Macefield (1976) in Chickpea; Ganeshaiah (1979) in horsegram; Nayar (1980) in field bean; Pillai (1980) in blackgram and Sigamani (1981) in groundnut.

Days to maturity was found to be important in discrimination of genotypes in various crops as is evident from the results obtained by Ram and Panwar (1970) in rice; Srivastava (1970) in wheat, Ramanujam et al. (1974) in Mungbean;

Malhotra et al. (1974) in green gram; Verma et al. (1973) in soybean; Jayaprakash et al. (1974) and Angadi et al. (1979) in cowpea; Trehan et al. (1974) in sesamum; Shoran (1975) in pigeon pea; Ganeshaiah (1979) in Horsegram; Nayar (1980) in field bean; Pillai (1980) in blackgram and Sigamani (1981) in groundnut.

Number of productive tillers per plant was found to be contributing towards the genetic divergence. Similar results were obtained by Srivastava (1970) in wheat, Maurya and Singh (1977) in rice, Nagarajan and Prasad (1980) in foxtail millet and Singh et al. (1980) in barley.

Grain yield per plant was observed to be another character in discriminating of genotypes. This was also observed by Nagarajan and Prasad (1980) in foxtail millet, Das and Brothakur (1973) in rice.

Number of seeds was observed to be a character which influences in discrimination of genotypes. Similar result was found by Nagarajan and Prasad (1980), as number of branches per spikelets in foxtail millet and seeds per pod in chickpea by Narayan and Macfield (1976).

In general, plant height, flowering, tiller number and number of seeds were the largest contributors to genetic diversity in Brassica, linseed, wheat, Nicotiana and sorghum (Murty and Arunachalam, 1966).

In the present study in addition to the above leaf angle, panicle exertion, panicle length, panicle breadth and panicle weight were also observed to be the other attributes contributing for the genetic diversity and in discrimination of the genotypes. This clearly indicates that besides stature and maturity other plant characteristics also play a pivotal role in differentiation of the population.

Distribution of entries

On the first principal component axis (Z_1) the entries which accumulated towards the right of the axis indicated in general to be late flowering, late maturing, possessing more number of tillers, larger panicle length, more panicle weight with average number of seeds, lower leaf angle, lower to medium sized panicle exertion and lower to medium sized peduncle length. The entries towards the left of the axis were found to be early flowering, early maturing, medium tillering, medium sized panicle length, medium sized panicle breadth with less number of seeds, greater leaf angle and medium sized peduncle length. The other remaining entries were found to be distributed between the two extremes, indicated the variable trends for most of the characters.

The clustering pattern of the entries on the canonical graph indicate, in general the pattern of relation between the geographic origin and the distribution of entries in the space.

Fifty six primary clusters were formed on the two dimensional graph and tested for any such association (Fig. 1). Since the perfect association was not found the whole space between the two variates was divided into 80 parts such that the Z_1 axis which extracted 29.05 per cent was divided into eight equal parts and Z_2 which extracted 13.90 per cent was divided into 10 equal parts along the Z_2 axis. Based on the distribution of the entries in such parts 46 clusters were formed (Fig. 2). The entries included in each of these clusters and the source of their collection are indicated in Table 7. It was observed that there was no perfect pattern between the origin of the entry and the cluster in which it was included. In this type of clustering, thirty six out of forty three exotic genotypes revealed random distribution along with the indigenous types. Thus there was no perfect correlation between the geographic origin and genetic diversity. However, 13 genotypes representing 7 exotics and 6 indigenous formed solitary clusters indicating the significant correlation between genetic diversity and diverse geographic origin.

It is interesting to note that such of the entries which did not remain isolated as separate entities representing the diversified geographic regions of their origin were grouped in clusters possessing entries from heterogenous origin and is due to overlapping and gene flow in the material (Table 6).

Hence there was no apparent parallelism between the genetic divergence and the geographic origin. This could be due to the free movement of the breeding material from place to place (Moore and Dumbor, 1969; Verma et al., 1973; ...; Angadi et al., 1979) and or due to selection forces acting in different regions of the world (Zohavary, 1965; Gupta and Singh, 1970).

D²- Analysis

The actual distance between entries are obtained in Mahalanobis' D²-analysis. It is possible to cluster the entries based on D² values, as D² values represents the index of genetic diversity among the clusters. D²-statistics has been employed widely to resolve genetic divergence at inter varietal, subspecies and species levels in classificatory problems in crop plants (Murty et al., 1965 in Nicotiana rustica; Murty et al., 1967 in sorghum; Goodman, 1968 in maize; Ram and Panwar, 1970 in rice; Siddiqui and Swaminathan, 1971 in cotton; Joshi and Singh, 1979 in tetraploid Triticum).

The genetic distance of all the possible entries were calculated and tested for significance. It was found that the combinations which had less than 167.04 as their D² value were not significant, accordingly 33 per cent of the combinations were significant. This may be due to the fact that the

germ-plasm is redundant because of the exchange and introduction of the materials or due to similar selection pressure by both natural and human forces might have operated in the same direction at different places. Dispersion of the entries into 33 clusters indicated the presence of large amount of diversity in the material chosen for study.

In D^2 analysis the variables that were found to contribute more towards the discrimination of the entries were Grain weight, days to maturity, panicle weight, number of seeds, leaf angle and peduncle length.

Clustering of the entries.

Based on the D^2 values, 225 entries of foxtail millet were clustered into 33 clusters. Figure 2 and Table 9 indicate the cluster number, entries included in each cluster and source of collection. It is interesting to note that out of 43 exotic entries from diverse geographic origin, there was overlapping of more than one entries in different clusters as indicated in Fig. 3 and Table 9. The entries from U.S.A. were found to present along with the entries from Africa, Turkey and Kenya in Cluster I with the entries from India. The entries from U.S.A., Ethiopia and China grouped in cluster II with entries from India. The entries from U.S.A., Africa, Ethiopia and China were grouped with Indian collections in Cluster III. Clusters IV, V, VI, VII, X and XII possessed

entries from U.S.A. along with the Indian collections, whereas cluster XVI had entries of China and Indian origin. It is observed that there is no perfect relation between genetic diversity and geographic diversity. The grouping of varieties from heterogeneous geographic origin in one cluster is to be expected because of the free exchange of breeding material from one place to another. Similar results were obtained by Arunachalam and Jawahar Ram (1967); Govil et al. (1973) in sorghum; Bhatt (1970, 1973), Lee and Kaltsikes (1973) in wheat; Gupta and Singh (1970) in green gram; Jayaprakash et al. (1974) and Verma et al. (1976) in cowpea; Ganeshiah (1979) in Horsegram; Nayar (1980) in fieldbean and Sigamani (1981) in groundnut.

Seven clusters viz. cluster VIII, IX, XI, XIV, XV, XVII and XVIII have the overlapping of entries from different States of India. This may perhaps be due to free exchange of material from one place to another (Verma and Mehta, 1976). The material of the same eco-geographic region were found to be one or more components of the cluster. Clausen and Heisey (1958) and Singh et al. (1971) felt that even the temperature and rainfall pattern respectively could influence crop characters of the same races.

The pattern of clustering were similar with canonical variate analysis except for a few entries when the 33 clusters

were formed using D^2 -values and were superimposed on the 46 clusters of the canonical variate analysis (Fig. 2). The absence of the exact similarity between the D^2 clusters and canonical variate analysis is due to the fact that the clustering through D^2 analysis is based on the criteria fixed subjectively whereas in canonical variate analysis it is based on the arbitrary scale. Thus it could be concluded that there is almost a perfect agreement of the clusters formed through D^2 analysis and canonical variate analysis. Mahalanobis' et al. (1949) also observed similar pattern while analysing the Anthropometric data of United Provinces of India. Similar results were obtained by Murty and Pavate (1962) in Tobacco, Ramanujam et al. (1974) in Mungbean; Verma et al. (1973) in Soybean; Siddiqui et al. (1973) in cotton, Ganeshiah (1979) in Horsegram; Nayar (1980) in field bean.

Out of 15 solitary clusters formed, 7 solitary clusters were of exotic origin viz., 4 solitary clusters were of U.S.A entries, 2 solitary clusters were of entries from Turkey and single solitary cluster of an entry from Kenya. The remaining 8 solitary clusters have the entries of Indian origin. Two solitary clusters were of the entries from Uttar Pradesh; one each solitary cluster have the entries from Himachal Pradesh, Bihar, Jammu and Kashmir, Tamil Nadu, Karnataka and Bengal respectively. The formation of 15 distinct solitary clusters may be due to the fact that geographic barriers preventing

gene flow or intensive natural or human selection for diverse adaptive gene complexes must be responsible for this genetic diversity. Amongst the solitary clusters representing the diverse genetic material from varied geographic sources the clusters XXIV (entry I.Sc.89 from Turkey), cluster XXVI(entry I.Sc. 504 from Turkey), Cluster XXVII (entry I.Sc.389 from Bihar), cluster XXX(entry I.Sc.182 from Tamil Nadu), Cluster XXXI(entry I.Sc. 264 from Karnataka) and cluster XXXII(entry I.Sc.456 from U.S.A) were found to be superior in respect of yield and yielding attributes to be considered in the hybridization programme.

The mean values of each cluster for all the 16 characters are given in Table 11. It could be seen that the clusters differ very much in respect of character mean values, thus the clusters formed are very distinct in respect of these characters from one another. The mean values of the two nearest clusters (12 and 18) and the two distant clusters (29 and 32) for the 16 characters were converted into Z values and were plotted in Fig. 4. The study of the profile graph indicates that the nearest clusters have their Z values nearer while the Z values of the distant clusters were distant apart. They almost occupy an opposite extreme from the grand mean values. This indicates the high magnitude of diversity among the clusters for these characters. Hence, the divergence between the genotypes in the distant clusters is

indicative of the divergence of characters contributing for the genetic divergence. This again supports the conclusion from canonical variate analysis that such characters accounted more or less equally for the variability produced.

Inter-cluster and Intracluster D^2 values

The inter-cluster and intra-cluster D^2 values are given in Table 11. The inter-cluster D^2 value of any cluster is less than the intercluster D^2 value of any two closely related clusters. The intracluster D^2 values ranged from 25.50 (Cluster 4) to 57.00 (Cluster 18). The intercluster D^2 values ranged from 53.78 (between cluster 12 and 18) to 981.70 (between cluster 29 and 32). Fifteen entries remained as solitary clusters out of which 7 entries were exotic (4 from U.S.A; 2 from Turkey and 1 from Kenya). The remaining 8 were from different States of India.

It could be concluded that significant genetic diversity exists among the 225 genotypes selected for study for most of the important characters. This could be as a result of the long term selection in different direction by both natural and human forces. Such diversity can conveniently be represented on a canonical variate graph to get equally good and informative idea as through D^2 analysis. However, as many as six clusters

(Cluster Nos. XXIX; XI, XXIII; XXV; XXVI and XXXII) were common in both preliminary canonical grouping and in final grouping by D^2 analysis. This brings out the importance of preliminary grouping by canonical variate analysis in analysing diversity of large collection. Similar results were obtained by Varavan et al. (1973) in rice.

The results of canonical variate analysis were similar to that obtained by D^2 analysis. The little discrepancy in the relative disposition of the genotypes in the canonical graph compared to D^2 analysis could be probably due to the fact that the first two canonical variate accounted for 42.95 per cent hence the third vector is considered and the total 55.99 per cent of the total variation was accounted (Table 3).

The choice of parent is of paramount importance in any breeding programme. Selection of parents based on the extent of genetic divergence has been successfully utilised in different crop species by Moll et al. (1962); Miller and Marani (1963) Murty and Anand (1966) and Bhatt (1970). It is highly desirable that the extent of genetic divergence is reflected through any analysis. The D^2 statistics and principal component analysis in selecting divergent parents for successful hybridization programme have been successfully adopted (Matzinger et al., 1962; Chandrashekharaiiah et al., 1969; Ram and Panwar, 1970; Bhatt, 1973). Mahalanobis's generalized distance

(Mahalanobis, 1930; 1936; Rao, 1952) occupied a unique place in plant breeding. Singh and Ramanujam (1981) observed no correspondance between genetic divergence of parents as measured by generalized distance between and the extent of superiority of hybrids over parents. On the other hand canonical analysis showed that greater the heterosis the greater the differences between the parents and hybrids in respect of the canonical vectors.

Genetic divergence is dependent on geographic as well as phenotypic components of cultivars and its quantitative assessment could provide a rational basis for selection of parents in breeding programmes. In general, divergence is attempted to identify suitable parents for realising heterosis and recombinations. In a bid to generate genotypes possessing those attributes the breeder would like to choose genetically distant parent for hybridization. These studies may help in modelling the varieties in a desired genetic architecture.

In the present study, it is observed that considerable amount of genetic diversity is present amongst the entries in respect of yield and yield attributes. The entries from Turkey, U.S.A., Karnataka, Tamil Nadu and Bihar which formed the solitary clusters were genetically more diverse. These entries were high yielding, with greater panicle length.

panicle weight, panicle exertion and peduncle length. Such superior clusters were cluster XXIV (entry I.Sc.89 from Turkey), Cluster XXVI (entry I.Sc.504 from Turkey) Cluster XXVII (entry I.Sc.389 from Bihar), Cluster XXX (entry I.Sc.182 from Tamil Nadu), Cluster XXXI (entry I.Sc.264 from Karnataka) and cluster XXXII (entry I.Sc.456 from U.S.A). The inter-crossing of these genotypes should generate large variability and selection could be adopted for high yielding varieties.

SUMMARY

CHAPTER VI

SUMMARY

Two hundred and twenty five genotypes of foxtail millet (Setaria italica Beauv.) of diverse origin were studied for genetic divergence based on sixteen quantitative characters through canonical variate and Mahalanobis' D^2 -statistic .

The analysis revealed significant spectrum of variability among the genotypes studied. The canonical variate 3-Vector analysis per se accounted for 55.99 per cent of the total variability. Days to flowering, days to maturity, number of productive tillers, panicle weight, panicle length, panicle exertion, leaf angle and peduncle length were the characters which contributed significantly for the genetic diversity in the material.

Thirty six of the forty three exotic genotypes revealed random distribution along with indigenous types. No significant correlation could therefore, be accounted between genetic diversity and geographical diversity in this study. However, 13 out of the 46 clusters had occupied distinct cluster grouping. These were regarded as clusters with genotypes of distinct genetic background of different geographic regions.

The Mahalanobis' D^2 - statistics for 225 genotypes studied resulted in 33 clusters. The intra-cluster divergence (D^2) ranged from 25.50 to 57.00, while that of inter-cluster grouping varied from 53.78 to 981.70. The characters which contributed for maximum divergence in the Mahalanobis' D^2 -statistics were in conformity with those of canonical analysis.

The exotic and indigenous genotypes could be recovered in one and the same cluster grouping in 10 clusters out of 33 clusters. Fifteen clusters comprised genotypes of diverse geographical origin. These genotypes were also found to exhibit significant variability for yield and associated characters.

The study revealed on one hand the absence of association between genetic diversity and geographic distance in one set of cluster grouping, while in the other, the study confirms the earlier reports on positive correlation between genetic diversity and genetic distance.

A critical analysis of the grouping indicates the following:

- a) The reasons for absence or presence of significant correlation between genetic diversity and geographic origin could be more than one.

- b) If the natural selection pressure operating at different regions are of similar nature then there could be no genetic diversity between and among the genotypes.
- c) The duplication of genotypes accrued through exchange programmes will be similar in their genetic background. When such genotypes are analysed negative association between genetic diversity and geographical distance could result.
- d) Therefore, it is not advisable to generalize the information drawn from onset of sample to the entire population of setaria genotypes.

The study resulted in the identification of 15 solitary clusters representing widely diverse types with respect to the yield and yield components studied. The inter-crossing of these genotypes should result in generating sufficient variability to operate selection in segregating populations. This should help in synthesising new setaria varieties to substantially increase production.

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CHAPTER VII

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* Original not seen.

APPENDIX

Appendix I.

List of 225 entries included in the study and their place of origin

Sl. No.	I.Sc. Numbers of the entry	Origin/source
1	214	Maharashtra
2	274	Karnataka
3	84	Bihar
4	145	Maharashtra
5	324	Uttar Pradesh
6	158	Madhya Pradesh
7	137A	Jammu and Kashmir
8	509	Turkey
9	378	Assam
10	108	Himachal Pradesh
11	89	Bihar
12	459	U.S.A.
13	253	Karnataka
14	222A	Maharashtra
15	223B	Maharashtra
16	359	Uttar Pradesh
17	172	Madhya Pradesh
18	68	Bihar
19	234	Karnataka
20	265	Karnataka
21	323	Uttar Pradesh
22	581	U.S.A

Sl. No.	I.Sc. Numbers of the entry	Origin/source
23	183	Tamil Nadu
24	386	Bihar
25	69	Bihar
26	345	Uttar Pradesh
27	146	Madhya Pradesh
28	RS.118	Karnataka
29	519	U.S.A.
30	160	Madhya Pradesh
31	103	Himachal Pradesh
32	164	Madhya Pradesh
33	363	Uttar Pradesh
34	131	Jammu and Kashmir
35	518	U.S.A.
36	186.B	Tamil Nadu
37	150	Uttar Pradesh
38	342	Uttar Pradesh
39	176	Tamil Nadu
40	154	Madhya Pradesh
41	369	Uttar Pradesh
42	410 B.	Ethiopia
43	531	U.S.A.
44	483	China
45	63	Bihar
46	135	Jammu and Kashmir

Appendix I
(continued)

Sl. No.	I.Sc. Numbers of the entry	Origin/source
47	62	Bihar
48	231	Maharashtra
49	352	Uttar Pradesh
50	329	Uttar Pradesh
51	276	Karnataka
52	388	Bihar
53	99.B	Gujarat
54	133	Jammu and Kashmir
55	60	Bihar
56	396	Madhya Pradesh
57	184	Tamil Nadu
58	392	Madhya Pradesh
59	236	Karnataka
60	203	Tamil Nadu
61	263	Karnataka
62	373	Assam
63	256	Karnataka
64	215.A	Maharashtra
65	173	Tamil Nadu
66	59	Bihar
67	162	Madhya Pradesh
68	380	Assam
69	189	Tamil Nadu

Sl. No.	I. Se. No. of the entry	Origin/source
70	370	Uttar Pradesh
71	460	U.S.A.
72	193	Tamil Nadu
73	582	U.S.A.
74	153	Madhya Pradesh
75	148	Madhya Pradesh
76	573	U.S.A.
77	456	U.S.A.
78	482	China
79	471	U.S.A.
80	455	U.S.A.
81	406.A	Assam
82	K.222-1	Karnataka
83	226	Maharashtra
84	643.A	U.S.A.
85	405.A	Assam
86	217	Maharashtra
87	251	Karnataka
88	389	Bihar
89	507	Turkey
90	106	Himachal Pradesh
91	406.B	Assam
92	264	Karnataka

Appendix I
(continued)

Sl. No.	I. Se. No. of the entry	Origin/source
93	270	Karnataka
94	432	U.S.A.
95	326	Uttar Pradesh
96	448	U.S.A.
97	505	Kenya
98	331	Uttar Pradesh
99	521	U.S.A.
100	325	Uttar Pradesh
101	360	Uttar Pradesh
102	267	Karnataka
103	508.A	Kenya
104	168	Madhya Pradesh
105	340	Uttar Pradesh
106	192	Tamil Nadu
107	169	Madhya Pradesh
108	253	Karnataka
109	259	Karnataka
110	39.B	Bengal
111	268	Karnataka
112	504	Turkey
113	140	Kerala
114	371	Uttar Pradesh
115	469	U.S.A.

Appendix I
(continued)

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Sl. No.	I. So. No. of the entry	Origin/source
116	46	Bihar
117	211.B	Maharashtra
118	458	U.S.A.
119	255	Karnataka
120	156	Madhya Pradesh
121	354	Uttar Pradesh
122	138	Kerala
123	417.B	Africa
124	210	Maharashtra
125	398	Madhya Pradesh
126	320	Uttar Pradesh
127	410.A	Ethiopia
128	165	Madhya Pradesh
129	350	Uttar Pradesh
130	197	Tamil Nadu
131	34	Bengal
132	101.A	Himachal Pradesh
133	232	Uttar Pradesh
134	202	Tamil Nadu
135	377	Assam
136	508.A	Kenya
137	472	U.S.A.

Appendix I
(continued)

Sl. No.	I.Sc.No.of the entry	Origin/source
138	234	Uttar Pradesh
139	525	U.S.A.
140	235	Karnataka
141	343	Uttar Pradesh
142	335	Uttar Pradesh
143	137	Jammu and Kashmir
144	142	Madhya Pradesh
145	385	Assam
146	465.B	U.S.A.
147	238	Karnataka
148	155	Madhya Pradesh
149	376	Assam
150	101	Himachal Pradesh
151	107	Himachal Pradesh
152	180	Tamil Nadu
153	90	Bihaar
154	58	Bihaar
155	1	Andhra Pradesh
156	102	Himachal Pradesh
157	178	Tamil Nadu
158	397	Madhya Pradesh
159	260	Karnataka
160	136	Karnataka

Appendix I
(continued)

Sl. No.	I, Se. No. of the entry	Origin/source
161	99.C	Gujarat
162	80	Bihar
163	245	Karnataka
164	190	Tamil Nadu
165	200	Tamil Nadu
166	52	Bihar
167	127	Jammu and Kashmir
168	257	Karnataka
169	35.B	Bengal
170	40	Bihar
171	198.A	Tamil Nadu
172	45	Bihar
173	159.A	Madhya Pradesh
174	73	Bihar
175	221	Maharashtra
176	141	Kerala
177	405.B.	Assam
178	212.A	Maharashtra
179	375	Assam
180	132	Jammu and Kashmir
181	254	Karnataka
182	64	Bihar
183	362	Uttar Pradesh

Appendix I
(continued)

Sl. No.	I. Se. No. of the entry	Origin/source
184	Arjuna	Andhra Pradesh
185	266	Karnataka
186	262	Karnataka
187	417.A	Africa
188	96	Gujarat
189	66	Bihar
190	464	U.S.A.
191	104	Himachal Pradesh
192	339	Uttar Pradesh
193	417.B	Africa
194	457	U.S.A.
195	400	Madhya Pradesh
196	271	Karnataka
197	70	Karnataka
198	358	Uttar Pradesh
199	181	Tamil Nadu
200	474	U.S.A.
201	95	Bihar
202	334	Uttar Pradesh
203	97	Gujarat
204	143	Madhya Pradesh
205	248	Karnataka

Appendix I
(continued)

Sl. No.	I. So. No. of the entry	Origin/source
206	101.B	Himachal Pradesh
207	182	Tamil Nadu
208	354	Uttar Pradesh
209	161	Madhya Pradesh
210	481	China
211	395	Madhya Pradesh
212	35.A	Bengal
213	152	Madhya Pradesh
214	642	U.S.A.
215	Co.3	Tamil Nadu
216	36	Bengal
217	643	U.S.A.
218	196	Tamil Nadu
219	374	Assam
220	171	Madhya Pradesh
221	642	U.S.A.
222	470	U.S.A.
223	475	U.S.A.
224	175	Tamil Nadu
225	473	U.S.A.

Appendix I

Summarized list of 225 entries included
in the study

I.	<u>Indian collections</u>	:	182
	a. Andhra Pradesh		2
	b. Assam		11
	c. Bengal		5
	d. Bihar		21
	e. Gujarat		4
	f. Himachal Pradesh		10
	g. Jammu & Kashmir		7
	h. Kerala		3
	i. Madhya Pradesh		27
	j. Maharashtra		12
	k. Tamil Nadu		21
	l. Uttar Pradesh		29
	m. Karnataka		30
II.	<u>Exotic collection</u>	:	43
	a. Africa		3
	b. China		3
	c. Ethiopia		2
	d. Kenya		3
	e. Turkey		3
	f. U.S.A.		29