# GENETIC DIVERGENCE IN SOYBEAN
# [*Glycine max* (L.) Merrill] GENOTYPES

**By**

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**DEPARTMENT OF**
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**AGRICULTURAL COLLEGE, BAPATLA**

**ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY**
**RAJENDRANAGAR, HYDERABAD – 500 030.**

**2009**

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THESIS SUBMITTED TO THE
ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

**MASTER OF SCIENCE IN AGRICULTURE**

**DEPARTMENT OF GENETICS AND PLANT BREEDING**
**AGRICULTURAL COLLEGE, BAPATLA**
**ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY**
**RAJENDRANAGAR, HYDERABAD – 500 030.**

**2009**

# CERTIFICATE

**Mrs. Y. Pushpareni** has satisfactorily prosecuted the course of research and that the thesis entitled **"Genetic divergence in soybean [*Glycine max* (L.) Merrill] genotypes"**submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part there of has not been previously submitted by her for a degree of any University.

**Place: Bapatla**

**Date:**

**(Dr.Y.KOTESWARA RAO )**
Major Advisor
Principal Scientist (Pulses)
Regional Agricultural Research Station
Lam, Guntur.

# CERTIFICATE

This is to certify that the thesis entitled "**Genetic divergence in soybean [*Glycine max* (L.) Merrill] genotypes"** submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture in the major field of Genetics and Plant Breeding of the Acharya N.G. Ranga Agricultural University, Hyderabad, is a record of the bonafide research work carried out by Mrs. Y. Pushpareni under my guidance and supervision. The subject of thesis has been approved by the Student's Advisory Committee.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part has been fully acknowledged. All the assistance and help received during the course of investigation have been duly acknowledged by the author of the thesis.

**( Dr.Y.KOTESWARA RAO )**
Chairman of the Advisory Committee.

Thesis approved by the Student's Advisory Committee.

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# ACKNOWLEDGEMENTS

Accomplishment of this thesis is the result of benevolence of Almighty, blessings of my teachers and love of parents.

I humbly place on record my respect and profound sense of gratitude to the esteemed Chairman of my Advisory Committee, **Dr. Y.Koteswara Rao**, Principal scientist (Plant Breeding), Regional Agricultural Research Station, Lam Farm, Guntur for suggesting this present research work, rendering incessant guidance and giving valuable suggestions during entire course of my post graduate study.

I humbly express my profound gratitude to **J.V.Ramana,** Scientist, Rice Research Unit, Bapatla and **Dr.V. Srinivasa Rao**, Associate Professor and Head, Department of Statistics and Mathematics, members of my Advisory Committee for their constant support, timely suggestions and kind cooperation which greatly contributed to the enrichment of the thesis.

I am deeply indebted to **Dr. C. Panduranga Rao,** Professor and Head, Department of Genetics and Plant Breeding, Agricultural College, Bapatla for his encouragement in conducing research and meticulous reasoning to refine the dissertation to recon with set standards.

I owe respectable regards and heartful thanks to the staff members of Genetics and Plant Breeding **Dr. J.S.V. Samba Murthy**, Professor, **Dr. P.V. Ram Kumar**, Professor, **Dr. V.Satyanarayana Rao,** Associate Professor, and **Dr. Lal Ahamed**, Assistant Professor for the constant encouragement and valuable comments timely help and cooperate during the course of my study.

My sincere respect to **Associate Director of Research, Farm superindent and Staff** of RARS, Lam Farm, Guntur for extending all facilities in conducting the experiment in the farm.

*I express my special thanks to* ***Dr.M.V.Ramana*** *Senior Scientist (Breeding) ARS, Vuyyur****, Dr. Krishna Veni*** *, Scientist(Breeding),RRU, Bapatla and* ***Dr.B.PrameelaRani,*** *Senior Scientist (Agronomy),RARS, Lam for their generous help and valuable suggestions.*

*I am in dearth of words to express my heartfelt feelings to my beloved parents* ***Sri. Y.Sagareswara Rao*** *and* ***Smt. Y.Sesharatnam****, Sisters* ***Padmaja and Madhavi*** *Brother* ***Chandra Sekar*** *husband* ***G.Prasada Rao*** *daughters* ***Sai Sravya and Sai Sreya****, whose love and constant encouragement have always been a source of inspiration for me.*

*It is time to surface out my affection and gratitude to my friends,* ***Hema,Ch.Mallikarjuna Rao, Swaroopa, Indira, P.V.Padmavathi,*** *and* ***Kiran*** *for her friendly opulence and help during the course of my study.*

*I extend my sincere thanks to* ***Uma Devi****, Librarian and other staff of library for their help during my study.*

*I extend my sincere thanks to ANGRAU for sanctioning study leave during my study.*

*Finally, a word of appreciation goes to Eswar Digitals for typing of my thesis.*

***Place : Bapatla*** **( Y.PUSHPA RENI)**

***Date :***

# DECLARATION

I, Mrs.**Y.PUSHPA RENI,** hereby declare that the thesis entitled **"Genetic divergence in soybean [*Glycine max* (L.) Merrill] genotypes"** submitted to the Acharya N. G. Ranga Agricultural University for the degree of **Master of Science in Agriculture** in the major field of **GENETICS AND PLANT BREEDING** is the result of original research work done by me. I also declare that the thesis or any part there of has not been published earlier in any manner.

**Place: Bapatla**

**Date:** (**Y.PUSHPA RENI)**

# ABSTRACT

| | | |
|---|---|---|
| Name of the Author | : | **Pushpa Reni.Y** |
| Title of Thesis | : | **Genetic divergence in soybean [ *Glycine max* (L.) Merrill] genotypes** |
| Degree to which it is submitted | : | Master of Science in Agriculture |
| Faculty | : | Agriculture |
| Discipline | : | Genetics and Plant Breeding |
| Major Advisor | : | **Dr.Y.Koteswara Rao** |
| University | : | ACHARYA N G RANGA AGRICULTURAL UNIVERSITY |
| Year of submission | : | 2008 |

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An investigation was conducted during *kharif*, 2007 at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh to elicit information on the nature and extent of the genetic variability, divergence, correlations and path analysis in 45 soybean genotypes for 13 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%), protein content (%), oil content (%) and seed yield per plant (g).

The analysis of variance revealed significant differences among the genotypes for all the characters studied.

- The genotypic coefficients of variation for all characters studied were lesser than phenotypic coefficients of variation indicating the masking effects of the environment.

- High PCV coupled with high GCV, observed for number of branches per plant, number of pods per plant, biological yield, harvest index and seed yield per plant indicate the presence of wider variability for these traits in the genotypes studied.

- High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, biological yield, harvest index and seed yield per plant indicating operation of additive gene action in these traits and indicating that improvement is possible is possible through simple selection.

- The results of multivariate analysis indicated the presence of considerable genetic divergence among the 45 genotypes studied. The 45 genotypes were grouped into 6 clusters. Clustering pattern of genotypes did not follow geographical origin, suggesting that geographical isolation may not be the only factor causing genetic diversity. Based upon the divergence studies, crosses may be made between the genotype of cluster III (PS 1421) and cluster VI (VLS 69) to isolate good recombinants.

- Out of 13 characters studied days to maturity followed by pods per plant contributed maximum towards divergence.

- The principal component analysis identified 5 principal components with eigen value more than one. The contribution by the first ($PC_1$) is maximum and loaded with maximum contributing variables *i.e* days to maturity, pods per plant and days to 50% flowering.

- The clustering pattern is in accordance with the PCA analysis during *kharif*, 2007. Hierarchical cluster analysis revealed the subgroups in the major group of genotypes through Ward's minimum variance dendrogram.

- Correlation studies indicated that the seed yield per plant was positively correlated with biological yield per plant (g), number of pods per plant and harvest index (%).

- The results of path coefficient analysis further suggested that selection of the characters biological yield per plant (g), number of pods per plant and harvest index (%) will have positive influence on seed yield per plant. As these characters exhibited both direct effects and positive correlation with seed yield.

- Thus, the present study, revealed that major emphasis should be laid on selection for more number of pods per plant with simultaneous improvement of biological yield per plant (g) and harvest (%) index through their component traits  for yield improvement of seed yield in soybean.

# LIST OF SYMBOLS AND ABBREVIATIONS

| | | |
|---|---|---|
| $\overline{X}$ | : | Mean value |
| % | : | Per cent |
| $^{o}c$ | : | Degree Celsius |
| 2D | : | Two dimentional |
| 3D | : | Three dimentional |
| A.O.A.C | : | Official methods of Analysis of the Association of Agricultural chemists |
| ANOVA | : | Analysis of variance |
| CD | : | Critical difference |
| cm | : | Centimeter |
| CV | : | Coefficient of variation |
| d.f | : | Degree of freedom |
| g | : | gram |
| GA | : | Genetic advance |
| GCV | : | Genotypic coefficient of variation |
| ha | : | hectare |
| $K_2O$ | : | Potassium |
| MSS | : | mean sum of squares |
| N | : | Nitrogen |
| No. | : | Number |
| $P_2O_5$ | : | Phosphorous |
| PCA | : | Principal component analysis |
| PCV | : | Phenotypic coefficient of variation |
| RARS | : | Regional Agricultural Research Station |
| RBD | : | Randomised block design |
| S.Ed | : | Standard error of difference |
| S.Em | : | Standard error of mean |

# CHAPTER - I

# INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is a major oil seed crop in the world and is called as a golden bean or miracle bean because of its versatile nutritional qualities having about 20% oil and 40% protein, which has biological value as meat and fish protein (Quayam *et al.*, 1985) and rich in amino acids like lysine and tryptophan. The productivity of soybean crop is nearly 2 to 3 times higher than traditional pulses. It has good adaptability towards a wide range of soils, climate and fetches good returns to farmers and hence gained importance in foreign trade due to export of the deoiled cake (Anonymous, 2005).

In India, it is cultivated in an area of 5.68 m ha with production and productivity of 7.61 million tones and 1171 kg $ha^{-1}$, respectively. Madhya Pradesh contributes about 65% and 57% of the total area and production of soybean in the country. In Andhra Pradesh, soybean is cultivated in 1.4 lakh ha mainly in Adilabad, Nizamabad, Medak and Guntur districts (Anonymous, 2007). Soybean has emerged as a potential alternate crop to cash crops viz., cotton, tobacco, chilli *etc.* in Andhra Pradesh as the climatic conditions are congenial for its successful cultivation both in *kharif* and *rabi* seasons.

In India, per capita consumption of pulses is below 40 g per day as against World Health Organization (W.H.O) recommendation of 85 g per day. This protein deficit can be fulfilled when a high protein yielding soybean crop is encouraged in larger areas for cultivation.

Genetic variability is the basic requirement for improvement in any crop and information on the association among the yield and yield components is essential for improvement of the genotypes. Genetic divergence is a useful technique in selecting diverse parents for purposeful hybridization programme. Multivariate analysis based on Mahalanobis' $D^2$ statistic as well as principal component analysis are widely used for estimating the genetic diversity. Genetic divergence coupled with information on genetic parameters and genetic gain obtained by selection for yield and its components are the important pre-requisites for a systematic crop improvement programme.

Yield is a polygenically controlled complex character and is determined by number of character components, which are also quantitatively inherited. The knowledge of the association between yield and its components and among components themselves is of immense practical value in crop improvement through selection. Path coefficient analysis (Wright, 1921) brings out the direct and indirect effects of components traits on yield. The present investigation was carried out with 45 soybean germplasm collection of diverse origin to explore the extent of genetic variability, association of certain characters, their direct contribution to yield and indirect effects through other characters on yield.

Hence, the present investigation is undertaken with the following objectives.

**Objectives**

1. To study the magnitude of variability, heritability and genetic advance for yield and yield component characters.

2. To estimate the genetic divergence through $D^2$ analysis, cluster analysis and principal component analysis to find out diverse parents for crossing programme and the important characters contributing to the genetic divergence.

3. To study the association of various characters with yield and among themselves through correlation studies.

4. To estimate the direct and indirect effects of different component traits on seed yield per plant.

# CHAPTER – II

# REVIEW OF LITERATURE

Soybean [*Glycine max* (L.) Merrill] is called as a miracle crop / golden bean containing about 40% protein and 20% oil in its seed due to which it became the major source of vegetable oil, protein, feed and food supplements in the world. It belongs to the family Fabaceae and sub family of Papilionaceae with a diploid chromosome number of 2n = 40. The genus *Glycine* is sub divided into two sub-genera viz., *Glycine* and *Soja*. The sub genus *Glycine* includes seven wild perennial species. The sub-genus *Soja* includes two species viz. the cultivated type, *Glycine max (L.)* Merrill and annual wild type, *Glycine soja*, which is the ancestor of the cultivated soybean (Hymowitz and Newell, 1981).

Soybean ranks first among the oil seeds in the global scale. However, overall improvement in yield, oil and protein content in soybean remains as challenge task to the plant breeders. This can be achieved through selection, efficiency of which mainly depends on the extent of variability existing in the material.

The literature available on the main objectives of the present study have been comprehensively reviewed in this chapter under the following heads.

2.1 Variability, heritability and genetic advance

2.2 Genetic divergence

2.3 Correlation analysis

2.4 Path analysis

## 2.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

### 2.1.1 Variability

The information on the nature and magnitude of variability of different quantitative and qualitative traits in any crop species plays a vital role while formulating an efficient breeding programme. Superior genotypes can be isolated by selection if considerable genetic variation exists in the population. The progress in breeding for the economic traits which are mostly polygenically controlled and environmentally influenced is determined by the nature and magnitude of their genotypic variability.

Hence, it is essential to partition the overall variability into heritable and non-heritable components with the help of genetic parameters like genotypic and phenotypic coefficients of variation, heritability and genetic advance. The magnitude of heritability on one hand and nature and extent of variability on the other hand gives an idea for effective genetic improvement through selection (Allard, 1960).

The available literature on variability studies in soybean is furnished in Table 1.

### 2.1.2 Heritability, genetic advance and genetic advance as percent of mean

Heritability is defined as the ratio of additive genetic component of variance to total phenotypic variance (Wright, 1921). Heritability measures the relative amount of the heritable portion of the variability, while the genetic advance helps to measure the amount of progress that could be expected with selection in a character. Estimates of heritability along with estimates of genetic advance are more useful in choice of selection method rather than heritability or genetic advance alone (Johnson *et al.*, 1955). High heritability is not always an indication of high genetic gain ( Swarup and Chaugle, 1962). Whereas high heritability coupled with high genetic advance indicates that the improvement could be made for a character by simple selection based on phenotypic performance. The available literature on heritability and genetic advance is presented in Table 2.

**Table 1: Review of literature on genetic variability in soybean [*Glycine max* (L.) Merrill]**

| S.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 1 | Days to 50% flowering | Tiwari and Bhatnagar (1991)<br>Mehetre *et al.* (1994 a)<br>Taware *et al.* (1995)<br>Maharaddi (1996)<br>Taware *et al.* (1997)<br>Thorat *et al.* (1999)<br>Sood and Sood (2001) | Nirmala Kumari and Balasubramanian (1993)<br>Mehetre *et al.* (1995)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.* (2000)<br>Bangar *et al*. (2003)<br>Ramana (2003) |
| 2 | Days to maturity | Nirmala Kumari and Balasubramanian (1993)<br>Mehetre *et al.* (1994a)<br>Mehetre *et al.* (1995)<br>Taware *et al.* (1995)<br>Mehetre *et al.* (1997)<br>Taware *et al.* (1997) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Harer and Deshmukh (1992)<br>Sailaja (1997)<br>Taware *et al.* (1997)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.* (2000)<br>Agarwal *et al.* (2001)<br>Sood and Sood (2001)<br>Bangar *et al*. (2003)<br>Ramana (2003) |

| S.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 3 | Plant height (cm) | Harer and Deshmukh (1992)<br>Mahajan *et al.*(1993)<br>Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.* (1994a)<br>Mehetre *et al.* (1995)<br>Taware *et al.* (1995)<br>Maharaddi (1996)<br>Sailaja (1997)<br>Taware *et al.* (1997)<br>Mehetre *et al.* (1998)<br>Shrivastava and Shukla (1998)<br>Thorat *et al.* (1999)<br>Ramana *et al.* (2000)<br>Agarwal *et al.*(2001)<br>Bangar *et al.* (2003)<br>Ramana (2003)<br>Praveen Kumar *et al.* (2005)<br>Sriranjani *et al.* (2007) | Singh and Singh (1999) |
| 4 | Number of branches per plant | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992)<br>Mahajan *et al.* (1993)<br>Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagatap and Mehetre (1994)<br>Sailaja (1997)<br>Taware *et al.* (1997)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Bangar *et al.*(2003)<br>Ramana (2003)<br>Praveen Kumar *et al.* (2005)<br>Sriranjani *et al.* (2007) | Mehetre *et al.* (1994a)<br>Mehetre *et al.* (1995)<br>Maharaddi (1996)<br>Mehetre *et al.* (1998)<br>Shrivastava and Shukla (1998) |

| S.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 5 | Number of `pods per plant | Amarnath *et al.*(1991)<br>Harer and Deshmukh (1992)<br>Mahajan *et al.*(1993)<br>Jagatap and Mehetre (1994)<br>Mehetre *et al.* (1994a)<br>Srivastava and Jain (1994)<br>Mehetre *et al.* (1995)<br>Mehetre *et al.* (1997)<br>Sailaja (1997)<br>Mehetre *et al.* (1998)<br>Singh and Singh (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Bangar *et al.*(2003)<br>Ramana (2003)<br>Chettri *et al.*(2005)<br>Praveen Kumar *et al.*(2005)<br>Gohil *et al.*(2006)<br>Sriranjani *et al* (2007) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Thorat *et al.* (1999) |
| 6 | Pod length (cm) | Thorat *et al.*(1999) | Maharaddi (1996)<br>Ramana *et al.* (2000)<br>Mishra and Rao (2005)<br>Hina Kausar (2006) |
| 7 | Number of seeds per pod | Malik and Singh (1987) | Srivastava and Jain (1994)<br>Maharaddi (1996)<br>Sailaja (1997)<br>Thorat *et al.*(1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Ramana (2003)<br>Hina Kausar (2006) |

| S.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 8 | 100 seed weight (g) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Harer and Deshmukh (1992)<br>Mahajan *et al.* (1993)<br>Mehetre *et al.* (1994a)<br>Srivastava and Jain (1994)<br>Taware *et al.* (1995)<br>Maharaddi (1996)<br>Mehetre *et al.* (1997)<br>Sailaja (1997)<br>Taware *et al.* (1997)<br>Mehetre *et al.* (1998)<br>Thorat *et al.* (1999)<br>Sood and Sood (2001)<br>Bangar *et al.*(2003)<br>Ramana (2003) | Mehetre *et al.* (1995)<br>Shrivastava and Shukla (1998)<br>Singh and Singh (1999)<br>Ramana *et al.* (2000) |
| 9 | Biological yield per plant (g) | Nirmala Kumari and Balasubramanian (1993)<br>Srivastava and Jain (1994)<br>Mehetre *et al.* (1997)<br>Sailaja (1997)<br>Shrivastava and Shukla (1998)<br>Dixit *et al.*(2002)<br>Ramana (2003)<br>Praveen Kumar *et al.*(2005) | – |
| 10 | Harvest index (%) | Nirmala Kumari and Balasubramanian (1993)<br>Srivastava and Jain (1994)<br>Mehetre *et al.* (1997)<br>Mehetre *et al.* (1998)<br>Dixit *et al.*(2002) | Sailaja (1997)<br>Shrivastava and Shukla (1998)<br>Ramana (2003) |

| S.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 11 | Seed protein content (%) | Arora *et al.*(1970)<br>Musorina (1987)<br>Nirmala Kumari and Balasubramanian (1993) | Malik and Singh (1987)<br>Sailaja (1997)<br>Thorat *et al.* (1999)<br>Ramana (2003) |
| 12 | Oil content (%) | Weber and Moorthy (1952)<br>Malik and Singh (1987)<br>Taware *et al.* (1997) | Sharma *et al.* (1986)<br>Mehetre *et al.* (1995)<br>Thorat *et al.* (1999)<br>Ramana (2003) |
| 13 | Seed yield per plant (g) | Jagtap and Mehetre (1994)<br>Mehetre *et al.* (1995)<br>Maharaddi (1996)<br>Mehetre *et al.* (1997)<br>Sailaja (1997)<br>Taware *et al.* (1997)<br>Mehetre *et al.* (1998)<br>Shrivastava and Shukla (1998)<br>Singh and Singh (1999)<br>Thorat *et al.* (1999)<br>Ramana *et al.* (2000)<br>Agarwal *et al.* (2001)<br>Sood and Sood (2001)<br>Dixit *et al.* (2002)<br>Bangar *et al.* (2003)<br>Ramana (2003)<br>Gohil *et al.* (2006)<br>Sriranjani *et al.* (2007) | Kalaimagal (1991)<br>Nirmala Kumari and Balasubramanian (1993) |

| | | | | | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| | | | | | |
| | | | | | |
| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
| | | | | | |
| | | | | | |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 4 | Number of branches per plant | Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagatap and Mehetre (1994)<br>Rajarathinam *et al.* (1996)<br>Sailaja (1997)<br>Roy and Raquib (1998)<br>Agarwal *et al.* (2001)<br>Bangar *et al.* (2003)<br>Ramana (2003)<br>Hina Kausar (2006) | Rajasekaran *et al.* (1980)<br>Taware *et al.* (1997) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Harer and Deshmukh (1992)<br>Maharaddi (1996) | Mehetre *et al* (1994a)<br>Mehetre *et al.* (1995)<br>Shrivastava and Shukla (1998) Ramana *et al.* (2000) |
| 5 | Number of pods per plant | Amarnath *et al.* (1991)<br>Nirmala Kumari and Balasubramanian (1993)<br>Jagatap and Mehetre (1994) | -- | Harer and Deshmukh (1992)<br>Mahajan *et al.* (1994)<br>Mehetre *et al.* (1994a) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Shrivastava and Shukla |

| | | | | | |
|---|---|---|---|---|---|
| | | Mehetre *et al.* (1994a)<br>Rajarathinam *et al.* (1996)<br>Mehetre *et al.* (1997)<br>Sailaja (1997)<br>Taware *et al.* (1997)<br>Mehetre *et al.* (1998)<br>Roy and Raquib (1998)<br>Maharaddi *et al.* (1999)<br>Singh and Singh (1999);<br>Jain and Ramgiry (2000);<br>Ramana *et al.* (2000);<br>Agarwal *et al.* (2001);<br>Gohil *et al.* (2006)<br>Hina Kausar (2006); Sriranjani *et al* (2007) | | Thorat *et al.* (1999)<br>Sood and Sood (2001)<br>Bangar *et al.* (2003) | (1998)<br>Ramana *et al.* (2000)<br>Mishra and Rao (2005) |
| 6 | Pod length (cm) | Thorat *et al.* (1999) | Agarwal *et al.* (2001) | -- | Rana Khurana and Sandhu (1972)<br>Maharaddi (1996)<br>Ramana *et al.* (2000) |
| 7 | Number of seeds per pod | -- | Rashid and Islam (1982)<br>Sailaja (1997) | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992) | Kalaimagal (1991)<br>Vimala Devi (1993)<br>Srivastava and Jain (1994) |

| | | | | | |
|---|---|---|---|---|---|
| | | | Chettri *et al.* (2005) | | Maharaddi (1996)<br>Thorat *et al.* (1999)<br>Ramana *et al.* (2000)<br>Ramana. (2003)<br>Praveen Kumar *et al.* (2005) |
| 8 | 100 seed weight (g) | Nirmal Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Mahajan *et al.* (1994)<br>Mehetre *et al.* (1994a)<br>Srivastava and Jain (1994)<br>Taware *et al.* (1995)<br>Maharaddi (1996)<br>Rajarathinam *et al.* (1996)<br>Mehetre *et al.* (1997),<br>Taware *et al.* (1997)<br>Mehetre *et al.* (1998)<br>Throat *et al.* (1999)<br>Basavaraja *et al.* (2005)<br>Jyothi Sethi and Tyagi (2005)<br>Hina Kausar (2006) | Sailaja (1997)<br>Nehru *et al.* (1999)<br>Singh and Singh (1999)<br>Ramana *et al.* (2000)<br>Sood and Sood (2001)<br>Chettri *et al.* (2005) | Shrivastava and Shukla (1998)<br>Bangar *et al.* (2003) | -- |

| | | | | | |
|---|---|---|---|---|---|
| 9 | Biological yield per plant (g) | Mehetre *et al.* (1994a)<br>Sailaja (1997), Mehetre *et al.* (1998)<br>Ramana *et al.* (2003)<br>Jyothi Sethi and Tyagi (2005)<br>Hina Kausar (2006)<br>Sriranjani *et al* (2007) | Shrivastava and Shukla (1998) | Srivastava and Jain (1994) | -- |
| 10 | Harvest index (%) | Nirmala Kumari and Balasubramanian (1993)<br>Sailaja (1997), Mohana Rao (1999)<br>Basavaraja *et al.* (2005)<br>Hina Kausar (2006)<br>Sriranjani *et al* (2007) | -- | -- | Srivastava and Jain (1994)<br>Shrivastava and Shukla (1998)<br>Praveen Kumar *et al.* (2005) |
| 11 | Seed protein content (%) | Thorat *et al.* (1999)<br>Ramana (2003) | Malik and Singh (1987)<br>Nirmala Kumari and Balasubramanian (1993)<br>Sailaja (1997) | -- | Sharma *et al.* (1986) |
| 12 | Oil content (%) | Thorat *et al.* (1999) | Taware *et al.* (1997) | -- | Mehetre *et al.* (1995)<br>Ramana . (2003) |
| 13 | Seed yield per plant (g) | Nirmala Kumari and Balasubramanian (1993) | Sailaja (1997)<br>Taware *et al.* (1997) | Amarnath *et al.* (1991)<br>Kalaimagal (1991) | Thorat *et al.* (1999)<br>Bangar *et al.* (2003) |

| | | | | | |
|---|---|---|---|---|---|
| | | Jagatap and Mehetre (1994)<br>Mehetre *et al.* (1994a)<br>Singh and Singh (1999)<br>Ramana *et al.* (2000)<br>Jain and Ramgiry (2000)<br>Basavaraj *et al.* (2005)<br>Gohil *et al.* (2006)<br>Sriranjani *et al* (2007) | | Shrivastava and Shukla (1998)<br>Sood and Sood (2001) | |

## 2.3 CORRELATION ANALYSIS

Correlation refers to the degree and direction of association between two or more variables. Correlation studies are useful in developing an effective basis of phenotype selection in plant populations. Since yield is polygenically controlled character with low heritability, phenotype selection is not effective, and can only be achieved by indirect selection. Further knowledge of genetic correlations among the characters contributing to the yield helps to adopt to the most effective method of selection. By this way combinations of favourable characters could be brought together by minimizing the retarding effect of antagonistic relations. When attempts are made to establish correlations, it is essential to calculate the coefficient of correlation between the characters of interest with regard to the type of variability viz., environmental, genotypic and phenotypic.

The literature available on the association of component characters with seed yield are presented in Table 3 and the association among the yield component characters are presented in Table 4.

**Table 3: Review of literature on the association of yield component characters with seed yield in soybean** [*Glycine max* (L.) Merrill]

| Sl. No. | Character | Correlation | Reference |
|---|---|---|---|
| 1 | Days to 50% flowering | Positive | Harer and Deshmukh (1992), Mahajan *et al.* (1993), Mehetre *et al*, (1994a), Taware *et al.* (1995), Rajarathinam *et al.*(1996), Sailaja (1997), Taware *et al.* (1997), Mohana Rao (1999), Nehru *et al.* (1999), Pooranchand (1999), Ramana *et al.* (2000), Bangar *et al.* (2003), Ramana (2003); Mukhekar *et al.* (2004) |
| | | Negative | Kalaimagal (1991), Singh *et al.* (1994), Mehetre *et al.* (1995), Mehetre *et al.* (1998), Basavaraja *et al.* (2005) |
| 2 | Days to maturity | Positive | Amarnath *et al.* (1991) Harer and Deshmukh (1992), Jagtap and Choudhary (1993), Lakhani (1993); Mahajan *et al.* (1993); Singh *et al.* (1994), Taware *et al.* (1995), Taware *et al.* (1997), Dogney *et al.* (1998), Nehru *et al.* (1999), Poornachand (1999), Singh and Yadava (2000), Agarwal *et al.* (2001), Bangar *et al.* (2003), Ramana. (2003), Mukhekar *et al.* (2004), Praveen Kumar (2005) |
| | | Negative | Kalaimagal (1991), Mehetre *et al.* (1995), Sailaja (1997), Mehetre *et al.* (1998), Mohana Rao (1999) |
| 3 | Plant height (cm) | Positive | Amarnath *et al.* (1991) Harer and Deshmukh (1992), Mahajan *et al.* (1993), Wu *et al.* (1995), Rajarathinam *et al.* (1996), Shinde *et al.* (1996) Taware *et al.* (1997), Koti and Chetti (1999), Mohana Rao (1999), Nehru *et al.* (1999), Pooranchand (1999), Rajput *et al.* (2000), Ramana *et al.* (2000), Singh and Yadava (2000), Agarwal *et al.* (2001), Bangar *et al.* (2003), Mukhekar *et al.* (2004), Turkec (2005), Hina Kausar (2006) |

| Sl. No. | Character | Correlation | Reference |
|---|---|---|---|
| | | Negative | Kalaimagal (1991), Singh *et al.* (1994), Mehetre *et al.* (1995), Dogney *et al.* (1998), Singh and Singh (1999), Kulvir Singh *et al.* (2000), Basavaraja *et al.* (2005) |
| 4 | Number of branches per plant | Positive | Deshmukh *et al.* (1991), Kalaimagal (1991), Nirmala Kumari and Balasubramanian (1991), Harer and Deshmukh (1992), Jagtap and Choudhary (1993), Lakhani (1993), Mahajan *et al.* (1993), Mehetre *et al.* (1994a), Jadhav *et al.* (1995), Mehetre *et al.* (1995), Wu *et al.* (1995), Major Singh *et al.* (1996), Rajarathinam *et al.* (1996), Mehetre *et al.* (1997), Dogney *et al.*(1998), Mehetre *et al.* (1998), Pooranchand (1999), Singh and Singh (1999), Agarwal *et al.* (2001), Ramana. (2003), Mukhekar *et al.*(2004), Turkec (2005), Hina Kausar (2006) |
| | | Negative | Shinde *et al.*(1996), Ramana *et al.* (2000), Chamundeswari and Aher (2003) |
| 5 | Number of pods per plant | Positive | Amarnath and Viswanatha (1990), Deshmukh *et al.* (1991), Harer and Deshmukh (1992), Jagtap and Choudhary (1993), Lakhani (1993), Mahajan *et al.*(1993), Prabhakar Tiwari (1993), Vimala Devi (1993), Mehetre *et al.* (1994a), Srivastava and Jain (1994), Mehetre *et al.* (1995), Taware *et al.* (1995), Wu *et al.* (1995), Rajarathinam *et al.*(1996), Sailaja (1997), Taware *et al.* (1997), Shukla *et al.*(1998), Koti and Chetti (1999), Maharaddi *et al.* (1999), Nehru *et al.* (1999), Pooranchand (1999), Singh and Phul (1999), Singh and Singh (1999), Thorat *et al.* (1999), Ayub Khan *et al.* (2000), Kulvir Singh *et al.* (2000), Rajput *et al.* (2000), Ramana *et al.* (2000), Singh and Yadava (2000), Agarwal *et al.* (2001), Namrata Jain *et al.* (2002), Narne *et al.* (2002), Bangar *et al.* (2003), Ramana (2003), Mukhekar *et al.* (2004), Mishra and Rao (2005), Praveen Kumar *et al.* (2005), Turkec (2005), Hina Kausar (2006), Sriranjani *et al.* (2007) |

| Sl. No. | Character | Correlation | Reference |
|---|---|---|---|
| | | Negative | Kalaimagal (1991), Singh *et al.* (1994), Kushal Chandel *et al.* (2005) |
| 6 | Pod length (cm) | Positive | Major Singh *et al.* (1996), Singh and Singh (1999), Ramana *et al.* (2000), Basavaraja *et al.* (2005) |
| | | Negative | Dixit and Patil (1982), Mukhekar *et al.* (2004) |
| 7 | Number of seeds per pod | Positive | Kalaimagal (1991), Prabhakar and Tiwari (1993), Mishra *et al.* (1994), Srivastava and Jain (1994), Jadhav *et al.* (1995), Shinde *et al.* (1996), Sailaja (1997), Taware *et al.* (1997), Nehru *et al.*(1999), Kulvir Singh *et al.* (2000), Ramana *et al.* (2000), Singh and Yadava (2000), Agarwal *et al.* (2001), Namrata Jain *et al.* (2002), Mishra and Rao (2005) |
| | | Negative | Gopani and Kabaria (1970) |
| 8 | 100 seed weight (g) | Positive | Kalaimagal (1991), Nirmala Kumari and Balasubramanian (1991), Harer and Deshmukh (1992), Mahajan *et al.* (1993), Mehetre *et al.* (1994 a), Srivastava and Jain (1994), Mehetre *et al.* (1995), Maharaddi (1996), Major Singh *et al.* (1996), Mehetre *et al.* (1997), Sailaja (1997), Taware *et al.* (1997), Dogney *et al.* (1998), Mehetre *et al.* (1998), Maharaddi *et al.* (1999), Kulvir Singh *et al.* (2000), Singh and Yadava (2000), Ramana *et al.* (2000), Namrata Jain *et al.* (2002), Bangar *et al.* (2003); Ramana (2003), Mukhekar *et al.* (2004), Basavaraja *et al.* (2005), Kushal Chandel *et al.* (2005) |
| | | Negative | Jagatap and Choudhary (1993), Shinde *et al.* (1996), Pooranchand (1999), Praveen Kumar *et al.* (2005) |

| Sl. No. | Character | Correlation | Reference |
|---|---|---|---|
| 9 | Biological yield per plant (g) | Positive | Nirmala Kumari and Balasubramanian (1993), Srivastava and Jain (1994), Shrivastava and Shukla (1998), Nehru *et al.*(1999), Singh and Yadava (2000), Radha Krishna Murthy *et al.*(2001), Narne *et al.* (2002), Chamundeswari and Aher (2003), Ramana. (2003), Kushal Chandel *et al.* (2005), Praveen Kumar *et al.*(2005), Hina Kausar (2006), Sriranjani *et al* (2007) |
| | | Negative | Kulvir Singh *et al.* (2000) |
| 10 | Harvest index (%) | Positive | Bharadwaj and Bhagsari (1990), Nirmala Kumari and Balasubramanian (1991), Srivastava and Jain (1994), Sailaja (1997), Radha Krishna Murthy *et al.* (2001), Ramana (2003), Basavaraja *et al.* (2005), Kushal Chandel *et al.* (2005), Mishra and Rao (2005), Praveen Kumar *et al.* (2005), Hina Kausar (2006), Sriranjani *et al* (2007) |
| | | Negative | Yao (1989) |
| 11 | Seed protein content (%) | Positive | Devraj Sood *et al.*(1980), Wilcox (1986), Gai *et al.* (1994), Sailaja (1997), Mohana Rao (1999), Nehru *et al.* (1999) |
| | | Negative | Fontes *et al.* (1980), Maharaddi *et al.* (1999), Kushal Chandel *et al.* (2005) |
| 12 | Oil content (%) | Positive | Harer and Deshmukh (1992), Song Qijan *et al.* (1996), Taware *et al.* (1997), Maharaddi *et al.* (1999), Kushal Chandel *et al.* (2005) |
| | | Negative | Mehetre *et al.* (1995), Praveen Kumar *et al.*(2005) |

**Table 4: Review of literature on the association among the yield component characters in soybean [*Glycine max(* L.) Merrill]**

| Character | Correlation | Reference |
|---|---|---|
| **Days to 50% flowering with** | | |
| Days to maturity | Positive | Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh (1992), Mehetre *et al.* (1994a), Mehetre *et al.* (1995), Taware *et al.* (1995), Taware *et al.* (1997), Mohana Rao (1999), Pooranchand (1999), Ramana *et al.* (2000), Praveen Kumar (2005), Sriranjani *et al.* (2007) |
| | Negative | Sharma *et al.* (1983), Konieczny (1986) |
| Plant height (cm) | Positive | Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh (1992), Mehetre *et al.* (1995), Taware *et al.* (1995), Shinde *et al.* (1996) Taware *et al.* (1997), Shrivastava *et al.* (1998), Mohana Rao (1999), Pooranchand (1999), Ramana *et al.* (2000), Ramana (2003), Praveen Kumar *et al.* (2005), Sriranjani *et al.* (2007) |
| | Negative | Mehetre *et al.* (1994a) |
| Number of branches per plant | Positive | Amarnath *et al.* (1991) Kalaimagal (1991), Harer and Deshmukh (1992), Maharaddi (1996), Taware *et al.* (1997), Mohana Rao (1999), Pooranchand (1999), Ramana (2003) |
| | Negative | Mehetre *et al.* (1994a), Ramana *et al.* (2000) |
| Number of pods per plant | Positive | Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh (1992), Taware *et al.* (1995), Maharaddi (1996), Shinde *et al.* (1996), Ramgiry and Raha (1997), Taware *et al.* (1997); Mohana Rao (1999), Ramana *et al.* (2000), Ramana (2003), Kushal Chandel *et al.* (2005), Praveen Kumar *et al.* (2005) |
| | Negative | Mehetre *et al.* (1994a), Mehetre *et al.* (1995) |

| Character | Correlation | Reference |
|---|---|---|
| Pod length (cm) | Positive | Ramana *et al.* (2000) |
| | Negative | Maharaddi (1996) |
| Number of seeds per pod | Positive | Mehetre *et al.* (1995), Taware *et al.* (1997) |
| | Negative | Harer and Deshmukh (1992), Ramana *et al.* (2003) |
| 100 seed weight (g) | Negative | Mehetre *et al.* (1994a), Mehetre *et al.* (1995), Maharaddi (1996); Taware *et al.* (1997), Shrivastava and Shukla (1998), Mohana Rao (1999), Pooranchand (1999), Ramana *et al.* (2000), Ramana . (2003) |
| Biological yield per plant (g) | Positive | Srivastava and Jain (1994), Ramana (2003) |
| Harvest index (%) | Negative | Mohana Rao (1999), Ramana. (2003) |
| Seed protein content (%) | Negative | Mohana Rao (1999), Ramana (2003) |
| Oil content (%) | Positive | Narne *et al.* (2002), Ramana (2003) |
| | Negative | Mohana Rao (1999) |

| Character | Correlation | Reference |
|---|---|---|
| **Days to maturity with** | | |
| Plant height (cm) | Positive | Amarnath *et al.* (1991), Harer and Deshmukh (1992), Taware *et al.* (1995), Sailaja (1997), Taware *et al.* (1997), Dogney *et al.* (1998), Pooranchand (1999), Ramana *et al.* (2000), Agarwal *et al.* (2001), Bangar *et al.* (2003), Ramana (2003) |
| | Negative | Mehetre *et al.* (1994a), Mehetre *et al.* (1995), Mohana Rao (1999) |
| Number of branches per plant | Positive | Kalaimagal (1991), Harer and Deshmukh (1992), Lakhani (1993), Shinde *et al.* (1996), Sailaja (1997), Dogney *et al.*(1998), Mohana Rao (1999), Nehru *et al.* (1999); Pooranchand (1999); Ramana *et al.* (2000), Agarwal *et al.* (2001), Ramana (2003) |
| | Negative | Mehetre *et al.* (1994a), Mehetre *et al.* (1995) |
| Number of pods per plant | Positive | Kalaimagal (1991), Harer and Deshmukh (1992), Taware *et al.* (1995), Taware *et al.* (1997), Dogney *et al.* (1998), Ramana *et al.* (2000), Agarwal *et al.* (2001), Bangar *et al.* (2003), Ramana (2003) |
| | Negative | Mehetre *et al.* (1995), Mohana Rao (1999), Pooranchand (1999) |
| Pod length (cm) | Negative | Ramana *et al.* (2000) |
| Number of seeds per pod | Positive | Sailaja (1997), Mohana Rao (1999), Ramana *et al.* (2000) |
| | Negative | Harer and Deshmukh (1992), Ramana (2003) |
| 100 seed weight (g) | Positive | Sailaja (1997), Dogney *et al.* (1998), Ramana *et al.* (2000), Bangar *et al.* (2003), Ramana (2003) |
| | Negative | Mehetre *et al.* (1995), Taware *et al.* (1997), Mohana Rao (1999), Agarwal *et al.* (2001) |
| Biological yield (g) | Positive | Srivastava and Jain (1994), Sailaja (1997), Ramana (2003) |
| Harvest index (%) | Positive | Srivastava and Jain (1994), Mohana Rao (1999), Radha Krishna Murthy *et al.* (2001) |

| Character | Correlation | Reference |
|---|---|---|
| Protein content (%) | Positive | Sailaja (1997) |
| | Negative | Mohana Rao (1999), Ramana (2003) |
| Oil Content (%) | Positive | Mehetre *et al.* (1995), Mohana Rao (1999), Narne *et al*. (2002), Ramana (2003) |
| | Negative | Johnson *et al.* (1995) |
| **Plant height (cm) with** | | |
| Number of branches per plant | Positive | Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh (1992), Maharaddi (1996), Taware *et al.* (1997), Dogney *et al.*(1998), Mohana Rao (1999), Pooranchand (1999), Agarwal *et al*. (2001), Narne *et al.*(2002), Mukhekar *et al.* (2004) |
| | Negative | Mehetre *et al.* (1995), Sailaja (1997), Ramana *et al.* (2000), Ramana (2003) |
| Number of pods per plant | Positive | Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh (1992), Lakshmi (1993), Taware *et al*. (1995), Maharaddi (1996), Ramgiry and Raha (1997), Sailaja (1997), Taware *et al.* (1997), Dogney *et al.* (1998), Shukla *et al.* (1998), Mohana Rao (1999), Pooranchand (1999), Agarwal *et al*. (2001), Narne *et al.* (2002), Mukhekar *et al.* (2004), Praveen Kumar *et al.* (2005) |
| | Negative | Mehetre *et al.* (1995), Ramana (2003) |
| Pod length (cm) | Positive | Ramana *et al.* (2000) |
| | Negative | Dixit and Patil (1982), Maharaddi (1996) |
| Number of seeds per pod | Positive | Amarnath *et al.* (1991), Kalaimagal (1991), Lakhani (1993), Ramana *et al.* (2000), Ramana (2003) |
| | Negative | Sailaja (1997), Nehru *et al.*(1999) |
| 100 seed weight (g) | Positive | Amarnath *et al.* (1991), Lakhani (1993), Mehetre *et al*. (1995), Sailaja (1997), Dogney *et al.* (1998), Mohana Rao (1999), Singh and Phul (1999), Ramana *et al*. (2000), Narne *et al.* (2002), Ramana (2003), Praveen Kumar *et al.* (2005) |

| Character | Correlation | Reference |
|---|---|---|
| | Negative | Kalaimagal (1991), Maharaddi (1996), Taware *et al.* (1997), Nehru *et al.* (1999), Pooranchand (1999), Agarwal *et al.*(2001), Narne *et al.* (2002) |
| Biological yield (g) | Positive | Paschal and Wilcox (1975), Sailaja (1997), Kushal Chandel *et al.* (2005) |
| | Negative | Ramana (2003) |
| Harvest index (%) | Positive | Sailaja (1997), Mohana Rao (1999) |
| | Negative | Paschal and Wilcox (1975), Ramana. (2003) |
| Protein content (%) | Positive | Sailaja (1997), Mohana Rao (1999), Ramana (2003) |
| Oil content (%) | Positive | Kushal Chandel *et al.* (2005) |
| **Number of branches per plant with** | | |
| Number of pods per plant | Positive | Amarnath *et al.* (1991), Harer and Deshmukh (1992), Jagtap and Choudhary (1993), Lakhani (1993), Mehetre *et al.* (1994a), Mehetre *et al.* (1995), Shinde *et al.* (1996), Ramgiry and Raha (1997), Dogney *et al.* (1998), Mohana rao (1999), Nehru *et al.* (1999), Pooranchand (1999), Ramana (2003), Kushal Chandel *et al.* (2005) |
| | Negative | Li *et al.* (1997), Sailaja (1997), Shrivastava *et al.* (1998), Ramana *et al.* (2000) |
| Pod length (cm) | Positive | Dixit and Patil (1982) |
| | Negative | Maharaddi (1996), Ramana *et al.* (2000) |
| Number of seeds per pod | Positive | Kalaimagal (1991), Lakhani (1993), Sailaja (1997), Ramana (2003) |
| | Negative | Sailaja (1997), Ramana *et al.* (2003), Ramana (2003) |
| 100 seed weight (g) | Positive | Amarnath *et al.* (1991), Mehetre *et al.* (1994a), Mehetre *et al.* (1995), Kulvir Singh *et al.* (2000), Ramana *et al.* (2000) |
| | Negative | Jagtap and Choudhary (1993), Maharaddi (1996), Shinde *et al.* (1996), Sailaja (1997), Taware *et al.* (1997), Mohana Rao (1999), Nehru *et al.* (1999), Agarwal *et al.* (2001), Ramana (2003) |

| Character | Correlation | Reference |
|---|---|---|
| Biological yield per plant (g) | Positive | Kulvir Singh *et al.* (2000), Radha Krishna Murthy *et al.*(2001), Ramana (2003) |
| | Negative | Sailaja (1997) |
| Harvest index (%) | Positive | Sailaja (1997), Mohana Rao (1999), Ramana *et al.* (2003) |
| | Negative | Radha Krishna Murthy *et al.* (2001) |
| Seed protein content (%) | Positive | Sailaja (1997), Mohana Rao (1999) |
| | Negative | Ramana (2003) |
| Oil content (%) | Positive | Johnson *et al.* (1955), Mehetre *et al.* (1995), Ramana (2003) |
| | Negative | Mohana Rao (1999) |
| **Number of pods per plant with** | | |
| Pod length (cm) | Negative | Maharaddi *et al.* (1996), Ramana *et al.* (2000) |
| Number of seeds per pod | Positive | Shinde *et al.* (1996), Kulvir Singh *et al.* (2000), Radha Krishna Murthy *et al.* (2001) |
| | Negative | Sailaja (1997), Mohana rao (1999), Ramana *et al.* (2000) |
| 100 seed weight (g) | Positive | Mehetre *et al.* (1994a), Li *et al* (1997), Ramana *et al.* (2000), Ramana (2003), Praveen Kumar *et al.* (2005) |
| | Negative | Amarnath *et al.* (1991), Kalaimagal (1991), Jagtap and Choudhary (1993), Srivastava and Jain (1994), Maharaddi (1996), Shinde *et al.* (1996), Sailaja (1997), Taware *et al.* (1997), Dogney *et al.* (1998), Nehru *et al.* (1999), Agarwal *et al.* (2001), Chamundeswari and Aher (2003) |
| Biological yield per plant (g) | Negative | Srivastava and Jain (1994), Sailaja (1997), Shukla *et al.* (1998), Ramana (2003) |
| Harvest index (%) | Positive | Srivastava and Jain (1994), Sailaja (1997), Mohana Rao (1999), Ramana *et al.* (2003) |
| Seed protein content (%) | Positive | Sailaja (1997), Mohana Rao (1999), Praveen Kumar *et al.* (2005) |
| | Negative | Ramana. (2003) |

| Character | Correlation | Reference |
|---|---|---|
| Oil content ( %) | Positive | Taware *et al.* (1997), Mohana Rao (1999), Ramana. (2003), Praveen Kumar *et al.* (2005) |
| **Number of seeds per pod with** | | |
| 100 seed weight (g) | Positive | Rajasekaran *et al.* (1980), Sailaja (1997) |
| | Negative | Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh (1992), Lakhani (1993), Srivastava and Jain (1994), Shinde *et al.* (1996), Dogney *et al.* (1998), Mohana Rao (1999), Ramana *et al.* (2000), Ramana (2003) |
| Biological yield (g) | Positive | Sailaja (1997) |
| | Negative | Ramana (2003) |
| Harvest index (%) | Positive | Srivastava and Jain (1994), Ramana. (2003) |
| | Negative | Sailaja (1997), Mohana Rao (1999) |
| Seed protein content (%) | Positive | Sailaja (1997), Mohana Rao (1999) |
| | Negative | Praveen Kumar *et al.* (2005) |
| **100 seed weight (g) with** | | |
| Biological yield per plant (g) | Positive | Srivastava and Jain (1994), Sailaja (1997), Ramana (2003), Kushal Chandel *et al.* (2005) |
| Harvest index (%) | Positive | Srivastava and Jain (1994), Sailaja (1997), Mohana Rao (1999) |
| | Negative | Ramana (2003) |
| Seed protein content (%) | Positive | Sailaja (1997), Mohana Rao (1999), Ramana (2003) |
| Oil content (%) | Positive | Mohana Rao (1999), Narne *et al.* (2002) |
| | Negative | Ramana (2003) |

| Character | Correlation | Reference |
|---|---|---|
| **Biological yield per plant (g) with** | | |
| Harvest index (%) | Positive | Srivastava and Jain (1994) and Ramana (2003) Sriranjani *et al* (2007) |
| | Negative | Sailaja (1997) and Radha Krishna Murhty *et al.* (2001) |
| Seed protein content ( %) | Positive | Sailaja (1997) |
| | Negative | Ramana (2003) |
| Oil content( %) | Positive | Ramana (2003) |
| **Harvest index (%) with** | | |
| Seed protein content (%) | Positive | Sailaja (1997) and Mohana Rao (1999) |
| | Negative | Ramana (2003) |
| Oil content (%) | Positive | Mohana Rao (1999) and Ramana (2003) |
| **Seed protein content (%) with** | | |
| Oil content | Positive | Wilcox (1998), Mohana Rao (1999) |
| | Negative | Mishra *et al.* (1994), Mohana Rao (1999), Nehru *et al.* (1999), Ramana (2003), Praveen Kumar *et al.* (2005) |

## 2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis as devised by Wright (1921) is a standardized partial regression coefficient, which helps in partitioning the correlation coefficient into direct and indirect effects of independent variables on the dependent variable. The path coefficient analysis further helps to elucidate the intrinsic nature of the observed associations and imparts a degree of confidence in the selection scheme adopted for a given situation. It may help to minimize the number of attributes for which simultaneous selection must be exercised (Dewey and Lu, 1959).

The available literature on direct and indirect effects of yield components on yield in soybean are reviewed here in Table 5 and 6.

**Table 5: Review of literature on direct effects of component characters on seed yield in soybean [*Glycine max* (L.) Merrill]**

| Sl. No. | Characters | Positive direct effects | Negative direct effects |
|---|---|---|---|
| 1 | Days to 50% flowering | Deshmukh *et al.* (1991),<br>Sailaja (1997),<br>Mohana Rao (1999),<br>Mukhekar *et al.* (2004),<br>Dev Vart *et al.* (2005),<br>Kushal Chandel *et al.* (2005),<br>Mishra and Rao (2005) | Mehetre *et al.* (1994a)<br>Raut *et al.* (2001),<br>Narne *et al.* (2002),<br>Ramana *et al.* (2000) |
| 2 | Days to maturity | Taware *et al.* (1997),<br>Dogney *et al.* (1998),<br>Mohana Rao (1999),<br>Ramana *et al.* (2000),<br>Singh and Yadava (2000),<br>Raut *et al.* (2001),<br>Ramana. (2003) | Mehetre *et al.* (1994a),<br>Narne *et al.* (2002),<br>Dev Vart *et al.* (2005) |

| Sl. No. | Characters | Positive direct effects | Negative direct effects |
|---|---|---|---|
| 3 | Plant height (cm) | Sailaja (1997), Singh and Phul (1999), Ramana *et al.* (2000), Narne *et al.*(2002), Ramana (2003), Dev Vart *et al.* (2005), Mishra and Rao (2005) | Dogney *et al.* (1998), Mohana Rao (1999), Raut *et al.* (2001) |
| 4 | Number of branches per plant | Dogney *et al.* (1998), Mohana Rao (1999), Raut *et al.* (2001), Ramana (2003) | Mehetre *et al.* (1994a) Sailaja (1997), Ramana *et al.* (2000) |
| 5 | Number of pods per plant | Mehetre *et al.* (1994a), Sailaja (1997),Taware *et al.* (1997), Mohana Rao (1999), Singh and Phul (1999), Ayub Khan *et al.* (2000), Ramana *et al.* (2000), Singh and Yadava (2000), Raut *et al.* (2001), Narne *et al.*(2002), Ramana (2003), Mukhekar *et al.* (2004), Mishra and Rao (2005), Sriranjani *et al* (2007) | -- |
| 6 | Pod length (cm) | Kumar and Nadarajan (1992) | Dixit and Patil (1984), Mukhekar *et al.* (2004) |
| 7 | Number of seeds per pod | Sailaja (1997), Mohana Rao,(1999), Ramana *et al.* (2000), Ball *et al.* (2001), Narne *et al.* (2002), Ramana (2003), Mishra and Rao (2005) | Dev Vart *et al.* (2005) |
| 8 | 100 seed weight (g) | Singh *et al.* (1996), Sailaja (1997), Dogney *et al.* (1998), Mohana Rao (1999), Ayub Khan *et al.* (2000), Ramana *et al.* (2000), Raut *et al.* (2001), Narne *et al.* (2002), Ramana . (2003), Dev Vart *et al.* (2005), | Mehetre *et al.* (1994a) |

| Sl. No. | Characters | Positive direct effects | Negative direct effects |
|---|---|---|---|
| | | Mishra and Rao (2005),<br>Trukec (2005) | |
| 9 | Biological yield per plant (g) | Sailaja (1997),<br>Singh and Yadava (2000),<br>Narne *et al*. (2002), Chamundeswari and Aher (2003), Ramana (2003), Dev Vart *et al.* (2005), Jyothi Sethi and Tyagi (2005), Kushal Chandel *et al.* (2005), Hina Kausar (2006),<br>Sriranjani *et al* (2007) | Narne *et al.* (2002) |
| 10 | Harvest index (%) | Sailaja (1997),<br>Mohana Rao (1999),<br>Singh and Yadava (2000),<br>Raut *et al.* (2001),<br>Narne *et al*. (2002),<br>Ramana (2003),<br>Chamundeswari and Aher (2003),<br>Dev Vart *et al.* (2005),<br>Kushal Chandel *et al.* (2005), Mishra and Rao (2005),<br>Hina Kausar (2006),<br>Sriranjani *et al* (2007) | Narne *et al.* (2002) |
| 11 | Seed protein content (%) | Gai *et al*. (1994),<br>Song Qijan *et al.* (1996),<br>Sailaja (1997),<br>Mohana Rao (1999),<br>Narne *et al.* (2002),<br>Ramana (2003) | |
| 12 | Oil content (%) | Prabhakar and Tiwari (1993),<br>Song Qijan *et al.* (1996),<br>Mohana Rao (1999),<br>Narne *et al.* (2002),<br>Ramana (2003) | Raut *et al.* (2001) |

**Table 6: Review of literature on indirect effects of component characters on seed yield in soybean [*Glycine max* (L.) Merrill]**

| Character showing indirect effect on seed yield | Character through which effect is expressed | Direction of indirect effect | References |
|---|---|---|---|
| Days to 50% flowering | Plant height and branches per plant | Positive | Deshmukh *et al.* (1991) |
| | Branches per plant and days to maturity | Negative | Mehetre *et al.* (1994a) |
| | Pods per plant | Positive | Sailaja (1997) |
| | Branches per plant | Negative | Sailaja (1997) |
| | Days to maturity | Positive | Mohana Rao (1999) |
| | Oil content | Negative | Mohana Rao (1999) |
| | Plant height | Positive | Ramana *et al.* (2000) |
| | 100 seed weight | Negative | Ramana *et al.* (2000) |
| | 100 seed weight and days to maturity | Positive | Raut *et al.* (2001) |
| | Oil content | Negative | Raut *et al.* (2001) |
| | Branches per plant and days to maturity | Negative | Kushal Chandel *et al.* (2005) |
| | Biological yield per plant | Positive | Praveen Kumar *et al.* (2005) |
| Days to maturity | Plant height | Positive | Taware *et al.* (1997) |
| | Branches per plant | Positive | Dogney *et al.* (1998) |
| | 100 seed weight and oil content | Negative | Mohana Rao (1999) |
| | 100 seed weight | Positive | Ramana *et al.* (2000) |
| | Days to 50% flowering and pod length | Negative | Ramana *et al.* (2000) |

| Character showing indirect effect on seed yield | Character through which effect is expressed | Direction of indirect effect | References |
|---|---|---|---|
| | 100 seed weight and harvest index | Negative | Praveen Kumar *et al.* (2005) |
| Plant height | Seeds per pod | Positive | Sailaja (1997) |
| | 100 seed weight and pods per plant | Negative | Dogney *et al.* (1998) |
| | Days to maturity | Negative | Mohana Rao (1999) |
| | Pods per plant and harvest index | Positive | Mohana Rao (1999) |
| | Pods per plant | Negative | Singh and Phul (1999) |
| | Pods per plant | Positive | Raut *et al.* (2001) |
| | 100 seed weight | Negative | Raut *et al.* (2001) |
| | Pods per plant and harvest index | Negative | Kushal Chandel *et al.* (2005) |
| | Biological yield | Positive | Praveen Kumar *et al.* (2005) |
| | Harvest index | Negative | Praveen Kumar *et al.* (2005) |
| Number of branches per plant | Pods per plant | Positive | Sailaja (1997) |
| | Days to maturity | Negative | Sailaja (1997) |
| | Plant height | Negative | Dogney *et al.* (1998) |
| | Pods per plant | Positive | Mohana Rao (1999) |
| | Oil content | Negative | Mohana Rao *et al.*(1999) |
| | Pods per plant, pod length and seeds per pod | Negative | Ramana *et al.* (2000) |
| | 100 seed weight, harvest index and days to maturity | Negative | Kushal Chandel *et al.* (2005) |
| | Biological yield | Positive | Praveen Kumar *et al.* (2005) |

| Character showing indirect effect on seed yield | Character through which effect is expressed | Direction of indirect effect | References |
|---|---|---|---|
| Number of pods per plant | Plant height and seeds per pod | Negative | Ayub khan *et al.* (2000) |
| | Days to 50% flowering | Negative | Mehetre *et al.* (1994a) |
| | Plant height | Positive | Taware *et al.* (1997) |
| | Harvest index | Positive | Mohana Rao (1999) |
| | Seeds per pod | Negative | Mohana Rao (1999) |
| | Plant height and Seeds per pod | Negative | Ayub Khan *et al.* (2000) |
| | Days to 50% flowering, seeds per pod and pod length | Negative | Ramana *et al.* (2000) |
| | 100 seed weight | Negative | Raut *et al.* (2001) |
| | 100 seed weight | Negative | Kushal Chandel *et al.* (2005) |
| | Biological yield | Positive | Praveen Kumar *et al.* (2005) |
| Pod length (cm) | Pods per plant | Negative | Mukhekar *et al.* (2004) |
| Number of seeds per pod | Branches per plant | Positive | Sailaja (1997) |
| | Plant height | Negative | Mohana Rao (1999) |
| | Pods per plant | Negative | Ramana *et al.* (2000) |
| | 100 seed weight | Negative | Mukhekar *et al.* (2004) |
| 100 seed weight (g) | Days to maturity | Positive | Mehetre *et al.* (1994a) |
| | Biological yield | Positive | Sailaja (1997) |
| | Branches per plant | Negative | Dogney *et al.* (1998) |

| Character showing indirect effect on seed yield | Character through which effect is expressed | Direction of indirect effect | References |
|---|---|---|---|
| | Days to maturity and branches per plant | Negative | Mohana Rao (1999) |
| | Harvest index | Positive | Mohana Rao (1999) |
| | Pods per plant | Positive | Ramana *et al.* (2000) |
| | Seeds per plant | Positive | Ramana *et al.* (2000) |
| | Harvest index | Positive | Praveen Kumar *et al.* (2005) |
| | Biological yield | Negative | Praveen Kumar *et al.* (2005) |
| Biological yield per plant (g) | Pods per plant | Positive | Narne *et al.* (2002) |
| | Days to maturity and plant height | Negative | Sailaja (1997) |
| | Harvest index and branches per plant | Positive | Ramana. (2003) |
| | Harvest index | Positive | Praveen Kumar *et al.* (2005) |
| Harvest index (%) | Pods per plant | Positive | Sailaja (1997) |
| | Pods per plant and oil content | Positive | Mohana Rao (1999) |
| | Days to maturity | Negative | Mohana Rao (1999) |
| | Days to maturity | Negative | Praveen Kumar *et al.* (2005) |
| Seed protein content (%) | Pods per plant and seeds per pod | Positive | Sailaja (1997) |
| | Days to 50% flowering and seeds per pod | Negative | Mohana Rao (1999) |
| | 100 seed weight, harvest index and plant height | Negative | Praveen Kumar *et al.* (2005) |

| **Character showing indirect effect on seed yield** | **Character through which effect is expressed** | **Direction of indirect effect** | **References** |
|---|---|---|---|
| | Biological yield | Positive | Praveen Kumar *et al.* (2005) |
| Oil content (%) | Pods per plant | Positive | Prabhakar Tiwari (1993) |
| | 100 seed weight and pods per plant | Positive | Song Qijian *et al.* (1996) |
| | Protein content | Positive | Mohana Rao (1999) |
| | Biological yield | Negative | Praveen Kumar *et al.* (2005) |

## 2.2 GENETIC DIVERGENCE

The information on the nature and the magnitude of genetic variability present in a crop species will play an important role in formulating a successful breeding programme. It is known that the greater the genetic variability present in the plant population the greater will be the chances of obtaining the desirable gene combinations. Mahalanobis' $D^2$ statistic is an effective tool in quantifying the degree of genetic divergence at the genotypic level and provides a measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1936). Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding.

Divergence analysis is performed to identify the diverse genotypes for hybridization purposes. Clustering by $D^2$ statistic is useful in this matter. The genotypes grouped together are less divergent than the ones, which fall into different clusters. Three important points are to be considered while selecting genotypes for hybridization purpose.

1. Choice of the particular cluster from which genotypes are to be used as parents.
2. Selection of particular genotype from selected cluster.
3. Relative contribution of characters towards total divergence.

Clusters separated by largest statistical distance ($D^2$) show maximum divergence (Singh and Chaudhary, 1977).

Nair and Mukharjee (1960) for the first time used $D^2$ statistic as a measure of genetic divergence in the classification of natural and plantation Teak. The basic importance of genetic diversity in breeding for higher yield has long been recognized and is evident from the results supported by several workers.

Chikhale *et al.*(1992) studied genetic divergence among 25 soybean genotypes for 8 traits through $D^2$ statistics and grouped them into 8 clusters and reported that characters *viz.*, 100 seed weight followed by plant height, number of pods per plant have contributed more towards the total genetic divergence.

The quantitative assessment of genetic diversity among 58 soybean genotypes obtained from different ecogeographical regions for 16 characters through $D^2$ statistics was worked out by Ghatge and Kadu (1993). They reported substantial genetic diversity with $D^2$ values ranging from 4.34 to 7772.22. The genotypes were grouped into 7 clusters and the clustering pattern revealed that genetic diversity was not necessarily associated with the geographical diversity.

Jaylal (1994) evaluated 40 soybean genotypes through $D^2$ statistic and grouped into 9 clusters. The constellations obtained were confirmed by canonical root analysis with three canonical vectors accounted for 95.9% of total divergence. He reported pods per node followed by seed yield per plant contributed maximum towards total genetic divergence.

Kumar and Nadarajan (1994) studied 64 genotypes for genetic divergence through $D^2$ statistic and grouped into 11 clusters. They reported 100 seed weight followed by pods per plant and plant height contributed high oil content while protein content contributed moderate and seeds per pod contributed minimum towards total genetic divergence.

Mehetre *et al.*(1994b) evaluated 51 soybean genotypes collected from different sources through $D^2$ statistic and grouped into 10 clusters and reported maximum genetic diversity by plant height, pods per plant, grain yield per plant, branches per plant, days to maturity and days to flowering.

Dobhal (1995) studied 65 genotypes using Mahalanobis' $D^2$ statistic and grouped them into 17 clusters. Further, the constellations were confirmed by canonical root analysis with 4 canonical vectors and reported that seed yield per plant followed by number of pods per plant and seeds per pod contributed more towards the total genetic divergence.

Sharma *et al.* (1995) estimated the genetic divergence in 60 indigenous and exotic soybean genotypes using Mahalanobis' $D^2$ statistic and grouped them into 6 clusters. They reported no significant relationship between geographical and genetic diversity. The genotypes at the same place also showed wider genetic diversity.

Genetic divergence among 30 soybean genotypes was estimated by using $D^2$ statistic and canonical root analysis by Chowdhary *et al.* (1996) and reported that 100 seed weight and seed yield per plant are the main characters contributed to total genetic divergence.

Mehetre *et al.* (1997) grouped 41 soybean genotypes in to 12 clusters using $D^2$ statistic and reported that genetic diversity was independent of geographical origin.

Ramgiry and Raha (1997) studied genetic divergence among 49 genotypes of soybean through $D^2$ statistic and grouped into 6 clusters and reported the highest inter-cluster distance between I and V clusters which serve as potential parents for hybridization.

Mohan Rao (1999) studied 20 genotypes of soybean for genetic divergence through $D^2$ statistic and grouped them into 6 clusters and also reported protein content followed by seed yield per plant and seeds per pod contributed maximum towards genetic divergence.

Das *et al.* (2000) studied genetic divergence among 65 genotypes of soybean from 18 diverse origins for eleven characters through $D^2$ values and the genotypes were grouped into 13 clusters out of which 6 were Monogenotypic. Grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of genotypes. Pods per plant and plant height had maximum contribution towards genetic divergence.

Sharma (2000) performed multivariate analysis among 60 genotypes of soybean under 4 different environments grouped into 9 clusters from pooled data and reported that the traits *viz.,* plant height, number of branches per plant, number of pods per plant, 100 seed weight, seed yield per plant and protein content contributed more towards total genetic divergence.

Shrivastava *et al.* (2000) evaluated 50 soybean genotypes through genetic divergence using Mahalanobis $D^2$ analysis with 9 component characters. All the genotypes could be grouped in to five clusters and the maximum and minimum distances were observed between cluster II and III and cluster III and IV respectively.

Chandankar *et al.* (2002) evaluated 25 genotypes of soybean for genetic divergence through $D^2$ statistic and were grouped into 9 clusters. Further, the constellations were confirmed by canonical root analysis with 3 canonical vectors accounting for 99.9% of total variation and reported that traits *viz.,* days to 50% flowering, branches per plant, pods per plant, biological yield per plant and oil content contributed maximum to the total genetic divergence.

Ganesamurthy and Seshadri (2002) studied 50 soybean genotypes for genetic divergence through $D^2$ statistic and grouped them into 10 clusters and also reported that 100 seed weight followed by plant height and pods per plant contributed maximum where as days to maturity and days to 50% flowering contributed minimum towards the total genetic divergence.

Gawande *et al.* (2002) studied 50 soybean genotypes for genetic divergence through $D^2$ statistic and canonical root analysis. The population was grouped into 10 clusters and also reported that traits *viz.,* plant height followed by pods per plant and days to maturity contributed maximum towards genetic divergence.

Ramana (2003) evaluated 70 soybean genotypes for genetic divergence through $D^2$ statistics and grouped them into 9 clusters. There was no linear relationship between geographic and genetic divergence while, plant height, plant dry weight and 100 seed weight contributed maximum to the total genetic divergence.

Chamundeswari and Aher (2003) evaluated 90 germplasm lines through $D^2$ analysis and the clustering pattern revealed that there is no relationship between the genetic divergence and geographical distribution. The genotypes were grouped based on 9 clusters and characters *viz.,* Plant height (cm), number of pods per plant, protein content (%) and oil content (%) contributed maximum towards genetic divergence.

Praveen Kumar (2004) studied 84 soybean genotypes through Mahalanobis' $D^2$ statistic and revealed that that distribution of genotypes among clusters is independent of its geographical origin. The characters plant height followed by seed protein content, days to maturity, 100 seed weight and total biomass per plant contributed maximum towards the total genetic divergence.

Sriranjani (2006) studied 38 soybean genotypes through $D^2$ statistic and grouped them into 9 clusters. Clustering pattern of genotypes did not follow geographic origin, suggesting that geographical isolation may not be the only factor causing genetic diversity. Out of 13 characters studied, days to maturity followed by plant height contributed maximum towards divergence.

Truong *et al.* (2005) evaluated 20 soybean genotypes quantitatively by image analysis using elliptic Fourier descriptors and their principal components for pod shape. The cumulative contribution at the fifth principal component was higher than 95%, indicating that the first, second, third, fourth and fifth principal components represented the aspect ratio of the pod, the location of the pod centriod, the sharpness of two pod tips and the roundness of the base in the pod contour, respectively. Analysis of variance revealed significant genotypic differences in these principal components and seed number per pod.

**Principal Component Analysis:**

Ghafoor *et al.* (2001) evaluated 484 accessions of blackgram (*Vigna mungo* L. Hepper) for genetic diversity. Data collected on quantitative traits were subjected for cluster and principal component analysis. The first four principal components with eigen values more than one contributed 79.5 per cent of variability amongst accessions. The germplasm was categorized into five clusters based on average linked and cluster II and IV were more clearly separated from I and V.

Altaher and Singh (2003) assessed the genetic divergence among 40 different upland cotton varieties of India for different agronomical and fiber quality traits using Mahalanobis' $D^2$ statistic and principal component analysis.

On the basis of these two clustering methods, six clusters were obtained, genotypes form different agro-climatic zones grouped together in same cluster indicating that geographical diversity is always not necessarily associated with genetic diversity.

Yadav *et al.* (2004) in their study on 109 forage sorghum genotypes with 30 characters identified nine principal components which explained 79 per cent variability. PCA applying varimax rotation enabled loading of similar type of variables on a common principal component. Genotypes S 1999, IS 3359, G 127, G 143 and IS 3075 were found better performers with regard to fodder yield based on principal component scores of the genotypes.

Twenty-five genotypes of mungbean were evaluated by Bhattacharaya and Vijayalakshmi (2005) using principal component analysis and the genotypes were grouped into ten clusters. Cluster VIII was the largest cluster having five genotypes, where as clusters I, II, VI and X were large having three genotypes each and these cluster accounted 68% of the genotypes. Geographical origin of genotypes did not show any relationship with genetic diversity.

Sriranjani (2006) evaluated 38 soybean genotypes for genetic diversity. Data collected on quantitative traits were subjected for cluster and principal component analysis. The first five principal components with eigen values more than one contributing 79.39 per cent of variability amongst 38 soybean genotypes. On the basis of principal component analysis the genotypes were grouped into seven clusters. Cluster III had maximum number of genotypes i.e. 10 and cluster VII had minimum only single genotype.

**Table 1: Review of literature on genetic variability in soybean**

| Sl.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 1. | Days to 50% flowering | Tiwari and Bhatnagar (1991)<br>Mehetre *et al.*(1994 a)<br>Taware *et al.*(1995)<br>Maharaddi.(1996)<br>Taware *et al.*(1997)<br>Thorat *et al.*(1999)<br>Sood and Sood (2001) | Nirmala Kumari and Balasubramanian (1993)<br>Mehetre *et al.*(1995)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.*(2000)<br>Bangar *et al.*(2003)<br>Ramana (2003) |
| 2. | Days to maturity | Nirmala Kumari and Balasubramanian (1993)<br>Mehetre *et al.*(1994 a)<br>Mehetre *et al.*(1995)<br>Taware *et al.*(1995)<br>Mehetre *et al.*(1997)<br>Taware *et al.*(1997) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Harer and Deshmukh (1992)<br>Sailaja (1997)<br>Taware *et al* (1997)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Sood and Sood (2001)<br>Bangar *et al.*(2003)<br>Ramana (2003) |

| Sl.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 3. | Plant height | Harer and Deshmukh (1992)<br>Mahajan *et al.*(1993)<br>Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1994 a)<br>Mehetre *et al.*(1995)<br>Taware *et al.*(1995)<br>Maharaddi.(1996)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Shrivastava and Shukla (1998)<br>Thorat *et al.*(1999)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Bangar *et al.*(2003)<br>Ramana (2003)<br>Praveen Kumar *et al.*(2005) | Singh and Singh (1999) |

| Sl.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 4. | Number of branches per plant | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992)<br>Mahajan *et al* (1993)<br>Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Ramana *et al.*(2000)<br>Agarwal *et al (*2001)<br>Bangar *et al.*(2003)<br>Ramana (2003)<br>Praveen Kumar *et al* (2005) | Mehetre *et al.*(1994 a)<br>Mehetre *et al.*(1995)<br>Maharaddi.(1996)<br>Mehetre *et al.*(1998)<br>Shrivastava and Shukla (1998) |
| 5. | Number of pods per plant | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992)<br>Mahajan *et al* (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1994 a)<br>Shrivastava and Shukla (1998)<br>Mehetre *et al.*(1995)<br>Mehetre *et al.*(1997)<br>Sailaja (1997)<br>Mehetre *et al.*(1998)<br>Singh and Singh (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Bangar *et al.*(2003)<br>Ramana (2003)<br>Chettri *et al* (2005)<br>Praveen Kumar *et al* (2005)<br>Gohil *et al* (2006) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Thorat *et al* (1999*)* |

| Sl.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 6. | Pod length (cm) | Thorat *et al* (1999) | Maharaddi.(1996)<br>Ramana *et al.*(2000)<br>Mishra and Rao (2005)<br>Hina Kausar (2006) |
| 7 | Number of seeds per pod | Malik and Singh (1987) | Shrivastava and Jain (1994)<br>Maharaddi.(1996)<br>Sailaja (1997)<br>Thorat *et al* (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Ramana (2003)<br>Hina Kausar (2006) |
| 8. | 100 seed weight (g) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Harer and Deshmukh (1992)<br>Mahajan *et al* (1993)<br>Mehetre *et al.*(1994 a)<br>Shrivastava and Jain (1994)<br>Taware *et al.*(1995)<br>Maharaddi.(1996)<br>Mehetre *et al.*(1997)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Thorat *et al* (1999)<br>Sood and Sood (2001)<br>Bangar *et al.*(2003)<br>Ramana (2003) | Mehetre *et al.*(1995)<br>Shrivastava and Shukla (1998)<br>Singh and Singh (1999)<br>Ramana *et al.*(2000) |

| Sl.No. | Character | Wider genetic variability | Narrow genetic variability |
|---|---|---|---|
| 9. | Biological yield per plant | Nirmala Kumari and Balasubramanian (1993)<br>Shrivastava and Jain (1994)<br>Sailaja (1997)<br>Shrivastava and Shukla (1998)<br>Dixit *et al* **(**2002)<br>Ramana (2003)<br>Praveen Kumar *et al* (2005) | |
| 10. | Harvest index (%) | Nirmala Kumari and Balasubramanian (1993)<br>Shrivastava and Jain (1994)<br>Mehetre *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Dixit *et al* ***(***2002) | Sailaja (1997)<br>Shrivastava and Shukla (1998)<br>Ramana (2003) |
| 11. | Seed protein content (%) | Arora *et al* (1970)<br>Musorina (1987)<br>Nirmala Kumari and Balasubramanian (1993) | Malik and Singh (1987)<br>Sailaja (1997)<br>Torat *et al* (1999)<br>Ramana (2003) |
| 12. | Oil content (%) | Weber and Moorthy (1952)<br>Malik and Singh (1987)<br>Taware *et al.*(1997) | Sharma *et al* (1986)<br>Mehetre *et al.*(1995)<br>Torat *et al* (1999)<br>Ramana (2003) |

| **Sl.No.** | **Character** | **Wider genetic variability** | **Narrow genetic variability** |
|---|---|---|---|
| 13. | Seed yield per plant (g) | Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1995)<br>Maharaddi.(1996)<br>Mehetre *et al.*(1997)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Shrivastava and Shukla (1998)<br>Singh and Singh (1999)<br>Thorat *et al* (1999)<br>Ramana *et al* (2000)<br>Agarwal *et al* (2001)<br>Sood and Sood (2001)<br>Dixit *et al* (2002)<br>Bangar *et al.*(2003)<br>Ramana (2003)<br>Gohil *et al* (2006) | Kalaimagal (1991)<br>Nirmala Kumari and Balasubramanian (1993) |

**Table 2: Review of literature on heritability ($h^2$) and genetic advance (GA) in soybean.`**

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 1. | Days to 50% flowering | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Mahajan *et al* (1993)<br>Maharaddi.(1996)<br>Thorat *et al* (1999)<br>Sood and Sood (2001)<br>Mishra and Rao (2005) | Mehetre *et al.*(1994a)<br>Mehetre *et al.*(1995)<br>Taware *et al.*(1995)<br>Nehru *et al* (1999)<br>Ramana *et al.*(2000)<br>Ramana (2003) | Nirmala Kumari and Balasubramanian (1993)<br>Bangar *et al* (2003) | --- |
| 2. | Days to maturity | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992)<br>Nirmala Kumari and Balasubramanian (1993)<br>Mahajan *et al* (1993)<br>Bangar *et al* (2003) | Tiwari and Bhatnagar (1991)<br>Mehetre *et al.*(1994a)<br>Mehetre *et al.*(1995)<br>Taware *et al.*(1995)<br>Nehru *et al* (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Ramana (2003) | --- | Kalaimagal (1991)<br>Shrivastava and Shukla (1998) |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 3. | Plant height (cm) | Harer and Deshmukh (1992)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Mahajan *et al.*(1994)<br>Maharaddi.(1996)<br>Rajarathinam *et al* (1996)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Roy and Raquib (1998)<br>Thorat *et al.*(1999)<br>Jain and Ramgiry (2000)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Ramana (2003)<br>Basavaraja *et al* (2005)<br>Chettri *et al* (2005)<br>Jyothi sethi and Tyagi (2005)<br>Mishra and Rao (2005)<br>Gohil *et al* (2006)<br>Hina kausar (2006) | Singh and Singh (1999) | Kalaimagal (1991)<br>Mehetre *et al.*(1994a)<br>Mehetre *et al.*(1995)<br>Shrivastava and Shukla (1998)<br>Sood and Sood (2001)<br>Bangar *et al (*2003) | --- |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 4. | Number of branches per plant | Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Rajarathinam *et al* (1996)<br>Sailaja (1997)<br>Roy and Raquib (1998)<br>Agarwal *et al.*(2001)<br>Bangar *et al.*(2003)<br>Hina kausar (2006) | Rajasekaran *et al* (1980)<br>Taware *et al.*(1997) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Harer and Deshmukh (1992)<br>Maharaddi.(1996) | Mehetre *et al.*(1994 a)<br>Mehetre *et al.*(1995)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.*(2000) |
| 5. | Number of pods per plant | Amarnath *et al.* (1991)<br>Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1994 a)<br>Rajarathinam *et al* (1996)<br>Mehetre *et al.*(1997)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Roy and Raquib (1998)<br>Maharaddi.(1999)<br>Singh and Singh (1999)<br>Jain and Ramgiry (2000)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Gohil *et al* (2006)<br>Hina kausar (2006) | --- | Harer and Deshmukh (1992)<br>Mahajan *et al.*(1994)<br>Mehetre *et al.*(1994 a)<br>Thorat *et al.*(1999)<br>Sood and Sood (2001)<br>Bangar *et al* (2003) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.*(2000)<br>Mishra and Rao (2005) |

| S.No. | Character | High heritability with high | High heritability | Low heritability with | Low heritability with |
|---|---|---|---|---|---|

| | | genetic advance | with low genetic advance | high genetic advance | low genetic advance |
|---|---|---|---|---|---|
| 6. | Pod length | Thorat *et al.*(1999) | Agarwal *et al.*(2001) | | Rana Khurna and sandhu (1972)<br>Maharaddi.(1999)<br>Ramana *et al.*(2000) |
| 7. | Number of seed per pod | --- | Rashid and Islam (1982)<br>Sailaja (1997)<br>Chettri *et al* (2005) | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992) | Kalaimagal (1991)<br>Vimala Devi (1993)<br>Shrivastava and Jain (1994)<br>Maharaddi.(1999)<br>Thorat *et al.*(1999)<br>Ramana *et al.*(2000)<br>Ramana (2003)<br>Praveen Kumar *et al* (2005) |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 8. | 100 seed weight (g) | Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Mahajan *et al.*(1993)<br>Mehetre *et al.*(1994 a)<br>Shrivastava and Jain (1994)<br>Taware *et al.*(1995)<br>Maharaddi.(1996)<br>Rajarathinam *et al* (1996)<br>Mehetre *et al.*(1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Thorat *et al.*(1999)<br>Basavaraja *et al* (2005)<br>Jyothi sethi and Tyagi (2005)<br>Hina kausar (2006) | Sailaja (1997)<br>Nehru *et al (1999)*<br>Singh and Singh (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Chettri *et al* (2005) | Shrivastava and Shukla (1998)<br>Bangar *et al.*(2003) | -- |
| 9. | Biological yield per plant (g) | Mehetre *et al.*(1994 a)<br>Sailaja (1997)<br>Mehetre *et al.*(1998)<br>Ramana (2003)<br>Jyothi sethi and Tyagi (2005)<br>Hina kausar (2006) | Shrivastava and Shukla (1998) | Shrivastava and Jain (1994) | -- |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 10. | Harvest index (%) | Nirmala Kumari and Balasubramanian (1993)<br>Sailaja (1997)<br>Mohan Rao (1991)<br>Basavaraja *et al* (2005)<br>Hina kausar (2006) | --- | --- | Shrivastava and Jain (1994)<br>Shrivastava and Shukla (1998)<br>Praveen Kumar *et al* (2005) |
| 11. | Seed protein content (g) | Thorat *et al.*(1999)<br>Ramana (2003) | Malik and Singh (1987)<br>Nirmala Kumari and Balasubramanian (1993)<br>Sailaja (1997) | --- | Sharma *et al* (1986) |
| 12. | Oil content (%) | Thorat *et al.*(1999) | Taware *et al.*(1997) | -- | Mehetre *et al.*(1995)<br>Ramana (2003) |
| 13. | Seed yield per plant (g) | Nirmala Kumari and Balasubramanian (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1994 a)<br>Singh and singh (1999)<br>Ramana *et al.*(2000)<br>Jain and Ramgiry (2000)<br>Basavaraja *et al.* (2005)<br>Gohil *et al.* (2006) | Sailaja (1997)<br>Taware *et al.*(1997) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Shrivastava and Shukla (1998)<br>Sood and Sood (2001) | Thorat *et al.*(1999)<br>Bangar *et al.*(2003) |

**Table 2 : Review of literature on heritability ($h^2$) and genetic advance (GA) in soybean.`**

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 1. | Days to 50% flowering | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Mahajan *et al.* (1993)<br>Maharaddi.(1996)<br>Thorat *et al.* (1999)<br>Sood and Sood (2001)<br>Mishra and Rao (2005) | Mehetre *et al.*(1994a)<br>Mehetre *et al.*(1995)<br>Taware *et al.*(1995)<br>Nehru *et al.* (1999)<br>Ramana *et al.*(2000)<br>Ramana (2003) | Nirmala Kumari and Balasubramanian (1993)<br>Bangar *et al.* (2003) | --- |
| 2. | Days to maturity | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992)<br>Nirmala Kumari and Balasubramanian (1993)<br>Mahajan *et al.* (1993)<br>Bangar *et al.* (2003) | Tiwari and Bhatnagar (1991)<br>Mehetre *et al.*(1994a)<br>Mehetre *et al.*(1995)<br>Taware *et al.*(1995)<br>Nehru *et al.* (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Ramana (2003) | --- | Kalaimagal (1991)<br>Shrivastava and Shukla (1998) |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 3. | Plant height (cm) | Harer and Deshmukh (1992)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Mahajan *et al.*(1994)<br>Maharaddi.(1996)<br>Rajarathinam *et al.* (1996)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Roy and Raquib (1998)<br>Thorat *et al.*(1999)<br>Jain and Ramgiry (2000)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Ramana (2003)<br>Basavaraja *et al.* (2005)<br>Chettri *et al.* (2005)<br>Jyothi sethi and Tyagi (2005)<br>Mishra and Rao (2005)<br>Gohil *et al.* (2006)<br>Hina Kausar (2006)<br>Sriranjani *et al.* (2007) | Singh and Singh (1999) | Kalaimagal (1991)<br>Mehetre *et al.*(1994a)<br>Mehetre *et al.*(1995)<br>Shrivastava and Shukla (1998)<br>Sood and Sood (2001)<br>Bangar *et al.* (2003) | --- |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 4. | Number of branches per plant | Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Rajarathinam *et al.* (1996)<br>Sailaja (1997)<br>Roy and Raquib (1998)<br>Agarwal *et al.*(2001)<br>Bangar *et al.*(2003)<br>Hina Kausar (2006) | Rajasekaran *et al.* (1980)<br>Taware *et al.*(1997) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Harer and Deshmukh (1992)<br>Maharaddi.(1996) | Mehetre *et al.*(1994 a)<br>Mehetre *et al.*(1995)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.*(2000) |
| 5. | Number of pods per plant | Amarnath *et al.* (1991)<br>Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1994 a)<br>Rajarathinam *et al.* (1996)<br>Mehetre *et al.*(1997)<br>Sailaja (1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Roy and Raquib (1998)<br>Maharaddi.(1999)<br>Singh and Singh (1999)<br>Jain and Ramgiry (2000)<br>Ramana *et al.*(2000)<br>Agarwal *et al.*(2001)<br>Gohil *et al.* (2006)<br>Hina Kausar (2006) | --- | Harer and Deshmukh (1992)<br>Mahajan *et al.*(1994)<br>Mehetre *et al.*(1994 a)<br>Thorat *et al.*(1999)<br>Sood and Sood (2001)<br>Bangar *et al.* (2003) | Kalaimagal (1991)<br>Tiwari and Bhatnagar (1991)<br>Shrivastava and Shukla (1998)<br>Ramana *et al.*(2000)<br>Mishra and Rao (2005) |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 6. | Pod length | Thorat *et al.*(1999) | Agarwal *et al.*(2001) | --- | Rana Khurna and sandhu (1972)<br>Maharaddi.(1996)<br>Ramana *et al.*(2000) |
| 7. | Number of seed per pod | --- | Rashid and Islam (1982)<br>Sailaja (1997)<br>Chettri *et al.* (2005) | Amarnath *et al.* (1991)<br>Harer and Deshmukh (1992) | Kalaimagal (1991) Vimala Devi (1993)<br>Srivastava and Jain (1994)<br>Maharaddi.(1999)<br>Thorat *et al.*(1999)<br>Ramana *et al.*(2000)<br>Ramana (2003)<br>Praveen Kumar *et al.* (2005) |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 8. | 100 seed weight (g) | Nirmala Kumari and Balasubramanian (1993)<br>Vimala Devi (1993)<br>Mahajan *et al.*(1993)<br>Mehetre *et al.*(1994 a)<br>Srivastava and Jain (1994)<br>Taware *et al.*(1995)<br>Maharaddi.(1996)<br>Rajarathinam *et al* (1996)<br>Mehetre *et al.*(1997)<br>Taware *et al.*(1997)<br>Mehetre *et al.*(1998)<br>Thorat *et al.*(1999)<br>Basavaraja *et al.* (2005)<br>Jyothi sethi and Tyagi (2005)<br>Hina Kausar (2006) | Sailaja (1997)<br>Nehru *et al. (1999)*<br>Singh and Singh (1999)<br>Ramana *et al.*(2000)<br>Sood and Sood (2001)<br>Chettri *et al.* (2005) | Shrivastava and Shukla (1998)<br>Bangar *et al.*(2003) | -- |
| 9. | Biological yield per plant (g) | Mehetre *et al.*(1994 a)<br>Sailaja (1997)<br>Mehetre *et al.*(1998)<br>Ramana (2003)<br>Jyothi sethi and Tyagi (2005)<br>Hina Kausar (2006)<br>Sriranjani *et al.* (2007) | Shrivastava and Shukla (1998) | Srivastava and Jain (1994) | -- |

| S.No. | Character | High heritability with high genetic advance | High heritability with low genetic advance | Low heritability with high genetic advance | Low heritability with low genetic advance |
|---|---|---|---|---|---|
| 10. | Harvest index (%) | Nirmala Kumari and Balasubramanian (1993)<br>Sailaja (1997)<br>Mohan Rao (1999)<br>Basavaraja *et al.* (2005)<br>Hina Kausar (2006)<br>Sriranjani *et al.* (2007) | --- | --- | Srivastava and Jain (1994)<br>Shrivastava and Shukla (1998)<br>Praveen Kumar *et al* (2005) |
| 11. | Seed protein content (g) | Thorat *et al.*(1999)<br>Ramana (2003) | Malik and Singh (1987)<br>Nirmala Kumari and Balasubramanian (1993)<br>Sailaja (1997) | --- | Sharma *et al* (1986) |
| 12. | Oil content (%) | Thorat *et al.*(1999) | Taware *et al.*(1997) | -- | Mehetre *et al.*(1995)<br>Ramana (2003) |
| 13. | Seed yield per plant (g) | Nirmala Kumari and Balasubramanian (1993)<br>Jagtap and Mehetre (1994)<br>Mehetre *et al.*(1994 a)<br>Singh and singh (1999)<br>Ramana *et al.*(2000)<br>Jain and Ramgiry (2000)<br>Basavaraja *et al.* (2005)<br>Gohil *et al.* (2006)<br>Sriranjani *et al.* (2007) | Sailaja (1997)<br>Taware *et al.*(1997) | Amarnath *et al.* (1991)<br>Kalaimagal (1991)<br>Shrivastava and Shukla (1998)<br>Sood and Sood (2001) | Thorat *et al.*(1999)<br>Bangar *et al.*(2003) |

# CHAPTER – III

# MATERIALS AND METHODS

## 3.1 MATERIAL

The material used in the present investigation consisted of 45 soybean genotypes obtained from different research centers under the All India Coordinated Research Project on Soybean and studied at Regional Agricultural Research Station, Lam, Guntur during *Kharif*, 2007.

## 3.2 METHODS

The experiment was conducted at Regional Agricultural Research Station, Lam, Guntur located at 16.18 $^0$ North latitude and 80.29 $^0$ East longitude at an altitude of 31.5 m above MSL (Mean Sea Level) during *Kharif*, 2007 in a randomized complete block design with three replications. Each plot comprised four rows of 3m length with a spacing of 30 cm between the rows and 7.5 cm within the row in black cotton soils.

The crop was provided with 30 kg N, 60 kg $P_2O_5$ and 40 kg $K_2O$ ha $^{-1}$. All necessary prophylactic measures were adopted against pests and diseases and standard agronomic practices recommended to the region were followed.

List of soybean genotypes used in the present study and their source of origin are given in table 7.

**Table 7 : List of soybean genotypes and their source of origin used in the present study.**

| S.No. | Genotype | Pedigree | Source |
|---|---|---|---|
| 1 | JS(SH) 2001-04 | JS 93-01 X EC 39081 | Jabalpur |
| 2 | LSb 23 | PK 416 X JS 335 | Lam |
| 3 | VLS 70 | NA | Almora |
| 4 | DSb 10 | Hardee X MACS 450 | Dharwad |
| 5 | PS 1437 | JS 335 X PS - 1024 | Pantnagar |
| 6 | NSO 111 | Mutant of MACS -450 | Pachora |
| 7 | DS 2402 | NA | Delhi |
| 8 | SL 752 | SL 495 X SL 565 | Ludhiana |
| 9 | JS 20 - 01 | JS 335 X EC 109541 | Jabalpur |
| 10 | DSb 12 | JS 335 X PS 73 -7 | Dharwad |
| 11 | MACS 1126 | Selection from IR - 1 | Pune |
| 12 | PS 1421 | PS 1029 X JS 335 | Pantnagar |
| 13 | KDS 167- 9 | Selection from AGS 134 | Sangali |
| 14 | MAUS 285 | UGM 52 X Hardee | Parbhani |
| 15 | HIMSO 1608 | SL 284 X Bragg | Palampur |
| 16 | DS 2410 | NA | Delhi |
| 17 | NSO 78 | JS 335 X MACS 450 | Pachora |
| 18 | AMS 4-4 | MACS 450 X JS 93-95-2 | Amaravathi |
| 19 | PS 1433 | Jupitor X VLS 40 | Pantnagar |
| 20 | NRC 78 | NRC 7 X JS 335 | Indore |
| 21 | JS 20- 06 | DSb1 X SL 603 | Jabalpur |
| 22 | MAUS 295 | MAUS1 X Jawra 16-2 | Parbhani |
| 23 | MACS 1148 | MACS 684 X MACS 124 | Pune |
| 24 | HIMSO 1609 | PK-1053 X HIMSO 107 | Palampur |
| 25 | TS 94 | TS 9 X EC 34160 | Trombay |

**Contd….**

**Table 7 contd…**

| S.No. | Genotype | Pedigree | Source |
|---|---|---|---|
| 26 | NRC 77 | JS -335 X TGX 835-53D | Indore |
| 27 | SL 790 | PK 1162 X SL 523 | Ludhiana |
| 28 | AMS 4- 63 | TAMS 38 X MAUS -61-2 | Amaravathi |
| 29 | RCS 9 | JS 80-21 X Bragg | Ranchi |
| 30 | NRC 76 | NRC 37 X L-129 | Indore |
| 31 | SL 744 | SL 457 X SL 459 | Ludhiana |
| 32 | VLS 69 | NA | Almora |
| 33 | RKS 45 | NRC 37 X PK 472 | Kota |
| 34 | JS 20-09 | Mutant of NRC -37 | Jabalpur |
| 35 | TS 56 | Bragg X TS 107 | Trombay |
| 36 | VLS 68 | NA | Almora |
| 37 | RKS 48 | PK 1024 X NRC 37 | Kota |
| 38 | MACS 1139 | PK 416 X JS (SH) 89-98 | Pune |
| 39 | RCS 1 | PK 416 X UGM 52 | Ranchi |
| 40 | NSO 15 | Ankur X JS 335 | Pachora |
| 41 | AMS 99-33 | Hardee X Pb 1 | Amaravathi |
| 42 | JS 93-05 | Selection from PS 73-22 | Jabalpur |
| 43 | Bragg | Jackson X D49 2491 | Introduced from USA |
| 44 | RKS 18 | MACS 450 X Monetta | Kota |
| 45 | JS 335 | JS 78-77 X JS 71-05 | Jabalpur |

**NA = Not available**

## 3.3 RECORD OF OBSERVATIONS

The observations were recorded on five randomly selected plants from each genotype per replication for the following characters and the mean of five plants were used for statistical analysis. However, days to 50% flowering, days to maturity, 100 seed weight, protein content and oil content were recorded on plot basis.

### 3.3.1 Days to 50% flowering

The number of days from sowing to 50 percent of the plants to flower was recorded as days to flowering on plot basis.

### 3.3.2 Days to maturity

The number of days from sowing to physiological maturity of the crop was recorded as days to maturity on plot basis.

### 3.3.3 Plant height (cm)

The plant height was measured from the base to the tip of the plant at maturity in centimeters.

### 3.3.4 Number of branches per plant

The number of branches of each plant arising from the main stem was counted at maturity.

### 3.3.5 Number of pods per plant

The number of well filled pods per plant was counted at the time of harvest.

### 3.3.6 Pod length (cm)

Pod length was measured from the base of the pod to the base of the beak on five randomly selected pods from each plant; the mean value of the sample was recorded as the length of the pod in centimeters at harvest.

### 3.3.7 Number of seeds per pod

The seeds of five randomly selected pods from a plant were counted and averaged to obtain the number of seeds per pod.

### 3.3.8 100-Seed weight (g)

One hundred randomly selected seeds from the bulk of seed yield were calculated and weighed in grams.

### 3.3.9 Biological yield per plant (g)

Sample plants were collected at physiological maturity and dried in an oven at 72 $^{0}$C for 24 hours and weighed in grams.

### 3.3.10 Harvest index (%)

The harvest index was estimated by using the formula

$$HI (\%) = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield}} \times 100$$

### 3.3.11 Seed protein content (%)

The nitrogen content in the seeds was estimated on plot basis using micro-kjeldahl technique (AOAC, 1980) and protein content was calculated by the formula.

Per cent Protein = Per cent nitrogen x 5.71

(Sadasivam and Manickam, 1992)

### 3.3.12 Oil content (%)

Oil content in seeds was estimated on plot basis using NIR (Nuclear Infrared Resonance) and expressed as percentage.

### 3.3.13 Seed yield Per Plant (g)

The seed yield harvested from sample plants were dried and weighed in grams.

## 3.4 STATISTICAL TECHNIQUES

The data collected on thirteen characters from 45 genotypes were subjected to the following statistical analysis.

### 3.4.1 Genetic Variability

**Analysis of variance**

The analysis of variance for each character was performed as per the standard statistical procedure for CRBD Proposed by Cochran and Cox (1950).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

$Y_{ij}$ = Performance of $j^{th}$ genotype in $i^{th}$ block

$\mu$ = General mean

$b_i$ = True effect of $i^{th}$ block

$t_j$ = True effect of $j^{th}$ genotype

$e_{ij}$ = Random error

**ANOVA Table for R.B.D.**

| **Source of variation** | **Degree of freedom (d.f.)** | **Mean sum of squares** | | **F Cal.** |
|---|---|---|---|---|
| | | **Observed** | **Expected** | |
| Blocks | (r-1) | Mr | $\sigma^2 r + \sigma^2 e$ | Mr/Me |
| Treatments | (t-1) | Mt | $\sigma^2 t + \sigma^2 e$ | Mt/Me |
| Error | (r-1) (t-1) | Me | $\sigma^2 e$ | |

Where,

r = Number of replications

t = Number of treatments

Mr = Mean sum of squares of replications

Mt = Mean sum of squares of treatments

Me = Mean sum of squares of error.

$$\sigma^2 g = \frac{Mt - Me}{r}$$

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

**Estimation of genetic parameters**

**Coefficient of variation**

Phenotypic and Genotypic Coefficients of Variation (PCV and GCV) were computed as suggested by Burton (1952).

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean (X)}} \times 100$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean (X)}} \times 100$$

As suggested by Sivasubramanian and Menon (1973), GCV and PCV were categorized

| | | |
|---|---|---|
| Low | = | Less than 10% |
| Moderate | = | 10-20% |
| High | = | More than 20% |

**Heritability in Broad sense [$h^2$ (b)]**

Heritability in broad sense was estimated as per Allard (1960).

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

As suggested by Johnson *et al.* (1955), $h^2$ (b) was categorized

| | | |
|---|---|---|
| Low | = | 0- 30% |
| Moderate | = | 30-60% |
| High | = | More than 60% |

**Genetic advance (GA)**

This was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

$$GA = K \times \sigma_p \times h^2 (b)$$

Where,

K = selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

$h^2$ (b) = Heritability in broad sense

$\sigma_p$ = phenotypic standard deviation

**Genetic Advance as per cent of Mean (GAM)**

$$GAM = \frac{\text{Genotypic advance}}{\text{General mean } (\bar{X})} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.*(1955).

| | | |
|---|---|---|
| Low | = | Less than 10% |
| Moderate | = | 10-20% |
| High | = | More than 20% |

**3.4.2 Genetic divergence**

**Mahalanobis' $D^2$ analysis**

The data collected on different characters were analysed through Mahalanobis' $D^2$ analysis to determine the genetic divergence among the genotypes.

$D^2$ value between $i^{th}$ and $j^{th}$ genotypes for 'P' characters was calculated as

$$D^2_{ij} = \sum_{t=1}^{P} (Y_i^t - Y_j^t)^2$$

Where,

$Y_i^t$ = Uncorrelated mean value of $i^{th}$ genotype for't' characters

$Y_j^t$ = Uncorrelated mean value of $j^{th}$ genotype for't' characters

$D^2_{ij}$ = $D^2$ value between $i^{th}$ and $j^{th}$ genotypes.

The various steps involved in estimation of $D^2$ values are given below.

#### 3.4.2.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1961). After testing difference between genotypes for each of the characters, a simultaneous test of significance for the differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using V statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error and error + variety, variance and covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using following relationship.

$$\wedge = \frac{|E|}{|E + V|}$$

Where,

$\wedge$ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E + V|$ = Determinant of error + variety matrix

V(Stat) = $-m \log_e \wedge = -[n - (P + Q + 1) / 2] \log_e$ '$\wedge$'

Where, $m = n-(P + Q +1) / 2$

P = Number of characters *i.e.*, 13

$Q$ = Number of varieties -1 (or d.f. for populations) *i.e.*, 45-1 = 44

$n$ = degree of freedom for error + varieties

$\text{Log}_e$ '^' = 2.3026 $\log_{10}$ '^'

V (Stat) is distributed as $\chi^2$ with PQ degrees of freedom *i.e.*, (13 x 45) = 585 in the present study.

**3.4.2.2 Transformation of correlated variables**

In the present model computation of $D^2$ values were reduced to simple summation of the differences in mean values of various characters of the two genotypes *i.e.*, $\sum d^2_i$. Therefore, transformation of correlated variables into uncorrelated ones was done before working out the $D^2$ values. Transformation was done using pivotal condensation method.

**3.4.2.2 Computation of $D^2$ values**

For the given combination of i and j genotype, the mean deviation *i.e.*, $Y_i^t - Y_j^t$ for t = 1, 2…p variables are computed and the $D^2$ values were calculated as

$$D^2_{ij} = \sum_{t=1}^{P} (Y_i^t - Y_j^t)^2$$

### 3.4.2.3 Testing the significance of $D^2$ values

The $D^2$ value obtained for a pair of population is taken as calculated value of $\chi^2$ and is tested against the tabulated value of $\chi^2$ for P degree of freedom where P is the number of characters considered. In the present study P is 13.

### 3.4.2.5 Contribution of individual characters towards divergence

In all combinations each character was ranked based on their contribution towards divergence between two entries ($d_i = Y_i^t - Y_j^t$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

$$\text{Percentage contribution of a character X} = \frac{N \times 100}{M}$$

Where,

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered 990 in the present study.

### 3.4.2.6 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster should at least on an average show a smaller $D^2$ value than those belonging to different clusters. For this purpose $D^2$ values of all combinations of each genotype were arranged in ascending order of magnitude in tabular form as described by Singh and Chaudhary (1977). To start with, two populations having the smallest $D^2$ value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an increase in the average $D^2$, that population was not considered for including in that cluster. The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued until all the genotypes were included into one or other clusters.

### 3.4.2.7 Average intra-cluster distance

For the measurement of intra-cluster distance, the formulae used was $\sum D^2_i/n$ where, $\sum D^2_i$ was the sum of distances between all possible combinations (n) of the populations included in a cluster.

### 3.4.2.8 Average inter-cluster distance

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of $D^2$ values between the genotypes of one cluster to each of the genotypes of the other cluster divided by the product of number of genotypes in both the clusters under consideration.

$$\text{Average-inter cluster distance} = \frac{D^2}{\quad}$$

$$(n_1 \times n_2)$$

Where,

$D^2$ = Divergence value

$n_1$ and $n_2$ = number of genotypes of two clusters.

### 3.4.2 Cluster analysis

Agglomerative hierarchical clustering technique was followed as given by Anderberg (1993).

#### 3.4.3.1 Obtaining data matrix

A data matrix was obtained by recording the data on 45 genotypes for 13 yield component characters.

#### 3.4.3.2 Standardizing the data matrix

To compare the similarities among the genotypes the data matrix was standardized with a column standardizing function i.e., Q analysis. The data matrix is standardized in cluster analysis to make the characters contribute more equally to the similarities among genotypes and to nullify the arbitrarily affect of the units chosen for measuring the attributes among the genotypes.

Column standardizing function CA-Q analysis was carried by the following formula.

$$Z_{ij} = X_{ij} – X_j / S_{ij}$$

Where,

$$X_i = \sum_{i=1}^{n} X_{ij} / n$$

Where,

$$S_{ij} = \frac{\sum_{i=1}^{n} X_{ij} - X_j / n}{n-1}$$

For i = genotypes *i.e.,* 45 in this case

j = total variables *i.e.,* 13 in this case

The resulting data after standardization is unit less and have mean zero and variance one.

### 3.4.3.3 Computing the resemblance matrix

A resemblance coefficient, which measures the over all resemblance between a pair of genotypes was computed. Here 45 genotypes were taken in data matrix therefore resemblance coefficient was computed for total 990 combinations.

The data matrix was transformed to distance matrix (resemblance matrix) based on the dissimilarity coefficients using Squared Euclidean distance method.

$$\text{Squared Euclidean distance } (d_{ij}) = \sum_{K=1}^{P} (X_{ik} - X_{jk})^2$$

Where, P = Number of genotypes *i.e.*, 45

$X_{ik}$ = Value of $i^{th}$ genotype for k characters

$X_{jk}$ = Value of $j^{th}$ genotype for k characters

### 3.4.3.4 Execution of the clustering method

Distance matrix was converted into dendogram by using Ward's method where the distance between two clusters summed over all variables. At each stage in the clustering procedure, the within cluster sum of squares is minimized over all partitions obtained by combining two clusters from previous stage.

### 3.4. 4 Principal component analysis

Principal component analysis was carried out with the data collected from the plants according to Jackson (1991). A data matrix of all 45 genotypes over 13 variables of each genotype was prepared and used for analysis by SPSS computer programme.

A covariance matrix derived from the data matrix is converted to correlation matrix as suggested by Jackson (1991). The eigen value and eigen vector pairs correlated from data matrix is utilized to identify the principal components.

### 3.4. 4.1 Eigen values and eigen vectors

The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal components. The proportion of variation accounted for each Principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

$$\text{Per cent variance explained for } PC_1 = \frac{\text{eigen value } (PC_1)}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components.

The $j^{th}$ principal component ($Y_i$) of the observations X is the linear combination given as follow:

$$Y_j = A_{1j}X_1 + \ldots\ldots\ldots + A_{pj}X_p$$

Where,

$A_{ij}$ are found such that $Y_j$ is uncorrelated

$Y_1, Y_2 \ldots\ldots\ldots\ldots Y_{j-1}$ the $j^{th}$ largest variance.

The variance of the $j^{th}$ principal component of the $\lambda_j$ and the total system variance trace (S) = $\lambda_{1} + \lambda_{2} + \ldots + \lambda_{p}$.

The important of the $j^{th}$ principal component is given by

$$\frac{\lambda_1}{\text{Trace (S)}}$$

This is informative about the proportion of total variation that can be accounted for the $i^{th}$ principal component. The correlation between the $i^{th}$ original variable $X_i$ and the $j^{th}$ principal component $Y_j$ is given by

$$(X_i, Y_j) = \frac{A_{ij} \cdot \sqrt{\lambda_1}}{\sqrt{S_i}}$$

Where,

$S_i$ is the standard deviation of $X_i$

Thus, a principal component is linear function of the test variables given as follow

$$\text{Principal component} = ax_1 + bx_2 + \ldots\ldots\ldots + hx_8 .$$

Where, a,b,…. are coefficient and $x_1$, $x_2$ ………..etc., are the variables in such a way that the principal component has a unit variance as reported by Ehrenberg (1985).

PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D or 3D scatter diagram as plot of genotypes.

## 3.5 CORRELATION

Phenotypic and genotypic correlations were calculated by using covariance technique (Falconer, 1981).

### 3.5.1 Phenotypic coefficients of correlation ($r_p$)

$$r(x_i x_j)_p = \frac{Cov(x_i . x_j)_p}{\sqrt{V(x_i)_p . V(x_j)_p}}$$

Where,

$r(x_i,x_j)_p$ = Phenotypic correlation between i[th] and j[th] character.

$Cov(x_i,x_j)_p$ = Phenotypic correlation between i[th] and j[th] character.

$V(x_i)_p$ = Phenotypic variance for i[th] character.

$V(x_j)_p$ = Phenotypic variance for j[th] character.

### 3.5.2 Genotypic coefficients of correlation ($r_g$)

$$r(x_i x_j)_g = \frac{Cov(x_i . x_j)_g}{\sqrt{V(x_i)_g . V(x_j)_g}}$$

Where,

r (xi,xj)g = Genotypic correlation between i[th] and j[th] character.

Cov (xi,xj)g = Genotypic correlation between i[th] and j[th] character.

V(xi)g = Genotypic variance for i[th] character.

V(xj)g = Genotypic variance for j[th] character.

**Test of significance**

Significance of correlation coefficients was tested by comparing phenotypic genotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degree of freedom at 5% and 1% level where 'n' denotes the number of genotypes tested.

## 3.6 PATH COEFFICIENT ANALYSIS

Path coefficient analysis, suggested by Wright (1921) as elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contribution of various traits to yield.

For estimation of various direct and indirect effects, a set of simultaneous equations were formed

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots + r_{1k}P_{ky}$$

$$r_{2y} = r_{21} P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots\ldots + r_{2k}P_{ky}$$

$$r_{iy} = r_{i1} P_{1y} + P_{i2} P_{2y} + r_{i3}P_{3y} + \ldots\ldots + r_{ik}P_{ky}$$

$$r_{ky} = P_{k1} P_{1y} + P_{k2}P_{2y} + r_{k3}P_{3y} + \ldots\ldots + r_{kk}P_{ky}$$

$r_{1k}$ to $r_{ky,}$ k = coefficient of correlation among causal factors.

$P_{1y}$ to $P_{ky}$ = Direct effects of characters 1 to k on character y.

The above equations were written in a matrix from as under:

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ r_{ky} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{13} \ldots\ldots r_{1} \\ r_{21} & 1 & r_{23} \ldots\ldots r_{2} \\ \ldots\ldots\ldots & \ldots\ldots\ldots & \ldots\ldots\ldots \\ \ldots\ldots\ldots & \ldots\ldots\ldots & \ldots\ldots\ldots \\ r_{k1} & r_{k2} & r_{k3} \quad 1 \end{pmatrix} \times \begin{pmatrix} P_{1y} \\ P_{2y} \\ \vdots \\ P_{ky} \end{pmatrix}$$

$$\text{Where } (C)^{-1} \qquad \begin{pmatrix} C_{11} & C_{12} \ldots\ldots\ldots\ C_{1k} \\ C_{21} & C_{22} \ldots\ldots\ldots\ C_{2k} \\ C_{k1} & C_{k2} \ldots\ldots\ldots\ C_{kk} \end{pmatrix}$$

Then direct effects are calculated as follows.

$$P_1y \sum_{i=1}^{k} = C_{1i} \, . \, r_{iy}$$

$$P_2y \sum_{i=1}^{k} = C_{2i} \, . \, r_{iy}$$

$$P_{ky} \sum_{i=1}^{k} = C_{ki} \, . \, r_{iy}$$

### 3.6.1 Residual Effect

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effects measure the role of other possible independent variables which were not included in the study on the dependent variable. The residual effect is estimated with the help of direct effects and simple correlation coefficients.

$$I = P^2\ Ry + \sum P_{iy}\ r_{iy}$$

Where, $P^2\ R_y$ is the square of residual effect.

# CHAPTER – IV

# RESULTS

The data collected from 45 soybean genotypes on 13 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%), protein content (%), oil content (%) and seed yield per plant (g) were statistically analysed for the estimation of mean, range, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), heritability, genetic advance, genetic divergence, correlations and path analysis and character wise results are presented below.

## 4.1 ANALYSIS OF VARIANCE

Analysis of variance was carried out for all the 13 characters and presented in Table 8. The results indicated highly significant differences among the genotypes for all the characters studied. Replication difference was non-significant for all characters, except pod length.

### Means

The mean performance of 45 soybean genotypes for 13 characters was presented in the Table 9. The results indicated the presence of considerable variability among the genotypes for the all the characters studied. The estimates of mean, range, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), heritability, genetic advance as per cent of mean (GAM) were calculated and presented in the Table 10.

#### 4.1.1.1 Days to 50% flowering

The Mean values for days to 50% flowering ranged from 30.00 (VLS 70) to 46.00 (PS 1421) with a mean of 38.35 indicating considerable variability among the genotypes. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were moderate (11.18 and 10.89) for this trait. High heritability (94.88%) coupled with moderate genetic advance as per cent of mean (21.86) was recorded for this trait.

#### 4.1.1.2 Days to maturity

Days to maturity recorded a mean of 105.78 ranging from 81.00 (VLS 69) to 118.66 (AMS 4-63) showing considerable degree of variability among the genotypes. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were low (8.30 and 8.37) for this trait. High heritability (98.33%) coupled with high genetic advance as per cent of mean (16.97) was recorded for this trait.

#### 4.1.1.3 Plant height (cm)

The mean plant height ranged from 30.53cm (VLS 69) to 67.07cm (RKS 45) with a general mean of 50.38cm.

The phenotypic coefficient of variation and genotypic coefficient of variation were moderate (19.05 and 18.13) for this trait. High heritability (90.57%) coupled with high genetic advance as per cent of mean (35.54) was recorded for this trait.

#### 4.1.1.4 Number of branches per plant

Mean values of number of branches per plant ranged from 1.00 (RCS 1) and to 4.96 (RKS 18) with a mean of 2.51.

The phenotypic and genotypic coefficients of variation (31.92 and 30.56) were high for this trait. High heritability (91.63%) coupled with high genetic advance as per cent of mean (60.27) was recorded for this trait.

#### 4.1.1.5 Number of pods per plant

Mean values of number of pods per plant ranged from 12.35 (HIMSO 1608) to 49.57 (NSO 15) with a mean of 29.94 indicating considerable variability among the genotypes. The high phenotypic and genotypic coefficients of variation (38.19 and 37.26) were recorded for this trait. High heritability (95.20%) coupled with high genetic advance as per cent of mean (74.90) was recorded for this trait.

#### 4.1.1.6 Pod length (cm)

Mean of 3.21cm was recorded for this trait ranging from 1.26 cm (VLS 69) to 4.32 cm (JS 20-09) among the genotypes. Moderate phenotypic coefficient of variation (16.35) and genotypic coefficient of variation (15.79) was recorded for this trait. High heritability (93.19%) coupled with high genetic advance as per cent of mean (31.40) was recorded for this trait.

#### 4.1.1.7 Number of seeds per pod

Mean values for number of seeds per pod ranged from 1.00 (VLS 69) to 3.00 (NRC 77) with a mean of 2.35 indicating considerable differences among the genotypes studied. Phenotypic and genotypic coefficient of variation were moderate (18.57 and 15.50). High heritability (69.71%) coupled with high genetic advance as per cent of mean (26.66) was recorded for this trait.

#### 4.1.1.8 100 Seed weight (g)

Mean values for 100 seed weight ranged from 7.26 g (VLS 69) to 15.28 g (DSb 10) with a mean of 12.79 g indicating considerable differences among the genotypes studied. Phenotypic and genotypic coefficients of variation were moderate (13.90 and 12.76). High heritability (84.26%) coupled with high genetic advance as per cent of mean (24.13) was recorded for this trait.

#### 4.1.1.9 Biological yield per plant (g)

Mean values of biological yield per plant ranged from 12.30 g (RCS 1) to 33.42 g (NSO 15) with a mean of 21.18 g indicating considerable differences among the genotypes studied.

High phenotypic and genotypic coefficients of variation were recorded (23.98 and 22.10) for this trait. High heritability (84.97%) coupled with high genetic advance (41.97) was recorded for this trait.

#### 4.1.1.10 Harvest index (%)

The mean values of harvest index ranged from 19.63 (HIMSO 1608) to 51.85 (JS 20-09) with a mean of 36.57. The genotypic and phenotypic coefficients of variation (24.70 and 22.72) were high for this trait. High heritability (84.62%) coupled with high genetic advance as per cent of mean (43.07) was recorded for this trait.

#### 4.1.1.11 Protein content (%)

Mean values of protein content ranged from 33.52% (MACS 1148) to 41.55% (HIMSO 1609) with a mean of 37.83% indicating differences among the genotypes. The estimates of phenotypic and genotypic coefficient of variation (6.59 and 5.70) were low for this trait. High heritability (74.90%) coupled with moderate genetic advance as per cent of mean (10.17) was recorded for this trait.

#### 4.1.1.12 Oil content (%)

Mean values of oil content ranged from 18.00% (PS 1421) to 22.48% (NSO 78) with a general mean of 20.35% indicating differences among the genotypes.

The estimates of phenotypic and genotypic coefficient of variation (6.01 and 5.81) were low for this trait. High heritability (88.18 %) coupled with moderate genetic advance as per cent of mean (11.24) was recorded for this trait.

#### 4.1.1.13 Seed yield per plant (g)

High variability was recorded for this trait with a mean of 8.00 ranging from 3.34 (MACS 1148) to 14.99 (NSO 15) among the genotypes.

High phenotypic and genotypic coefficients of variation (40.44 and 38.51) were recorded for this character. High heritability (90.69%) coupled with high genetic advance as per cent of mean (75.55) was recorded for this trait.

## 4.2 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was carried out in 45 soybean genotypes for 13 characters studied in the present investigation by using Mahalanobis' $D^2$ statistic and principal component analysis.

### 4.2.1 Test with Wilk's Criterion

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes of all the characters were carried out by using the Wilk's criterion '$\Lambda$'. The Wilk's criterion thus obtained was used in calculations of 'V' statistic. The 'V' calculated statistic was highly significant (2807.10) at 572 d.f which was much more than the table value (around 197.05) revealing that genotypes differed significantly when the all characters were considered simultaneously.

### 4.2.2 Mahalanobis'$D^2$ Values

The correlated unstandardized means of 13 characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance ($D^2$) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes were considered at a time. Thus, the possible 990 combinations and the corresponding $D^2$ values are obtained for final grouping of the genotypes.

Since each genotype can produce 44 combinations with all other genotypes, 990 possible $D^2$ values were obtained. Based on these $D^2$ values, percentage contribution of different characters towards genetic divergence was presented in Table 12. Days to maturity showed maximum contribution (40.91%) towards genetic divergence followed by number of pods per plant (15.25%) and days to 50% flowering (12.73%). While the lowest contribution from the traits number of seeds per pod (0.00%), 100 seed weight (0.30%), protein content (0.51%), harvest index (0.91%), seed yield per plant (1.92%), biological yield per plant (3.03%), plant height (4.75%), number of branches per plant (5.96%), pod length (6.46%) and oil content (7.27%).

#### 4.2.2.1 Grouping of genotypes into various clusters

Tocher's method (Singh and Chaudhary, 1977) was followed to group the genotypes into different clusters, considering the estimated $D^2$ values as the squares of the generalized distance. The 45 genotypes were grouped into 6 clusters. The distribution of genotypes into 6 clusters is presented in the Table 11. The mutual relation ships between the clusters were represented diagrammatically by using the average intra-cluster and inter-cluster $D^2$ values.

### 4.2.2.2 Average Intra-and inter-cluster $D^2$ Values

The average intra-cluster and inter-cluster $D^2$ values estimated as per the procedure given by Singh and Choudhary (1977) were presented in the Table 13.

Based on the $D^2$ values, the 45 genotypes were grouped into 6 clusters. Cluster II showed maximum intra-cluster distance of 90.05 followed by cluster I (74.07). The clusters (Cluster III, IV, V, and VI) were solitary possessing single entries; they had no intra-cluster distances.

The inter-cluster distances varied from 102.759 (between cluster I and III) to 531.948 (between cluster III and VI)

Cluster I was the largest comprising of 29 genotypes. It was relatively closer to cluster III (102.759) followed by cluster V (147.143) and was farthest from cluster VI (460.209).

Cluster II was the second largest with 12 accessions and was nearest to cluster IV (150.635) and farthest to cluster VI (255.742).

Cluster III had solitary genotype (PS 1421) and was close to cluster I (102.759) and farthest to cluster VI (531.948) followed by cluster II (221. 821).

Cluster IV consisted of only one genotype (NSO 15). It was nearest to cluster II (150.635) followed by cluster I (151.847) and farthest from cluster VI (396.123).

Cluster V with solitary genotype (VLS 68) was close to the cluster I (147.143) followed by cluster III (162.417) and farthest to cluster VI (370.55).

Cluster VI comprised of only one genotype (VLS 69) and was close to cluster II (255.742) and farthest to cluster III (531.948).

**Table 11: Clustering pattern of 45 soybean genotypes during *Kharif*, 2007.**

| Cluster No | No.of genotypes | Genotypes |
|---|---|---|
| 1 | 29 | MACS 1126, MAUS 285, MAUS 295, SL 744, RCS 9, RCS 1, MACS 1148, NSO 78, SL 752, PS 1437, KDS 167-9, TS 94, AMS 4-4, LSb 23, DS 2402, AMS 99-33, SL 790, JS 335, DS 2410, JS 20-06, NSO 111, DSb 10, JS 20-09, NRC 77, RKS 45, AMS 4-63, MACS 1139, RKS 18, JS 93-05. |
| 2 | 12 | HIMSO 1608, NRC 78, Bragg, VLS 70, TS 56, DSb 12, HIMSO 1609, NRC 76, JS 20-01, JS(SH) 2001-04, PS 1433, RKS 48 |
| 3 | 1 | PS 1421 |
| 4 | 1 | NSO 15 |
| 5 | 1 | VLS 68 |
| 6 | 1 | VLS 69 |

**Table 12: Contribution of different characters towards genetic divergence among 45 soybean genotypes during *Kharif*, 2007.**

| S.No | Characters | Contribution towards divergence (%) | Rank |
|---|---|---|---|
| 1 | Days to 50% flowering | 12.73 | 3 |
| 2 | Days to maturity | 40.91 | 1 |
| 3 | Plant height (cm) | 4.75 | 7 |
| 4 | Branches/ plant | 5.96 | 6 |
| 5 | Pods/ plant | 15.25 | 2 |
| 6 | Pod length (cm) | 6.46 | 5 |
| 7 | seeds/ pod | 0.00 | 13 |
| 8 | 100 seed weight (g) | 0.30 | 12 |
| 9 | Biological yield (g) | 3.03 | 8 |
| 10 | Harvest Index (%) | 0.91 | 10 |
| 11 | Protein content (%) | 0.51 | 11 |
| 12 | Oil content (%) | 7.27 | 4 |
| 13 | Seed yield/plant (g) | 1.92 | 9 |

### 4.2.2.3. Clustering pattern in relation to geographic diversity

The constellations of genotypes into different clusters are furnished in Table 11. Distribution of genotypes into different clusters was at random and no relationship was observed between geographic origin and genetic diversity as the genotypes developed from different geographic regions were included in the same cluster.

### 4.2.2.4. Cluster Mean Values

Cluster means were computed for the 13 characters studied and reported in the Table 14.

Days to 50% flowering recorded mean values ranged from 30.66 for cluster VI to 46.00 for cluster III. Days to maturity recorded a range of 81.00 for cluster VI to 114.33 for cluster V. Plant height recorded a range of 30.53 cm for cluster VI to 51.97 cm for cluster I. Branches per plant showed a range of 2.00 for cluster III to 4.00 for cluster VI. Pods per plant recorded a range of 20.07 for cluster V to 49.57 for cluster IV. Pod length recorded a range of 1.26 cm for cluster VI to 3.53cm for cluster IV. Seeds per pod showed a range of 1.00 for cluster VI to 2.73 for cluster IV. 100 seed weight recorded a range of 7.26 g for cluster VI to 15.13 g for cluster IV. Biological yield per plant exhibited a range of 15.02 g for cluster VI to 33.42 g for cluster IV. Harvest index recorded a range of 21.66 % for cluster V to 44.57 % for cluster IV. Seed protein content showed a range of 35.10 % for cluster III to 41.45 % for cluster V. Oil content exhibited a range of 18.00 % for cluster III to 21.28 % for cluster VI. Seed yield per plant recorded a range of 3.49 g for cluster VI to 14.99 g for cluster IV.

### 4.2.3 Principal Component Analysis

The eigen values (variances), per cent variability, cumulative per cent variability and component loading of the different characters are given in Table 15 and the genotypic mean for the first three principal components are given in Table 16.

In the present studies, the first five components with eigen values more than one contributed 84.51 percent of cumulative variability amongst 45 soybean genotypes evaluated for 13 traits. The first principal component ($PC_1$) contributed maximum (38.02%) towards variability characters *viz* ., days to maturity (0.877), biological yield per plant (0.269), days to 50% flowering (0.175), oil content (0.161), 100 seed wt (0.158), pod length (0.151), pods per plant (0.112), harvest index (0.007), seeds per pod (-0.154), protein content (-0.091), branches per plant (-0.064), yield per plant (-0.063) and plant height (-0.036) explained the maximum variance in first principal component ($PC_1$). Positive correlation were observed for days to 50% flowering, days to maturity, pod per plant , pod length , 100 seed weight , biological yield per plant, harvest index and oil content, while plant height, branches per plant, seeds per pod, protein content and yield per plant were negatively correlated.

The second principal component ($PC_2$) which described 20.63 percent of total variance, third principal component ($PC_3$) 10.78 percent of total variance, forth principal component ($PC_4$) 8.77 percent of total variance and fifth principal component ($PC_5$) described 6.28 percent of total variance.

During *kharif* 2007, the 2D and 3D plot indicated the grouping of genotypes of same cluster nearer to each other and presented in fig 1 and fig 2. For example the genotypes AMS 4-4 and LSb 23 of cluster V fall nearer to each other. There are also indication that genotypes of different clusters falling nearer to each other *i.e* DSb 10 (cluster VI) and AMS 4-4 (cluster V), while the genotypes NSO 15, VLS 69, VLS 70 and NRC 78 fall away from other genotypes indicating their specificity in clustering.

### 4.2.4 Hierarchical cluster analysis

The extent of genetic diversity among the 45 genotypes studied during *kharif*, 2007 was assessed and the results presented here under.

#### 4.2.4.1 Grouping of genotypes into various clusters

Forty five genotypes were grouped into seven clusters using the Ward's minimum variance procedure (Anderberg, 1993) and the distributions of the genotypes into different clusters are presented in the Table 17.

The hierarchical cluster analysis of 45 soybean genotypes during *kharif* 2007 identified seven clusters. Cluster V had maximum number of genotypes *i.e* 18 and cluster IV had minimum number of genotypes only single genotype *i.e*

VLS 69 and the clusters VII, I, II, III,VI comprised 10,5,4,4 and 3 genotypes respectively.

### 4.2.4.2 Intra-cluster and inter-cluster distances

The Euclidean$^2$ values within (intra) and in between (inter) clusters were estimated and are presented in Table 18 for *kharif*, 2007. The cluster diagram showing mean intra and inter-cluster distances among seven clusters are given in figure 3 and 4.

The intra-cluster distances average ranged from 0.000 (cluster IV) to 195.030 (cluster II).The inter-cluster distances ranged from 265.477 (between cluster V and cluster VI) to 1394.821 (between cluster IV and cluster V).

Cluster I consists of 5 genotypes. It is closest to cluster II (326.576) and farthest to cluster IV (838.768).

Cluster II consists of 4 genotypes. It is closest to cluster I (326.576) followed by cluster III (344.670) and farthest to the cluster IV (676.664).

Cluster III consists of 4 genotypes. It is closest to cluster II (344.670) and farthest to the cluster IV (873.645).

Cluster IV consists of 1 genotype. It is closet to cluster II (676.644) and farthest to the cluster V (1394.821).

Cluster V is the largest cluster consists of 18 genotypes. It is closest to cluster VI (265.477) and farthest to the cluster IV (1394.821).

Cluster VI consists of 3 genotypes. It is closest to cluster VI (265.477) and farthest to the cluster IV (1340.391).

Cluster VII is the second largest cluster consists of 10 genotypes. It is closest to cluster V (295.939) and farthest to the cluster IV (1361.772).

#### 4.2.4.3 Cluster mean values of characters

The cluster means in respect of 13 characters are presented in Table 19. The grouping of 45 genotypes into different clusters was based on hierarchical cluster analysis. Days to 50% flowering varied from as low as 30.66 for cluster IV to as high as 45.00 for cluster VI. Days to maturity recorded as low as 81.00 for cluster IV and as high as 111.93 days for cluster VII. Plant height varies from 30.53cm for cluster IV to 53.41cm for cluster V. Number of branches per plant varied from 1.86 for cluster II to 4.00 for cluster IV. Numbers of pods per plant recorded high mean value for cluster I (45.21) and low mean value (15.21) for cluster III. Pod length varied from as low as 1.26 for cluster IV to as 3.45 for cluster III. Number of seeds per pod varied from 1.00 for cluster IV to as high as 2.53 for cluster III. Cluster IV recorded low mean for 100 seed weight value (7.26) where as high mean value of 14.05 by cluster III. For biological yield per plant, cluster I recorded high mean value (25.40) where as cluster III recorded low mean value (15.02). Cluster IV recorded high mean value (41.74) and low mean value (27.94) for cluster VII for harvest index. For protein content, cluster II showed low mean value (36.82) and cluster IV showed high mean value (41.25). For oil content, cluster VI showed low mean (18.63) and cluster IV showed high mean value

(21.28). Yield per plant varied from as low as 3.49 for cluster IV to as high as 11.06 for cluster I.

## 4.3 CORRELATION

The phenotypic and genotypic correlations between seed yield and other yield component characters and among themselves were estimated and presented in Table 20.

### 4.3.1 Days to 50% flowering

This trait showed significant positive correlation both at phenotypic and genotypic levels with days to maturity ($r_g$= 0.3222 and $r_P$= 0.3157) and 100 seed weight ($r_g$= 0.2928 and $r_P$= 0.2582), while this trait showed significant negative association with branches per plant ($r_g$= -0.2600 and $r_P$= -0.2395) and protein content ($r_g$= -0.2200 and $r_P$= -0.1913) at phenotypic and genotypic level. This trait also showed non-significant positive association with plant height, pods per plant, pod length, seeds per pod, biological yield per plant, harvest index and seed yield per plant and non-significant negative association with oil content ($r_g$= -0.0879 and $r_P$= - 0.0775).

### 4.3.2. Days to maturity

Days to maturity showed significant positive association with 100 seed weight ($r_g$= 0.3320 and $r_P$= 0.2987), pod length ($r_g$= 0.2732 and $r_P$= 0.2613) and seeds per pod ($r_g$= 0.2549 and $r_P$= 0.2252). A non-significant positive association with plant height ($r_g$= 0.1204 and $r_P$= 0.1172), number of branches per plant ($r_g$= 0.0558 and $r_P$= 0.0563), biological yield per plant ($r_g$= 0.0621 and $r_P$= 0.0472) and seed yield per plant ($r_g$= 0. 0889 and $r_P$= 0.0890) at both genotypic and phenotypic levels. While non-significant negative correlation was recorded with pods per plant ($r_g$= -0.1602 and $r_P$= -0.1596), oil content ($r_g$= -0.1361 and $r_P$= -0.1336) protein content ($r_g$= -0.1041 and $r_P$= -0.0866) and harvest index ($r_g$= -0.0348 and $r_P$= -0.0306).

### 4.3.3 Plant height (cm)

This character recorded significant positive correlation with seeds per pod ($r_g$= 0.3880 and $r_P$=0.2965), seed yield per plant ($r_g$= 0.3079 and $r_P$= 0.2913) biological yield per plant ($r_g$= 0.2834and $r_P$=0.2540), protein content ($r_g$= 0.3176 and $r_P$= 0.2409), 100 seed weight ($r_g$= 0.2131 and $r_P$= 0.1812), harvest index ($r_g$= 0.2117 and $r_P$= 0.1753), and pod length ($r_g$= 0.1942 and $r_P$= 0.1729) while non-significant positive correlation with branches per plant at phenotypic level ($r_P$= 0.1633) and significant positive correlation at genotypic level ($r_g$= 0.1730), oil content had negative non significant correlation with this trait at both genotypic and phenotypic level level ($r_g$= -0.0170 and $r_P$= -0.0285).

### 4.3.4 Number of branches per plant

This character recorded significant positive correlation with seed yield per plant ($r_g$= 0.2901and $r_P$= 0.2795), biological yield per plant ($r_g$= 0.2654 and $r_P$= 0.2384), harvest index ($r_g$= 0.2549 and $r_P$= 0.2270), pods per plant ($r_g$= 0.2447 and $r_P$= 0.2254), protein content ($r_g$= 0.2233 and $r_P$= 0.1710), while seeds per pod ($r_g$= 0.1338 and $r_P$= 0.1180), pod length ($r_g$= 0.0264 and $r_P$= 0.0161) showed non-significant positive correlation with this trait at both genotypic and phenotypic levels. However, the remaining characters, 100 seed weight ($r_g$= -0.1373 and $r_P$= -0.1171) and oil content ($r_g$= - 0.0346 and $r_P$= -0.0254) showed non-significant negative correlation at phenotypic and genotypic level.

### 4.3.5 Number of pods per plant

This trait showed a highly significant positive correlation with yield plant ($r_g$= 0.7801 and $r_P$= 0.7289), biological yield per plant ($r_g$= 0.7226 and $r_P$= 0.6442), harvest index ($r_g$= 0.5852 and $r_P$= 0.5318), pod length ($r_g$= 0.2196 and $r_P$= 0.2076) and seeds per pod ($r_g$= 0.2472 and $r_P$= 0.1965) both at phenotypic and genotypic levels. The traits, 100 seed weight ($r_g$= -0.1432 and $r_P$= -0.1332), protein content ($r_g$= -0.0148 and $r_P$= -0.0027) showed non-significant negative correlation and the trait, oil content showed significant negative correlation ($r_g$= -0.1728) at genotypic level and non-significant negative correlation at phenotypic level ($r_p$= -0.1458).

### 4.3.6 Pod length (cm)

This trait showed a highly significant positive correlation with seeds per pod ($r_g$= 0.8868 and $r_P$= 0.7412), 100 seed weight ($r_g$= 0.5632 and $r_P$= 0.5094), biological yield per plant ($r_g$= 0.3324 and $r_P$= 0.3138), yield per plant ($r_g$= 0.4021 and $r_P$= 0.3667). This trait protein recorded negative significant correlation ($r_g$= -0.3341 and $r_P$= -0.2664) with protein content, while positive non-significant correlation with oil content ($r_g$= 0.1132 and $r_P$= 0.1105) and harvest index ($r_g$=0.0743 and $r_P$= 0.0459)

### 4.3.7 Number of seeds per pod

This trait showed significant positive correlation with 100 seed weight ($r_g$= 0.6253 and $r_P$= 0.4695), yield per plant ($r_g$= 0.4812 and $r_P$= 0.3986) and biological yield per plant ($r_g$= 0.4696 and $r_P$= 0.3698). However Positive non-significant correlation was also recorded with harvest index ($r_g$= 0.1662 and $r_P$= 0.1386). Negative significant correlation with protein content ($r_g$= -0.2372 and $r_P$= -0.1760) while observed and non significant negative correlation with oil content ($r_g$= -0.0372 and $r_P$= -0.0171).

### 4.3.8 100 seed weight(g)

This trait has significant positive correlation with yield per plant ($r_g$= 0.2444 and $r_P$= 0.2339) at both genotypic and phenotypic levels while biological yield shows significant positive correlation ($r_g$= 0.1984) at genotypic level and positive non-significant correlation at phenotypic level ($r_P$= 0.1386). However, harvest index shows non-significant positive correlation ($r_g$= 0.0657 and $r_P$= 0.0436) at both genotypic and phenotypic levels

Protein content shows significant negative correlation at genotypic level ($r_g$= -0.2131) and non-significant negative correlation at phenotypic level ($r_P$= -0.1671). The character oil content recorded non-significant negative correlation with this trait ($r_g$= -0.0028) and ($r_p$= - 0.0317) at both genotypic and phenotypic levels.

### 4.3.9 Biological yield per plant(g)

At phenotypic and genotypic levels, this trait exhibited high significant positive correlation with seed yield per plant ($r_g$= 0.8939 and $r_P$= 0.7854) and harvest index ($r_g$= 0.3705 and $r_P$= 0.3146) while the trait, protein content ($r_g$=0.0421 and $r_P$=0.0126) and oil content ($r_g$= -0.0588 and $r_P$= -0.0504) at both the levels exhibited non-significant positive and negative correlations respectively.

### 4.3.10 Harvest index (%)

This trait showed a high significant positive correlation with seed yield per plant ($r_g$= 0.6998 and $r_P$= 0.5891) and non-significant negative correlation with protein content ($r_g$= -0.0564 and $r_P$= -0.0799) and oil content ($r_g$= -0.1084 and $r_P$= - 0.0713) at both levels.

### 4.3.11 Protein content (%)

This trait exhibited non-significant positive correlation with seed yield per plant ($r_g$= 0.0555 and $r_P$=0.0504) and non-significant negative correlation with oil content ($r_g$= -0.0710 and $r_P$= -0.0624).

### 4.3.12 Oil content (%)

A non-significant negative correlation was exhibited by this trait with seed yield per plant ($r_g$= -0.0725 and $r_P$= -0.0820).

**Table 17 : Clustering pattern of 45 soybean genotypes as per hierarchical cluster analysis**

| Cluster | Number of Genotypes | Genotypes |
|---|---|---|
| I | 5 | JS(SH) 2001-04, RKS 48, DSb 12, NRC 76, NSO 15 |
| II | 4 | JS 20-01, PS 1433, HIMSO 1609, TS 56 |
| III | 4 | HIMSO 1608, NRC 78, Bragg, VLS 70 |
| IV | 1 | VLS 69 |
| V | 18 | LSb 23, AMS 4-4, DS 2410, JS 20-09, PS 1437, SL 752, JS 20-06, RKS 45, DS 24-04, AMS 99-33, RKS 18, SL 790, JS 93-05, AMS 4-63, JS 335,TS94, NRC 77, MACS 1139 |
| VI | 3 | DSb 10, NSO 111, PS 1421 |
| VII | 10 | MACS 1126, MAUS 285, MAUS 295, RCS 1, RCS 9, SL 744, MACS 1148, NSO 78, VLS 68, KDS 167-9 |

## 4.4 PATH COEFFICIENT ANALYSIS

The correlation studies do not project a complete picture especially when the casual factors are interrelated. Such inter-dependence of the contributory factors often affects their direct relationship with yield there by making correlation coefficients unreliable as selection indices. Path coefficient analysis permits the separation of direct effect from the indirect effects through other related characters by partitioning correlation coefficients. The direct and indirect effects of yield components on yield were given in Table 21 and presented here under character wise. A path diagram showing cause and effect relationship was presented in Fig.5

### 4.4.1 Days to 50% flowering

Days to 50% flowering showed negative direct effect (-0.0591) on seed yield per plant. The negative indirect effect were manifested via protein content (-0.0205), branches per plant (-0.0049) and oil content (-0.0016). This trait also showed positive indirect effect via biological yield /plant (0.0508), 100 seed weight (0.0468), days to maturity (0.0274), pods/plant (0.0115), harvest index (0.0100), pod length (0.0025), seeds per pod (0.0004) and plant height (0.0002) and finally resulted in positive phenotypic correlation (0.0634) with seed yield per plant.

### 4.4.2 Days to maturity

This trait exhibited positive direct effect (0.0868) on seed yield per plant. The positive indirect effects were manifested via 100 seed weight (0.0541), biological yield per plant (0.0209), pod length (0.0148), seeds per pod (0.0014), branches per plant (0.0012) and plant height (0.0006) and these were counter balanced by negative indirect effects of pods per plant (-0.0515), days 50% flowering (-0.0187), protein content (-0.0093), harvest index (-0.0085) and oil content (-0.0028) which finally resulted in positive phenotypic correlation (0.0890) with seed yield per plant.

### 4.4.3 Plant height (cm)

Plant height showed positive direct effect (0.0048) on seed yield. The positive indirect effects were manifested via biological yield per plant (0.1122), harvest index (0.0485), pods per plant (0.0447), 100 seed weight (0.0328), protein content (0.0258), days to maturity (0.0102), pod length (0.0098), branches per plant (0.0034) and seeds per pod (0.0019) and these were counter balanced by negative indirect effects of days to 50% flowering (-0.0022) and oil content (-0.0006) which could finally resulted in positive phenotypic correlation (0.2913) with seed yield per plant.

### 4.4.4 Number of branches per plant

This trait observed positive direct effect (0.0206) on seed yield per plant. Negative indirect effects were manifested through 100 seed weight (-0.0212) and oil content (-0.0005) and these were cancelled by positive indirect effects of biological yield per plant ((0.1053), pods per plant (0.0726), harvest index (0.0628), protein content (0.0183), days to 50% flowering (0.0142) days to maturity (0.0049), pod length (0.0009), plant height (0.0008) and seeds per pod (0.0007) which finally resulted in positive phenotypic correlation (0.2795) with seed yield per plant.

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### 4.4.5. Number of pods per plant

Number of pods per plant showed positive direct effect (0.3223) on seed yield per plant. Positive indirect effects were recorded through biological yield per plant (0.2846), harvest index (0.1471), pod length (0.0117), branches per plant (0.0047), seeds per pod (0.0012), plant height (0.0007) and negative indirect effects through 100 seed weight (-0.0241), days to maturity (-0.0139), oil content (-0.0031), days to 50% flowering(-0.0021) protein content (-0.0003) which finally resulted in positive phenotypic correlation (0.7289) with seed yield per plant.

### 4.4.6 Pod length (cm)

Positive direct effect (0.0565) was exhibited by pod length on seed yield per plant. The positive indirect effects were manifested through biological yield per plant (0.1386), 100 seed weight (0.0923), pods per plant (0.0669), days to maturity (0.0227), harvest index (0.0127), seeds per pod (0.0047), oil content (0.0023), plant height (0.0008) and branches per plant (0.0003) and negative indirect effect were manifested through protein content (-0.0285) and days to 50% flowering (-0.0026) resulting in positive phenotypic correlation (0.3667) with seed yield per plant.

### 4.4.7 Number of seeds per pod

This trait showed positive direct effect (0.0063) on seed yield per plant. Positive indirect effects were manifested through biological yield per plant (0.1634), 100 seed weight (0.0851), pods per plant (0.0633), pod length (0.0419), harvest index (0.0383), days to maturity (0.0195), branches per plant (0.0024) and plant height (0.0014) and these were counter balanced by negative indirect effects of protein (-0.0188), days to 50% flowering (-0.0039) and oil content (-0.0004) which finally resulted positive phenotypic correlation (0.3986) with seed yield per plant.

### 4.4.8 100 seed weight (g)

This trait showed positive direct effect (0.1812) on seed yield. Positive indirect effects were manifested through biological yield per plant (0.0612), pod length (0.0288), days to maturity (0.0259), harvest index (0.0121), seeds per pod (0.0030), plant height (0.0009) and these were counter balanced by negative indirect effects of pods per plant (-0.0429), protein content (-0.0179), days to 50%flowering (-0.0153), branches per plant (-0.0024), oil content (-0.0007) resulted positive phenotypic correlation (0.2339) with seed yield per plant.

### 4.4.9. Biological yield per plant (g)

This trait exhibited high positive direct effect (0.4418) on seed yield. The negative indirect effect were manifested through days to 50% flowering (-0.0068) and oil content (-0.0011) and these were neutralized through positive indirect effect of pods per plant (0.2077), harvest index (0.0870), 100 seed weight (0.0251), pod length (0.0177), branches per plant (0.0049), days to maturity (0.0041), seeds per pod (0.0023), protein content (0.0013) and plant height (0.0012) resulted in positive phenotypic correlation (0.7854) with seed yield per plant.

### 4.4.9 Harvest index (%)

This trait showed positive direct effect (0.2767) on seed yield. The positive indirect effects were manifested through pods per plant (0.1714), biological yield per plant (0.1390), 100 seed weight (0.0079), branches per plant (0.0047), pod length (0.0026), seeds per pod (0.0009) and plant height (0.0008) and these were nullified by negative indirect effects of the protein content (-0.0086), days to maturity (-0.0027), days to 50% flowering (-0.0021), oil content (-0.0015) finally resulted in positive phenotypic correlation (0.5891) with seed yield per plant.

### 4.4.11 Protein content (%)

Positive direct effect was observed by the protein content (0.1070) on seed yield per plant. Negative indirect effect were manifested through 100 seed weight (-0.0303), harvest index (-0.0221), pod length (-0.0150), days to maturity (-0.0075), oil content (-0.0013), seeds per pod (-0.0011) and pods per plant (-0.0009) and these effects are counter balanced through positive indirect effects of days to 50% flowering (0.0113), biological yield per plant (0.0056), branches per plant (0.0035) and plant height (0.0012) finally resulted in positive phenotypic correlation (0.0504) with seed yield per plant.

### 4.4.12 Oil content (%)

Oil content showed positive direct effect (0.0210) on seed yield per plant. Negative indirect effects were manifested through pods per plant (-0.0470), biological yield per plant (-0.0223), harvest index (-0.0197) days to maturity (-0.0116), protein content (-0.0067), 100 seed weight (-0.0057), branches per plant (-0.0005) and seeds per pod (-0.0001). These effects were counter balanced through positive indirect effects of pod length (0.0062) and days to 50% flowering (0.0046) and finally resulted in negative phenotypic correlation (-0.0820) with seed yield per plant.

**Table 19: Mean Values of hierarchical clusters (Ward's method) of 45 soybean genotypes**

| S.No | characters | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|---|
| 1 | Days to 50% flowering | 35.133 | 41.167 | 31.417 | 30.667 | 38.000 | 45.000 | 41.033 |
| 2 | Days to maturity | 95.400 | 92.333 | 99.917 | 81.000 | 110.593 | 107.778 | 111.933 |
| 3 | Plant height (cm) | 52.518 | 45.865 | 51.283 | 30.530 | 53.413 | 46.844 | 48.379 |
| 4 | Branches/ plant | 2.720 | 1.867 | 2.400 | 4.000 | 2.850 | 2.156 | 2.093 |
| 5 | Pods/ plant | 45.213 | 27.132 | 15.218 | 24.990 | 34.382 | 38.872 | 19.178 |
| 6 | Pod length (cm) | 3.409 | 3.109 | 3.457 | 1.267 | 3.375 | 3.036 | 3.024 |
| 7 | Seeds/ pod | 2.487 | 2.233 | 2.533 | 1.000 | 2.463 | 2.400 | 2.180 |
| 8 | 100 seed wt (g) | 12.127 | 12.333 | 14.050 | 7.267 | 12.865 | 13.983 | 12.886 |
| 9 | Biological yield /plant (g) | 25.400 | 19.779 | 15.355 | 15.023 | 23.438 | 24.722 | 17.488 |
| 10 | Harvest index (%) | 40.977 | 36.847 | 28.036 | 41.740 | 41.192 | 39.647 | 27.945 |
| 11 | Protein content (%) | 38.903 | 36.827 | 37.582 | 41.250 | 37.699 | 38.290 | 37.570 |
| 12 | Oil content (% ) | 19.973 | 20.841 | 20.504 | 21.280 | 20.540 | 18.639 | 20.396 |
| 13 | Seed yield/plant (g) | 11.067 | 6.627 | 4.261 | 3.490 | 9.967 | 9.750 | 4.929 |

**Table 8: Analysis of variance for yield and yield attributing characters of 45 soybean genotypes during *kharif* , 2007**

| | | Mean squares | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Source | df | Days to 50% flowering | Days to maturity | Plant height (cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight (g) | Biological Yield (g) | Harvest index (%) | Protein content (%) | Oil content (%) | Seed yield/ plant (g) |
| Replications | 2 | 1.155 | 1.118 | 7.726 | 0.061 | 8.223 | 0.055** | 0.057 | 0.152 | 4.736 | 2.901 | 2.029 | 0.121 | 1.154 |
| Treatments | 44 | 53.35** | 233.03** | 259.12** | 1.832** | 380.05** | 0.789** | 0.456** | 8.501** | 69.705** | 219.91** | 15.547** | 4.390** | 29.511** |
| Error | 88 | 0.943 | 1.307 | 8.687 | 0.054 | 6.284 | 0.018 | 0.057 | 0.498 | 3.880 | 12.55 | 1.562 | 0.187 | 0.976 |

**** Significant at 1% level**

**Table 13 : Average intra-and inter-cluster $D^2$ values among 13 characters for 45 soybean genotypes during *Kharif*, 2007.**

| Cluster number | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | **74.079** | 150.965 | 102.759 | 151.847 | 147.143 | 460.209 |
| II | | **90.051** | 221.821 | 150.635 | 234.874 | 255.742 |
| III | | | ----- | 163.865 | 162.417 | 531.948 |
| IV | | | | ---- | 274.637 | 396.123 |
| V | | | | | ---- | 370.550 |
| VI | | | | | | ---- |

Values in the bold indicate intra-cluster distances
'-' Single genotype in particular cluster.

**Table 20: Estimates of phenotypic and genotypic correlation coefficient between yield and yield components in 45 soybean genotypes**

| Characters | Days to maturity | Plant height (cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight (g) | Biological yield/ plant (g) | Harvest index (%) | Protein content (%) | Oil content (%) | Yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 0.3157** **(0.3222)** | 0.0364 **(0.0380)** | -0.2395** **(-0.2600)** | 0.0356 **(0.0345)** | 0.0441 **(0.0439)** | 0.0664 **(0.0731)** | 0.2582** **(0.2928)** | 0.1151 **(0.1177)** | 0.0361 **(0.0281)** | -0.1913* **(-0.2200)** | -0.0775 **(-0.0879)** | 0.0634 **(0.0669)** |
| Days to maturity | | 0.1172 **(0.1204)** | 0.0563 **(0.0558)** | -0.1596 **(-0.1602)** | 0.2613** **(0.2732)** | 0.2252** **(0.2549)** | 0.2987** **(0.3320)** | 0.0472 **(0.0621)** | -0.0306 **(-0.0348)** | -0.0866 **(-0.1041)** | -0.1336 **(-0.1361)** | 0.0890 **(0.0889)** |
| Plant height (cm) | | | 0.1633 **(0.1730)** | 0.1386 **(0.1430)** | 0.1729* **(0.1942)** | 0.2965** **(0.3880)** | 0.1812* **(0.2131)** | 0.2540** **(0.2834)** | 0.1753* **(0.2117)** | 0.2409** **(0.3176)** | -0.0285 **(-0.0170)** | 0.2913** **(0.3079)** |
| Branches/ plant | | | | 0.2254** **(0.2447)** | 0.0161 **(0.0264)** | 0.1180 **(0.1338)** | -0.1171 **(-0.1373)** | 0.2384** **(0.2654)** | 0.2270** **(0.2549)** | 0.1710* **(0.2233)** | -0.0254 **(-0.0346)** | 0.2795** **(0.2901)** |
| Pods/ plant | | | | | 0.2076* **(0.2196)** | 0.1965* **(0.2472)** | -0.1332 **(-0.1432)** | 0.6442** **(0.7226)** | 0.5318** **(0.5852)** | -0.0027 **(-0.0148)** | -0.1458 **(-0.1728)** | 0.7289** **(0.7801)** |
| Pod length (cm) | | | | | | 0.7412** **(0.8868)** | 0.5094** **(0.5632)** | 0.3138** **(0.3324)** | 0.0459 **(0.0743)** | -0.2664** **(-0.3341)** | 0.1105 **(0.1132)** | 0.3667** **(0.4021)** |
| Seeds/ pod | | | | | | | 0.4695** **(0.6253)** | 0.3698** **(0.4696)** | 0.1386 **(0.1662)** | -0.1760* **(-0.2372)** | -0.0171 **(-0.0372)** | 0.3986** **(0.4812)** |
| 100 Seed weight (g) | | | | | | | | 0.1386 **(0.1984)** | 0.0436 **(0.0657)** | -0.01671 **(-0.2131)** | -0.0317 **(-0.0028)** | 0.2339** **(0.2444)** |
| Biological yield / plant (g) | | | | | | | | | 0.3146** **(0.3705)** | 0.0126 **(0.0421)** | -0.0504 **(-0.0588)** | 0.7854** **(0.8939)** |
| Harvest index (%) | | | | | | | | | | -0.0799 **(-0.0564)** | -0.0713 **(-0.1084)** | 0.5891** **(0.6998)** |
| Protein content (%) | | | | | | | | | | | -0.0624 **(-0.0710)** | 0.0504 **(0.0555)** |
| Oil content (%) | | | | | | | | | | | | -0.0820 **(-0.0725)** |

* Significant at 5% level ** Significant at 1% level Values in the parenthesis are genotypic correlation coefficients

**Table 15 : Eigen values, percent and cumulative variance, factors loading of different characters in soybean**

| | $PC_1$ | $PC_2$ | $PC_3$ | $PC_4$ | $PC_5$ |
|---|---|---|---|---|---|
| Eigen Value (Root) | 1063.076 | 576.865 | 301.570 | 245.430 | 175.795 |
| % Variance Explained | 38.025 | 20.634 | 10.787 | 8.779 | 6.288 |
| Cum. Variance Explained | 38.025 | 58.658 | 69.445 | 78.224 | 84.512 |
| Days to 50% flowering | 0.175 | 0.108 | 0.827 | 0.064 | 0.212 |
| Days to maturity | 0.877 | 0.098 | -0.217 | -0.126 | 0.085 |
| Plant height (cm) | -0.036 | -0.142 | -0.061 | 0.414 | 0.605 |
| Branches/ plant | -0.064 | -0.230 | -0.375 | -0.202 | 0.274 |
| Pods/ plant | 0.112 | -0.646 | 0.168 | -0.287 | -0.059 |
| Pod length (cm) | 0.151 | -0.276 | -0.125 | 0.570 | -0.448 |
| Seeds/ pod | -0.154 | -0.091 | 0.028 | 0.202 | -0.001 |
| 100 seed wt (g) | 0.158 | -0.017 | 0.150 | 0.314 | 0.002 |
| Biological yield/plant(g) | 0.269 | -0.322 | 0.080 | -0.090 | 0.130 |
| Harvest index (%) | 0.007 | -0.277 | -0.076 | 0.189 | 0.049 |
| Protein content (%) | -0.091 | -0.032 | -0.108 | 0.030 | 0.526 |
| Oil content (%) | 0.161 | 0.243 | -0.142 | 0.394 | 0.078 |
| Seed yield/plant (g) | -0.063 | -0.404 | 0.118 | 0.144 | -0.023 |

**Table 10 : Variability, heritability and genetic advance for yield and yield components of 45 soybean genotypes during *kharif*, 2007.**

| S.No | Characters | Mean ± SEM | Range | | PCV (%) | GCV (%) | $h^2$ (b) (%) | GAM |
|---|---|---|---|---|---|---|---|---|
| | | | Min | Max | | | | |
| 1 | Days to 50% flowering | 38.35 ± 0.55 | 30.00 | 46.00 | 11.18 | 10.89 | 94.88 | 21.86 |
| 2 | Days to maturity | 105.78 ± 0.65 | 81.00 | 118.66 | 8.37 | 8.30 | 98.33 | 16.97 |
| 3 | Plant height (cm) | 50.38 ± 1.68 | 30.53 | 67.07 | 19.05 | 18.13 | 90.57 | 35.54 |
| 4 | Branches/ plant | 2.51 ± 0.13 | 1.00 | 4.96 | 31.92 | 30.56 | 91.63 | 60.27 |
| 5 | Pods/ plant | 29.94 ± 1.43 | 12.35 | 49.57 | 38.19 | 37.26 | 95.20 | 74.90 |
| 6 | Pod length (cm) | 3.21 ± 0.07 | 1.26 | 4.32 | 16.35 | 15.79 | 93.19 | 31.40 |
| 7 | Seeds/ pod | 2.35 ± 0.13 | 1.00 | 3.00 | 18.57 | 15.50 | 69.71 | 26.66 |
| 8 | 100 seed weight (g) | 12.79 ± 0.40 | 7.26 | 15.28 | 13.90 | 12.76 | 84.26 | 24.13 |
| 9 | Biological yield/plant (g) | 21.18 ± 1.12 | 12.30 | 33.42 | 23.98 | 22.10 | 84.97 | 41.97 |
| 10 | Harvest index (%) | 36.57 ± 2.02 | 19.63 | 51.85 | 24.70 | 22.72 | 84.62 | 43.07 |
| 11 | Protein content (%) | 37.83 ± 0.71 | 33.52 | 41.55 | 6.59 | 5.70 | 74.90 | 10.17 |
| 12 | Oil content (%) | 20.35 ± 0.24 | 18.00 | 22.48 | 6.01 | 5.81 | 88.18 | 11.24 |
| 13 | Seed yield/plant (g) | 8.00 ± 0.56 | 3.34 | 14.99 | 40.44 | 38.51 | 90.69 | 75.55 |

PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; $h^2$(b) = Heritability;
GAM = Genetic advance as percent of mean

**Table 9: Performance of 45 soybean genotypes for 13 characters during *Kharif* , 2007.**

| No | Character | Days to 50% flowering | Days to maturity | Plant height (cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight (g) | Biological yield/ plant (g) | Harvest index (%) | Protein content (%) | Oil content (%) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | JS(SH) 2001-04 | 39.66 | 93.66 | 57.66 | 2.13 | 47.33 | 3.36 | 2.40 | 11.46 | 23.21 | 46.82 | 41.04 | 19.34 | 10.96 |
| 2 | LSb 23 | 38.00 | 109.00 | 55.00 | 2.80 | 34.00 | 3.67 | 2.66 | 14.69 | 24.52 | 40.50 | 39.01 | 22.07 | 10.00 |
| 3 | VLS 70 | 30.00 | 102.00 | 33.93 | 1.33 | 15.25 | 3.46 | 2.20 | 14.43 | 13.15 | 31.92 | 34.05 | 21.32 | 4.17 |
| 4 | DSb- 10 | 45.00 | 104.33 | 45.00 | 1.86 | 40.05 | 3.03 | 2.40 | 15.28 | 23.69 | 36.93 | 38.66 | 18.64 | 8.82 |
| 5 | PS 1437 | 37.00 | 105.33 | 48.60 | 2.66 | 33.30 | 3.14 | 2.20 | 11.48 | 26.21 | 28.85 | 36.35 | 21.58 | 7.70 |
| 6 | NSO 111 | 44.00 | 106.00 | 63.00 | 2.60 | 38.67 | 3.04 | 2.60 | 14.60 | 24.07 | 45.52 | 41.11 | 19.27 | 11.03 |
| 7 | DS 2402 | 45.00 | 109.66 | 61.00 | 3.60 | 34.50 | 3.18 | 2.33 | 11.86 | 22.71 | 34.65 | 34.07 | 20.00 | 8.03 |
| 8 | SL 752 | 37.00 | 109.66 | 52.00 | 1.86 | 30.98 | 3.15 | 2.46 | 13.16 | 25.55 | 31.81 | 37.63 | 22.42 | 8.18 |
| 9 | JS 20 - 01 | 40.00 | 86.66 | 54.06 | 1.60 | 37.76 | 2.91 | 2.26 | 11.13 | 25.44 | 33.94 | 36.66 | 20.67 | 8.82 |
| 10 | DSb 12 | 34.66 | 96.00 | 42.00 | 1.93 | 38.88 | 3.44 | 2.43 | 11.53 | 22.61 | 40.22 | 38.85 | 21.02 | 9.23 |
| 11 | MACS 1126 | 42.00 | 109.66 | 47.00 | 1.60 | 19.86 | 3.20 | 2.33 | 14.96 | 20.21 | 33.00 | 36.71 | 19.09 | 6.72 |
| 12 | PS 1421 | 46.00 | 113.00 | 32.53 | 2.00 | 37.89 | 3.03 | 2.20 | 12.06 | 26.40 | 35.43 | 35.10 | 18.00 | 9.40 |
| 13 | KDS 167- 9 | 41.00 | 117.33 | 57.06 | 3.20 | 18.32 | 3.52 | 2.73 | 12.40 | 22.22 | 19.82 | 40.15 | 19.88 | 4.36 |
| 14 | MAUS 285 | 44.66 | 110.33 | 57.80 | 1.46 | 21.00 | 3.12 | 2.33 | 14.17 | 20.37 | 25.55 | 36.39 | 19.19 | 5.40 |
| 15 | HIMSO 1608 | 31.00 | 96.66 | 55.40 | 2.53 | 12.35 | 3.55 | 2.60 | 15.03 | 18.72 | 19.63 | 39.19 | 20.90 | 3.71 |
| 16 | DS 2410 | 35.33 | 106.00 | 43.93 | 2.06 | 40.99 | 3.51 | 2.46 | 12.26 | 22.66 | 45.31 | 35.35 | 21.06 | 10.32 |
| 17 | NSO 78 | 41.00 | 114.33 | 50.00 | 2.80 | 23.12 | 3.77 | 2.66 | 13.73 | 22.25 | 27.45 | 36.69 | 22.48 | 6.31 |
| 18 | AMS 4-4 | 38.66 | 110.00 | 50.33 | 3.06 | 31.71 | 3.46 | 2.40 | 14.20 | 25.32 | 40.90 | 35.83 | 19.37 | 10.31 |
| 19 | PS 1433 | 44.00 | 93.33 | 33.40 | 2.53 | 37.80 | 3.38 | 2.40 | 13.80 | 21.97 | 43.71 | 34.66 | 21.68 | 9.65 |

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| No | Character | Days to 50% flowering | Days to maturity | Plant height (cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight (g) | Biological yield/ plant (g) | Harvest index (%) | Protein content (%) | Oil content (%) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 20 | NRC 78 | 33.00 | 97.66 | 56.80 | 3.46 | 15.99 | 3.12 | 2.66 | 13.20 | 15.32 | 28.32 | 38.27 | 19.28 | 4.37 |
| 21 | JS 20-06 | 38.00 | 103.33 | 60.00 | 2.53 | 44.33 | 3.34 | 2.26 | 12.20 | 24.28 | 43.73 | 37.62 | 21.46 | 10.67 |
| 22 | MAUS 295 | 43.66 | 114.00 | 61.00 | 2.26 | 19.00 | 2.82 | 2.33 | 14.40 | 14.12 | 36.41 | 38.85 | 20.53 | 5.17 |
| 23 | MACS 1148 | 41.00 | 113.66 | 32.00 | 2.26 | 14.98 | 3.29 | 2.40 | 11.93 | 15.57 | 21.24 | 33.52 | 21.10 | 3.34 |
| 24 | HIMSO 1609 | 40.00 | 92.66 | 43.00 | 1.86 | 15.95 | 2.88 | 1.86 | 11.83 | 18.20 | 21.63 | 41.55 | 20.35 | 3.99 |
| 25 | TS 94 | 38.00 | 115.33 | 59.06 | 2.73 | 30.60 | 2.88 | 2.13 | 14.20 | 22.41 | 42.42 | 38.08 | 20.32 | 9.56 |
| 26 | NRC 77 | 38.66 | 114.33 | 62.06 | 2.60 | 22.66 | 2.98 | 3.00 | 14.80 | 28.26 | 48.40 | 39.95 | 20.09 | 13.90 |
| 27 | SL 790 | 36.00 | 115.66 | 41.73 | 2.20 | 30.22 | 3.25 | 2.33 | 10.86 | 17.19 | 35.81 | 41.22 | 18.38 | 6.27 |
| 28 | AMS 4- 63 | 39.00 | 118.66 | 54.86 | 3.46 | 41.06 | 3.77 | 2.73 | 12.66 | 23.25 | 44.56 | 39.28 | 20.94 | 10.31 |
| 29 | RCS 9 | 42.33 | 107.33 | 44.93 | 1.33 | 18.05 | 3.00 | 2.26 | 11.53 | 14.12 | 28.51 | 36.39 | 21.58 | 4.03 |
| 30 | NRC 76 | 35.00 | 94.66 | 51.33 | 3.46 | 42.07 | 3.22 | 2.26 | 12.00 | 22.11 | 45.40 | 41.16 | 21.80 | 10.05 |
| 31 | SL 744 | 41.66 | 106.00 | 44.00 | 2.13 | 22.98 | 2.99 | 2.13 | 13.22 | 18.32 | 30.46 | 37.75 | 21.62 | 5.73 |
| 32 | VLS 69 | 30.66 | 81.00 | 30.53 | 4.00 | 24.99 | 1.26 | 1.00 | 7.26 | 15.02 | 23.55 | 41.25 | 21.28 | 3.49 |
| 33 | RKS 45 | 37.00 | 104.66 | 67.07 | 2.66 | 46.00 | 2.60 | 2.06 | 11.00 | 24.36 | 41.51 | 38.62 | 20.17 | 10.11 |
| 34 | JS 20-09 | 37.33 | 107.00 | 54.00 | 2.33 | 40.25 | 4.32 | 2.83 | 13.40 | 24.67 | 51.85 | 38.83 | 20.18 | 12.74 |
| 35 | TS 56 | 40.66 | 96.66 | 53.00 | 1.46 | 17.01 | 3.26 | 2.40 | 12.56 | 13.50 | 29.80 | 34.44 | 20.66 | 4.05 |
| 36 | VLS 68 | 31.66 | 114.33 | 46.00 | 2.86 | 20.07 | 1.90 | 1.33 | 8.73 | 15.40 | 23.11 | 41.45 | 18.08 | 3.56 |
| 37 | RKS 48 | 31.66 | 93.33 | 63.00 | 2.53 | 48.21 | 3.48 | 2.60 | 10.50 | 25.64 | 39.05 | 35.65 | 19.57 | 10.09 |
| 38 | MACS 1139 | 37.33 | 112.66 | 60.00 | 3.26 | 14.50 | 3.42 | 2.26 | 13.36 | 26.16 | 46.78 | 40.48 | 22.47 | 12.30 |
| 39 | RCS 1 | 41.33 | 112.33 | 44.00 | 1.00 | 14.40 | 2.60 | 1.26 | 13.76 | 12.30 | 37.11 | 37.80 | 20.39 | 4.64 |
| 40 | NSO 15 | 34.66 | 99.33 | 48.60 | 3.53 | 49.57 | 3.53 | 2.73 | 15.13 | 33.42 | 44.90 | 37.81 | 18.13 | 14.99 |

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| No | Character | Days to 50% flowering | Days to maturity | Plant height (cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight (g) | Biological yield/ plant (g) | Harvest index (%) | Protein content (%) | Oil content (%) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 41 | AMS 99-33 | 38.33 | 107.66 | 55.00 | 3.00 | 28.00 | 3.13 | 2.40 | 12.40 | 15.18 | 48.38 | 37.26 | 19.00 | 7.30 |
| 42 | JS 93-05 | 35.00 | 116.00 | 37.80 | 2.86 | 35.98 | 3.81 | 2.96 | 13.73 | 22.95 | 46.01 | 34.05 | 19.25 | 10.60 |
| 43 | Bragg | 31.66 | 103.33 | 59.00 | 2.26 | 17.28 | 3.69 | 2.66 | 13.53 | 14.23 | 33.46 | 38.81 | 20.51 | 4.79 |
| 44 | RKS 18 | 38.33 | 112.00 | 49.00 | 4.96 | 34.52 | 3.76 | 2.53 | 13.73 | 20.07 | 47.08 | 36.53 | 20.06 | 9.53 |
| 45 | JS 335 | 40.00 | 105.66 | 50.00 | 2.60 | 45.27 | 3.32 | 2.26 | 11.53 | 26.09 | 44.01 | 38.40 | 20.87 | 11.56 |
| | **Mean** | **38.35** | **105.78** | **50.38** | **2.51** | **29.94** | **3.21** | **2.35** | **12.79** | **21.18** | **36.57** | **37.83** | **20.35** | **8.00** |
| | **S.Em.** | **0.560** | **0.660** | **1.701** | **0.134** | **1.447** | **0.079** | **0.138** | **0.407** | **1.137** | **2.046** | **0.721** | **0.250** | **0.570** |
| | **C.D. (0.05)** | **1.57** | **1.85** | **4.78** | **0.37** | **4.06** | **0.22** | **0.39** | **1.14** | **3.19** | **5.75** | **2.02** | **0.70** | **1.60** |
| | **C.V.(%)** | **2.53** | **1.08** | **5.84** | **9.23** | **8.37** | **4.26** | **10.22** | **5.51** | **9.29** | **9.68** | **3.30** | **2.12** | **12.34** |

**Table 18: Mean intra and inter-hierarchical cluster (Euclidean$^2$) distances of seven clusters of soybean**

| Cluster number | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | **156.481** | 326.576 | 381.604 | 838.768 | 375.707 | 391.939 | 611.983 |
| II | | **195.030** | 344.670 | 676.664 | 563.606 | 447.619 | 526.510 |
| III | | | **139.928** | 873.645 | 409.755 | 548.061 | 379.809 |
| IV | | | | **0.000** | 1394.821 | 1340.391 | 1361.772 |
| V | | | | | **176.772** | 265.477 | 295.939 |
| VI | | | | | | **172.927** | 307.678 |
| VII | | | | | | | **179.048** |

Values in the bold letter indicate the intra-cluster distances

**Table 17 : Clustering pattern of 45 soybean genotypes as per hierarchical cluster analysis**

| Cluster | Number of Genotypes | Genotypes |
|---|---|---|
| I | 5 | JS (SH) 2001-2004, RKS 48, DSb12, NRC 76, NSO 15 |
| II | 4 | JS 20-01, PS 1433, HIMSO 1609, TS 56 |
| III | 4 | HIMSO 1608, NRC 78, Bragg, VLS 70 |
| IV | 1 | VLS 69 |
| V | 18 | LSb 23, AMS 4-4, DS 2410, JS 20-09, PS 1437, SL-752, JS 20-06, RKS 45, DS 24-04, AMS 99-33, RKS 18, SL 790, JS-93-05, AMS 4-63, JS 335,Ts 94, NRC 77, MACS 1139 |
| VI | 3 | DSb 10, NSO 111, PS1421 |
| VII | 10 | MACS 1126, MAUS 285, MAUS 295, RCS 1, RCS 9, SL7 44, MACS 1148, KDS 167-9, NSO78, VLS 68 |

**Table 14: Mean values of clusters for 45 soybean genotypes during *Kharif*, 2007**

| Cluster | Days to 50% flowering | Days to maturity | Plant height (cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight (g) | Biological yield/plant (g) | Harvest index (%) | Protein content (%) | Oil content (%) | Seed Yield/ Plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 39.71 | 110.55 | 51.97 | 2.54 | 29.97 | 3.28 | 2.40 | 13.15 | 21.69 | 37.32 | 37.67 | 20.46 | 8.44 |
| II | 35.94 | 95.55 | 50.21 | 2.26 | 28.82 | 3.31 | 2.39 | 12.58 | 19.51 | 34.98 | 37.86 | 20.59 | 6.99 |
| III | 46.00 | 113.00 | 32.53 | 2.00 | 37.89 | 3.03 | 2.20 | 12.06 | 26.40 | 35.72 | 35.10 | 18.00 | 9.40 |
| IV | 34.66 | 99.33 | 48.60 | 3.53 | 49.57 | 3.53 | 2.73 | 15.13 | 33.42 | 44.57 | 37.81 | 18.13 | 14.99 |
| V | 31.66 | 114.33 | 46.00 | 2.86 | 20.07 | 1.90 | 1.33 | 8.73 | 15.40 | 21.66 | 41.45 | 18.08 | 3.56 |
| VI | 30.66 | 81.00 | 30.53 | 4.00 | 24.99 | 1.26 | 1.00 | 7.26 | 15.02 | 41.74 | 41.25 | 21.28 | 3.49 |

**Table 21: Estimates of direct and indirect effects of yield components in soybean during *Kharif*, 2007.**

| S.No | Character | Days to 50% flowering | Days to maturity | Plant height ( cm) | Branches/ plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight ( g) | Biological yield/ plant ( g) | Harvest index (%) | Protein content (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Days to 50% flowering | **-0.0591** | -0.0187 | -0.0022 | 0.0142 | -0.0021 | -0.0026 | -0.0039 | -0.0153 | -0.0068 | -0.0021 | 0.0113 | 0.0046 |
| 2 | Days to maturity | 0.0274 | **0.0868** | 0.0102 | 0.0049 | -0.0139 | 0.0227 | 0.0195 | 0.0259 | 0.0041 | -0.0027 | -0.0075 | -0.0116 |
| 3 | Plant height (cm) | 0.0002 | 0.0006 | **0.0048** | 0.0008 | 0.0007 | 0.0008 | 0.0014 | 0.0009 | 0.0012 | 0.0008 | 0.0012 | -0.0001 |
| 4 | Branches/ plant | -0.0049 | 0.0012 | 0.0034 | **0.0206** | 0.0047 | 0.0003 | 0.0024 | -0.0024 | 0.0049 | 0.0047 | 0.0035 | -0.0005 |
| 5 | Pods/ plant | 0.0115 | -0.0515 | 0.0447 | 0.0726 | **0.3223** | 0.0669 | 0.0633 | -0.0429 | 0.2077 | 0.1714 | -0.0009 | -0.0470 |
| 6 | Pod length (cm) | 0.0025 | 0.0148 | 0.0098 | 0.0009 | 0.0117 | **0.0565** | 0.0419 | 0.0288 | 0.0177 | 0.0026 | -0.0150 | 0.0062 |
| 7 | Seeds/ pod | 0.0004 | 0.0014 | 0.0019 | 0.0007 | 0.0012 | 0.0047 | **0.0063** | 0.0030 | 0.0023 | 0.0009 | -0.0011 | -0.0001 |
| 8 | 100 seed wt (g) | 0.0468 | 0.0541 | 0.0328 | -0.0212 | -0.0241 | 0.0923 | 0.0851 | **0.1812** | 0.0251 | 0.0079 | -0.0303 | -0.0057 |
| 9 | Biological yield / plant (g) | 0.0508 | 0.0209 | 0.1122 | 0.1053 | 0.2846 | 0.1386 | 0.1634 | 0.0612 | **0.4418** | 0.1390 | 0.0056 | -0.0223 |
| 10 | Harvest index (%) | 0.0100 | -0.0085 | 0.0485 | 0.0628 | 0.1471 | 0.0127 | 0.0383 | 0.0121 | 0.0870 | **0.2767** | -0.0221 | -0.0197 |
| 11 | Protein content (%) | -0.0205 | -0.0093 | 0.0258 | 0.0183 | -0.0003 | -0.0285 | -0.0188 | -0.0179 | 0.0013 | -0.0086 | **0.1070** | -0.0067 |
| 12 | Oil content (%) | -0.0016 | -0.0028 | -0.0006 | -0.0005 | -0.0031 | 0.0023 | -0.0004 | -0.0007 | -0.0011 | -0.0015 | -0.0013 | **0.0210** |
| | Correlation on seed yield/plant (g) | **0.0634** | **0.0890** | **0.2913**** | **0.2795**** | **0.7289**** | **0.3667**** | **0.3986**** | **0.2339**** | **0.7854**** | **0.5891**** | **0.0504** | **-0.0820** |

Residual effect = 0.4179 ** Significant at 1% level

**Table 21. Estimates of direct and indirect effects (phenotypic) of yield components in soybean during *Kharif* 2007.**

| S.No | Character | Days to 50% flowering | Days to maturity | Plant height ( cm) | Branches / plant | Pods/ plant | Pod length (cm) | Seeds/ pod | 100 seed weight ( gm) | Biological yield/ plant ( gm) | Harvest index (%) | Protein content (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Days to 50% flowering | **-0.0591** | -0.0187 | -0.0022 | 0.0142 | -0.0021 | -0.0026 | -0.0039 | -0.0153 | -0.0068 | -0.0021 | 0.0113 | 0.0046 |
| 2 | Days to maturity | 0.0274 | **0.0868** | 0.0102 | 0.0049 | -0.0139 | 0.0227 | 0.0195 | 0.0259 | 0.0041 | -0.0027 | -0.0075 | -0.0116 |
| 3 | Plant height (cm) | 0.0002 | 0.0006 | **0.0048** | 0.0008 | 0.0007 | 0.0008 | 0.0014 | 0.0009 | 0.0012 | 0.0008 | 0.0012 | -0.0001 |
| 4 | Branches/ plant | -0.0049 | 0.0012 | 0.0034 | **0.0206** | 0.0047 | 0.0003 | 0.0024 | -0.0024 | 0.0049 | 0.0047 | 0.0035 | -0.0005 |
| 5 | Pods/ plant | 0.0115 | -0.0515 | 0.0447 | 0.0726 | **0.3223** | 0.0669 | 0.0633 | -0.0429 | 0.2077 | 0.1714 | -0.0009 | -0.0470 |
| 6 | Pod length (cm) | 0.0025 | 0.0148 | 0.0098 | 0.0009 | 0.0117 | **0.0565** | 0.0419 | 0.0288 | 0.0177 | 0.0026 | -0.0150 | 0.0062 |
| 7 | Seeds/ pod | 0.0004 | 0.0014 | 0.0019 | 0.0007 | 0.0012 | 0.0047 | **0.0063** | 0.0030 | 0.0023 | 0.0009 | -0.0011 | -0.0001 |
| 8 | 100 seed wt (g) | 0.0468 | 0.0541 | 0.0328 | -0.0212 | -0.0241 | 0.0923 | 0.0851 | **0.1812** | 0.0251 | 0.0079 | -0.0303 | -0.0057 |
| 9 | Biological yield / plant (g) | 0.0508 | 0.0209 | 0.1122 | 0.1053 | 0.2846 | 0.1386 | 0.1634 | 0.0612 | **0.4418** | 0.1390 | 0.0056 | -0.0223 |
| 10 | Harvest index (%) | 0.0100 | -0.0085 | 0.0485 | 0.0628 | 0.1471 | 0.0127 | 0.0383 | 0.0121 | 0.0870 | **0.2767** | -0.0221 | -0.0197 |
| 11 | Protein content (%) | -0.0205 | -0.0093 | 0.0258 | 0.0183 | -0.0003 | -0.0285 | -0.0188 | -0.0179 | 0.0013 | -0.0086 | **0.1070** | **-0.0067** |
| 12 | Oil content (%) | -0.0016 | -0.0028 | -0.0006 | -0.0005 | -0.0031 | 0.0023 | -0.0004 | -0.0007 | -0.0011 | -0.0015 | -0.0013 | 0.0210 |
| | Correlation with seed yield/plant (g) | **0.0634** | **0.0890** | **0.2913**** | **0.2795**** | **0.7289**** | **0.3667**** | **0.3986**** | **0.2339**** | **0.7854**** | **0.5891**** | **0.0504** | **-0.0820** |

** Significant at 1% level     Bold and diagonal values are direct effect

**Table 16: Genotypic mean (PCA) on the first three principal components for 45 soybean genotypes**

| S.NO. | Gennotype | PCAI X -axis | PCAII Y -axis | PCAIII Z-axis |
|---|---|---|---|---|
| 1 | JS(SH) 2001-04 | 58.435 | -7.743 | 5.711 |
| 2 | LSb 23 | 67.921 | -4.976 | 2.024 |
| 3 | VLS 70 | 63.347 | 0.696 | -0.537 |
| 4 | DSb 10 | 65.044 | -3.912 | 8.511 |
| 5 | PS 1437 | 65.596 | -3.171 | 2.252 |
| 6 | NSO 111 | 65.272 | -5.347 | 6.427 |
| 7 | DS 2402 | 67.014 | -3.420 | 5.218 |
| 8 | SL 752 | 68.314 | -2.345 | 2.441 |
| 9 | JS 20 - 01 | 55.064 | -3.776 | 6.798 |
| 10 | DSb 12 | 60.229 | -5.642 | 2.759 |
| 11 | MACS 1126 | 67.272 | 0.001 | 5.468 |
| 12 | PS 1421 | 69.401 | -3.715 | 8.510 |
| 13 | KDS 167- 9 | 70.798 | 0.253 | 1.622 |
| 14 | MAUS 285 | 67.486 | 1.017 | 6.649 |
| 15 | HIMSO 608 | 60.159 | 0.486 | -1.491 |
| 16 | DS 2410 | 66.012 | -6.238 | 2.486 |
| 17 | NSO 78 | 70.494 | -0.822 | 2.412 |
| 18 | AMS 4-4 | 67.879 | -5.263 | 2.807 |
| 19 | PS 1433 | 59.300 | -4.599 | 7.632 |
| 20 | NRC 78 | 59.304 | -0.684 | -0.948 |
| 21 | JS 20-06 | 64.517 | -6.626 | 3.323 |
| 22 | MAUS 295 | 68.782 | 1.619 | 4.465 |
| 23 | MACS 1148 | 69.025 | 2.727 | 3.291 |
| 24 | HIMSO 1609 | 57.279 | 2.165 | 4.671 |
| 25 | TS 94 | 70.522 | -3.516 | 2.009 |
| 26 | NRC 77 | 69.679 | -4.359 | 2.485 |
| 27 | SL 790 | 69.416 | -2.966 | 1.298 |
| 28 | AMS 4- 63 | 72.473 | -6.801 | 1.383 |
| 29 | RCS 9 | 65.332 | 2.881 | 5.155 |
| 30 | NRC 76 | 59.409 | -5.973 | 1.429 |
| 31 | SL 744 | 65.411 | 1.286 | 4.672 |
| 32 | VLS 69 | 49.564 | -0.149 | -0.437 |
| 33 | RKS 45 | 64.419 | -6.786 | 2.899 |
| 34 | JS 20-09 | 66.583 | -7.337 | 2.837 |
| 35 | TS 56 | 59.294 | 0.685 | 4.864 |
| 36 | VLS 68 | 67.640 | 1.276 | -1.632 |
| 37 | RKS 48 | 58.547 | -9.143 | 1.235 |
| 38 | MACS 1139 | 68.886 | -2.929 | -0.168 |
| 39 | RCS 1 | 68.215 | 3.358 | 4.870 |
| 40 | NSO 15 | 62.942 | -11.664 | 2.695 |
| 41 | AMS 99-33 | 64.896 | -3.406 | 2.182 |
| 42 | JS 93 05 | 71.124 | -6.871 | 1.000 |
| 43 | Bragg | 63.042 | -1.087 | -1.464 |
| 44 | RKS 18 | 68.329 | -6.761 | 0.135 |
| 45 | JS 335 | 70.104 | -6.739 | 3.854 |

| S.No | Characters | Contribution towards divergence (%) | Rank |
|---|---|---|---|
| 1 | Days to 50% Flowering | 12.73 | 126 |
| 2 | Days to Maturity | 40.91 | 405 |
| 3 | Plant height cm | 4.75 | 47 |
| 4 | Branches/ plant | 5.96 | 59 |
| 5 | Pods/ plant | 15.25 | 151 |
| 6 | Pod length (cm) | 6.46 | 64 |
| 7 | seeds/ pod | 0.00 | 0 |
| 8 | 100 seed wt (gm) | 0.30 | 3 |
| 9 | Biological yield /plant (gm) | 3.03 | 30 |
| 10 | Harvest Index (%) | 0.91 | 9 |
| 11 | Protein (%) | 0.51 | 5 |
| 12 | Oil content (%) | 7.27 | 72 |
| 13 | Yield/plant (gm) | 1.92 | 19 |

**Table 12 Contribution of different characters towards genetic divergence among 45 soybean genotypes during Kharif 2007.**

| S.No | Characters | Contribution towards divergence (%) | Rank |
|---|---|---|---|
| 1 | Days to 50% Flowering | 12.73 | 126 |
| 2 | Days to Maturity | 40.91 | 405 |
| 3 | Plant height cm | 4.75 | 47 |
| 4 | Branches/ plant | 5.96 | 59 |
| 5 | Pods/ plant | 15.25 | 151 |
| 6 | Pod length (cm) | 6.46 | 64 |
| 7 | seeds/ pod | 0.00 | 0 |
| 8 | 100 seed wt (gm) | 0.30 | 3 |
| 9 | Biological yield /plant (gm) | 3.03 | 30 |
| 10 | Harvest Index (%) | 0.91 | 9 |
| 11 | Protein (%) | 0.51 | 5 |
| 12 | Oil content (%) | 7.27 | 72 |
| 13 | Yield/plant (gm) | 1.92 | 19 |

**Table 12 Contribution of different characters towards genetic divergence among 45 soybean genotypes during Kharif 2007.**

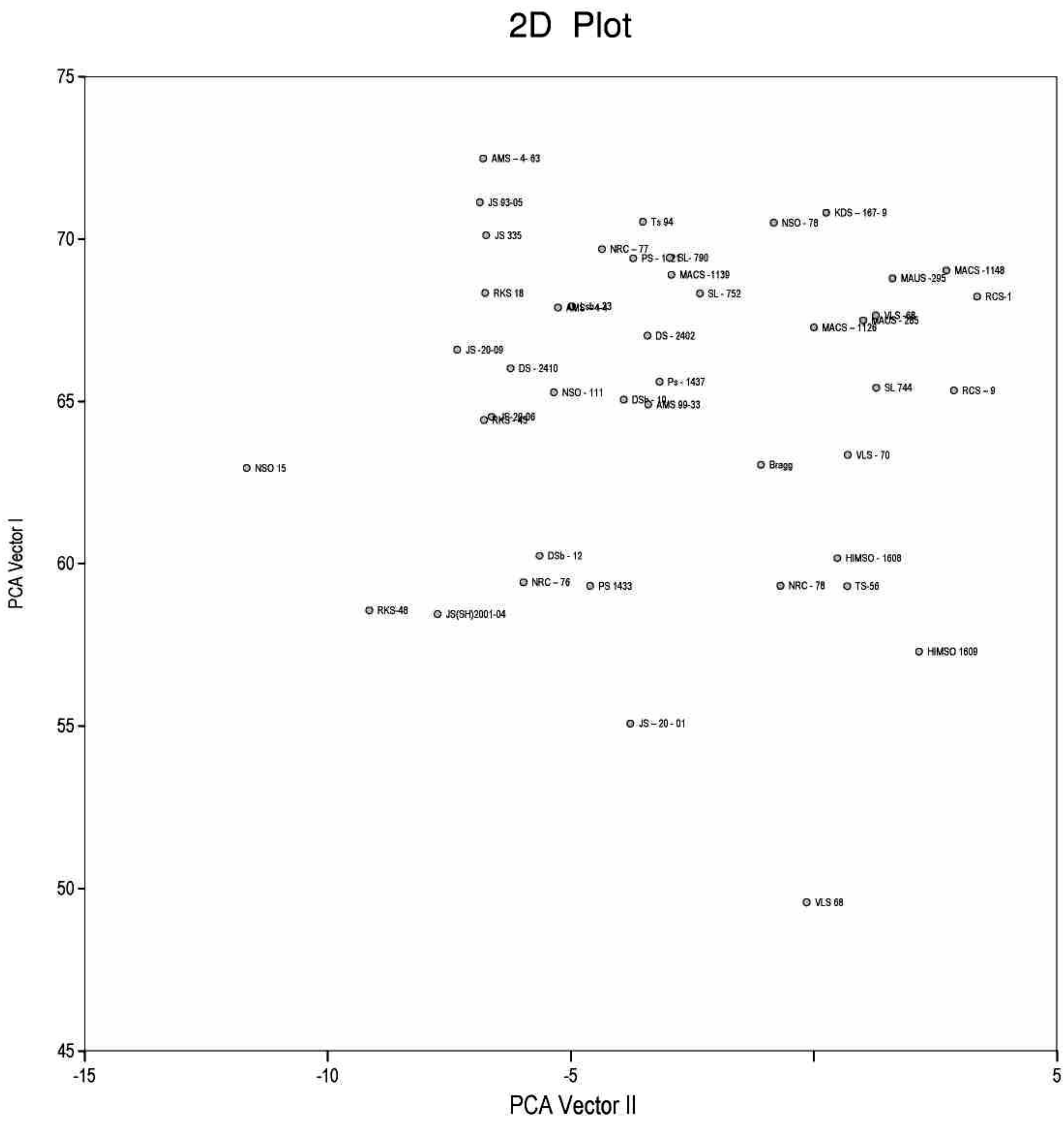



**Fig.1: Two dimensional graph showing relative position of genotypes of soybean based on scores (numbers as per Table 7)**

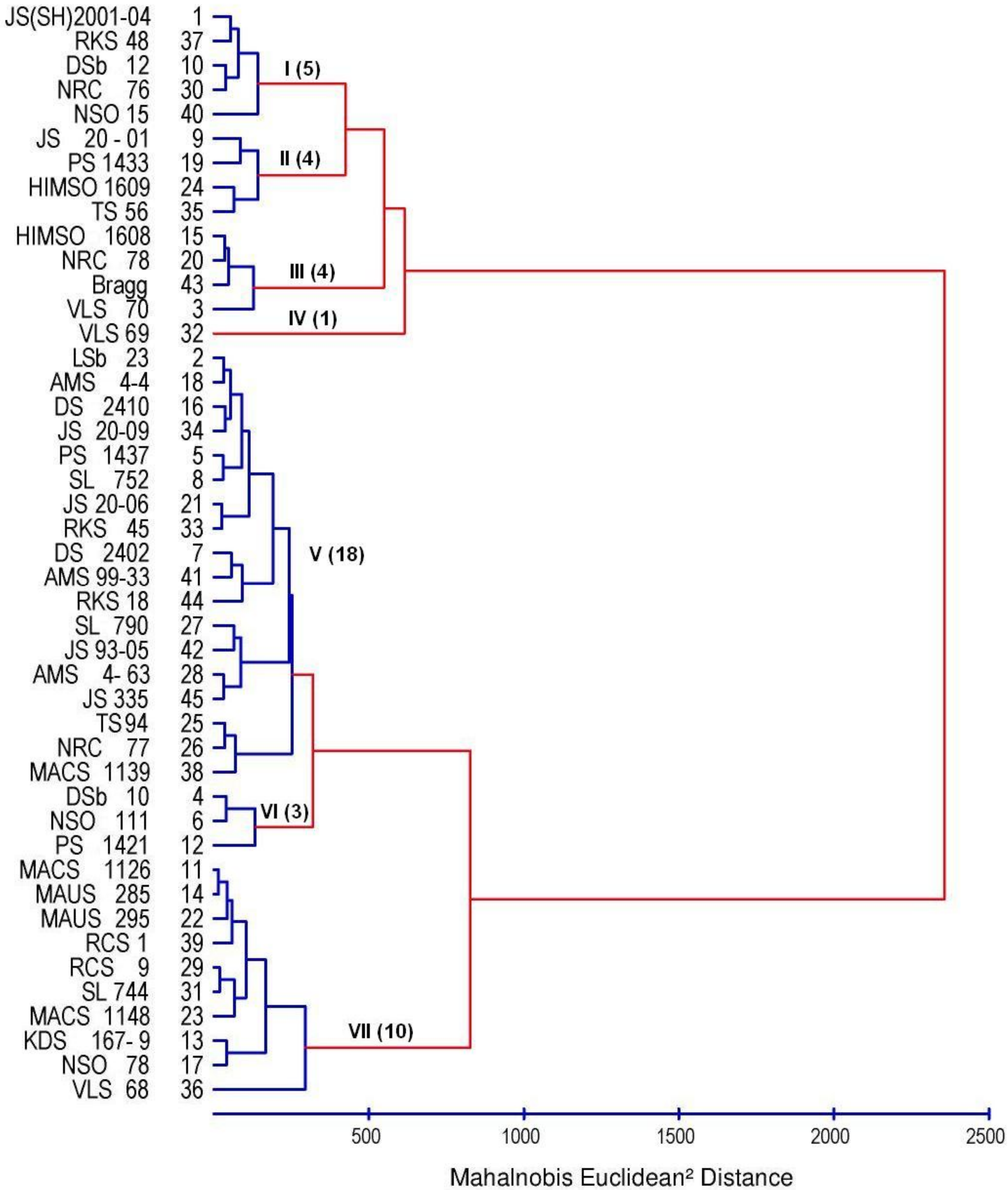



**Fig.3: Diagram illustrating the clustering pattern by Ward's minimum variance**

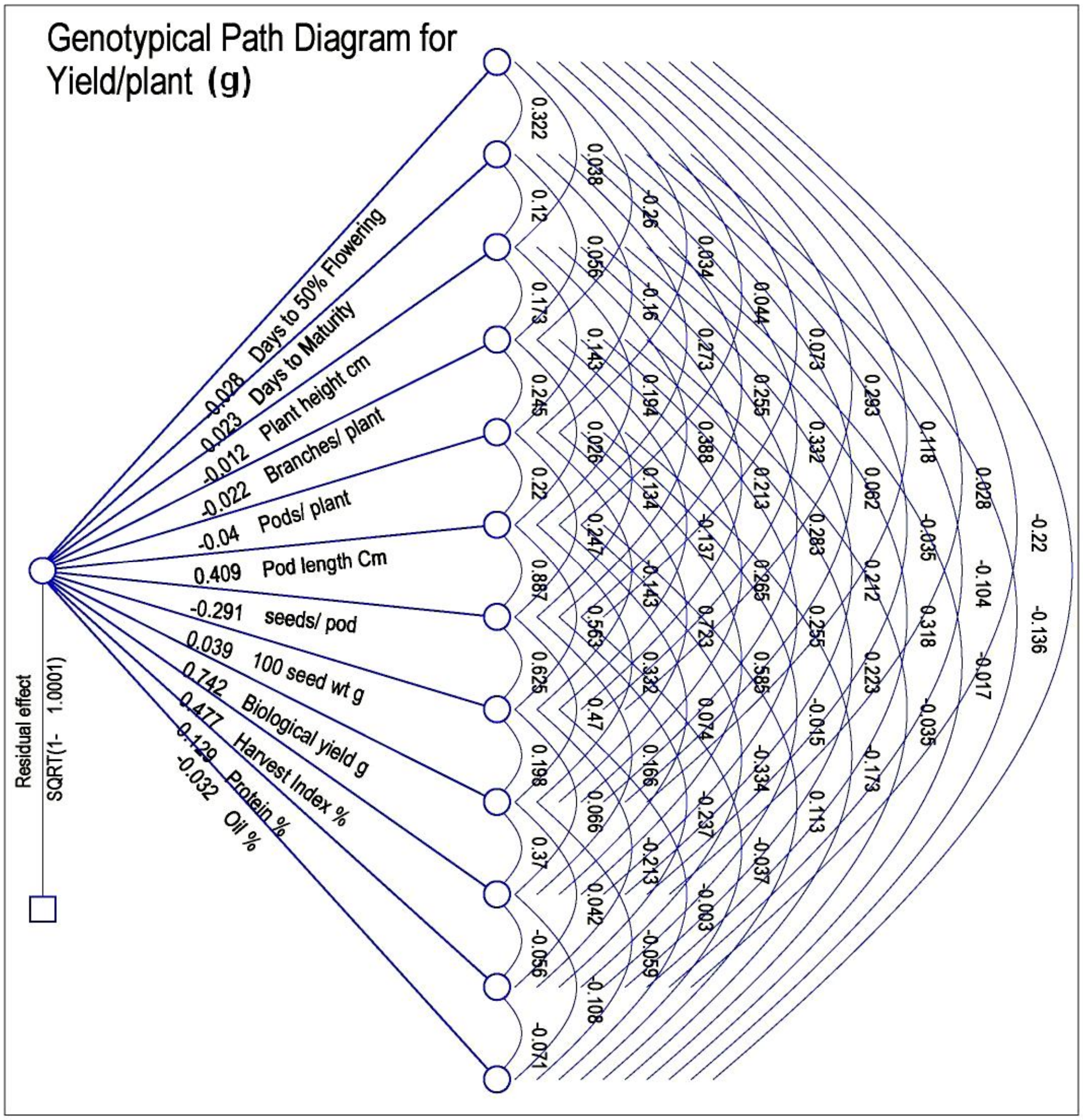



**Fig.9: Path diagram showing cause and effect relationship in soybean**

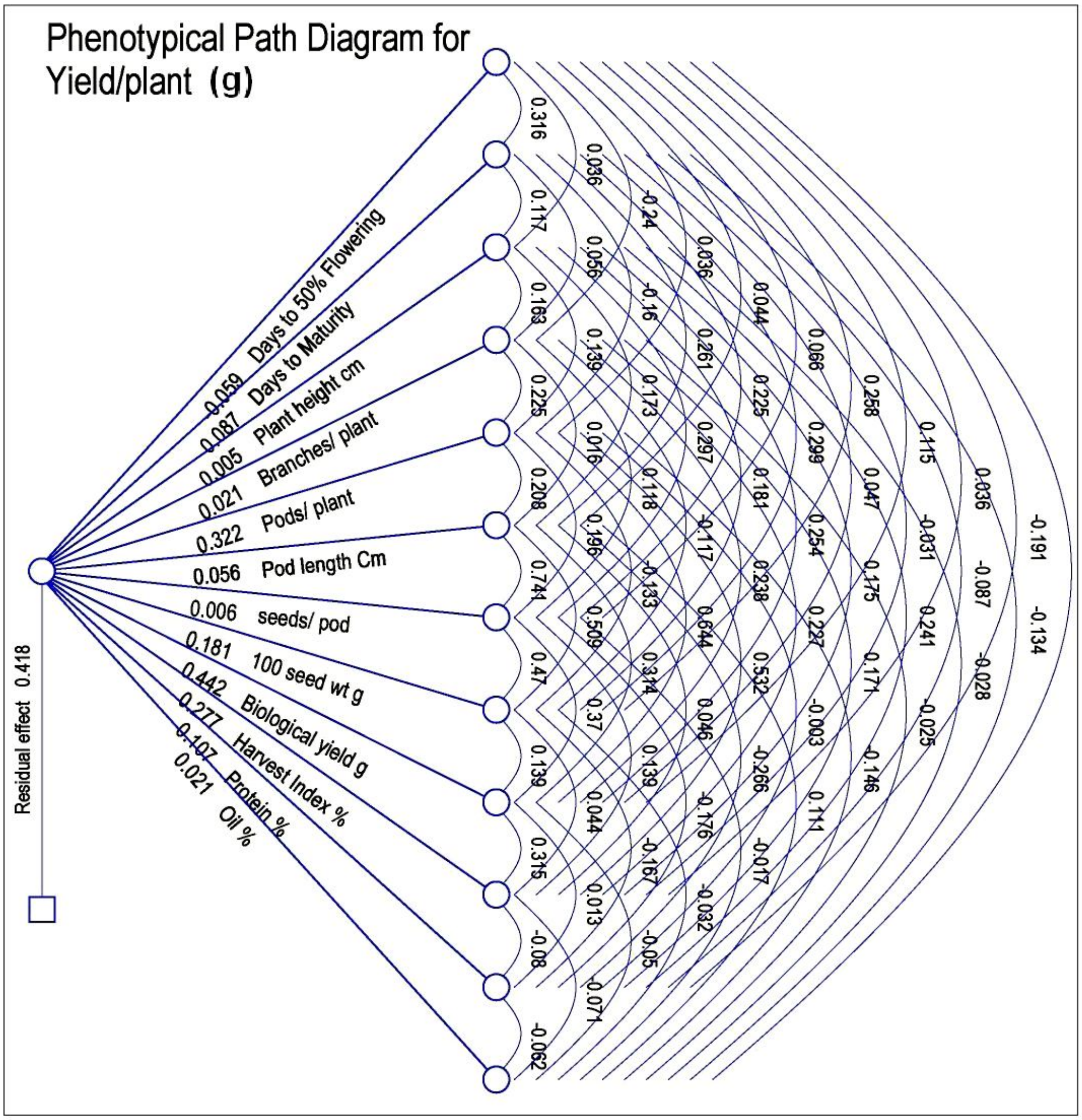



**Fig.5 : Path diagram showing cause and effect relationship in soybean**

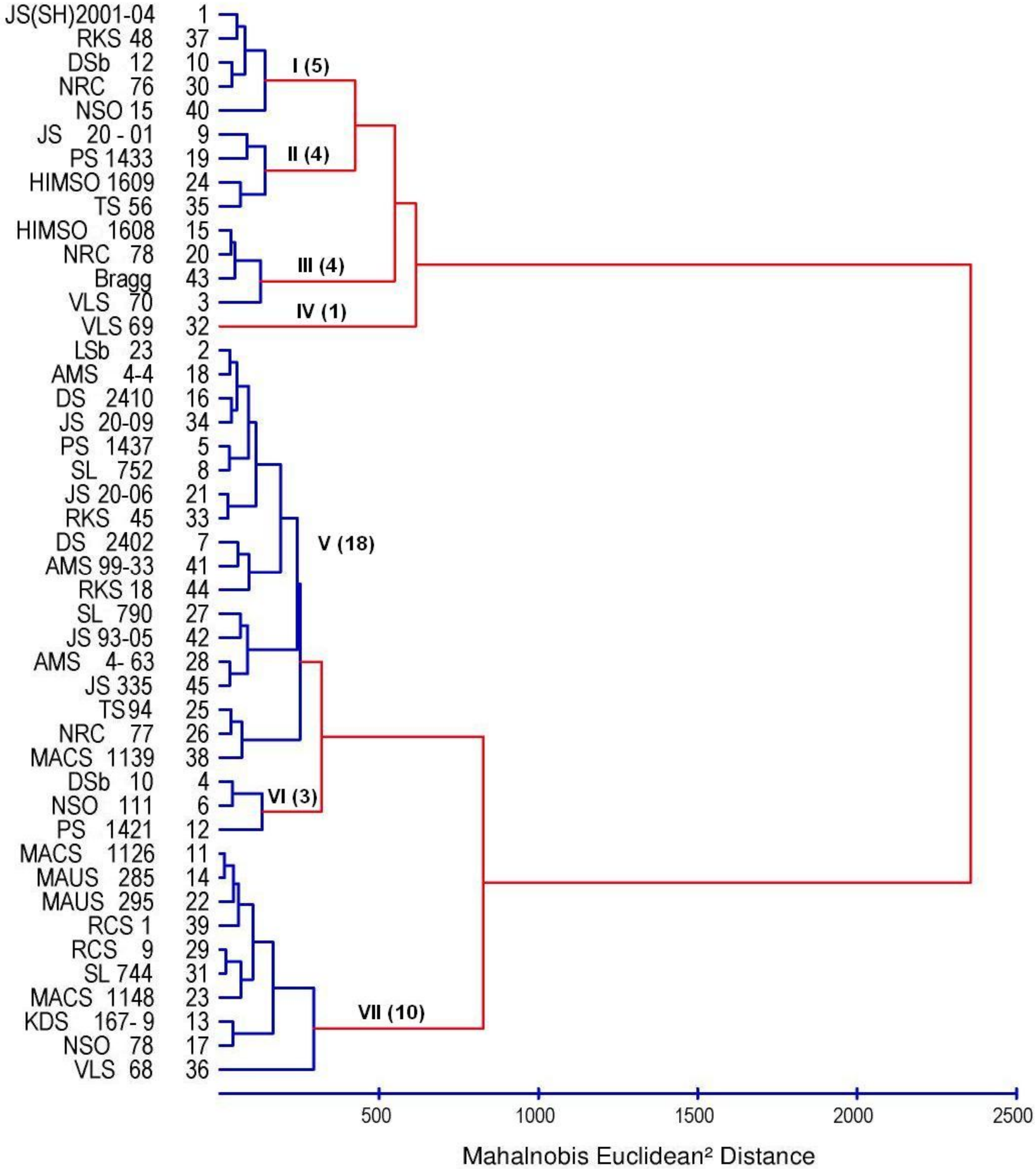
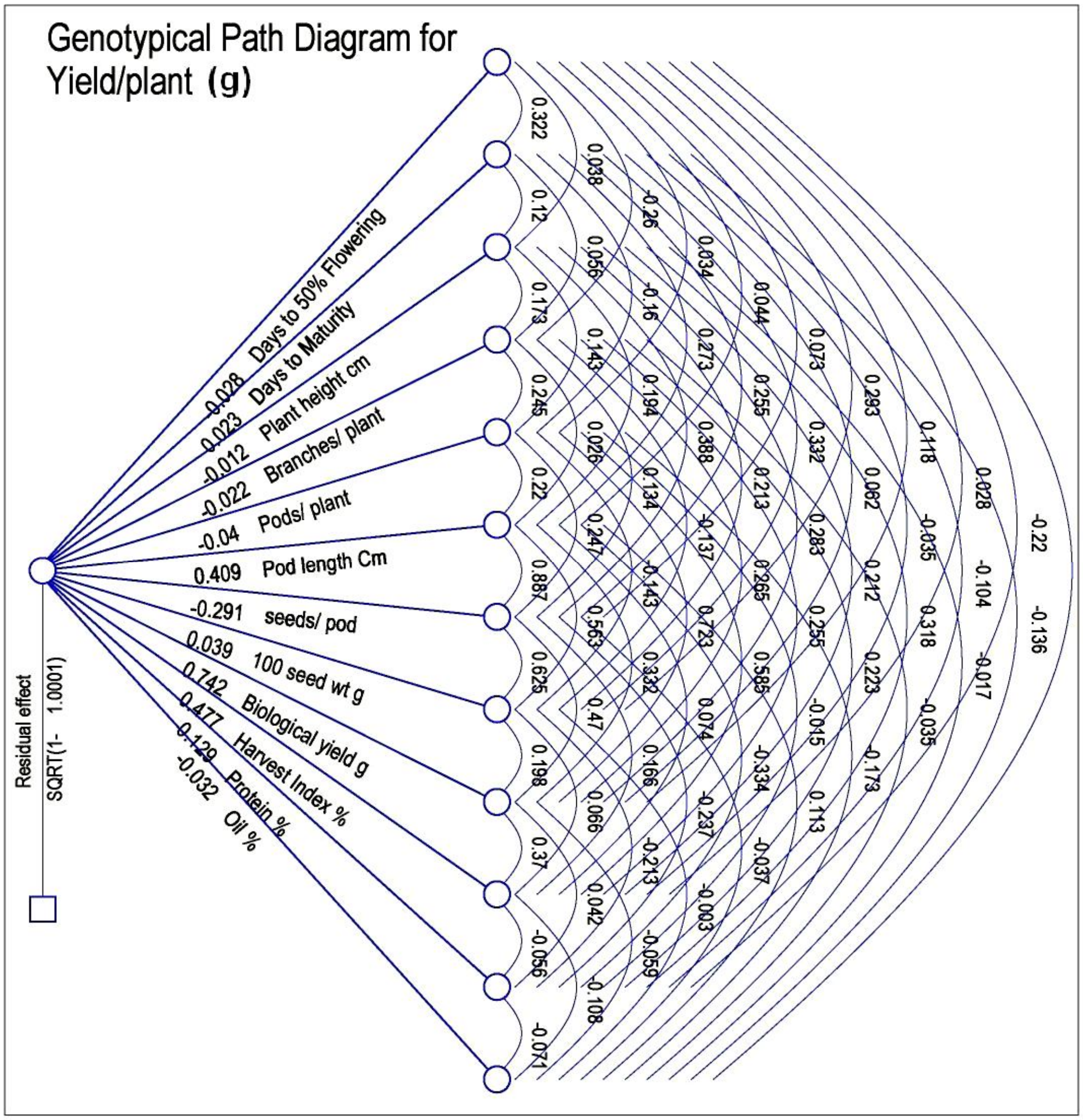
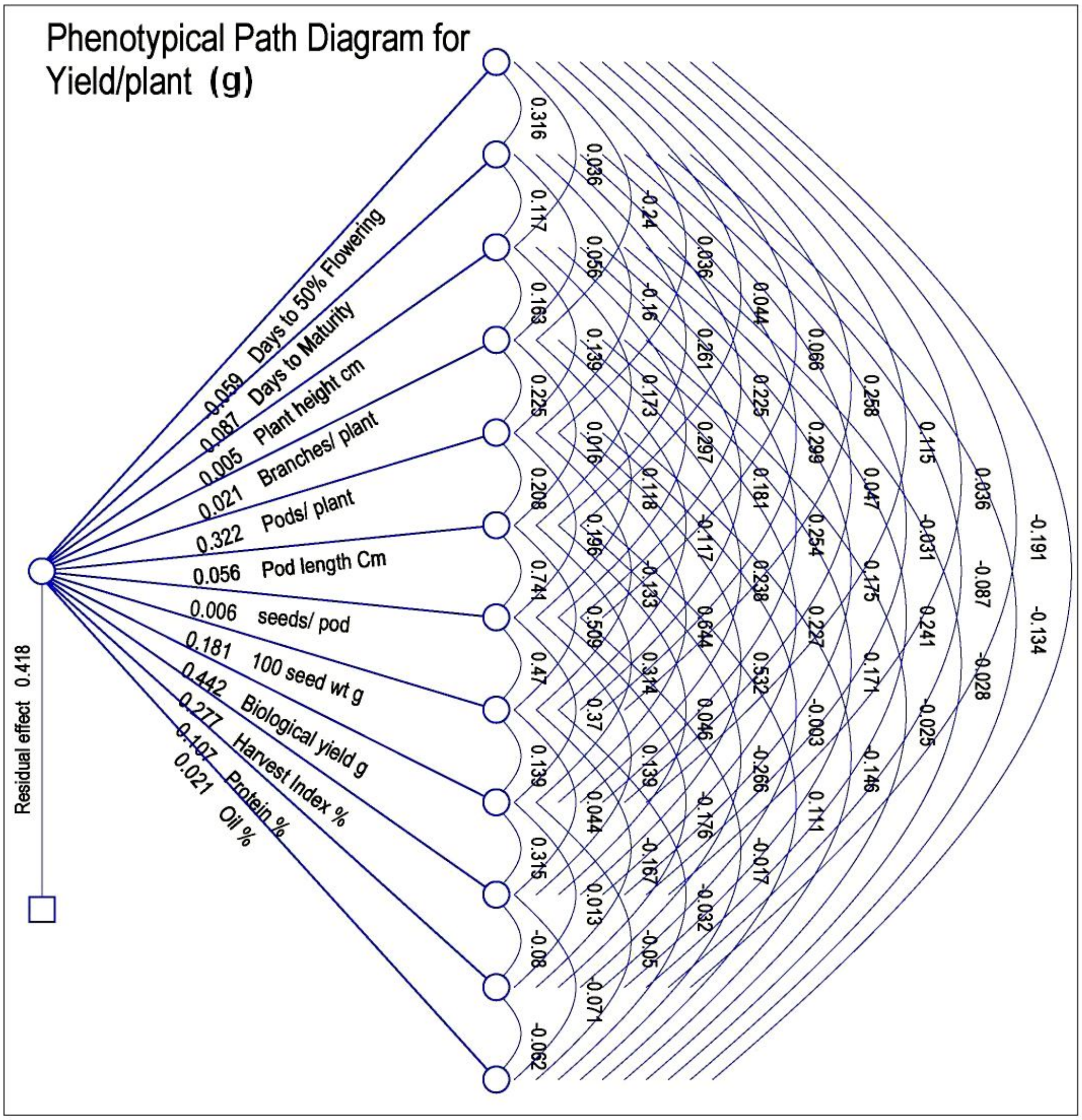



**Fig : Ward's minimum variance dendrogram of soybean based on Euclidean$^2$ distance during *kharif,* 2007.**



Genotypical Path Diagram for Yield/plant (g)
0.028 Days to 50% Flowering
0.023 Days to Maturity
-0.012 Plant height cm
-0.022 Branches/ plant
-0.04 Pods/ plant
0.409 Pod length Cm
-0.291 seeds/ pod
0.039 100 seed wt g
0.742 Biological yield g
0.477 Harvest Index %
0.129 Protein %
-0.032 Oil %
Residual effect
SQRT(1- 1.0001)


Phenotypical Path Diagram for Yield/plant (g)
0.059 Days to 50% Flowering
0.087 Days to Maturity
0.005 Plant height cm
0.021 Branches/ plant
0.322 Pods/ plant
0.056 Pod length Cm
0.006 seeds/ pod
0.181 100 seed wt g
0.442 Biological yield g
0.277 Harvest Index %
0.107 Protein %
0.021 Oil %
Residual effect 0.418

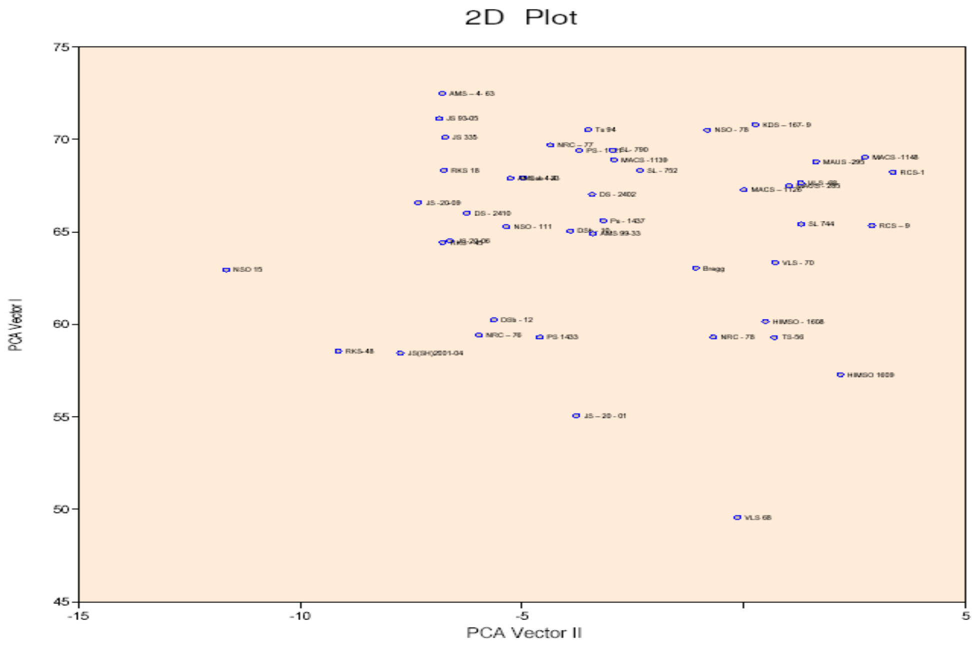



**Fig 5: 2D Plot showing scattering of soybean genotypes based on PCA scores during *Kharif*,2007.**

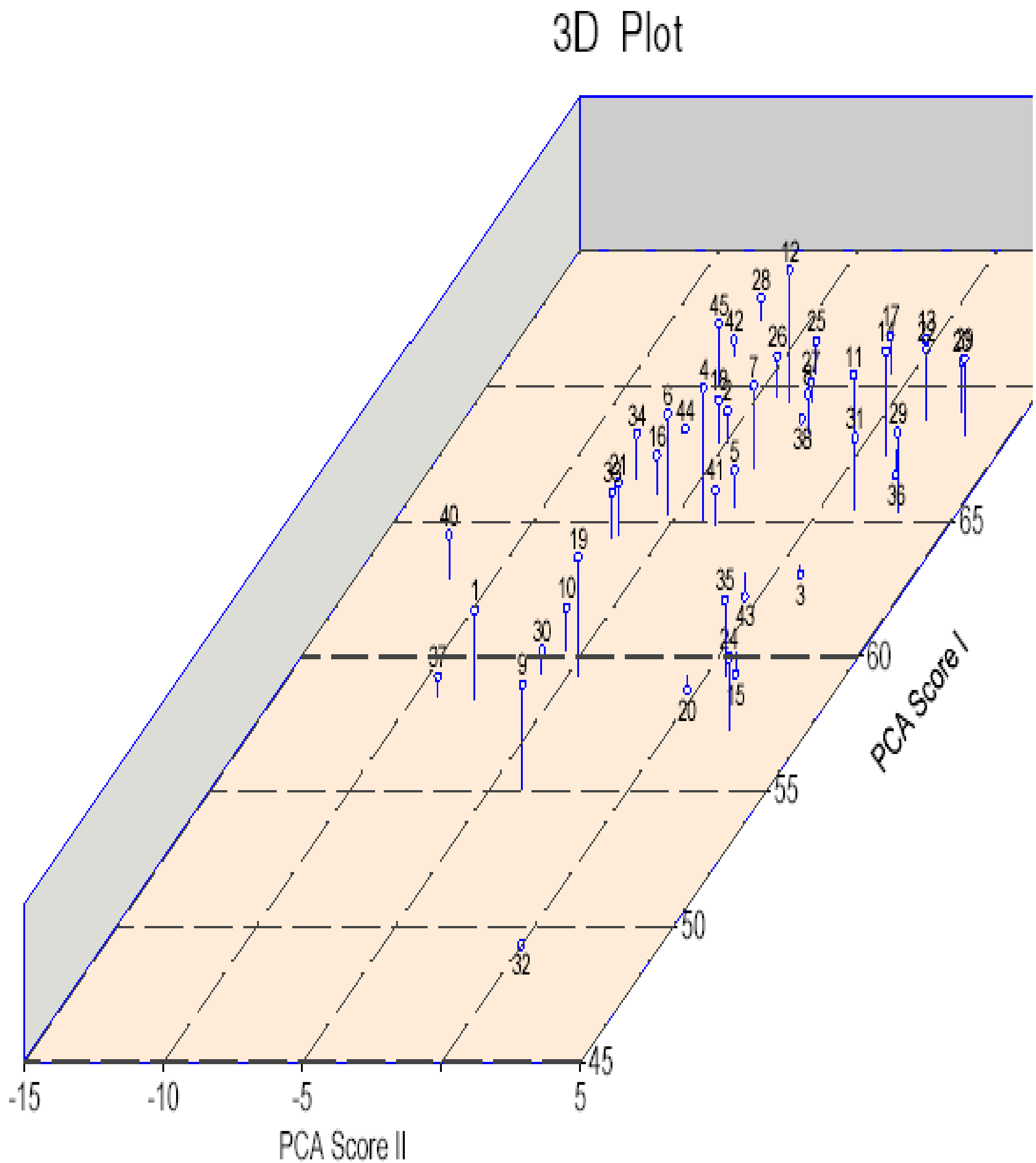



**Fig.2: 3D Plot showing scattering of soybean genotypes based on PCA scores during *Kharif,* 2007.**

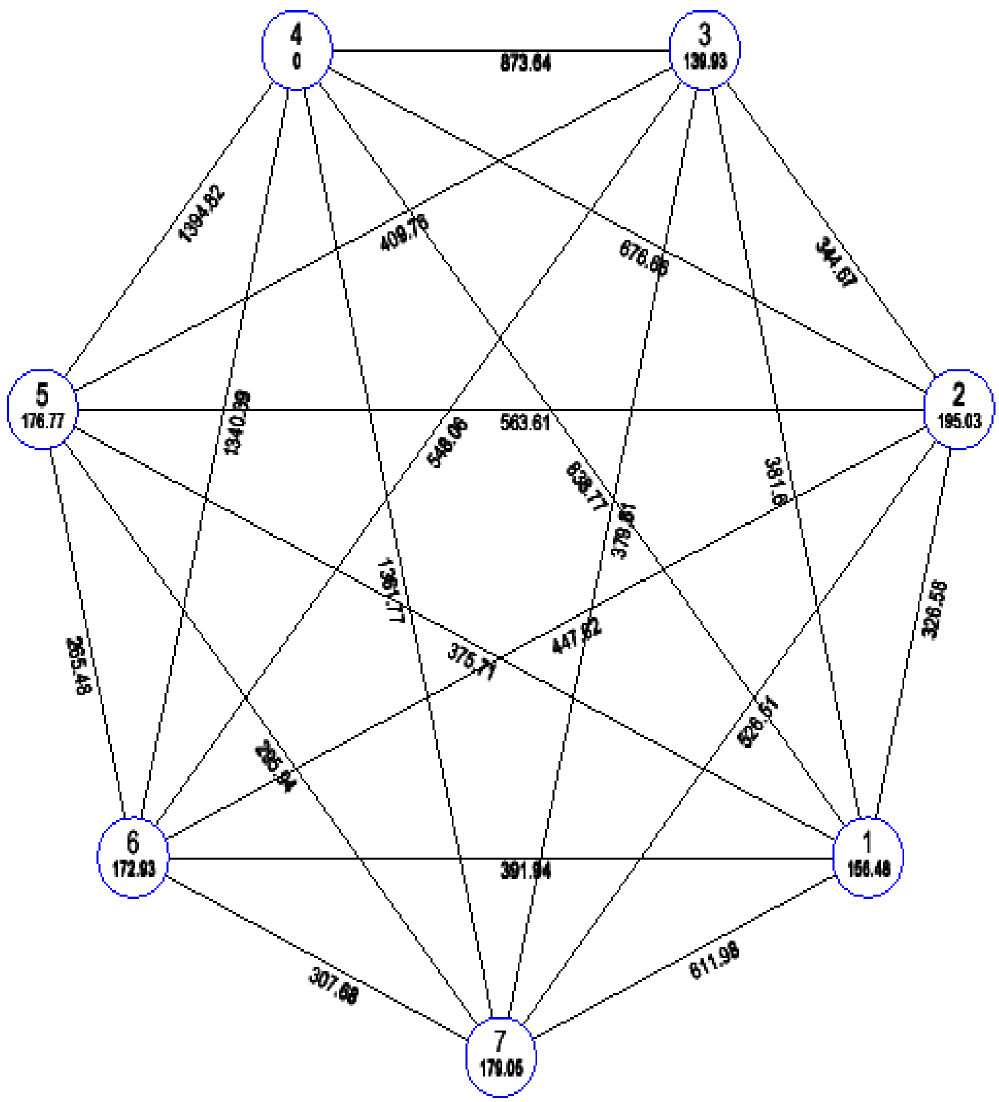



**Fig.4: Cluster diagram showing intra-and inter-cluster distance in soybean using Euclidean$^2$ distance during *kharif,* 2007.**

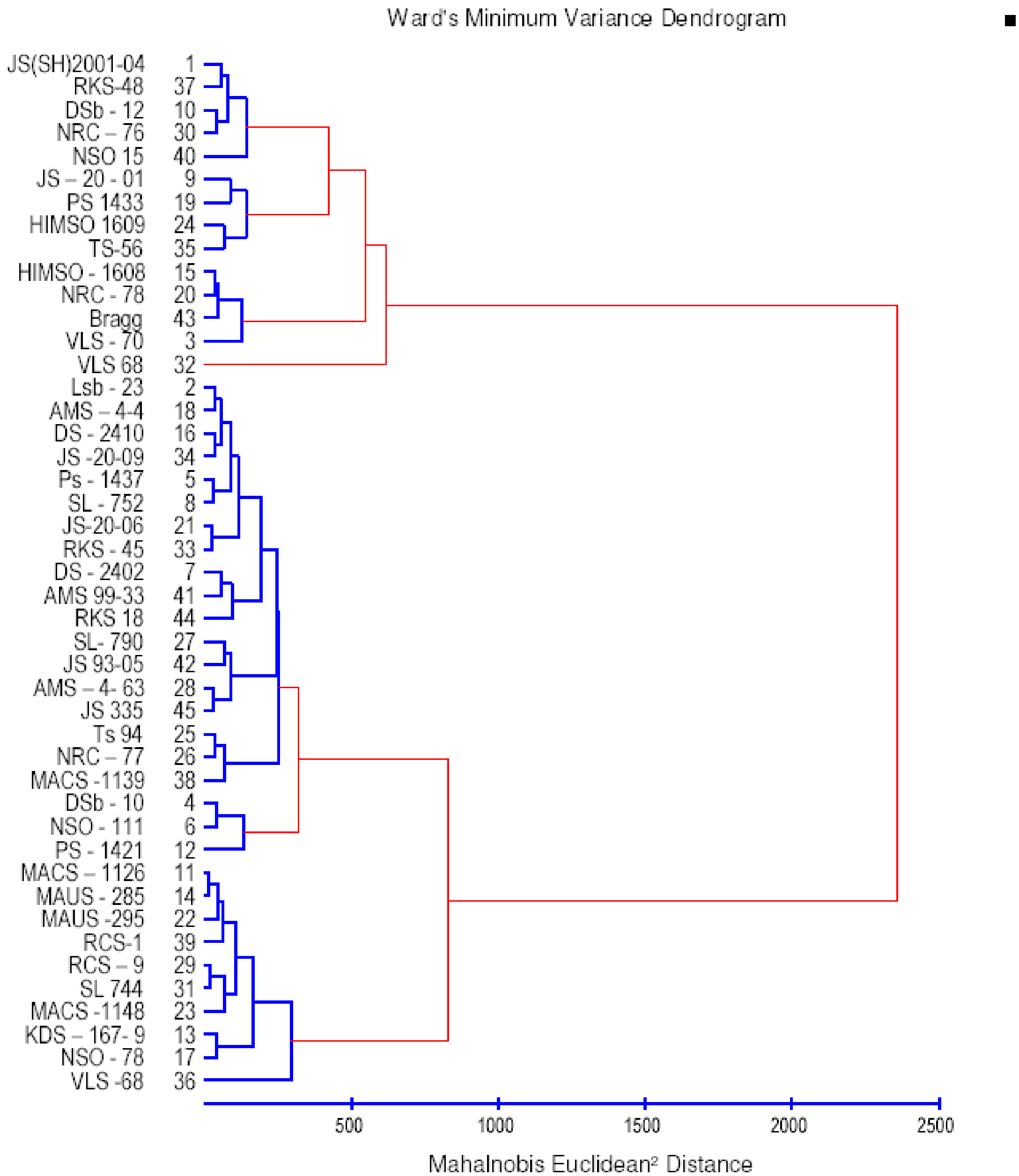



**Fig7 : Ward's minimum variance dendrogram of soybean based on Euclidean$^2$ distance during *kharif*, 2007.**

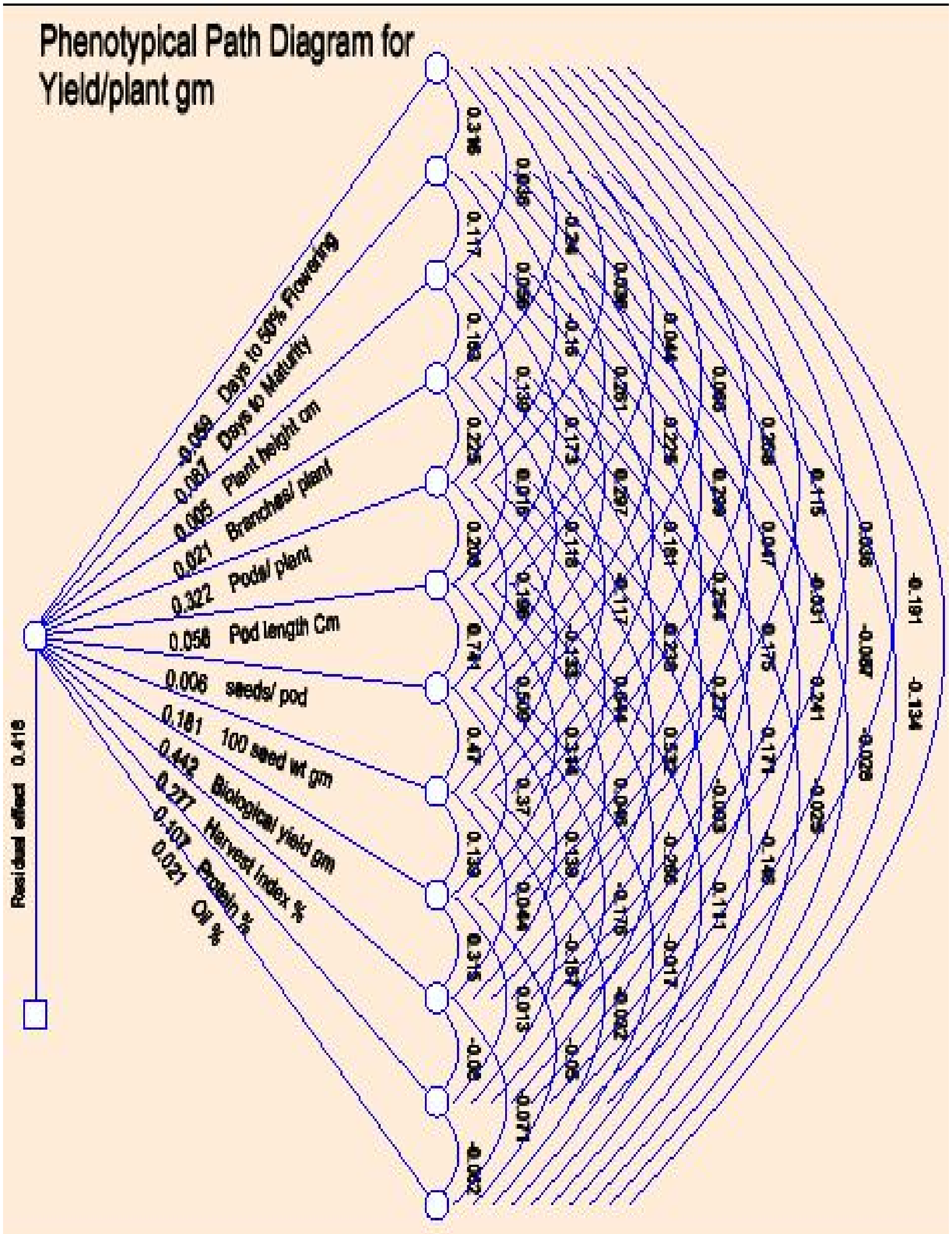



**Fig.9: Path diagram showing cause and effect relationship in soybean during *kharif*, 2007**

# CHAPTER –V

# DISCUSSION

In the present investigation, 13 quantitative characters of 45 genotypes of Soybean [*Glycine max* (L.) Merrill] were studied and the results of the study are discussed under the following headings:

5.1 Genetic variability

5.2 Genetic divergence

5.3 Correlations

5.4 Path coefficient analysis

## 5.1 GENETIC VARIABILITY

Presence of wider spectrum of variability will enhance the chances of selecting desired genotypes. Besides genetic variability, knowledge on heritability and genetic advance indicate the extent to which a character is transmitted to progeny, there by helping the breeder to employ a suitable breeding strategy to achieve objective quickly. It is necessary to have a thorough knowledge on the variability present in the available breeding material for successful improvement of any crop.

Burton (1952) and Swarup and Chaugle (1962) indicated that genetic variability together with the heritability would give a better idea about the extent of genetic advance expected out of selection. The magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has close relationship, on its response to selection (Panse, 1957).

The 45 genotypes of soybean studied in the present investigation differed statistically for all the characters studied. The results obtained on the variability, heritability and genetic advance as percent of mean are discussed here under.

### 5.1.1 Days to 50% flowering

Days to 50% flowering recorded moderate phenotypic and genotypic coefficient of variation indicating that there is a scope for improvement of this trait. Similar results were also reported by Mehetre *et al.* (1994a), Taware *et al.* (1997), Thorat *et al.* (1999) and Sood and Sood (2001) conforming the present findings.

High heritability coupled with high genetic advance as percent of mean of this trait indicates the operation of additive genes and offer the best possibility for improvement of this trait through mass selection, progeny selection, family selection on any other suitable modified selection procedure aiming to exploit the additive gene effects. Similar results were reported by Sood and Sood (2001), Basavaraja *et al.* (2005) and Dev Vart *et al.* (2005).

### 5.1.2 Days to maturity

The estimates of PCV and GCV were low for this trait indicating the narrow range of variability and provide little scope for selection. The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Sailaja (1997), Shrivastava and Shukla (1998), Ramana *et al*. (2000), Agarwal *et al.* (2001) and Ramana (2003).

High heritability coupled with moderate genetic advance as percent of mean recorded in the present investigation indicates the predominance of additive gene action in the expression of this trait. Harer and Deshmukh (1992), Nirmala Kumari and Balasubramanian (1993), Mahajan *et al.* (1994), and Bangar *et al.* (2003) reported similar findings.

### 5.1.3 Plant height (cm)

Plant height recorded moderate phenotypic and genotypic coefficient of variation indicating that there is a scope for improvement of this trait. Similar results were reported by Harer and Deshmukh (1992), Mahajan *et al.* (1994), Nirmala Kumari and Balasubramanian(1993), Vimala Devi (1993), Jagtap and Mehetre (1994), Sailaja (1997), Ramana *et al.* (2000), Agarwal *et al.* (2001), Bangar *et al.* (2003), Ramana (2003) and Praveen Kumar (2005).

High heritability coupled with high genetic advance as percent of mean was recorded for plant height indicates the predominance of additive gene action in the expression of this trait. Similar results were reported by Harer and Deshmukh (1992), Vimala Devi (1993), Jagtap and Mehetre (1994), Mahajan *et al.* (1994), Rajarathinam *et al.* (1996), Sailaja (1997), Ramana *et al.* (2000), Agarwal *et al.* (2001), and Ramana (2003), Chettri *et al.* (2005), Gohil *et al.* (2006), Hina Kausar (2006) and Sriranjani *et al.* (2007).

### 5.1.4 Number of branches per plant

The PCV and GCV were high for this trait. The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Amarnath *et al.* (1991), Harer and Deshmukh (1992), Mahajanet *et al.* (1994), Nirmala Kumari and Balasubramanian(1993), Vimala Devi (1993), Jagtap and Mehetre (1994), Sailaja (1997), Ramana *et al.* (2000) Agarwal *et al.* (2001), Bangar *et al.* (2003), Ramana (2003) and Praveen Kumar (2005).

High heritability coupled with high genetic advance as percent of mean recorded indicates the predominance of additive gene action in the expression of this trait. The results suggest that there is a wide scope for improvement of this trait through simple selection procedure. Similar results were reported by Nirmala Kumari and Balasubramanian (1993), Vimala Devi (1993), Jagtap and Mehetre

(1994), Rajarathinam *et al.* (1996) Sailaja (1997), Roy and Raquib (1998), Agarwal *et al.* (2001), Bangar *et al.* (2003), Ramana (2003) and Hina Kausar (2006).

### 5.1.5 Number of pods per plant

PCV and GCV were high for this trait. The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Amarnath *et al.* (1991), Harer and Deshmukh (1992), Mahajan *et al.* (1994), Jagtap and Mehetre (1994), Mehetre *et al.* (1994a), Shrivasthava and Shukla (1998), Mehetre *et al.* (1995), Mehetre *et al.* (1997), Sailaja (1997), Mehetre *et al.* (1998), Singh and Singh (1999), Ramana *et al.* (2000), Sood and Sood (2001), Bangar *et al.* (2003), Ramana (2003), Chettri *et al.* (2005), Praveen Kumar *et al.* (2005) and Gohil *et al.* (2006).

High heritability coupled with high genetic advance as percent of mean was recorded indicates the predominance of additive gene action in the expression of this trait. The results suggest that there is a wide scope for improvement of this trait through simple selection procedure. Similar results were reported by Amarnath *et al.* (1991), Nirmala Kumari and Balasubramanian(1993), Jagtap and Mehetre (1994), Mehetre *et al.* (1994a), Mehetre *et al.* (1997), Sailaja (1997), Mehetre *et al.* (1998), Maharaddi *et al.* (1999), Singh and Singh (1999), Jain and

Ramgiry (2000), Ramana *et al.* (2000), Agarwal *et al.* (2001), Gohil *et al.* (2006), Hina Kausar (2006) and Sriranjani *et al.* (2007).

### 5.1.6 Pod length (cm)

Pod length recorded moderate phenotypic and genotypic coefficient of variation indicating that there is a scope for improvement of this trait. Similar results were also reported by Thorat *et al.* (1999).

High heritability coupled with high genetic advance as percent of mean of this trait indicates the operation of additive genes and offer the best possibility for improvement of this trait through mass selection, progeny selection, family selection or any other suitable modified selection procedure aiming to exploit the additive gene effects. Similar results were reported by Thorat *et al.* (1999).

### 5.1.7 Number of seeds per pod

Number of seeds per pod recorded moderate phenotypic and genotypic coefficient of variation indicating that there is a scope for improvement of this trait. Similar results were reported by Malik and Singh (1987).

High heritability coupled with high genetic advance as percent of mean of this trait indicates the operation of additive genes and offer the best possibility for improvement of this trait through mass selection, progeny selection, family selection to any other suitable modified selection procedure aiming to exploit the additive gene effects. Similar results were reported by Rashid and Islam (1982), Sailaja (1997) and Chettri *et al*. (2005).

### 5.1.8 100 seed weight (g)

100 seed weight recorded moderate phenotypic and genotypic coefficient of variation indicating that there is a scope for improvement of this trait. Similar results were reported by Amarnath *et al.* (1991), Kalaimagal (1991), Harer and Deshmukh(1992), Shrivastava and Jain (1994), Sailaja (1997), Taware *et al.* (1997), Mehetre *et al.* (1998), Thorat *et al.* (1999), Bangar *et al*. (2003) and Ramana (2003).

High heritability coupled with high genetic advance as percent of mean of this trait indicates the operation of additive genes and offer the best possibility for improvement of this trait through mass selection, progeny selection, family selection to any other suitable modified selection procedure aiming to exploit the additive gene effects.Similar results were reported by Nirmala Kumari and Balasubramanian (1993), Vimala Devi (1993), Mahajan *et al.* (1994), Mehetre *et al*. (1994a), Rajarathinam *et al.* (1996), Mehetre *et al.* (1998), Basavaraja *et al.* (2005), Jyothi Sethi and Tyagi (2005) and Hina Kausar (2006).

### 5.1.9 Biological yield per plant (g)

PCV and GCV were high for the trait. The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Nirmala Kumari and Balasubramanian (1993), Srivastava and Jain (1994), Sailaja (1997), Shrivasthava and Shukla (1998), Dixit *et al.* (2002), Ramana (2003) and Praveen Kumar *et al.* (2005).

High heritability coupled with high genetic advance as percent of mean was recorded indicates the predominance of additive gene action in the expression of this trait. The results suggest that there is a wide scope for improvement of this trait through simple selection. Similar results were reported by Mehetre *et al.* (1994a), Sailaja (1997), Mehetre *et al.* (1998), Ramana *et al.* (2003), Hina Kausar (2006) and Sriranjani *et al*. (2007).

### 5.1.10 Harvest index (%)

PCV and GCV were high for the trait. The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Nirmala Kumari and Balasubramanian (1993), Srivastava and Jain (1994), Mehetre *et al.* (1997), Mehetre *et al.* (1998) and Dixit *et al.* (2002).

High heritability coupled with high genetic advance as percent of mean was recorded indicates the predominance of additive gene action in the expression of this trait. The results suggest that there is a wide scope for improvement of this trait through simple selection procedure. Similar results were reported by Nirmala Kumari and Balasubramanian (1993), Sailaja (1997), Mohana Rao (1999), Basavaraj *et al.* (2005), Hina kausar (2006) and Sriranjani *et al.* (2007).

### 5.1.11 Protein content (%)

The estimates of PCV and GCV were low for the trait indicating the narrow range of variability and provide little scope for selection The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Malik and Singh (1987), Sailaja (1997), Thorat *et al.* (1999) and Ramana (2003).

High heritability coupled with moderate genetic advance as percent of mean was recorded indicates the predominance of additive gene action in the expression of this trait. Similar results were reported by Malik and Singh (1987) and Sailaja (1997).

**Oil content (%)**

The estimates of PCV and GCV were low for this trait indicating the narrow range of variability and provide little scope for selection The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar results were reported by Sharma et al (1986), Mehetre *et al.* (1995), Thorat *et al.* (1999) and Ramana (2003).

High heritability coupled with moderate genetic advance as percent of mean was recorded indicates the predominance of additive gene action in the expression of this trait. These results are in agreement with Taware *et al.* (1997).

**5.1.12 Seed yield per plant (g)**

The estimates of PCV and GCV were high for this trait. The low difference between PCV and GCV indicates the greater role of genetic factors in influencing the expression of the character and it was confirmed by high heritability of the trait. Similar findings were also reported by Jagtap and Mehetre (1994), Mehetre *et al.* (1995), Sailaja (1997), Taware *et al.* (1997), Mehetre *et al*. (1998), Shrivasthava and Shukla (1998), Singh and Singh (1999), Ramana *et al.* (2000), Sood and Sood (2001), Bangar *et al.* (2003) and Ramana (2003).

High heritability coupled with high genetic advance as percent of mean was recorded indicates the predominance of additive gene action in the expression of this trait. The results suggest that there is a wide scope for improvement of this trait through simple selection procedure.Singh and Singh (1999), Jain and Ramgiry (2000), Ramana *et al.* (2000), Basavaraja *et al.* (2005) and Sriranjani *et al.* (2007) also reported similar results.

## 5.2 GENETIC DIVERGENCE

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence would more likely yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm (Singh, 1998).

Generally geographic diversity was considered as a measure of genetic diversity when no scientific tools were available. However, this is an inferential criterion and may not be useful for discrimination among the populations occupying ecologically marginal habitats (Singh and Choudhary, 1997).

### 5.2.1 Mahalanobi's $D^2$ Analysis

The multivariate $D^2$ analysis using Mahalanobi's $D^2$ statistic provides an useful statistical tool for measuring the genetic diversity in germplasm collection with respect to the characters considered together. Further the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between the populations (Rao, 1952).

The data collected on 13 yield contributing characters from 45 genotypes studied during *kharif*, 2007 was subjected to multivariate analysis and genetic divergence was estimated by using Mahalanobis'$D^2$ statistic. The magnitude of $D^2$values suggested that there was considerable variability in the material studied, which led to genetic diversity.

Based on $D^2$ analysis, the 45 genotypes were grouped into six clusters. 29 genotypes were grouped in cluster I, twelve genotypes in cluster II, one each in III, IV, V and VI clusters. The varietal composition of the clusters indicated that the geographic distribution of varieties from diverse sources were grouped into the same clusters.

Similar observation of non correspondence of genetic divergence and geographic diversity has been reported by Chikhale et al. (1992), Ghatge and Kadu (1993), Jaylal (1994), Mehetre *et al.* (1994b), Kumar and Nadarajan (1994), Dobhal (1995), Choudhary *et al.*(1996), Ramgiry (1998), Mohan Rrao (1999), Sharma (2000), Chandakar *et al.* (2002), Ganesamurthy and Seshadri (2002), Gawande *et al.* (2002), Ramana (2003), Praveenkumar (2004) and Sriranjani(2005)

The genotypes of common geographic origin or same location also were grouped into different clusters as evidenced by the distribution of genotypes from Dharwad into different clusters.

The analysis of contribution of various characters in the expression of divergence in the present investigation indicated that days to maturity (40.91%) followed by pods per plant (15.25%), days to 50% flowering (12.73%), oil content (7.27%), pod length (6.46%) and branches per plant (5.96%) contributed maximum to the total genetic divergence.

Mehetre *et al*. (1994b), Gawande *et al.* (2002), Sharma (2004) reported high contribution of days to maturity towards total genetic divergence.

Kumar and Nadarajan (1994), Mehetre *et al.* (1994b), Shrivasthava and Shukla *et al.* (1998), Sharma (2000), Ganesamurthy and Seshadri (2002), Gawande *et al.* (2002) and Ramana (2003) reported maximum contribution of plant height towards total genetic divergence.

The relative importance of yield components contributing towards divergence can be judged by comparing the means of 13 characters .Cluster III had high mean value for days to 50% flowering (46.00), days to maturity (113.00). Cluster IV had high mean value for pods per plant (49.57), pod length (3.53), seeds per pod (2.73)100 seed weight (15.13), biological yield per plant (33.42), harvest index (44.57) and seed yield per plant (14.99).Cluster I had high mean value for plant height (51.97). Cluster V had high mean value for protein content (41.45%) and days to maturity (114.33). Cluster VI had high mean value for oil content (21.28 %).

The inter-cluster distance was maximum between cluster III and cluster VI (531.94) and the minimum distance was observed between cluster I and cluster III (102.75). The intra cluster distance ranged from zero to 90.05. The crossing of varieties from widely divergent clusters may result in heterotic and desirable combinations. For example genotypes of cluster III (PS 1421) and cluster VI (VLS 69) may produce useful recombinants.

### 5.2.2 Principal Component Analysis

The principal component analysis identified the maximum contributing variables days to maturity (0.877), biological yield per plant (0.269), days to 50% flowering (0.175), oil content (0.161) and pod length (0.151) for the variance by loading in the $PC_1$ which contributed maximum to the variance.

The genotypes, AMS4 63, JS 93-05, KDS 167-9, TS 94, NSO 78 and NRC 77 showed maximum variance through $PC_1$ axis and these genotypes are considered to be highly divergent with required variability for further improvement using plant breeding. While the genotypes VLS 69 and JS 20-01 showed low variance through $PC_1$ axis, so it may be considered that these genotypes are less efficient in breeding programme to improve the yield unless they have special added advantage.

### 5.2.3 Hierarchical Cluster Analysis

The cluster analysis using Euclidean$^2$ distance provides an useful tool for measuring the genetic diversity in germplasm with respect to the characters considered together.

Based on Euclidean$^2$ distance and Ward's method of clustering the 45 genotypes were grouped into seven clusters.

Cluster V and VII had the maximum number of genotypes i.e.18 and 10 respectively. Cluster IV had only one genotype i.e. VLS 69 and cluster I, II, III and VI comprised of 5, 4, 4 and 3 genotypes respectively.

The genotypes of common geographic origin or same location were grouped into different clusters as evidenced by the distribution of genotypes from Jabalpur into different clusters. JS (SH) 2001-04 included in cluster I, JS 20-01 included in cluster II, JS 20-09 and JS 93-05 in cluster V. The relative importance of yield components contributing towards divergence can be judged by comparing the group means of 13 characters.

The intra-cluster distances ranged from 0 to 195.03 (cluster IV and cluster II) and the inter-cluster distances ranged from 265.47 (between cluster V and VI) to 1394.82 (between cluster IV and V).

## 5.3 CORRELATION

Direct selection for yield and quality traits is not effective as they are complex quantitative characters, highly influenced by environment. High genotype and environment interaction will restrict improvement, if selection is based on yield per se. Thus, effective improvement in yield may be brought through selection on yield component characters. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection on any particular trait may bring about undesirable changes in other associated characters (Singh, 1998).

Genotypic correlation in general were higher than phenotypic correlations. This may be due the relative stability of genotypes as majority of them were subjected to certain amount of selection (Johnson et al. 1955). Similar findings were also reported by Pooranchand (1999), Singh and Phul (1999), Singh and Singh (1999), Thorat et al. (1999), Kulvir Singh et al. (2000) and Ramana et al. (2000).

Yield is a quantitatively inherited complex character, highly influenced by the environment hence, if the selection based on yield as a single trait alone improvement will not be there where as the yield components are with less complex inheritance and influenced by the environment to a lesser extent. Thus effective improvement in yield may be brought about through selection for yield components.

In the present investigation, correlation estimates obtained for 13 characters of soybean [*Glycine max* (L.) Merrill] are discussed here under.

An overall perusal of the genotypic and phenotypic correlation in the present investigation indicated that seed yield per plant was found to be significantly and positively associated with biological yield per plant ($r_p$ = 0.7854 and $r_g$ = 0.8939), followed by pods per plant ($r_p$ = 0.7289 and $r_g$ = 0.7801), harvest index ($r_p$ = 0.5891 and $r_g$ = 0.6998); seeds per pod ($r_p$ = 0.3986 and $r_g$ = 0.4812), pod length ($r_p$ = 0.3667 and $r_g$ = 0.4021), plant height ($r_p$ = 0.2913 and $r_g$ = 0.3079), branches per plant ($r_p$ = 0.2795 and $r_g$ = 0.2901) and 100 seed weight ($r_p$ = 0.2339 and $r_g$ = 0.2444). Such associations are desirable and selection for above traits would be useful in simultaneous improvement of these traits. Positive association of biological yield per plant with seed yield per plant was obtained in the present study is in conformity with the results of Shrivastava and Shukla (1998), Nehru *et al.* (1999), Singh and Yadava (2000), Narne *et al.* (2002), Ramana (2003), Kushal Chandel *et al.* (2005), Praveen kumar *et al*. (2005)and Hina Kausar (2006).

Positive association of number of pods per plant with seed yield per plant was obtained in the present study is in conformity with the results of Sailaja (1997), Taware *et al.* (1997), Nehru *et al.* (1999), Pooranchand (1999), Sharma and Phul (1999) Singh and Singh (1999), Thorat *et al.* (1999), Kulvir Singh *et al.*

(2000), Ramana *et al.* (2000), Agarwal *et al.* (2001), Bangar *et al.* (2003) and Ramana (2003).

Positive association of harvest index with seed yield per plant obtained in the present investigation is in agreement with the results reported by Nirmala Kumari and Balasubramanian (1991), Sailaja (1997), Mohana Rao (1999), Kulvir Singh *et al.* (2000), Radha Krishna Murthy *et al.*(2001), Ramana (2003), Basavaraja. *et al.* (2005), Kushal Chandel *et al.* (2005), Mishra and Rao (2005) and Praveen Kumar *et al*.(2005).

Positive association of seeds per pod with seed yield per plant obtained in the present investigation is in agreement with the results of Kalaimagal (1991), Kulvir Singh *et al.* (2000), Ramana *et al*. (2000), Singh and Yadava (2000), Agarwal. *et al*. (2001), Namrata Jain *et al.* (2002) and Mishra and Rao (2005).

Days to 50% flowering showed significant positive association with days to maturity and 100 seed weight. These findings are agreement with Harer and Deshmukh (1992), Mohana Rao (1999), Ramana (2000) Praveen Kumar *et al*.(2005). It also showed significant negative association with number of branches per plant. These findings are in agreement with Mehetre *et al*.(1994a) and Ramana *et al* (2000) It also showed significant negative association with protein content. These findings are in agreement with Mohana Rao (1999), Ramana (2003).

Days to maturity showed significant positive association with 100 seed weight. These findings are in agreement with Sailaja (1997), Dogney *et al.* (1998)

Ramana *et al.* (2000), Bangar *et al.* (2003) Ramana *et al.* (2003). Positive association with seeds per pod was reported by Sailaja (1997), Mohana Rao *et al.* (1999) Ramana *et al.* (2000) and also positive association with pod length and negative association with pods per plant. These findings are in agreement with Mehetre *et al.* (1995), Mohana Rao *et al.* (1999), Pooranchand (1999) and negative association with oil content was reported by Johnson *et al.* (1955).

Plant height showed significant positive association with seeds per pod. These findings are in agreement with Amarnath *et al.* (1991), Lakhani (1993), Ramana *et al.* (2000) and Ramana *et al.* (2003).

Plant height showed significant positive association with biological yield per plant and the same was also reported by Paschal and Wilcox (1975), Sailaja (1997) and Kushal Chandel *et al.* (2005).

Plant height showed significant positive association with protein content and harvest index and the same was reported by Sailaja (1997), Mohana Rao *et al.* (1999), and Ramana *et al.* (2003).

Plant height showed significant positive association with 100 seed weight similar result was reported by Narne *et al.* (2002), Ramana (2003) and Praveen Kumar *et al.* (2005). Plant height showed significant positive association with pod length which was in agreement with Ramana *et al.* (2000).

Number of branches per plant showed significant positive association with biological yield per plant and these results are in agreement with Kulvir Singh et al (2000), Murthy *et al.* (2001) and Ramana (2003). Number of branches per plant also showed significant positive association with harvest index, protein content and these results are in agreement with Sailaja (1997), Mohana Rao *et al.* (1999). This clearly indicates that selection of these characters improve the yielding ability in soybean.

Number of pods per plant exhibited significant positive association with biological yield per plant and harvest index .These findings are in agreement with the results obtained by Nehru *et al.* (1999), Kulvir Singh *et al.* (2000), Agarwal *et al.* (2001), and Praveen Kumar *et al.* (2005). Number of pods per plant also showed negative correlation with 100 seed weight. These findings are in agreement with Agarwal *et al.* (2001), and Chamundeswari and Aher. (2003).

Pod length showed significant positive association with number seeds per pod. These results are in conformity with Ramana *et al.* (2000). Number of seeds per pod showed significant negative association with protein content. These results are in conformity with Praveen Kumar *et al.* (2005). Number of seeds per pod showed significant positive association with 100 seed weight. These results are in conformity with Rajasekharan *et al.* (1980) and Sailaja (1997).

100 seed weight showed positive association with biological yield per plant. These results are in conformity with Srivastava and Jain (1994), Sailaja (1997) Ramana. (2003) and Kushal Chandel *et al.* (2005).

Protein content showed negative association with oil content. Similar results were reported by Diaz-Carasco (1985), Nehru *et al.*(1999), Ramana (2003) and Praveen Kumar *et al.* (2005).

## 5.4 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and yield attributing characters is the net result of the direct effect of the yield component and indirect effect through other yield attributing characters.

The total correlation between grain yield and its component characters may sometimes be misleading. Since, it may be over or under estimates of its association with other characters. Hence direct selection on correlated response basis may not be useful. The correlation coefficient needs to be split into direct and indirect effects, using path coefficient analysis for critical evaluation as many characters affect a given trait. Thus the correlation and path analysis in combination, can give a better insight, into cause and effect relationship between different pairs of characters. As a guideline for interpretation of path analysis results, the following broad points may be kept in view (Singh and Chaudhary, 1997).

- If the correlation coefficient between a causal factor and the effect is almost equal to its direct effects, then correlation explains the true relationship through this trait will be effective.

- If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.

- Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed i.e. restrictions to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

- If the correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on the character.

- The residual effect determines how best the causal factors account for the variability of the dependent factor. If residual effect is high, some other factors, which have not been considered here, need to be included in this analysis to account fully for the variation in yield.

Based on the above criteria, path coefficient analysis was worked out for 12 characters with seed yield to obtain information of direct and indirect contribution of various yield components to yield and to formulate a sound basis for selection in soybean.

### 5.4.1 Days to 50% flowering

Days to 50% flowering exhibited a negative direct effect and positive correlation with seed yield per plant. Its positive indirect effects are through biological yield per plant, 100 seed weight, days to maturity, pods per plant, harvest index, pod length, seeds per pod and plant height. While, it had negative indirect effects through protein content, branches per plant and oil content. The magnitude of positive indirect effect is greater through biological yield per plant and 100 seed weight. Hence selection through these characters may bring about improvement in yield. These results are in conformity with the reports of Sailaja (1997), Mohana Rao (1999),Raut *et al.* (2001) and Praveen Kumar *et al.* (2005).

### 5.4.2 Days to maturity

Days to maturity exhibited a positive direct effect and positive correlation with seed yield per plant. This trait exhibited positive indirect effect through 100 seed weight, biological yield per plant, pod length, seeds per pod, branches per plant, plant height and negative indirect effect through pods per plant, days to 50% flowering, protein content, harvest index and oil content. Similar results were also reported by Harer and Deshmukh (1992), Ramana *et al.* (2000) and Praveen Kumar *et al.* (2005).

### 5.4.3 Plant height (cm)

Plant height exhibited positive direct effect on seed yield via biological yield, harvest index, pods per plant, 100 seed weight, protein content, days to maturity, plant height, seeds per pod and days to maturity and negative indirect effect through days to 50% flowering and oil content. These results are in conformity with Mohana Rao (1999), Raut *et al.* (2001) and Praveen Kumar *et al*. (2005).

### 5.4.4 Number of branches per plant

This trait exhibited positive direct effect and positive correlation with seed yield. The positive indirect effects are through biological yield per plant, harvest index, pods per plant, protein content, days to 50% flowering, days to maturity, pod length, plant height and seeds per pod. It had negative indirect effect through 100 seed weight and oil content. These results are in conformity with Sailaja (1997), Mohana Rao (1999) and Praveen Kumar *et al.* (2005).

### 5.4.5 Number of pods per plant

Pods per plant showed positive direct effect and highly significant positive correlation with yield. It has positive indirect effect through biological yield per plant, harvest index, pod length, seeds per pod, branches per plant, plant height. These results are in conformity with Mohana Rao (1999) and Praveen Kumar et al (2005).

Negative indirect effect through 100 seed weight, days to maturity, oil content, days to 50% flowering and protein content. Hence restriction has to be imposed to nullify the undesirable negative indirect effects while adopting selection in order to make use of direct effect. These results are in conformity with Raut *et al.* (2001) and Kushal Chandal *et al.* (2005).

### 5.4.6 Pod length (cm)

Pod length showed positive direct effect and positive correlation with yield. It has positive indirect effect through biological yield per plant, 100 seed weight, pods per plant, days to maturity, harvest index, seeds per pod, oil content, plant height, branches per plant and negative indirect effect through protein content, and days to 50% flowering Hence restriction has to be imposed to nullify the undesirable negative indirect effect while adopting selection in order to make use of direct effect. These results are in conformity with Kumar and Nadarajan (1994), Ramana *et al.* (2000) and Mukhekar *et al.* (2003).

**5.4.7 Number of seeds per pod**

Seeds per pod showed positive direct effect and a positive correlation with seed yield per plant. It had positive indirect effects through biological yield per plant, 100 seed weight, pods per plant, pod length, harvest index, days to maturity, number of branches per plant and plant height. It had negative indirect effect through protein content, days to 50% flowering and oil content. These results are in conformity with Sailaja (1997) and Kushal Chandal *et al*. (2005)..

**5.4.8 100 seed weight (g)**

This trait had positive direct effect and positive correlation with seed yield per plant. It had negative indirect effects through number of pods per plant, protein content, days to 50% flowering, number of branches per plant, oil content and had positive indirect effects through biological yield per plant, pod length, days to maturity, harvest index, number of seeds per pod and plant height. These findings are in close agreement with result obtained by Sailaja (1997), Mohana Rao (1999) and Dogney *et al.* (2003).

**5.4.9 Biological yield per plant (g)**

This trait had highest positive direct effect and positive correlation with seed yield per plant. It had positive indirect effects through pods per plant, harvest index, 100 seed weight, pod length, branches per plant, days to maturity, seeds per pod, protein content, plant height and had negative indirect effect through days to 50% flowering and oil content. These findings are in close agreement with results obtained by Narne *et al.* (2002), Ramana (2003) and Praveen Kumar *et al.* (2005).

### 5.4.9.10 Harvest index (%)

This trait exhibited positive direct effect and positive correlation with seed yield. It had high positive indirect effect through pods per plant and biological yield per plant. These findings are in close agreement with result obtained by Mohana Rao (1999), Ramana (2003) and Kushal Chandel *et al.* (2005).

### 5.4.11 Protein content (%)

This trait exhibited positive direct and positive correlation with seed yield. It had positive indirect effect through days to 50% flowering, biological yield per plant, number of branches per plant and plant height. It had negative indirect effect through 100 seed weight, harvest index, pod length, days to maturity, oil content, number of seeds per pod and number of pods per plant. These findings are in close agreement with results obtained by Sailaja (1997) and Praveen Kumar *et al.* (2005).

### 3.4.12 Oil content (%)

This trait exhibited positive direct and negative correlation with seed yield per plant. It had positive indirect effect through pod length, days to 50% flowering and negative indirect effect through number of pods per plant, biological yield per plant, harvest index, days to maturity, number of branches per plant, protein content, 100 seed weight, seeds per  pod and plant height. These findings are in close agreement with result obtained by Praveen Kumar *et al.* (2005).

Among the yield component characters biological yield contributed maximum positive direct effect. Hence selection through this trait along with more pods per plant and harvest index will be effective in yield improvement.

The overall perusal of results indicate that taller soybean genotypes with more number of pod bearing branches, high biological yield and harvest index appears to be an ideal genotype.

# CHAPTER –VI

## SUMMARY

The present investigation was carried out with 45 genotypes of soybean [*Glycine max* (L.) Merrill] during *kharif,* 2007 at Regional Agricultural Research Station, Lam.

The mean, variability, heritability, genetic advance, genetic divergence, character association and the magnitude of direct and indirect effects of yield components on yield were studied for 13 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%), protein content (%), oil content (%) and seed yield per plant (g).

The analysis of variance showed significant difference among the genotypes for all characters studied indicating that the data generated from the diverse material shall represent wide variability. The genotypic coefficient of variation for all characters studied were lesser than the phenotypic coefficient of variation. High PCV coupled with high GCV observed for number of branches per plant, number of pods per plant, biological yield per plant (g), harvest index (%) and seed yield per plant (g) indicating the presence of wider variability for these traits in the population studied. High heritability coupled with high genetic advance as percent of mean was observed for days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g),

harvest index (%) and seed yield per plant (g) indicate the operation of additive gene action in the inheritance of these traits and improvement in these characters is possible through simple selection.

The results of multivariate analysis indicated the presence of considerable genetic divergence among the 45 genotypes studied. The genotypes were grouped into 6 clusters. Clustering pattern of genotypes did not follow geographic origin, suggesting that geographical isolation may not be the only factor causing genetic diversity. Out of 13 characters studied, days to maturity followed by number of pods per plant contributed maximum towards divergence. Based upon the divergence studies crosses may be made between the genotypes of clusters III and cluster VI to get good recombinants. The maximum inter-cluster distance was observed between cluster III and cluster VI followed by cluster I and cluster VI. Selection of the genotypes from these distant clusters for hybridization programme may result into desirable recombinants. The principal component analysis identified 5 principal components. The contribution by the first PC is maximum (38.02 %) and is loaded with maximum contributing variables, days to maturity followed by biological yield per plant (g) while the second and the third principal components contributed 20.63 % and 10.78 % of total variance respectively.

Hierarchical cluster analysis through Ward's minimum variance dendrogram revealed the sub groups in the major group of genotypes in breeding programmes. The clustering pattern is in accordance with the PCA analysis.

The correlation study indicated that biological yield per plant (g) followed by number of pods per plant and harvest index (%) had positive association with seed yield indicating the possibility of simultaneous improvement of these characters along with seed yield.

The path analysis indicated that biological yield per plant (g), number of pods per plant, harvest index (%) exerted perfect direct positive effect on seed yield. As direct effects of these parameters are almost equal direct selection through these traits for improvement of seed yield is highly effective. The indirect selection through biological yield per plant (g), number of pods per plant, harvest index (%) exerted maximum indirect effects on seed yield per plant.

The present study revealed that major emphasis should be laid on selection for more biological yield per plant (g) coupled with more number of pods per plant and harvest index (%) for realizing higher seed yield in soybean.

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