GENETIC DIVERGENCE AND VARIABILITY STUDIES IN SOYBEAN (*Glycine max.* (L.) Merrill.

A Thesis Submitted to the
MAHATMA PHULE AGRICULTURAL UNIVERSITY
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IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF
MASTER OF SCIENCE (AGRICULTURE)
IN
CYTOGENETICS AND PLANT BREEDING

BY
RAJESH NILKANTHARAO KADU

MAHATMA PHULE AGRICULTURAL UNIVERSITY
COLLEGE OF AGRICULTURE
PUNE - 411 005

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APPROVED :

Dr. R.D. Ghatge
Research Guide

A.M. Pawar
Committee Member

Dr. M.M. Patil
Committee Member

V.R. Karandikar
Committee Member

Dr. R.N. Sabale
Committee Member

COLLEGE OF AGRICULTURE, PUNE 411005
MAHATMA PHULE AGRICULTURAL UNIVERSITY
RAHURI 413 722
1989

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part thereof has not been submitted by me or any other person to this or any other University or Institute for a Degree or Diploma.

Pune : Rajesh N. Kadu

Dated : 4/5/89

Dr. R.D. Ghatge,
Associate Professor,
Department of Botany,
College of Agriculture,
Kolhapur.

CERTIFICATE

This is to certify that the thesis entitled " Genetic divergence and variation studies in Soybean (Glycine max. (L.) Merrill) " submitted to the College of Agriculture, Pune, Mahatma Phule Agricultural University, Rahuri, District Ahmednagar (Maharashtra) for the award of Degree of MASTER OF SCIENCE (AGRICULTURE) in CYTOGENETICS AND PLANT BREEDING, embodies the results of a bonafide research carried out by Shri R.N. KADU, under my guidance and supervision and that no part of thesis has been submitted for any Degree or Diploma. The assistance and help received during the course of this investigation have been acknowledged.

Ghatge

Dr. R.D. Ghatge
Research Guide

PUNE

Dated : 14.1.1989

Dr. D.S. Ajri,
Associate Dean,
College of Agriculture, Pune,
Mahatma Phule Agricultural University,
Rahuri 413 722, District Ahmednagar,
(MAHARASHTRA).

CERTIFICATE

This is to certify that the thesis entitled " Genetic divergence and variation studies in Soybean (*Glycine max*. (L.) Merrill) " submitted in partial fulfilment of the requirements of the College of Agriculture, Pune, Mahatma Phule Agricultural University, Rahuri for the award of Degree of MASTER OF SCIENCE (AGRICULTURE) in CYTOGENETICS AND PLANT BREEDING, embodies the results of a bona fide research carried out by Shri R.N. KADU, under the guidance and supervision of Dr.R.D. Ghatge, Associate Professor, College of Agriculture, Kolhapur and that no part of the thesis has been submitted for any Degree or Diploma.

(Dr. D.S. Ajri)

PUNE :
Dated : 6 MAY 1989

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Pune : (Rajesh N. Kadu)

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" GENETIC DIVERGENCE AND VARIABILITY STUDIES IN SOYBEAN (Glycine max. (L.) Merrill) "

BY

Rajesh N. Kadu
College of Agriculture, Pune-5
Mahatma Phule Agricultural University,
Rahuri 413722
1989

Major Professor and Chairman, Advisory Committee	:	Dr. R.D. Ghatge
Department	:	Agricultural Botany
Major Field	:	Cytogenetics and Plant Breeding

The study of correlation, variability and genetic diversity for yield and its components in Soybean (Glycine max. (L.) Merrill) was aimed at estimation of genetic coefficient of variation, heritability, genetic advance and to measure the divergence between the different genetic stocks of Soybean.

Fifty eight genotypes of Soybean (<u>Glycine</u> <u>max</u>.(L.) Merrill) originating from different geographic regions were selected from the germplasm maintained by the Maharashtra Association for Cultivation of Sciences, Pune and were grown in a Kharif season (1988) in a Randomised Block Design with three replications. Observations were recorded for days to fifty per cent flowering, days to maturity, plant height, plant spread, plant index, leaf length, leaf breadth, harvest index, number of branches on main stem, number of pods per plant, number of seeds per plant, leaf length, number of seeds per pod, test weight (100 seed weight), biological weight and grain yield.

The data on range of variability and significance of means indicated sufficient variability present in the genotype. The estimates of G.C.V. were low as compared to P.C.V. Very high estimates of heritability were obtained for the character days to fifty per cent flowering, while higher heritability estimates were recorded for the characters days to maturity, plant height, plant index, leaf length, leaf breadth, and medium estimates were recorded for the characters plant spread and test weight. The estimates of genetic advance were high for the characters number of seeds per plant and plant height and moderate for days to fifty per cent flowering, days to maturity, number of pods per plant, biological weight. Moderate to high heritability values with high genetic advance were observed for the characters plant height, thus indicating additive genetic control for this character.

Grain yield per plant had highly significant positive association with the characters, days to maturity, plant spread, leaf length, number of pods per plant, number of seeds per pod, 100 seed weight and biological weight. Grain yield per plant had significant positive association with the characters days to fifty per cent flowering, leaf length and plant spread.

The D^2 statistics showed that there was adequate diversity among the strains with D^2 values ranging from 4.34 to 772.22, on the basis of these values fifty eight strains under study were grouped in seven clusters.

On the basis of D^2 values and cluster means a crossing programme has been suggested to evolve the better strain.

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1.- INTRODUCTION

CHAPTER 1

INTRODUCTION

Soybean (Glycine max (L.) Merrill) is often designated as a 'miracle bean' or 'golden bean' containing more than 40 per cent proteins and 20 per cent oil. It is one of the most efficient protein producing crops, yielding three times more proteins than wheat, rice or maize. Soya-proteins are richer in lysine and tryptophan contents than that of cereals (Cowan, 1973).

Soybean tops both in area and oil production among the oilseed crops of the world. In 1984-85, it was grown on an area of 52.67 million hectares with 87.722 million tonnes of production in the world (Bhatnagar, 1987). The main countries growing Soybean are U.S.A., Brazil and Argentina accounting for more than 80 per cent of the world production. Other countries are U.S.S.R., Bulgaria, Romania and Yugoslavia in Eastern Europe; Indonesia, Japan, China, Korea, Thiland and India in Asia; Egypt in North Africa and Mexico, Paraguay, Columbia, Uruguay and Equador in Latin America.

It is not a new crop in India. Black Soybean is being cultivated for ages in low hills of Kumaon and Garhwal regions of Uttar Pradesh, the foot hills of Himalayas and some scattered pockets of Central India. The total area under Soybean in India was 1.3 million hectares with annual production of 0.994 million tonnes (Bhatnagar, 1987). Madhya Pradesh and Uttar Pradesh are two leading States for Soybean production.

However, it is also grown in other States viz. Rajasthan, Himachal Pradesh, Bihar and Karnataka. In Maharashtra, it is grown on more than 15,000 hectares with annual production of 11,400 tonnes in 1985-86 (Godbole, 1986). The average yield is 0.76 tonnes per hectare which is very low compared to world average of 1.7 tonnes per hectare.

In 1967, Indian Council of Agricultural Research, New Delhi launched an Inter-disciplinary 'All India Co-ordinated Research Projects on Soybean' and the whole country was divided into the following four zones on the agro-climatic basis :

(1) Northern Hill Zone - Himachal Pradesh, Jammu and Kashmir and Delhi.
(2) Northern Plain Zone - Uttar Pradesh, Punjab, Bihar, Haryana and West Bengal.
(3) Central Zone - Maharashtra, Madhya Pradesh, Gujarat and Rajasthan.
(4) Southern Zone - Karnataka, Tamil Nadu, Andhra Pradesh and Orissa.

The exact origin of the cultivated form of the Soybean is unknown. Although a statement 'the Soybean is native of Eastern Asia' is frequently transferred from one publication to another, there is no unanimity. *Glycine ussuriensis*, the progenitor of *G. max* was known to occur in China, Manchuria, and Korea (Piper and Morse, 1923). Fukuda (1933) argued that Manchuria was the centre of origin of *G. gracilis*, a closely related species, as numerous varieties of soybean having primitive characters were grown in Manchuria. Vavillov (1949-50) considered central and western China as centres of origin. According to Hymowitz (1970) *G. ussuriensis* grows wild in Korea, Taiwan, Japan, throughout Yangtage Valley, the north-eastern provinces of China and adjacent areas of U.S.S.R.

Linnaeus (1737) in his book 'Genera Plantarum' proposed the name *Glycine*. He has described the Soybean plant (in his species 'Plantarum' (1753) as *Phaseolus max*. Later he changed it to *Dolichos soja*. However, other botanists did not agree with this nomenclature. The botanical name *Glycine max* was proposed by Merrill in 1917, which is accepted for the cultivated species of soybean. It belongs to family Leguminoseae, sub-family Papilionaceae. Verdcourt (1966, 1970) listed the following species of Glycine with their chromosome numbers shown against them.

I.	Sub-genus - *Glycine*	*2n*
	1) *G. clandestina*	40
	G. clandestina var. *sericea*	
	2) *G. falcata*	40
	3) *G. latrobeans*	40
	4) *G. canescens*	40
	5) *G. tabacina*	40, 80
	6) *G. tomentelia*	38, 40
II.	Sub-genus - *Soja*	
	7) *G. soja* (*G. ussuriensis*)	40
	8) *G. max*	40

Glycine max was suggested to be polyploid derived from one or more diploid ancesters with $2n = 20$. G. max appears to favour a polyploid origin due to its chromosome number and many species in the sub-family Papilionaceae have basic chromosome numbers of $X = 8, 10, 11$ and 12 (Darlington and Whylie, 1955).

Soybean is mainly used for oil and proteins. Soybean oil products are used in the preparation of antibiotics, margarin, salad oil, bakery products, pharmaceuticals, printing inks, soaps, yeast, alcohol, paints, rubber, gasoline and sterols (Howard, 1961), while proteins are used in confectionary, baby food, livestock and poultry feed, protein isolates (minimum 70 per cent proteins), protein concentrates (minimum 90 per cent proteins), milk substitutes and beverages. It is also used in the preparation of non-fermented Soyfoods like tofu, soymilk yuba, kinaco, sprouts and green soybean and fermented Soyfoods like misa, soya-sauce and temph.

Soybean is used in the field of medicine as growth media in production of antibiotics such as penicillin, streptomycin, novoliyamycin, nystalin, erythromycin, oxytetracyclin, meomycin, condicline, actidione etc. all over the world (Singh and Bajaj, 1969). Soyfat is used in the preparation of lecithin, soygurts, butter, soycoffee, sweets, grease, soy-sauce and soy-curds, etc.

Being a leguminous crop soybean acts as a natural soil fertilizer. The root nodule bacteria, Rhizobium japonicum fix and add about 50 kg nitrogen per hectare from atmosphere to the soil. These bacteria also synthesize a substance called

'Rhizobitoxine' which is poisonous to other neighbouring plants. Hence, it is considered as natural weed killer (Anonymous, 1969).

India imports 1.5 million tonnes of edible oil annually to meet domestic requirements. It is estimated that annual requirement of edible oil by 2,000 A.D. would be 4.2 to 6.2 million tonnes, for which 24 million tonnes of oil seeds would be required as against the present production of 12 million tonnes. Soybean is an important oil seed and protein crop. Hence, its cultivation is speedily increasing in the country, with 1.3 million hectares area and 0.994 million tonnes of annual production (Bhatnagar, 198

The studies reported in this dissertation were undertaken in 58 cultivars of soybean to investigate the extent of variability and correlation coefficients between the yield and its components and also amongst the different yield contributing characters, which would be helpful in selection of the variable material available and in formulating a successful breeding programme for the improvement of this crop.

The present study therefore was planned with the following objectives :

(1) To estimate the degree and magnitude of genetic variability in morphological characters.

(2) To work out the genotypic, phenotypic and environmental correlation coefficients among the various characters.

(3) To estimate the genetic parameter like heritability and genetic advance.

(4) To measure the divergence between different genetic stocks of soybean.

(5) To group different soybean lines in suitable clusters on their relative divergence.

(6) To suggest suitable hybridization programme on the basis of inter-cluster values and cluster mean.

2. - REVIEW OF LITERATURE.

CHAPTER 2

REVIEW OF LITERATURE

2.1 Origin and Geographical Distribution of Soybean :

Piper and Morse (1923) proposed that Soybean was a native of Eastern Asia as the wild form of Soybean (Glycine ussuriensis) is known to occur in China, Manchuria and Korea. According to Fukuda (1933) Manchuria was the centre of origin since it showed diversity in Soybean forms; while, Vavillov (1935) described that Soybean is native of China. Ting (1946) reported that the wild Soybean (Glycine ussuriensis) was widely distributed throughout the Yantze Valley, where it grows with the bushes. The species was prostrate in growth habit having long fine twining stems and small oblong hard seed with sooty black colour.

2.2 Assessment of Genetic Variability by Statistical criteria in crop plants :

Bartley and Weber (1952) made crosses among three varieties viz. Ottawa Mendrian, Hawkege and Lincoln of Glycine max for studying variability of agronomic characters in successive generations and they found that segregation for seed yield, maturity, plant height and degree of lodging showed differences between two F_4 progenies, within each F_3 family. While, within family, variances were significantly larger than environmental variances to permit selection within families in most of the cases

Johnson et al. (1955) estimated genetics and environmental variability in Soybean by using two F_3 populations of Soybean. They evaluated 24 characters in the F_4 and F_5 generations and concluded that genetic variance obtained in different environment were less consistent, and the estimates of genotype x environment interaction were higher for yield than other important characters Heritability of yield was lower than other important characters. But the expected genetic advance expressed in percentage of mean was higher for yield than for per cent oil and proteins and iodine number of the oil.

Sevcenko (1964) studied the intra-varietal variability for five characters of Soybean by using a number of progenies of Har'kar 149, divergent lines from the basic type and stated that most of them proved to be natural hybrids and the origin of some forms could be explained by spontaneous mutation. The family H-58-9 ripening 24 days earlier than the initial variety, had large seeds and high protein content, probably arose by mutation.

Mjakusko (1968) examined the role of intra-varietal variability in breeding Soybean for increasing oil and protein content. They selected single plant progenies from the cultivar VN11SK1, which were uniform in many morphological features but varied in growing period, height, number of pods per plant, 1000 seed weight, oil and protein content. In many lines, variation was confined to certain characters, and the lines with the best combinations were selected. Some of the progenies were found to be natural hybrids. Examination of other cultivars showed that the progenies with high oil content were more variable in oil content than protein, whereas for those with high protein content the opposite was true. Selection from Komsomolka produced lines with 25.0 - 26.2 per cent oil. Variation was greater in new cultivars having hybrid origin than old established forms.

Bulah and Aristrarkova (1970) studied the variability for quantitative characters in Soybean. The analysis of eighteen characters was carried out in ten cultivars, belonging to different ecotypes, grown under different conditions of photoperiod and other conditions. They reported that varietal differences were greatest for 100 seed weight. The variability was determined almost exclusively by cultivar rather than environment for the characters such as angle of a insertion of branches, stem diameter, and pod length.

Comacho (1971) worked on genetic variance and heritability of vegetative and reproductive characters of Soybean in three generations of the crosses, Hill x PI 274 and Hill x 474. He observed that variability was greater for plant height than for the reproductive period. The additive variances were sufficient to allow satisfactory progress in selection, although heritability was low. Lal and Haque (1972) studied 36 varieties of Soybean for genotypic and phenotypic variability, broad sense heritability and genetic advance for ten characters. The result showed that selection for leaf number, total leaf area, period of flowering, plant height, 100 seed weight and number of days to flowering was effective. Malhotra (1973) reported significant differences between 37 varieties of Soybean for all six characters studied. The number of pods/plant and seed yield had the highest coefficient of genetic variation.

Rao (1974) carried out analysis of genetic variability for eight characters in seven varieties and seven F_2 derivatives. He observed that plant height and number of pods or seed/plant showed the highest genetic variability, Similarly, plant height, seed yield and number of branches/plant, number of pods or seeds per plant gave high estimates of heritability and genetic advance Seed yield was significantly associated with all the other characters except 100 seed weight.

Kovacheva (1975) collected data on 80 plants from each of the varieties grown at Russia for three years to study the variability of some characters in Soybean and concluded that variability within varieties was greatest in respect of number of pods/plant, number of seeds/plant and seed yield/plant. The variety Kabul gave the highest yield while, the variability in seed yield/plant was greatest in Pavlikeni-2. Ala (1977) studied variation in seed weight in Soybean due to mutagenic treatment and found that genetic variation in seed weight was higher in population of irradiated seed than the control. From M_4 generation he selected seeds having higher and lower weight. He observed that the change in the mean value of the character was greater in all cases in the treated population. Tanaka et al. (1978) studied seasonal variation in seed yield of Soybean at two locations and found that the yield and number of pods/plant were correlated. They further observed that factors contributing to both variability and adaptability differed among the varieties.

Upadhyaya and Singh (1979) studied induced variability in M_3 populations grown from γ irradiated seed of seven cultivars of Soybean and concluded that it did not differ from corresponding control populations for each of the severalquantitative characters However, the total variances within populations were higher in the population grown from irradiated seed.

Kaing (1980) examined 175 cultivars of G. max. 39 collections of G. soja and five of G. javanica for analysis variation by gel electrophoresis. Four alleles (F, S, null-1 and null-2) were found at the Am_3 locus in G. max. and two (F and S) in G. soja. G. javanica was monomorphii for null. He further found that a total of 84.5 per cent of the cultivars were fixed for the F. allele, 15 per cent for the S allele and 0.5 per cent for the null-2 allele. Of the 39 collections of G. soja, 18 were monomorphii for the F allele and seven for the S allele while, fourteen were polymorphic. Heterozygous seeds were found in only seven of the fourteen polymorphic populations.

Mosca et al. (1981) studied the variation in the oil and protein content of the whole seed in 36 varieties of Soybean with two sowing dates for two years and concluded that sowing date had no consistent effect on oil and protein content.

Boerma and Hussey (1983) studied genetic variation in Soybean for tolerance to Soybean cyst nematode and pointed out the differences in tolerance to Heterodera glycines. They found that 81 cultivars were susceptible and new introduction in maturity group V-VIII PI 197100 was the most tolerant. Cokar 156 and Wright were more tolerant.

Sharma et al. (1984) studied genetic variation, correlation and regression in fourteen U.S. varieties and a local variety. They also worked on selection of exotic Soybean for yield/ha and four related traits, and reported that pods/plant and days to maturity contributed most to seed yield in the foreign varieties examined by them.

Upadhyaya (1985) reported induced genetic variability for oi content in Soybean. He found that seed treatment with 20 krad γ rays significantly increased seed oil content in Bragg. Patil and Raut (1985) studied induced variation in M_2 generation of variety Kalitur of Soybean and concluded that the 31 plants (out of 14957) had green seed coat, while remainder were grouped into yellow, green, brown or black seed coat.

Rasaily et al. (1986) studied genetic variability, in 20 genotypes of Soybean, on yield/plant and other twelve related characters. They observed that genotypic variability was considerable for height, seed yield and number of branches, nodes and pods/plant. Heritability was high for height, number of nodes, days to flowering and days to maturity.

Vidal (1986) worked on genetic variability in Soybean of Subgenera Glycine soja with Glycine max. They reported that there was slight variability among cultivars from the U.S.A. whereas, it was more in the material from China, Japan and the U.S.S.R. or Central Europe. The interesting characteristics in the latter group were cold resistance, earliness and insensitivity to photo-period.

Malik and Singh (1987) studied genetic variability in interspecific crosses between Glycine soja and three varieties of G. max. of Soybean for yield/plant and six yield related and quality characters, and found that the F_2 population was more variable than the parents and further observed that seed weight had the highest broad sense heritability (98 per cent).

2.3 Assessment of Correlation by Statistical Criteria in Crop plants :

The association of characters, which is statistically determined by correlation studies, has always been a useful tool for selecting desirable genotypes. The pod yield in groundnut, a complex character, depends on a number of component characters, therefore, direct selection for this character is often misleading. Hence indirect methods such as determining the association between less variable plant characteristics and yield are adopted. Moreover, a character is influenced by a series of other variables which are variously associated with one another and hence the estimation of correlation between pod yield and its components indicates their relative contribution to pod yield.

Some attempts are made here to review the published literature on correlation studies in groundnut genotypes of different growth habits.

Johnson *et al.* (1955) studied genotypic and phenotypic correlation of 24 characters in two population of the F_4 generation of Soybean. They evaluated one population at two locations and the other at three; and observed that the genotypic correlations were slightly higher than the phenotypic correlation for yield and oil content.

Bhatta *et al.* (1968) studied 130 indigenous and exotic divergent cultivars of Soybean for estimation of correlation for four characters and found that in general, genotypic coefficient was found to be higher than phenotypic and environmental. Pod number and 100 seed weight were suitable characters for selection for improvement in seed yield.

Arora *et al.* (1970) worked out the correlation in 50 genotypically diverse types and observed that correlation between oil and protein percentage and between oil and mineral content were negative and significant respectively.

Gopani and Kabaria (1970) estimated the correlation of yield with agronomic characters in Soybean by using six genotypes and reported positively significant, simple and multiple correlation coefficients of yield with number of seed, number of pods and number of branches per plant. The oil content, the 100 seed weight, height and the number of seeds per pod were negatively associated with yield in different varieties. Ahmad and Khan (1971) studied six characters in 72 varieties of Soybean and showed significant and positive correlations between seed yield per plant with plant height, time of maturity, seed index and the number of pods per plant, seeds per plant and seed per pod.

Thseng and Hosokawa (1972) reported the high positive correlations between node number, pod number on main stem and plant, seed number per plant and seed yield. Similarly, between petiole length, leaflet length, seed weight and growth habit index, while studying genetic correlation in F_2 generation of crosses between indeterminate and determinate types of Soybean varieties.

Kozak (1973) worked on phenotypic correlation between quantitative characters in wild and cultivated species of Soybean and their inter-specific hybrids. He studied eight characters in the cultivated species and <u>Glycine ussuriensis</u> and also their hybrids. He found that the correlation between phenotypic characters in the inter-specific hybrids were higher than in the parents.

Marin (1975) studied the crosses of Williams x T-68-686 and C-881 x T-68-474 in F_1, F_2, BC_1 and BC_2 generations of Soybean for correlation between some quantitative characters and reported that height was having slight correlation with the number of pods and seeds per plant while significant correlation was not found between the height of pod insertion and either yield or any component thereof.

Aristrarkova (1977) worked on correlation of ten characters of Soybean and found close positive intra-varietal correlations between length and width of leaf blade, yield and number of pods per plant, number of leaves per plant and number of pods per plant, length of inflorescence and number of flowers per inflorescence and duration of emerging flower and ripening. The reverse correlation between seed size and number of pods per plant was found to be an obstacle in breeding for yield and bold seedness.

Jyang (1977) observed positive correlation between protein and K_2O, ash, moisture and P_2O_5 and ash contents in seeds. Fat and Cao, ash, K_2O and moisture, CaO and moisture, M_gO and ash contents were negatively correlated during his study on correlation between various chemical contents.

Shettar _et al_. (1978) studied correlation in ten characters of 21 varieties of Soybean and reported that yield per plant was positively correlated with number of nodes, branches, and pods per plant, each of these three traits was highly correlated with the other two and also with height, height of first node above the ground and seed number per plant. Similarly, weight of 100 seed was negatively correlated with all traits except pod number per plant and seed yield per plant.

Lee (1980) worked on genetic correlation between leaf index and number of seeds per pod in F_1 and F_2 generation of three cultivars of Soybean and showed that the long narrow leaflet was controlled by a single recessive gene. Segregation for number of seeds per pod showed a normal distribution and there was a highly significant correlation between leaf index and number of seeds per pod.

Schpaugh and Wilcox (1980) studied relationship between harvest indices and other plant characteristics in Soybean by taking 24 indeterminate, semi-determinate and determinate varieties of *G. max*. They observed that harvest index was significantly correlated with actual harvest index while both harvest indices were negatively correlated with biological and vegetative yield, (above ground dry matter, including and excluding seed respectively), straw and leaf weight, maturity and plant height. Further, they observed that these six characters were positively correlated with each other. However, growth habit and harvest index were not correlated.

Barbind *et al.* (1981) studied the correlation and regression on six yield contributing characters in sixteen varieties in Soybean. They concluded from analysis of data that number of days to maturity was significantly and positively correlated with yield.

Alam *et al.* (1983) studied correlation between yield and som agronomic characters in two F_2 population from intra-varietal crosses of Soybean and concluded that earliness, height, the number of branches, and seed per plant, number of pods per pod an seed oil content showed significant correlation with seed yield.

Gai and Fehr (1984) worked on the response of genotypic correlation for yield in Soybean and found that correlation between yield and several of its components changed from significant to non-significant and vice versa between the parental population and the superior selection. Correlation between height and both maturity and lodging score were significant in all three cycles. The positive correlation between yield and 100 seed weight became closer leading to closer correlation between 100 seed weight and both lodging score and height.

Liu _et_ _al._ (1985) reported that the genotypic coefficient of variation was significant for nine yield components of 58 cultivars of Soybean. Path analysis indicated that number of seeds per plant and 100 seed weight had a positive direct effect on seed weight per plant. Musorina and Kovalevich (1986) worked on breeding Soybean for earliness. They selected 1700 forms of which 33 were very early, 49 as early and 47 as mid-early in growth period (79-122 days). They found high and negative correlation (r = -0.79) between shortness of vegetative period and yield. A vegetative period of 100-127 days proved to be best for productivity, K 7196 and I 419370 were identified as earlier (26-40 days), higher yielding and higher in seed oil and protein content than Komosomalka.

Musorina (1987) studied the variation in protein content of the seed among 18 varieties of Soybean and revealed that the character, protein content of seed was 46 per cent conditioned by genotype, environmental condition, duration of growth period was negatively correlated with oil content of the seed (r = -0.64 to -0.87) and yield (-0.28 to -0.73).

2.4 Assessment of Heritability by Statistical Criteria in crop plants :

The concept of heritability is widely used in plant breeding to estimate the contribution of genetic variance to the total phenotypic variance. In other words it measures the relative importance of heredity and environment.

In practice, heritability may be expressed as the ratio of additive genetic variance to the total phenotypic variance in 'narrow' sense and the ratio of genotypic variance to phenotypic variance in 'broad' sense. Theoretically, when the heritability is high, reliance should be placed relatively more on selection. Usefulness of heritability depends on their reliability in predicting progress under selection.

Caviness (1969) worked on heritability of pod dehiscence and its association with some agronomic characters in Soybean. They selected parents F_1, F_2, F_3 plants from four crosses involving G. max. and G. ussuriensis. Their results showed that broad sense heritability estimates for pod dehiscence, date of flowering, date of maturity and days from flowering to maturity were generally high. Comacho (1971) studied plant height at flowering, and length of reproductive period in F_2, F_3, F_4 of the crosses Hill x PI 274 and Hill x 474 and observed that heritabili was less for plant height than for the reproductive period.

Thseng and Hosokawa (1972) revealed from the crosses Sangowase x Horosoy, Saikai 22 x Kokuiku 44 and Takachinggaha x Horosoy that heritability of all seventeen characters was high 66.79 per cent, except for branch number.

Kaw and Menon (1978) studied the heritability of nine agronomic characters of 37 varieties in G. max. and reported moderate to high estimates of heritability and a genetic advance for the number of pods or branch per plant, seed yield, plant height and node number. Martin and Wilcox (1973) worked on heritability of lowest pod height in Soybean and noted that heritability estimates for lowest pod height in crosses were slightly greater than those for seed yield and seed size in the F generation, while in the third cross, although the heritability estimates for lowest pod weight was lower than in the other two crosses, it was higher than that for yield in both the F_2 and F_3 generation.

Nishida and Abe (1974) while studying linearity of heritability, observed the relationship between the skewness in the distribution of genotypic and environmental values. The linearity of heritability of genotypic values and phenotypic values shown that the skewness of the distribution was a cause of curvilinearity in heritability.

Vishwanatha et al. (1975) concluded from heritability studies in 21 varieties of Soybean, that yield would be most effectively improved by selection for number of beans and pods per plant,

plant height, node number per plant and 100 seed weight which were highly heritable and controlled by additive gene action.

Bays (1976) studied heritability of several quantitative characters in segregating population in the crosses Hill x Bragg and Hood x Bragg of Soybean and reported that, apart from yield, the heritabilities of characters were high and consistent.

Miku (1978) studied heritability in the eleven Soybean hybrids and observed that it was high for duration of the period from emergence to flowering, plant height, height of insertion of the lowest pods, number of lateral branches, fruiting nodes and pods and seed weight. Karazawa and Caviness (1979) worked on genetic variability for resistance to propanil injury in Soybean. They made crosses among resistant types (R) Lec 68 and Hill and Susceptible (S) Devis and York and found that broad sense heritability estimates for propanil injury in progeny from S x R crosses ranged from 38 per cent to 50 per cent, while for those from S x S and R x R crosses were almost 0 per cent.

Takagi <u>et al.</u> (1979) estimated heritabilities of 95 per cent for oleic and linoleic and 71 per cent for linoleic acid content in 172 varieties of Soybean. Ratan Sing <u>et al.</u> (1980) studied heritability for fodder yield and component characters in Soybean and they studied 15 fodder characters in 36 varieties sown at two sowing dates, and found that heritabilities and genetic advance were high for leaf number, green and dry leaf weights, green and dry stem weights and green fodder and dry matter yields after both sowing.

Harrison et al. (1981) worked on heritability of canopy apparent photo-synthesis and its relationship to seed yield in 34 F_3 lines from each of the crosses Dare x Forrest (Cross V) and Tracy x Davis (Cross VI) of Soybean. They found that heritabilities based on variance components were significantly correlated in both crosses. Fisenko (1982) studied heritability of characters in F_3 and F_4 generation of Soybean and observed the heritability estimates in the population derived by crossing the parents differed in most of the economic characters.

Alam et al. (1984) carried out the heritability studies of yield components, protein and oil content in six parental varietie of Soybean, three crosses and the F_1, F_2, BC_1 and BC_2 populations derived from them. The heritability of these characters were found to be low. The oil and protein content characters were highly heritable. Additivity being more important in their control than dominance or epistasis. The broad base coefficient reached $H = 0.64$ and 0.68 respectively in Corsoy x Merit and the narrow sense coefficient for protein percentage reached 0.67 in the same cross.

Ronis et al. (1985) studied heritability of total and fixed nitrogen content of the seed in the two Soybean population, one derived from a cross of high and low nitrogen fixing parents grown for two years and other derived from a cross of intermediate nitrogen fixing parents one year only. They measured the broad sense heritability estimates of fixed nitrogen content of the seed which was ranged from 0.53 to 0.60.

Belic et al. (1986) analysed heritability values of seed yield and its several components in six parental varieties and their F_1 and F_2 progenies from a half diallel cross in Soybean. Their studies revealed that selection for the characters viz. plant height and height of the lowest pod would be effective as early as in F_2 and F_3 generation but that for the other characters it should not be effective before the F_5 generation.

Pushpendra and Hariharram (1987) studied on genetic components of variation for certain yield contributing traits in Soybean and obtained the large heritability values for plant height, seed weight and days to flowering suggesting that selection for these traits would be more effective.

2.5 Concept of Genetic Divergence :

The concept of D^2 statistic for measuring the divergence between the two populations was first given by Mahalnobis (1930). The main cause of the divergence is ultimately the function of change in gene frequency between different populations. This extent of change in gene frequency depends on the differential effect of evolutionary forces, which act on the population. In natural pollination, the frequency of given gene is determined by its relative contribution in the total adaption of individuals to their environment. Individuals which show more fitness contribute more than those having less fitness to the population gene pool (Lush, 1949).

2.6 Assessment of Genetic Diversity by Statistical Criteria in crop plants :

Allard (1961) studied the relationship between genetic diversity and consistency of performance in different environments by using three distinct levels of genetic diversity. He concluded that genetic diversity and productivity were complexly related and further stated that many factors determined the productivity of mixed populations. While, genetic diversity and stability, appeared more simply related, irrespective of number of characteristics of the components involved.

Murty (1965) examined heterosis and combining ability in relation to genetic divergence in flue cured tobacco and found that degree of heterosis could be related to the magnitude of divergence between the parents as measured by D^2.

Murty and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater diversity among genotypes than their geographical distance.

Anand and Murty (1968) used D^2 statistics in 55 populations consisting of ten parents and all possible F_1 hybrid combinations in linseed. Their analysis revealed that the diversity amongst the parents was mostly reflected in the corresponding F_1's also. They observed considerable diversity amongst the parents which were not necessarily related to their geographical diversity.

Zimmer and Uris (1969) reported several new sources of rust resistance in Safflower. They found that F_1 plants of crosses between resistant lines, having different genetic sources for resistance and rust susceptible lines were more or less equal in resistance to the resistant parents.

Shwe et al. (1972) carried out the multi-variate analysis of the nature of divergence among sixteen varieties of Scybean for eleven characters. On the basis of the differences in the cluster means, the characters such as number of nodes, number of pods per plant, plant height, plant habit, 100 seed weight and days to fifty per cent flowering were found to be major factors of differentiation. They further observed that the clustering pattern of the varieties did not follow their geographic distribution.

Verma et al. (1972) showed the restricted distribution of Soybean mainly to its photo-sensitivity requiring a minimum period of eight to ten hours of darkness for flowering. They opined that there are wide fluctuations in maturity of the same variety in different locations within a narrow range of latitudes They felt that the information on the nature of adoption and the factors for divergence, among the elite varieties, found to be adopted to a range of environments. This would be useful to identify characters, other than photo-sensitivity, which are important in genetic diversity.

Verma et al. (1974) carried out t rsis of diversity among seventy eight varieti r thirteen characters from diverse geographical areas planted at three localities and two fertility levels. The centroid method of factor analysis showed that days to flowering, days to maturity, and days from flowering to maturity accounted for 91 per cent of the total communality in the genotypic matrix. The main difference was due to the contribution of the first factor, other important characters for genetic divergence were synchrony of flowering, primary branches, 100 grain weight, specific gravity of seed weight and pods number per plant.

Chaudhary and Singh (1975) studied generalized distance in some varieties of Barley and their F_1's including reciprocal crosses. They found that the reciprocal crosses included in separate groups, indicated the role of cytoplasmic effect in causing genetic diversity in metric traits. They also reported that there was no consistent relationship between the varietal divergence and heterosis for yield expressed by their hybrids.

Chauhan (1976) while studying genetic divergence and heterosis in Soybean, pointed out the importance of selection of parents on the basis of generalized distance to get heterotic effects in F_1 and larger frequency of better segregants in subsequent generations.

Narsinghani et al. (1978) used multi-variate analysis in pea and concluded that the grouping pattern of varieties was quite at random. They further showed that the geographic and genetic diversity were not related.

Singh et al. (1979) studied genetic divergence in thirty five spontaneous and induced mutatants of rice by D^2 analysis and speculated that genetic drift and selection in different environments caused greater diversity rather than geographic isolation.

Asthana and Pandey (1980) used D^2 analysis in a set of forty varieties of linseed for grouping them into different clusters. They revealed that the varieties from different sources were grouped into one cluster while the varieties from the same source were distributed over different clusters. They further suggested that the genotypic and genetic diversity were not necessarily related. They stated that it was due to frequent exchange of breeding material from one place to another, while its further selection in different geographic regions could result in genetic drift. Thus they emphasized the selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity.

Dixit (1980) observed that the genetic divergence for yield and its components was high in the six characters of 21 varieties of (Lentil culinaris). The number of primary branches contributed to the total divergence followed by yield per plant. Even though the varieties were assigned to eight clusters, the grouping did not follow geographical distribution.

Asawa et al. (1981) used D^2 to analyse divergence in yield and four yield components among seven pure lines and their F_2

derivatives of Cicer arietinum. Yield per plant and 100 seed weight contributed 85.9 per cent and 14 per cent respectively to genetic divergence. The varieties JC. 81 and JC. 82 were good general combiner for all these characters.

Chauhan and Singh (1982) studied twenty F_1 crosses and their seventeen F_2 populations involving high, moderate and low diverse parents in Soybean. They found that highly divergent varieties were having high heterosis for most of the characters but maximum heterosis was not observed in crosses of most divergent types, but it was shown by crosses between moderately divergent parents. They also noticed that crosses within clusters showed low heterosis. Similarly, they observed greater variability in F_2 for most of the characters in those crosses involving moderate to highly divergent parents.

Chauhan (1983) described the grouping of six parents, their fifteen hybrids and twelve F_2 populations of Glycine max by Mahalnobis D^2. He concluded that seed size had contributed maximum to the total divergence followed by days to fifty per cent flowering.

Raut et al. (1984) studied the thirty six genotypes of Soybean representing geographic regions for genetic divergence using D^2 statistics. They grouped variable genotypes in twelve clusters which were not specific to their geographic distribution or origin. They found that EC 2586, EC 1077, P1SO-24A and IC-10037 were most divergent parents and further stated the possibility of utilising them in future Soybean breeding programme

Bartual et al. (1985) worked out the multi-variate analysis in 125 lines of Soybean sown on two dates in each of two consecutive years. They observed that late maturing varieties showed the best adoption to the ecological condition. The days to maturity, plant height, protein per cent and oil content contributed relatively more to the genetic diversity.

Malik et al. (1985) revealed that in pigeon pea, though geographic distribution could not be taken as a sole criterian of genetic diversity, the importance of former could still be traced. They described that character constellation might be associated with a particular region in nature and may loose their individuality under human interference.

Balyan and Singh (1986) studied forty eight Indian genotypes of lentil for genetic divergence and they grouped the genotypes into twelve clusters using Mahalnobis D^2 statistics. The largest cluster contained fourteen genotypes while genotypes L-9-12, J.L. 53, L. 1205-A, PKVL-1 and L.G. 103 appeared genetically divergent from the rest and formed individual cluster. They found that the data are useful for choosing genetically diverse parents for hybridization.

3. - MATERIAL AND METHODS.

CHAPTER 3

MATERIALS AND METHODS

3.1 Material used for study :

The present studies were undertaken to know the genetic variability, correlation and divergence in the available germplasm of Soybean. The experimental material for the present investigation included fifty eight promising genotypes of Soybean (Glycine max (L.) Merrill.), which were obtained from Maharashtra Association for Cultivation of Sciences, Pune (Maharashtra State). They represented different Soybean types with respect to growth habit, height, seed size, seed colour, etc. and have been enlisted in Table 1.

3.2 Experimental design :

The fifty eight lines were sown on 2nd July, 1987 in randomised block design, with three replications in two tire system. Each replication was having 12 blocks and the size of each block was 3.0 to 2.7 m^2. Each block consisted of six rows spaced 45 cm apart. The plant to plant distance within a row was 10 cm. Five plants were randomly selected from each experimental block for recording observations. A basal dose of 20 kg N, and 80 kg phosphorus per hectare was given. Rizhobium culture was also used before sowing the seeds. One irrigation was given immediately after sowing to ensure good germination. The recommended agronomic practices such as weeding, interculturing and plant protection measures were followed as and

Table 1. Name of Genotype/Parentage with their origin.

Sr.No.	Genotype/Parentage	Geographic Source
1)	I.C. 2065	Kalimpong
2)	J.S. 72-451	Unknown
3)	E.C. 2581	U.S.A.
4)	E.C. 18594	Nepal
5)	I.C. 2043	Kanpur
6)	E.C. 95837	Gochar
7)	I.C. 9451	Sikkim
8)	E.C. 39757	Italy
9)	E.C. 34039	U.S.A.
10)	E.C. 7034	Australia
11)	E.C. 34082	Hungary
12)	E.C. 37941	U.S.A.
13)	E.C. 18735	Nepal
14)	I.C. 15088	Unknown
15)	E.C. 30194	U.S.A.
16)	E.C. 39494	Unknown
17)	E.C. 7027	Australia
18)	E.C. 16697	U.S.A.
19)	E.C. 57104	U.S.A.
20)	P.L.S.O. 32	Jogindarpur
21)	E.C. 14469	Australia
22)	I.C. 10675	Nefa
23)	E.C. 7025	Australia

Table 1. Contd .....

Sr.No.	Genotype/Parentage	Geographic Source
24)	P.K. 73-55	Unknown
25)	P.L.S.O. 56	Baramula
26)	E.C. 100785	U.S.A.
27)	E.C. 37065	U.S.S.R.
28)	I.C. 7217	Naga Hills
29)	E.C. 95807	U.S.A.
30)	E.C. 57043	Taiwan
31)	E.C. 7990	U.S.A.
32)	E.C. 26693	Italy
33)	P.L.S.O. 21	Yeotmal (India)
34)	E.C. 14451	Australia
35)	E.C. 36964	U.S.A.
36)	E.C. 39726	Italy
37)	E.C. 34114	Hungary
38)	E.C. 39795	Nigeria
39)	E.C. 39730	Italy
40)	Kalitur x Ankur	M.A.C.S.(Pune)
41)	J.S. 2 x I.P.	M.A.C.S.(Pune)
42)	E.C. 13005 x MACS 40	M.A.C.S.(Pune)
43)	Kalitur mutant	M.A.C.S.(Pune)
44)	M.A.C.S.23 x M.A.C.S.14	M.A.C.S.(Pune)
45)	Punjab-1 x I.P.	M.A.C.S.(Pune)
46)	E.C. 95289	U.S.A.

Table 1. Contd .....

Sr.No.	Genotype/Parentage	Geographic Source
47)	Davis x Kalitur	M.A.C.S. (Pune)
48)	Hampton x E.C. 7034	M.A.C.S. (Pune)
49)	E.C. 44437 x E.C. 39821	M.A.C.S. (Pune)
50)	Ankur x I.P.	M.A.C.S. (Pune)
51)	Ankur x Yellow Tur	M.A.C.S. (Pune)
52)	E.C. 37043	U.S.S.R.
53)	E.C. 39079	Germany
54)	Kalitur mutant	M.A.C.S. (Pune)
55)	Ankur x Monetta	M.A.C.S. (Pune)
56)	J.S. 2 x I.P.	M.A.C.S. (Pune)
57)	Bragg x Monetta	M.A.C.S. (Pune)
58)	D-60-564 x Bragg	M.A.C.S. (Pune)

Source of Collection :

MAHARASHTRA ASSOCIATION FOR CULTIVATION OF SCIENCES,
PUNE.

when required. The average data for each character from the five randomly selected plants were used for statistical analysis.

3.3 Character studied :

3.3.1 Days for fifty per cent flowering :

Number of days for fifty per cent flowering were recorded for individual plot in all the three replications. The period between the date of sowing and the date on which 50 per cent of the flowers emerged from the axil of the leaf was considered as days to fifty per cent flowering.

3.3.2 Days for maturity :

The period between the date of sowing and the date of harvesting was treated as days for maturity.

3.3.3 Plant height (cm) :

Plant height was measured in centimeters from the base of the plant i.e. ground level to the tip of the main axis of the selected five plants.

3.3.4 Plant spread (cm) :

The spread of the plant was recorded at the time of harvest.

3.3.5 Plant index :

It is calculated by dividing leaf spread, with leaf breadth in percentage.

3.3.6 Leaf length (cm) :

It was measured from the base to the apex of the leaf.

3.3.7 Leaf breadth :

It was recorded from the mid point of central axis towards the edges of leaf.

3.3.8 Harvest index :

It was calculated in percentage by dividing grain yield by biological weight.

3.3.9 Number of branches on main stem :

The branches arising from main axis were considered as a number of branches on main stem. This observation was recorded at the time of harvest.

3.3.10 Number of pods per plant :

The number of pods per plant were counted on five randomly selected plants and averaged to give the number of pods per plant at the time of harvest.

3.3.11 Number of seeds per pod :

The seed from the five randomly selected pods were counted and the average number of seeds per pod was calculated.

3.3.12 Pod length (cm) :

The average length of pod was calculated by taking measurements of five randomly selected pods from selected plants.

3.3.13 Number of seeds per plant :

The seed obtained from randomly selected plants were counted and the average of the same was calculated.

3.3.14 Test weight (100 seed weight) :

The 100 seed of each randomly selected plants were counted and their weight in grams was recorded for each selected plants separately.

3.3.15 Biological weight :

The biological weight of each selected plant at the time of harvest with root, pods, branches, leaves together was recorded as biological weight in gm.

3.3.16 Grain yield :

The randomly selected plants were harvested separately and the weight of seeds from individual plants was recorded, and averaged which represented the grain yield per plant in gm.

3.4 Statistical analysis :

The analysis of variance for each character and covariance for each character pair and combined analysis of the genotypes for diversity, based on the average of the five randomly selected plants, was carried out. The data were subjected to the computer analysis at the Indian Agricultural Statistical Research Institute (IASRI), New Delhi, 110012.

3.4.1 Genotypic coefficient of variation (G.C.V.) :

It was estimated by the formula suggested by Burton (1951).

$$\text{G.C.V.} = \sqrt{\frac{V_g}{\bar{x}}} \times 100$$

where, $\bar{x}$ = Mean of the character.

V_g = Genotypic variance.

3.4.2 Heritability percentage :

Heritability percentage in broad sense was calculated by the formula quoted by Singh and Chaudhary (1979).

$$h^2 = \frac{V_g}{V_p} \times 100$$

where, h^2 = Heritability percentage in broad sense.

V_g = Genotypic variance.

V_p = Phenotypic variance.

3.4.3 Genetic Advance :

Genetic advance was calculated by the formula suggested by Robinson *et al.* (1949).

$$G.A. = K \times \frac{V_g}{V_p} \times \sqrt{V_p}$$

where,

K = Selection differential as defined by Lush (1949).

V_g = Genotypic variance.

V_p = Phenotypic variance.

3.5 Correlation study :

Phenotypic and genotypic correlation among the yield and yield components were calculated as per the formula suggested by Croxton and Cowden (1964).

$$r_p = \frac{\text{Covariance } XY^{(p)}}{\sqrt{\text{Variance } X^{(p)} \cdot \text{Variance } Y^{(p)}}}$$

$$r_g = \frac{\text{Covariance } XY^{(g)}}{\sqrt{\text{Variance } X^{(g)} \cdot \text{Variance } Y^{(g)}}}$$

where,

r_p = Phenotypic correlation coefficient between characters, X and Y.

r_g = Genotypic correlation coefficient between characters, X and Y.

The significance of correlation coefficient was tested against 'r' values given by Fisher and Yates (1963) at (t-2) degrees of freedom at 5 per cent and 1 per cent level of significance.

3.6 Mahalnobis's Generalised Distance (D^2) :

The generalised distance between any two population is defined as,

$$\Delta^2 = \Sigma\Sigma \; \lambda^{ij} \delta_i \delta_j$$

where, λ^{ij} = is the reciprocal matrix to the common dispersion matrix and δ_i is the difference between the mean values of the two population for the i^{th} character This quantity is estimated by D^2 statistics, as,

$$D^2 = \Sigma\Sigma \; s^{ij} d_i \; d_j$$

where, s^{ij} is the sample estimation of (λ^{ij}) and d_i of d_j.

Since the formula requires the inversion of sixteenth order determinant and then evaluation of 16 $(\frac{16+1}{2})$ terms whose sum is D^2.

The actual value of D^2 between any two genetic stocks of sixteen characters was obtained by taking sum of squares of the differences of values Y_1, Y_2 ..... Y_{16} for the two genetic stocks. Thus the total D^2 values for all possible pairs from the fifty eight genotypes were obtained.

3.6.1 Determination of population constellation :

Cluster is not a well defined term hence no rigid rule can be laid out about the formation of cluster. The only criterion appears to be that any two groups belonging the same cluster should at least on an average show a smaller D^2 than those belonging to the different clusters. A simple device suggested by Tocher (Rao, 1952) was therefore, used for grouping. It was to start with two closely associated groups and find a third group which had the smallest average D^2 from the first two groups. Similarly, the fourth was chosen to have the smallest average D^2 from the first three and so on. If at any stage the average D^2 of a group from those already listed appears to be higher then this genotype does not fit in with the former stocks and was therefore, taken to be outside the former cluster. The genotypes of the first cluster were then omitted and the rest were treated with similar procedure.

3.6.2 Average Intra and inter-cluster distance wand cluster mean

The average intra-cluster distance was obtained by using following formula :

$$D^2 = \frac{\Sigma D^2 i}{n}$$

where, D^2 i = Sum of distance between all possible combinations (n) of genotypes involved in a cluster.

The average inter-cluster distance was calculated using all possible D^2 values between genotypes included in any two clusters.

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

4. - EXPRIMENTAL RESULTS

CHAPTER 4

EXPERIMENTAL RESULTS

The present study was undertaken to find out the genetic divergence in regard to field components namely days to fifty per cent flowering, days to maturity, plant height, plant spread, plant index, leaf length, leaf breadth, harvest index, number of branches on main stem, number of pods per plant, number of seeds per plant, pod length, number of seed per pod, test weight, biological weight and grain yield in fifty eight varieties of Soybean during kharif season of 1987.

The results obtained from the present investigations, in regard to G.C.V., P.C.V., correlation,heritability,genetic advance and genetic diversity are presented in this Chapter.

4.1 Mean performance and range of variability of the genotypes :

The mean performance of the genotypes for sixteen characters studied is presented in Table 2.

Wide range of variation was observed for all the characters in the genotypes studied. The general mean and the range of variation for all the genotypes are given below under the respective characters.

i) Days to fifty per cent flowering :

The general mean for this character was 46.39 and the range of variation was from 34.26 to 79.60 days.

Table 2. Mean performance of fifty eight genotype for sixteen characters in Soybean.

Sr. No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	Plant index	Leaf length (cm)	Leaf breadth (cm)	Harvest index
1.	P 708	41.53	90.46	69.13	13.13	5.36	9.56	6.50	35.33
2.	P 681	43.80	90.00	42.26	14.26	2.96	10.23	7.00	36.50
3.	P 25	43.06	87.60	64.66	26.33	2.50	9.43	6.23	17.53
4.	P 696	44.33	100.33	65.86	19.03	4.03	9.70	6.63	17.93
5.	P 333	39.06	91.60	62.26	20.43	3.70	9.43	6.20	21.16
6.	P 412	37.66	92.20	55.60	19.46	3.20	8.63	6.80	32.80
7.	P 644	51.66	101.66	71.73	13.73	5.43	10.30	7.16	37.96
8.	P 600	46.00	109.00	75.40	12.86	6.03	9.93	7.26	31.83
9.	P 544	60.06	100.33	99.93	12.20	8.26	11.63	7.36	41.88
10.	P 516	44.00	94.00	87.83	11.66	7.10	12.43	8.86	26.63
11.	P 552	43.00	90.66	65.26	15.80	4.56	10.76	6.86	23.46
12.	P 167	37.46	90.60	27.73	5.86	4.73	11.00	8.30	32.53
13.	P 169	39.20	83.00	58.00	24.70	2.36	8.73	7.16	24.70
14.	P 500	40.66	84.33	59.53	24.73	3.60	9.10	6.20	18.96
15.	P 83	39.00	91.33	51.20	14.40	6.50	11.06	7.93	27.56
16.	P 583	43.66	92.00	95.40	15.26	6.63	10.60	6.53	30.23
17.	P 514	42.00	94.33	93.73	15.40	7.60	13.83	8.60	29.66
18.	P 748	43.33	104.00	86.93	11.66	1.70	11.83	7.16	35.00
19.	P 229	37.00	63.06	25.33	15.10	2.26	11.26	7.36	34.13
20.	P 351	36.00	90.66	23.43	10.80	5.53	10.70	7.36	40.00
21.	P 745	39.93	104.20	63.06	11.73	5.53	11.73	6.96	34.63
22.	P 341	41.13	69.00	79.60	21.10	3.80	8.96	5.80	25.86
23.	P 34	37.26	86.20	50.50	24.73	2.06	8.30	6.00	25.13
24.	P 671	44.13	110.40	89.80	14.26	7.20	13.50	7.60	26.40
25.	P 407	< 34.26	84.20	66.46	15.46	4.33	8.36	5.56	45.60
26.	P 636	43.46	100.66	71.06	12.33	5.73	10.53	7.03	22.36
27.	P 572	44.73	100.60	93.86	11.40	8.33	11.23	7.63	40.46
28.	P 638	43.00	94.00	53.00	12.53	4.26	9.10	6.36	33.83
29.	P 619	> 79.60	100.66	84.73	13.33	6.23	11.16	5.86	34.43
30.	P 608	60.46	95.46	91.73	14.53	6.93	13.73	8.70	26.26
31.	P 418	44.00	102.00	69.86	14.66	4.76	12.63	6.33	35.43
32.	P 538	49.66	105.26	98.86	13.73	7.50	12.76	8.40	28.60
33.	P 788	60.73	108.53	92.86	14.06	6.43	13.06	7.23	32.53
34.	P 51	45.33	98.33	78.73	16.86	4.73	12.23	7.40	23.93
35.	P 569	59.66	103.00	85.26	12.33	7.10	10.36	5.73	27.40
36.	P 209	38.00	91.00	44.43 ✓	13.26	3.36	8.43	6.43	37.20
37.	P 105	35.26	67.13	45.53 ✓	16.60	2.70	10.40	8.66	38.70
38.	P 731	43.00	96.00	80.26	13.10	6.80	14.76	6.30	33.20
39.	P 594	60.53	103.53	82.73	11.03	8.26	12.06	9.06	42.83
40.	MACS 118	44.00	94.00	68.13	12.40	5.56	10.03	7.33	38.53
41.	MACS 92	61.66	95.40	102.20	13.73	7.73	9.76	7.53	28.73
42.	MACS 106	50.53	102.00	100.53	11.66	8.73	8.96	5.73	27.40
43.	MACS 273	45.66	95.00	85.93	14.26	6.10	8.86	5.53	27.06
44.	MACS 188	38.46	90.33	47.33	27.06	1.83	10.93	6.53	39.73
✓ ~~45.~~	~~MACS 46~~	~~38.46~~	~~93.33~~	~~91.66~~	16.66	5.73	12.96	8.16	34.20
46.	P 260	61.66	103.26	76.26	10.80	7.13	7.50	6.20	35.33
47.	MACS 98	44.53	102.46	95.66	12.93	7.40	10.46	6.43	32.83
✓ 48.	MACS 13	44.06	100.93	50.33	10.86	4.66	12.93	7.23	36.63
49.	MACS 41	43.00	94.80	68.20	13.46	5.16	10.26	6.30	31.06
50.	MACS 249	44.86	94.20	92.93	13.60	6.96	14.40	7.26	24.13
51.	MACS 214	60.00	92.00	83.40	19.06	4.76	11.10	8.10	31.40
52.	P 150	45.80	90.86	44.80	13.20	3.36	11.26	7.26	38.90
53.	P 156	47.00	91.00	47.80	12.60	3.93	10.40	7.50	38.66
54.	MACS 100	62.00	101.13	95.00	11.66	8.56	12.26	7.56	40.26
55.	MACS 138	38.13	89.93	47.80 ✓	13.53	3.66	10.13	8.83	39.40
✓ 56.	MACS 57	63.06	92.00	71.93	12.93	5.90	11.33	7.30	42.43
✓ 57.	MACS 124	38.06	94.20	33.26	9.93	3.40	9.36	7.03	36.73
58.	MACS 42	64.13	91.13	56.26	12.80	4.36	13.23	7.40	31.30

Table 2. (Contd .....)

Sr. No.	Genotype	Number of branches on main stem	Number of pods per plant	Number of seed per plant	Pod length (cm)	Number of seed per pod	Test wt. (100 seed wt.)	Biological weight (gm)	Grain yield (gm)
1.	P 708	4.93	109.53	219.83	3.86	2.23	12.96	70.60	28.26
2.	P 681	4.06	69.53	117.13	4.26	1.66	12.96	32.46	14.93
3.	P 25	7.60	98.93	137.46	4.43	1.53	10.46	73.53	16.53
4.	P 696	5.93	58.33	95.40	3.93	1.60	10.70	80.46	13.16
5.	P 333	5.73	79.40	106.26	4.40	1.60	10.96	74.33	17.26
6.	P 412	5.33	74.93	142.33	4.80	1.80	7.66	59.33	24.90
7.	P 644	4.06	87.06	130.46	4.00	1.56	11.03	28.93	20.40
8.	P 600	3.80	47.66	95.26	4.00	2.00	11.96	46.40	14.86
9.	P 544	3.86	79.86	149.53	3.43	1.76	9.96	45.60	22.13
10.	P 516	5.53	102.06	183.66	3.83	1.73	13.20	40.33	25.00
11.	P 552	4.93	104.46	198.06	4.00	1.80	9.00	32.40	19.40
12.	P 167	3.40	35.66	60.00	3.86	1.70	11.80	74.73	7.33
13.	P 169	5.86	66.33	119.00	4.40	1.76	9.46	47.06	15.46
14.	P 500	5.40	47.20	91.66	4.53	1.90	10.16	59.40	12.86
15.	P 83	4.20	61.06	118.73	4.43	1.90	10.13	35.00	17.00
16.	P 583	4.00	85.06	147.33	3.96	1.70	15.86	88.06	17.13
17.	P 514	4.40	108.43	208.46	3.33	1.86	17.40	69.06	29.30
18.	P 748	4.53	97.66	191.60	3.36	1.90	11.70	54.86	29.06
19.	P 225	4.13	46.46	84.96	5.50	1.63	10.96	34.80	11.33
20.	P 351	5.00	48.46	78.86	4.46	1.60	10.36	43.60	11.53
21.	P 745	2.83	65.73	117.40	4.00	1.83	11.60	69.13	20.73
22.	P 341	5.33	86.86	174.13	4.03	1.93	10.40	84.66	17.53
23.	P 34	5.33	77.40	137.73	4.10	1.66	13.40	40.40	18.26
24.	P 671	3.00	72.46	134.06	4.00	1.80	12.80	42.33	18.86
25.	P 407	4.46	80.86	169.93	4.00	2.00	14.63	45.60	9.26
26.	P 630	4.80	81.80	144.86	3.46	1.73	9.40	38.33	17.66
27.	P 572	3.80	90.60	160.06	3.50	1.80	11.10	56.53	26.66
28.	P 638	4.53	80.00	140.60	4.00	1.70	14.43	32.26	17.40
29.	P 619	4.86	77.00	120.40	3.96	1.56	11.76	52.13	12.86
30.	P 608	4.86	73.73	141.93	4.33	1.90	15.00	83.33	18.53
31.	P 418	5.00	48.60	100.06	5.36	2.03	12.16	41.00	13.60
32.	P 538	4.06	106.26	196.33	4.00	1.86	11.76	100.80	21.03
33.	P 768	5.40	125.93	237.20	3.90	1.86	13.66	89.46	27.13
34.	P 51	6.00	84.80	160.40	5.66	1.83	13.06	90.00	15.46
35.	P 569	5.20	92.33	154.20	3.50	1.56	17.06	81.86	18.46
36.	P 209	5.06	49.53	92.66	4.93	1.86	15.43	56.86	10.13
37.	P 105	4.73	79.40	150.53	4.40	1.73	15.86	49.26	15.73
38.	P 731	6.06	93.26	148.60	3.96	1.50	14.70	51.86	14.10
39.	P 594	3.33	68.33	96.86	3.50	1.93	13.50	103.60	18.33
40.	MACS 118	4.53	82.80	141.13	3.20	1.70	9.26	81.40	12.86
41.	MACS 92	5.46	76.40	147.20	3.36	1.96	13.06	22.60	18.26
42.	MACS 106	5.53	80.93	134.93	3.40	1.60	13.66	65.46	12.90
43.	MA CS 273	6.26	95.66	170.53	3.53	1.66	13.43	71.80	15.60
44.	MACS 188	3.20	73.93	126.80	4.03	1.70	13.86	54.73	12.80
45.	MACS 66	5.33	88.93	176.26	3.56	1.93	11.53	61.73	27.66
46.	P 260	4.06	80.06	129.26	4.16	1.56	13.66	100.46	23.00
47.	MACS 98	5.33	85.60	144.33	3.73	1.70	13.86	78.86	17.53
48.	MACS 13	6.00	73.60	121.53	3.00	1.60	13.43	33.86	14.06
49.	MACS 41	5.06	72.86	112.33	3.53	1.63	14.43	28.80	13.30
50.	MACS 249	5.20	80.13	138.66	4.43	1.66	17.40	71.53	16.10
51.	MACS 214	5.93	140.73	246.60	3.20	1.76	10.56	64.00	25.53
52.	P 150	5.26	73.26	119.66	3.46	1.60	12.73	67.53	15.40
53.	P 156	5.06	76.80	129.20	3.63	1.56	13.40	79.13	16.00
54.	MACS 100	4.93	72.26	125.00	3.26	1.66	5.56	20.53	18.43
55.	MACS 138	3.86	80.26	138.60	4.00	1.66	11.66	78.33	13.70
56.	MACS 57	5.13	105.13	193.46	3.90	1.80	16.30	66.86	21.73
57.	MACS 174	3.73	44.00	83.80	4.43	1.80	11.90	54.66	12.43
58.	MACS 142	5.00	81.80	146.00	3.23	1.73	10.56	40.40	17.30

ii) Days to maturity :

The general mean for this character was 95.70 in fifty eight genotypes. The range of variation was 83.00 to 110.40 days.

iii) Plant height :

The general mean of this character was 70.06 cm and the range of variation was from 23.43 to 102.20 cm.

iv) Plant spread :

The grand mean for plant spread was 14.77 cm and the variation ranged from 5.86 cm to 27.06 cm.

v) Plant index :

The general mean was 5.26, while the range of variation was from 1.70 to 8.73.

vi) Plant length :

The general mean for the fifty eight genotypes was 10.85 cm. The range of variation was maximum from 7.50 to 14.76 cm.

vii) Leaf breadth :

The grand mean for this character was 7.10 cm and the range of variation was from 5.53 cm to 9.06 cm.

viii) Harvest index :

The mean for all the genotypes was 32.18. The range of variation observed was from 17.53 to 45.60.

ix) Number of branches on main stem :

The grand mean for this character was 4.83. The variation was ranging from 2.83 to 7.60.

x) Number of pods per plant :

The general mean for this character was 79.45. The range of variation observed was from 35.66 to 125.93.

xi) Number of seeds per plant :

The mean for this character was 141.02 and the variation ranged for this character from 78.86 to 246.60.

xii) Pod length :

The general mean for this character was 3.95 cm. The variation ranged between 3.00 cm to 5.66 cm.

xiii) Number of seed per pod :

The general mean for this character was 1.75 with maximum variation ranging from 1.50 to 2.23.

xiv) Test weight (100 seed weight) :

The grand mean for this character was 12.41 and the variation ranged between 5.56 to 17.40.

xv) Biological weight :

The general mean for this trait was 59.52. The biological weight ranged from 20.53 to 103.60.

xvi) Grain yield :

The grand mean of grain yield for fifty eight genotypes was 17.66 gm while the variation was observed ranging from 7.33 to 29.30.

The highest mean was observed for seeds per plant, while, it was the lowest for the character days to maturity. Similarly, the range of variation was highest for the number of seeds per plant. While, comparatively smaller range of variation was observed for number of pods per plant.

4.2 Analysis of variance :

The analysis of variance for sixteen characters under study for 58 Soybean genotypes is presented in Table 3.

The mean sum of squares (M.S.S.) for treatment i.e. genotypes were significant at 0.01 and 0.05 probability for characters, namely days to fifty per cent flowering, Days to maturity, plant height, plant spread, plant index, leaf length, leaf breadth, harvest index, number of branches on main stem, number of pods per plant, pod length, 100 seed weight, biological weight, grain yield, while for number of seeds per pod those were non-significant.

4.3 Coefficient of variation (genotypic and phenotypic) heritability percentage and genetic advance :

Range of variability, estimates of genotypic and phenotypic coefficients of variation, heritability percentage in broad sense and genetic advance were worked out for the individual characters, which are presented in Table 4.

Table 3. Analysis of Variance (Mean sum of squares).

Source	Degree of freedom	Mean Sum of Squares for different characters							
		Days to 50 % flowering 1	Days to maturity 2	Plant height (cm) 3	Plant spread (cm) 4	Plant index 5	Leaf length (cm) 6	Leaf breadth (cm) 7	Harvest index 8
Replication	2	0.055	1.50	336.00**	4.82	2.16	0.22	0.13	683.12**
Treatment	57	267.02 **	141.82**	1307.55**	53.61*	10.83**	8.43**	2.14**	133.83**
Error	114	4.80	9.55	84.12	9.53	0.94	0.54	0.11	46.67

Source	Degree of freedom	Mean Sum of Squares for different characters							
		Number of branches on main stem 9	Numer of pods per plant 10	Number of seeds per plant 11	Pod length (cm) 12	Number of seed per pod 13	Test wt. (100 seed wt.) 14	Biolo-gical wt. (gm) 15	Grain yield (gm) 16
Replication	2	4.98**	6487.30**	23778.75**	0.22	0.11	37.73**	2853.50**	603.24**
Treatment	57	2.42**	1198.58**	4510.98**	0.93**	0.06	16.81**	1346.40**	79.72**
Error	114	0.91	422.26	1401.64	0.20	0.05	3.36	365.30	26.64

* = Significant at 5 % level

** = Significant at 1 % level.

Table 4. Parameters of genetic variability in Soybean genotypes.

Sr. No.	Character	Range	G.C.V.	P.C.V.	Heritability (B.S.)	Genetic Advance
1.	Days to 50 % flowering	34.26- 79.60	20.15	20.70	94.79	18.75
2.	Days to maturity	83.00-110.40	6.94	7.65	82.19	12.40
3.	Plant height (cm)	23.43-102.20	28.82	31.66	82.90	37.88
4.	Plant spread (cm)	5.86- 27.06	25.93	33.31	60.63	6.15
5.	Plant index	1.70- 8.73	34.51	39.15	77.71	3.30
6.	Leaf length (cm)	7.50- 14.76	14.94	16.42	82.76	3.04
7.	Leaf breadth (cm)	5.53- 9.06	12.14	13.05	86.65	1.65
8.	Harvest index	17.53- 45.60	16.75	27.04	38.37	6.88
9.	Number of branches on main stem	2.83- 7.60	14.64	24.59	35.41	0.87
10.	Number of pods per plant	35.66-140.73	20.25	32.85	38.00	20.43
11.	Number of seed per plant	60.00-246.60	22.61	35.30	41.02	42.06
12.	Pod length (cm)	3.00- 5.66	11.95	17.73	45.45	0.66
13.	Number of seed per pod	1.50- 2.23	4.06	13.50	9.06	0.04
14.	Test weight (100 seed weight)	5.56- 17.40	17.06	22.57	57.15	3.30
15.	Biological weight (gm)	20.53-103.60	30.38	44.20	47.24	25.60
16.	Grain yield (gm)	7.33- 29.30	23.82	37.70	39.90	5.47

G.C.V. = Genotypic Coefficient of Variation.

P.C.V. = Phenotypic Coefficient of Variation.

B.S. = Broad Sense.

The estimates for genotypic coefficient of variation were low as compared to phenotypic coefficient of variation for the sixteen characters studied. Genotypic as well as phenotypic coefficients of variation were the lowest for the character days to maturity (G.C.V. - 6.94, P.C.V. - 7.65) and highest for plant index (G.C.V. - 34.51, P.C.V.-39.15). Very high estimates to heritability (broad sense) $(h > 90)$ were obtained for the character days to fifty per cent flowering while it was high $(h > 70)$ for the characters days to maturity, plant height, plant index, leaf length, leaf breadth, while it was medium $(h > 50)$ for the character plant spread, test weight. Low estimates to heritability $(h > 30)$ were also obtained for the characters viz. harvest index, number of branches on main stem, number of pods per plant, number of seeds per plant, pod length, biological weight and grain yield. However, very low heritability estimate was also observed for number of seeds per pod (i.e. 09.06). Higher genetic advance was observed for the characters number of seed per plant and plant height and the estimates of this paramete were moderate for the days to fifty per cent flowering, days to maturity, number of pods per plant, biological weight, while lower estimates were observed for characters viz. plant spread, plant index, leaf length, leaf breadth, harvest index, test weight and grain yield and the estimates were the lowest for number of branches on main stem, pod length and number of seeds per pod.

4.4 Genotypic (G) and Phenotypic (P) Coefficients of correlation

The estimates of genotypic (G) correlation coefficients for sixteen characters are worked out from pooled data and are presented in Table 5.

It is revealed from the Table 5, that grain yield had highly significant positive association with the characters viz. days to maturity, plant height, plant spread, leaf length, number of pods per plant, number of seeds per plant, number of seeds per pod, 100 seed weight and biological weight and positive significant association was also observed for the characters, days to fifty per cent flowering, leaf length and pod length.

Biological weight in turn showed highly significant positive association with the characters plant height, harvest index, number of seeds per plant. However, 100 seed weight had highly significant negative association with number of pods per plant and number of branches on main stem.

Number of seeds per pod were positively correlated with plant height, pod length, leaf breadth and negatively correlated with number of branches on main stem. Pod length showed negative correlation with the other characters except plant spread.

Number of seeds per plant showed highly significant positive association with plant height. Number of pods per plant also had positive correlation with days to fifty per cent flowering, plant height. Number of branches on main stem had also shown highly

Table 5. Genotypic (G) correlation in fifty eight genotypes of Soybean.

	Days to 50 % flowering 1	Days to maturity 2	Plant height (cm) 3	Plant spread (cm) 4	Plant index 5	Leaf length (cm) 6	Leaf breadth (cm) 7	Harvest index 8	Number of branches on main stem 9	No. of pods/ plant 10	No. of seeds/ plant 11	Pod length (cm) 12	No. of seeds/ pod 13	Test wt. (100 seed wt.) 14	Biological wt.(gm 15
1	1.0000	0.4316**	0.5173	-0.2729*	0.5193**	0.2365	0.0731	0.1133	0.0893	0.3798**	0.2683*	-0.4541**	-0.1966	-0.0463	0.0723
2		1.0000	0.6116**	-0.4445**	0.6186**	0.3517**	0.0490	0.0427	-0.2848	0.2371	0.1775	-0.3359**	0.1717	0.2164	0.2273
3			1.0000	-0.1272	0.7453	0.3527	0.1274	-0.2291	0.1490	0.6988**	0.6748**	-0.3781**	0.3962**	-0.0484	0.5491**
4				1.0000	-0.5372**	-0.3101*	-0.2594*	-0.5338**	0.3655**	0.0605	0.0566	0.4343**	0.0187	-0.0678	0.3442*
5					1.0000	0.4007**	0.2753*	0.0711	-0.1252	0.3171*	0.2591*	-0.4708**	0.1225	0.0785	0.1641
6						1.0000	0.5641**	0.0638	-0.1367	0.2589*	0.2789*	-0.1237	0.1422	0.0198	0.1287
7							1.0000	0.1636	-0.3807**	0.1077	0.1356	-0.0840	0.3795**	0.3114	0.1282
8								1.0000	-0.6002**	-0.1251	-0.1233	-0.3363*	-0.2102	0.0287	0.7607**
9									1.0000	0.3350*	0.2792*	-0.0168	-0.3905**	-0.3945**	0.3137*
10										1.0000	0.9813	-0.4666**	0.1547	-0.3549**	0.5270*
11											1.0000	-0.3411*	0.3417*	0.3272*	0.5214**
12												1.0000	0.4069**	0.1601	0.0250
13													1.0000	0.2512	0.2840*
14														1.0000	0.3291*
15															1.0000
16															

* = Significant at 5 % level. ** = Significant at 1 % level.

significant positive association with plant spread and negative association with leaf breadth and harvest index. Harvest index only had negative association with plant spread. Leaf breadth were positively associated with leaf length, leaf length with days to maturity and plant index, plant index with days to fifty per cent flowering and days to maturity. Plant spread was negatively associated with days to maturity, plant height with days to maturity and days to maturity with days to fifty per cent flowering.

The data from the Table 6 showed that the phenotypic correlation of grain yield per plant, was positive and significant with the characters, plant height, number of pods per plant, number of seeds per plant, 100 seed weight. Biological weight also had significantly positive association with plant height, plant spread, number of branches on main stem, number of pods per plant, number of seeds per plant, while, it was negatively associated with harvest index.

Number of seeds per pod was positively associated with the character, number of seeds per plant, similarly pod length exhibited positive association with plant spread and negative with days to fifty per cent flowering, days to maturity, plant index, number of seeds per plant showed highly significant positive association with the characters plant height, and number of pods per plant. Number of pods per plant with plant height, number of branches on main stem with plant spread had highly negative correlation with harvest index. Harvest index was negatively

Table 6. Phenotypic (P) correlation in fifty eight genotypes of Soybean.

	Days to 50 % flowering 1	Days to maturity 2	Plant height (cm) 3	Plant spread (cm) 4	Plant index 5	Leaf length (cm) 6	Leaf breadth (cm) 7	Harvest index 8	Number of branches on main stem 9	Number of pods per plant 10	No. of seeds/ plant 11	Pod length (cm) 12	No. of seeds/ pod 13	Test wt. (100 seed wt.) 14	Biologoical wt.(gm 15
1	1.0000	0.3956**	0.5004**	-0.2206	0.4919**	0.2324	0.0618	0.0782	0.0093	0.2504	0.1776	-0.3448*	-0.0729	-0.0853	0.0423
2		1.0000	0.4820**	-0.5188**	0.5724**	0.3068*	0.1992	0.0831	0.2732*	0.0936	0.0888	-0.2555*	0.0544	0.2160	0.0840
3			1.0000	-0.0347	0.6950**	0.2986*	0.0825	-0.1261	0.0831	0.4140**	0.4192**	-0.2366	0.1531	-0.0662	0.3932**
4				1.0000	-0.5132**	-0.2462	-0.2671*	-0.3968**	0.4181**	0.1412	0.1018	0.2559*	0.0076	-0.0880	0.3562**
5					1.0000	0.3471**	0.2463	0.0751	-0.1988	0.1382	0.1441	-0.2922*	0.0688	0.0293*	0.0666
6						1.0000	0.5047**	0.0473	-0.0811	0.1683	0.1663	-0.0766	0.0196	0.0111	0.0987
7							1.0000	0.1346	-0.2741*	0.0406	0.1027	-0.0666	0.1620	0.2702*	0.1082
8								1.0000	-0.3474**	-0.0262	-0.0428	-0.1618	0.1962	0.0897	-0.5286**
9									1.0000	0.3140*	0.2053	0.0406	-0.1752	-0.1733	0.3489**
0										1.0000	0.9094**	-0.2301	0.0018	0.1988	0.5939**
1											1.0000	-0.1733	0.3106*	-0.1565	0.5769**
												1.0000	0.1117	0.1062	0.0372
													1.0000	0.1213	0.1524
														1.0000	0.2430
															1.0000

* - Significant at 5 % level. ** - Significant at 1 % level.

associated with plant spread, leaf breadth with leaf length, while it had positive correlation with plant index, plant index with days to fifty per cent flowering, days to maturity, plant height and negatively with plant spread. Plant spread was negatively associated with days to maturity, while plant height recorded positive associated with days to fifty per cent flowering and days to maturity and days to maturity with days to fifty per cent flowering.

The data from the Table 7 showed that the environmental correlation of grain yield had highly significant association with the characters plant height, number of pods per plant, number of seeds per plant and biological weight. Similarly, biological weight with plant spread, number of branches on main stem, number of pods per plant, number of seeds per plant while, it was negatively associated with harvest index. Number of seeds per plant exhibited highly positive association with number of pods per plant. Number of branches on main stem with plant spread had negatively significant association with days to maturity, plant index. Harvest index was positively correlated with leaf length, leaf breadth with days to maturity, plant index with days to fifty per cent flowering. Days to maturity, plant height was negatively correlated with plant spread. Plant spread was negatively associated with days to maturity, while plant height had significantly positive association with days to fifty per cent flowering.

Table 7. Environmental (E) correlation in fifty eight genotypes of Soybean.

Days to 50 % flowering 1	Days to maturity 2	Plant height (cm) 3	Plant spread (cm) 4	Plant index 5	Leaf length (cm) 6	Leaf breadth (cm) 7	Harvest index 8	Number of branches on main stem 9	Number of pods per plant 10	Number of seed per plant 11	Pod length (cm) 12	Number of seed per pod 13	Test wt. (100 seed wt.) 14	Biological wt. (gm) 15
1.0000	0.1526	0.4432**	-0.0957	0.4288**	0.2412	-0.0539	0.0551	-0.2312	0.1252	0.0585	-0.2771*	-0.0704	-0.3433*	-0.0367
	1.0000	-0.1307	-0.7744**	0.3918**	0.0953	0.4398**	0.1784	-0.3525**	-0.1171	-0.0440	-0.1610	0.0187	0.2448	-0.1860
		1.0000	0.2140	0.4956**	0.0380	-0.1489	0.0096	0.0072	0.0668	0.0810	-0.0149	0.1128	-0.1215	0.1651
			1.0000	-0.4878**	-0.1018	-0.3450*	-0.2829*	0.4932**	0.2271	0.1527	0.0601	0.0054	-0.1170	0.3775**
				1.0000	0.1312	0.1179	0.0978	-0.3507**	-0.0917	-0.0061	0.0355	0.0807	-0.0747	-0.0957
					1.0000	0.1778	0.0348**	-0.0212	0.0707	0.0119	0.0024	-0.0491	-0.0094	0.0603
						1.0000	0.1405	-0.2153	-0.0737	0.0780	-0.0514	0.1598	0.2132	-0.0460
							1.0000	-0.2475	0.0349	0.1521	-0.0368	0.3144*	0.1485	-0.3591**
								1.0000	0.3021*	0.1603	0.0797	-0.1373	0.0080	0.3778**
									1.0000	0.8632**	-0.0623	-0.0359	-0.0649	0.6481**
										1.0000	-0.0459	0.3342*	0.0038	0.6228**
											1.0000	0.0414	0.0515	0.0478
												1.0000	0.1028	0.1353
													1.0000	0.1516
														1.0000

* = Significant at 5 % level. ** = Significant at 1 % level.

4.5 Divergence :

An attempts were made to calculate D^2 values among the fifty eight genotypes. The data obtained for each of the sixteen characters were subjected to analysis. All the genotypes differed significantly with regard to the differences in the mean values for these sixteen characters. Therefore, further analysis was undertaken to estimate the D^2 values.

4.5.1 D^2 *Analysis* :

The D^2 value ranged from 4.34 to 772.22. The maximum D^2 value of 772.22 was observed between the pair of genotypes, P-341 and P-636, while the lowest D^2 value of 4.34 was noted in M-260 and M-98.

4.5.2 Cluster formation and inter and intra-cluster divergence

The fifty eight populations were grouped into seven clusters on the basis of D^2 values. The distribution of fifty eight strains in different clusters is given in Table 8.

Out of these seven clusters, cluster A was the largest having twenty four varieties, followed by cluster C with nineteen varieties and B with eleven varieties, while D, E, F and G, were single variety clusters showing wide divergence from the rest and from each other.

The inter- and intra-cluster D^2 values and D values are given in Table 9 and graphically presented in Fig. 1.

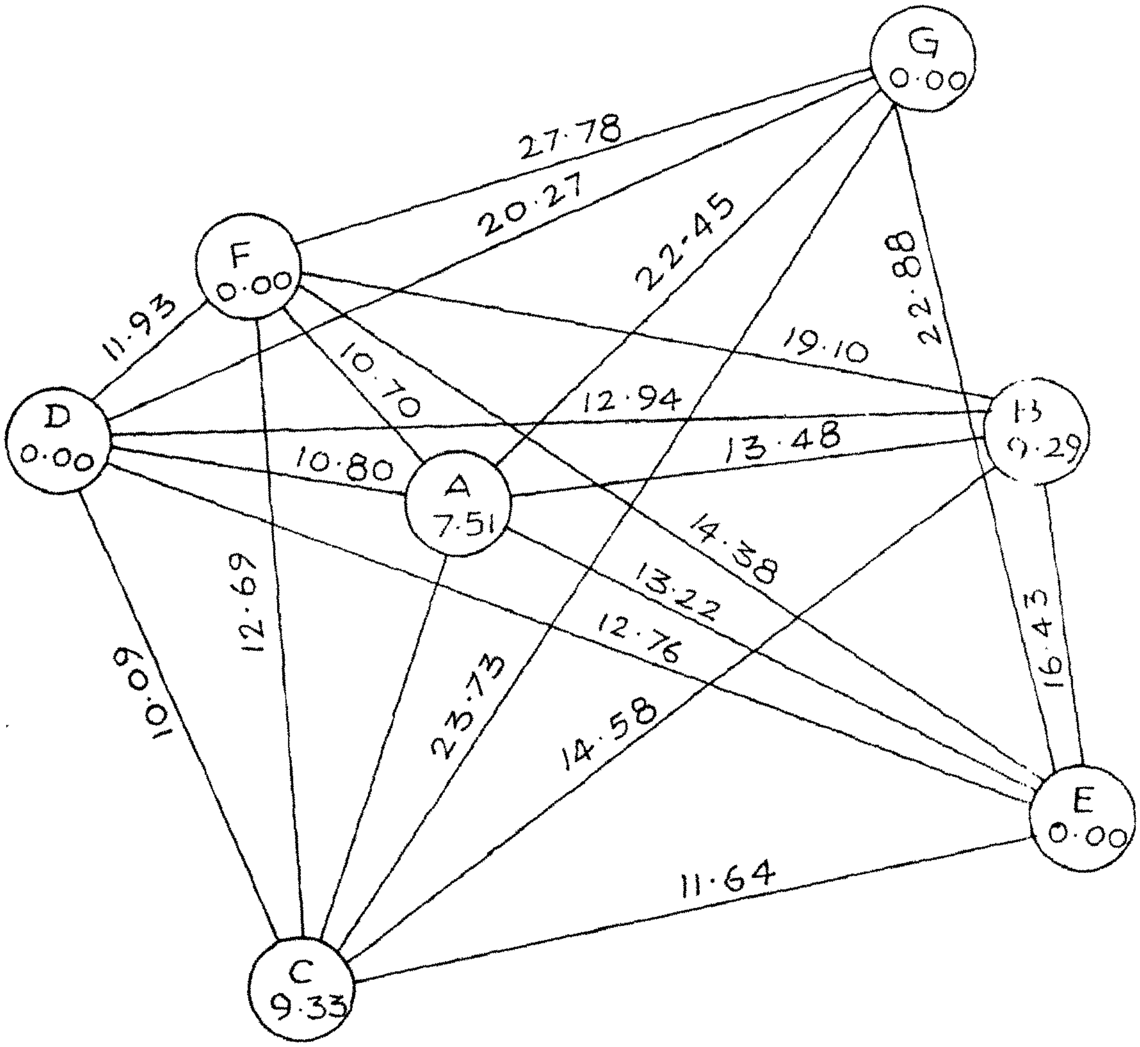
Table 8. Composition of D^2 clusters of fifty eight morphologically different genotypes in seven clusters.

Cluster	Number of genotypes	Genotype number included
A	24	52, 53, 57, 2, 28, 40, 19, 11, 13, 36, 55, 49, 48, 12, 14, 7, 3, 1, 6, 15, 20, 37, 5, 23.
B	11	9, 54, 41, 56, 30, 51, 39, 35, 33, 46, 58.
C	19	17, 45, 10, 16, 50, 32, 27, 38, 34, 21, 47, 26, 24, 22, 8, 4, 31, 43, 44.
D	1	18.
E	1	42.
F	1	25.
G	1	29.

Table 9. Intra (Diagonal) and inter cluster D^2 and D values of the seven clusters formed from fifty eight genotypes of Soybean.

	A	B	C	D	E	F	G
A	56.43 (7.51)	181.72 (13.48)	104.24 (10.20)	116.85 (10.80)	174.93 (13.22)	115.43 (10.74)	504.44 (22.45)
B		86.30 (9.29)	212.79 (14.58)	167.70 (12.94)	270.20 (16.43)	365.00 (19.10)	200.08 (14.14)
C			87.13 (9.33)	101.83 (10.09)	135.61 (11.64)	161.13 (12.69)	563.58 (23.73)
D				00.00 (00.00)	162.98 (12.76)	142.45 (11.93)	411.18 (20.27)
E					00.00 (00.00)	206.80 (14.38)	591.97 (22.80)
F						00.00 (00.00)	772.22 (27.78)
G							00.00 (00.00)

(Figures in parentheses indicate D values within and among the seven clusters)



CLUSTER DIAGRAM

FIG. 1 :- CLUSTERS AND THEIR INTER-RELETIONSHIP.

NOTE – A DIAGRAM IS NOT EXACTLY TO THE SCALE

The maximum inter cluster divergence (Table 8) was observed between cluster F and G (D = 27.78) followed by C and G (D = 23.73) while, it was the lowest between clusters C and D (D = 10.09). Out of 21 cluster combinations, four combinations viz. A with C, D, and C with D were within the inter cluster distance of 10.09 to 11.99.

Ten inter cluster combinations viz. A with B, E; B with C, D, G; C with E, F; D with E, F; E with F were within the inter cluster divergence of 12.00 to 15.99. While four inter cluster combinations viz. A with G, C with G, D with G, E with G were within the inter cluster divergence of 20.00 to 23.99. Cluster F with G had the inter cluster divergence of 27.78. Cluster A (7.51); B (9.29) and C (9.33) with their intra cluster D values given in the parentheses suggest substantial diversity within genotypes included in these clusters while the remaining clusters viz. D, E, F and G consisted of single strain hence had no intra-cluster divergence.

The mean values of sixteen characters for all clusters are given in Table 10.

The cluster means for number of days to fifty per cent flowering were maximum in cluster G (79.60), followed by B (61.23), intermediate in clusters A, C, D, E and the lowest in cluster F (34.26).

Table 10. Cluster mean formed from fifty eight genotypes of Soybean for sixteen characters.

Sr. No.	Character	Cluster A	B	C	D	E	F	G
1.	Days to fifty per cent flowering	41.20	61.23	43.43	43.33	50.53	34.26	79.60
2.	Days to maturity	90.82	98.72	99.15	104.00	102.00	84.20	100.66
3.	Plant height (cm)	51.24	85.23	82.12	86.93	100.53	66.46	84.73
4.	Plant spread (cm)	15.49	12.78	15.14	11.66	11.66	15.46	13.33
5.	Plant index	3.95	6.85	5.98	1.70	8.73	4.33	6.23
6.	Leaf length (cm)	13.93	11.45	11.70	11.83	8.96	8.36	11.16
7.	Leaf breadth (cm)	6.99	7.47	7.22	7.16	5.73	5.56	5.86
8.	Harvest index	32.31	34.66	29.74	35.00	27.40	45.60	34.33
9.	Number of branches on main stem	4.90	4.83	4.73	4.53	5.53	4.66	4.86
10.	Number of pods per plant	71.62	90.59	81.90	97.66	80.93	80.86	77.00
11.	Number of seeds per plant	123.67	160.65	145.71	191.60	134.93	169.93	120.40
12.	Pod length (cm)	4.10	3.61	4.04	3.36	3.40	4.00	3.36
13.	Number of seeds per pod	1.71	1.77	1.78	1.90	1.60	2.00	1.56
14.	Test weight (100 seed weight)	12.60	12.39	12.70	13.86	9.46	5.56	10.56
15.	Biological weight (gm)	53.47	62.29	68.24	78.86	47.06	20.53	40.40
16.	Grain yield (gm)	15.68	20.80	18.67	29.06	12.90	9.26	12.86

The clûster means for days to maturity were maximum in cluster D (104.00) followed by E (102.00), intermediate in clusters A, B, C, G and the lowest in cluster F (84.20). Similarly, for plant height was maximum in cluster E (100.53) followed by D (86.93), intermediate in clusters B, C, F, G and the lowest in cluster A (51.29).

The cluster mean for plant spread was maximum in cluster A (15.49), followed by F (15.46), intermediate in clusters B, C, G and lowest in cluster D and E (11.66). For the plant index, the mean of the cluster E (8.73) was high, which was followed by B (6.85), intermediate for the clusters A, C, F, G and low for the cluster D (1.70).

The cluster mean for leaf length was maximum in cluster A (13.93), followed by Cluster D (11.83), intermediate in clusters B, C, E, G and lowest in F (8.36). The maximum mean for the leaf breath was observed in the cluster B (7.47), followed by C (7.22), intermediate in the clusters A, D, E, G while low in the cluster F (5.56).

The cluster mean for harvest index was maximum in Cluster F (45.60), followed by cluster D (35.00), intermediate in clusters A, B, C, G and lowest in cluster E (27.40). The number of branches on main stem had high cluster mean in the cluster E (5.53) followed by A (4.90), intermediate for the clusters B, C, F, G and the lowest for the cluster D (4.53).

The cluster mean for number of pods per plant was maximum in cluster D (97.66), followed by B (90.59), intermediate in clusters C, E, F, G and lowest for the cluster A (71.62). The maximum mean was observed in the cluster D (191.60), followed by F (169.99), intermediate in clusters, A, B, C. E, while low in the cluster G (120.40) for the number of seeds per plant.

The cluster mean for pod length was maximum in cluster A (4.10), followed by cluster C (4.04), intermediate in clusters B, D, E, F and the lowest in cluster G (3.36). For the number of seeds per pod the cluster F (2.00) was high followed by C (1.78), intermediate for the clusters B, D, E, F and lowest for the cluster G (1.56).

The cluster mean for test weight was maximum in cluster D (13.86), followed by C (12.70), intermediate in clusters A. B, E, G and the lowest for the cluster F (5.56). Biological weight had its highest mean value in the cluster D (78.86) followed by C (68.24) and the lowest in the cluster F (20.53).

The cluster mean for grain yield were maximum in cluster D (23.06), followed by B (20.80), intermediate in clusters A, C, E, G and the lowest in cluster F (9.26).

5. - DISCUSSION

CHAPTER 5

DISCUSSION

In the present investigation, 58 entries of Soybean collected from different geographical origins (Table 1) were selected to assess the nature and magnitude of genetic divergence, and to know the clustering pattern with a view to establish the relationship between genetic and geographic diversity, as the above parameters are very useful tools in initiating the breeding programme in the crop plants.

The results obtained in the present investigations and presented in the Chapter 4 are discussed here in the light of already published literature.

5.1 Range of Variability :

Yield is the character of prime importance to the plant breeder. It is generally governed by polygenes which are complex in their behaviour and its expression is modified to a great extent by environmental factors. This is generally true for all other quantitative characters which are often directly associated with yield. Thus, the information regarding the variation present in respect of such characters is important from the plant breeding point of view which helps the breeder to assess and identify the superior genotypes. A wide range of variation was observed for almost all the characters viz., days to fifty per cent flowering, days to maturity, plant height, plant spread, plant index, leaf length, leaf breadth, harvest index, number of branches on main stem, number of pods per plant, number of seeds per plant, pod length, test weight, biological weight and grain yield. In the case of maturity date, plant height and grain yield the range of variation was maximum. Similar observations were also reported by Bartley and Weber (1952). The variation were also noted in case of time of maturity, number of pods per plant, number of seeds per plant and pod length. Similar results were also reported by Bulah and Aristrarkova (1970). The wide range of variation was observed in the characters like plant height, number of seeds per pod, grain yield by Malik and Singh (1987). Johnson _et al._ (1955) also reported a wide range of variation in the characters like days to fifty per cent flowering, plant spread, harvest index and test weight. Mjakusko (1968) observed a wide range of variability in the test weight. Since considerable variation exist for pod yield and other contributing characters it indicated scope for selection of the desirable genotypes from the respective botanical group.

5.2 Genetic Coefficient of Variation, Heritability Percentage and Genetic Advance :

It is useful to assess the genetic components of variability in the total variation before the variability can be utilised for further genetic improvement in crop plants.

Genetic variability is the basis for any heritable improvement in the crop plants. Additive genetic variance will be the heritable portion of the total variation. The genotypic and phenotypic coefficients of variation in the present study were the lowest for the characters, days to maturity and genotypic coefficient of variation was the highest for plant index followed by biological weight. Similarly phenotypic coefficient of variation was the highest for biological weight followed by plant index indicating low to highest variability in these characters respectively.

The genotypic and phenotypic coefficients of variation were also higher for grain yield, plant spread and plant height. The estimates of G.C.V. and P.C.V. for the characters studied were almost equal except plant spread, harvest index, number of branches on main stem, number of pods per plant, number of seeds per plant, number of seeds per pod, biological weight and grain yield. Thus indicating that the variability existing in these characters except the later group of characters was mainly due to genetic factors.

High G.C.V. and P.C.V. for the characters seed yield, number of pods per plant, plant height. Also observed high estimates of these parameters for number of branches on main stem, might be due to use of diverse material. High G.C.V. for the characters yield per plant, plant height, number of seeds per pod had been reported by Malik and Singh (1987). The results were in confirmation with the findings of Kovacheva (1975), Liu et al. (1985), Malhotra (1973), Bhatta et al. (1968) and Johnson et al. (1955).

However, genetic coefficient of variability alone would not indicate proportion of total heritable variation, the heritability estimates are better indication of heritable proportion of variation. The broad sense heritability percentage includes the contribution of additive gene effect, allelic interaction due to dominance and non-allelic due to epistasis. Very high estimates of heritability were obtained for almost all the characters studied except in number of seeds per pod. The results were in confirmation with the findings of Pushpendra and Ram (1987), Malik and Singh (1987), Alam et al. (1984),Fisenko (1982), Malik and Singh (1987) and Caviness (1969).

In the present investigation genetic advance was higher for the characters, number of seeds per plant and plant height, moderate for biological weight and number of pods per plant. Though heritability is a good indication of genetic control in the expression of character, heritability coupled with genetic advance can be of more use in predicting the effect of selecting types with such characters, days to fifty per cent flowering, leaf breadth, and leaf length have high heritability and fair estimates of genetic advance indicating additive gene effect in the inheritance of these characters as such selection of these characters would prove effective. These findings were in confirmation with those of Singh et al. (1979), Kaw and Menon (1978), Malhotra (1973) and Johnson et al. (1955).

5.3 Correlation :

Grain yield in the present study was positively significant environmental, genotypic and phenotypic correlation with plant height, number of pods per plant, number of seeds per plant, biological weight and test weight, days to maturity, plant index, leaf breadth and number of seeds per pod. Gai and Fehr (1984), Alam *et al.* (1983), Barbind and Reddy (1981), Kozak (1973), Kovacheva (1975), Malhotra (1972), Bhatta *et al.* (1968), Johnson *et al.* (1955) also reported positive association among these characters. Grain yield had positive but non-significant association with the characters plant spread, leaf length, leaf breadth, number of branches on main stem in environmental and phenotypic level. Days to fifty per cent flowering, pod length, harvest index in turn showed negative genotypic correlation with grain yield. These findings were in close confirmity with that of Tong (1986), Shettar *et al.* (1978), Arora *et al.* (1970) and Gopani and Kabaria (1970).

5.4 Genetic Divergence :

The concept of genetic distance has been of vital utility in many contexts. Particularly in differentiating well defined populations. Several measures of distance have been proposed in the past two decades to suit various objectives (Jacquard, 1974) of which Mahalnobis's generalised distance (Mahalnobis, 1930) occupied a unique place in plant breeding. Though unlike in biology its direct utilization fits well in more exact fields like mathematical statistics, physics and others when environmental influence is not a major component to deal with. In Biology, under the influence of random, unpredictable changes due to environments there appear certain limitations in the application of this concept.

The results obtained have been discussed under the following heads.

1) Relative importance of characters towards genetic divergence.
2) Cluster formation.
3) Relationship of geographic diversity and genetic diversity.

5.4.1 Relative importance of characters towards genetic divergence :

The relative importance of the individual character towards genetic divergence can be known on the basis of the size of the coefficients of the canonical vectors (Rao, 1952). The present investigation revealed the importance of 100 seed weight plant height, number of pods per plant and days to fifty per cent flowering. This supports the results of Shwe _et al._ (1972) Verma _et al._ (1973) in Soybean. Verma _et al._ (1974), Chauhan (1983), Bains and Sood (1984), Raut _et al._ (1984) in Soybean also reported that days to fifty per cent flowering contributed more to the total genetic divergence in Soybean.

Relative importance of the characters and the contribution of individual characters towards genetic divergence had been reported by several workers in different crops. However, Singh (1981) stated that this method of determining the influence of character on genetic divergence is incorrect. Because according to him, the transformed uncorrelated characters (Yi) do not have any biological meaning. He further pointed out that the workers who did use this method have wrongly taken characters (Yi) to be uncorrelated (Xi) implying a one to one correspondence between these two variables. In fact (Yi) is a linear function of several (Xi) values (Singh, 1981). Therefore, Bains and Sood (1984) used cluster means which are based on the correlated data, to know the relative importance of the characters in causing genetic divergence. In the present study also, the variances of cluster means were calculated for all the characters (Table 10 The results also indicated the importance of 100 seed weight, plant height, number of pods per plant and days to fifty per cent flowering which confirmed the results obtained on the basis of canonical methods. Thus, it can be concluded that if the parents are selected on the basis of these four traits, viz. 100 seed weight, plant height, number of pods per plant and days to fifty per cent flowering they are expected to be genetically diversed also which may be used in the hybridization programme to expect desired heterotic responses and the genetic improvement in desirable direction.

5.4.2 Cluster formation :

The aim of forming clusters and finding out the intra and inter cluster divergence is to provide the base for selecting parents for making crosses. The theoretical concepts in such grouping is that the strains grouped into the same clusters presumably are little diverse from each other and the crossing between the strains belonging to the same cluster is not expected to give desired heterotic response. Consequently, a breeding programme should be so diversed that the selected parents for crossing should belong to different clusters and appear logical to effect crosses between strains belonging to the clusters widely separated by high inter cluster diversity. It is assumed that the statistical distance (D^2) is an index of genetic diversity. It is, therefore, emphasized that while using this approach, the breeder should not ignore the biology of situation.

Cluster 'A' was very large and comprised of 24 strains while 'C' had 19 strains and 'B' had 11 strains. The maximum inter cluster distance was observed between clusters F and G (27.78), followed by C and G (23.73). An examination of Table 10 also showed that the means for different characters of cluster 'G' varied considerably from those of clusters F and C. This indicated that strains in Cluster 'G' might have entirely different genetic architecture from the strains included in clusters 'F' and 'C'.

It is suggested that varieties from diversed clusters and having high yield potential thus might be very useful in framing a suitable breeding programme since such crosses are expected to throw superior segregates.

5.4.3 Relationship of geographic diversity and genetic diversity :

The clustering pattern in the present study indicated that of the 24 genotypes with Indian majority (10 lines) have been grouped into Cluster-I suggesting that they are not genetically much diversed. It is interesting to find that all these genotypes are the Poona Soybean selections representing a common area of adoption. However, the other genotypes of Indian origin namely MACS-13 from Pune belonged to Cluster-II which also included other variety (S-788) of Indian origin, but coming from Vidarbha region. The remaining genotypes having India as their origin were included in Cluster-III and Cluster-IV

Thus, it is clear from the study that though the country of these genotypes is common, they represent different areas of adoption and thus, grouped into different clusters. The eleven U.S.A. genotypes were included into five different clusters. However, out of 4 genotypes of origin from Australia, three included in one Cluster seemed to be genetically relatively close, on the contrary, the constitution of the clusters revealed that genotypes coming from different geographic area are included into same cluster suggesting that geographic diversity does not necessarily represent the genetic diversity. These results are in close conformity to those reported by Murty and Arunachalam (1966), Shwe _et al._ (1972), Singh _et al._ (1979), Asthana and Pandey (1980), Jain _et al._ (1981), Raut _et al._ (1984), Malik _et al._ (1985).

This may be attributed to frequent exchange of breeding material from one place to another and its further selection in different geographic regions which could result in genetic diversity (Murty and Arunachalam, 1966; Bhatta et al. 1968; Narsinghani et al. 1976; Asthana and Pandey, 1980; Raut et al. 1984; and Malik et al. 1985). They have also stated that genetic drift and selection in different environments could cause greater diversity among the genotypes due to their geographic distances. Thus, the constellation that might be having association with the particular region in nature may loose their individuality under human intereference.

Thus, on the basis of the results obtained in the present study shared the relative importance of 100 seed weight, plant height, number of pods per plant and days to fifty per cent flowering in selecting the parents in the hybridization programme. And as indicated in the present investigation there appears no direct relationship between genetic diversity and geographic diversity in this crop.

5.5 Tentative Crossing Programme :

Based on the information from D^2 analysis, it is suggested that the genotypes from diversed clusters and having high yield potential for grain yield per plant with number of branches on main stem, plant height, and number of pods per plant might be very useful in forming a suitable breeding programme. Such crosses are expected to throw the superior segregates in any generation.

A crossing programme as given below is therefore suggested.

Cluster A with B, E, G.
Cluster B with C, E, F, G.
Cluster C with G.
Cluster D with G.
Cluster E with F, G.
Cluster F with G.

The inter cluster values of above combination are higher than 13. At this juncture, it is pointed out that if there is a greater diversity above critical limit, the crosses between clusters may not give the expected results as extremely divergent crosses, may result in decreased heterosis. Therefore, taking into account inter cluster divergence (Table 9), cluster means (Table 10) and character means (Table 2) of genotypes a breeding programme can be suggested.

6. - SUMMERY AND CONCLUSION

CHAPTER 6

SUMMARY AND CONCLUSIONS

The present investigations were undertaken in fifty eight varieties of Soybean collected from Maharashtra Association for Cultivation of Sciences, Pune, to study the nature and extent of variation, direction and magnitude of association of Soybean, during <u>Kharif</u> 1987.

The observations were recorded on days to fifty per cent flowering, days to maturity, plant height, plant spread, plant index, leaf length, leaf breadth, harvest index, number of branches on main stem, number of pods per plant, number of se per plant, pod length, number of seeds per pod, test weight, biological weight, grain yield. The data on range of variability and significance of mean indicated sufficient variability present in the genotypes under study.

The estimates of genotypic coefficient of variation were low as compared to the phenotypic coefficient of variation. The G.C.V. as well as P.C.V. were least for the characters, number of seeds per pod, days to maturity and highest for plant index and biological weight.

Very high estimates of heritability were obtained for almost all the characters while moderate heritability estimates were recorded for the character number of seeds per plant. The estimates of genetic advance were high for the characters plant height and number of seeds per plant and moderate for days to fifty per cent flowering and number of pods per plant and low for the characters number of branches on main stem, pod length and number of seeds per pod.

Moderate to high heritable values coupled with high genetic advance were observed for the characters, plant height and number of seeds per plant, thus indicating additive genetic control for these characters.

Grain yield per plant had highly significant positive association with the characters days to maturity, plant height. plant index, leaf breadth, number of pods per plant, number of seeds per plant, number of seeds per pod, test weight and biological weight, grain yield per plant had significant positive association with the characters days to fifty per cent flowering, leaf length. However, it had negative but non-significant association with the characters plant spread, harvest index, number of branches on main stem. Significant positive correlation of days to maturity and 100 seed weight, with grain yield and moderate to high heritability with fair estimates of genetic advance for these characters indicated that selection for these characters will be effective in increasing the yield potential of these crops.

The D^2 statistics showed that there was adequate diversity between strains with D^2 values ranging from 4.34 to 772.22. On the basis of D^2 analysis, strains studied were grouped in seven clusters with substantial genetic divergence between them. Cluster A was very large comprising 24 strains, C with 19 strains, B with 11 strains and D, E, F, G with one strains each. The clustering pattern of the genotypes was not necessarily as per geographic diversity.

Tentative crossing programmes based on the study is suggested as below :

Cluster A with B, E, G.
Cluster B with C, E, F, G.
Cluster C with G.
Cluster D with G.
Cluster E with F, G.
Cluster F with G.

7. - LITERATURE CITED

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* Originals not seen.

8. - VITA

VITA

RAJESH N. KADU
CANDIDATE FOR THE DEGREE
OF
MASTER OF SCIENCE (AGRICULTURE)

TITLE OF THESIS : " Genetic divergence and variation studies in Soybean (*Glycine max*. (L.) Merrill."

MAJOR FIELD : Agricultural Botany (Cytogenetics and Plant Breeding)

BIOGRAPHICAL INFORMATION

PERSONAL DATA : Born at Amravati, on June 29, 1965 son of Shri Nilkantharao A. Kadu at Amravati (Maharashtra State)

EDUCATION : Completed secondary and higher secondary school at Amravati, received Bachelor of Science (Agri.) degree with First Class from Anand Niketan College of Agriculture, Warora, District Chandrapur, Punjabrao Agricultural University, Akola, Maharastra State, 1985.