“Genetic Studies of Phenological and Yield Components in Promising Lines of Soybean”

THESIS

Submitted to the

Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur

In partial fulfillment of the requirement for the Degree of

MASTER OF SCIENCE

In

AGRICULTURE
(PLANT BREEDING AND GENETICS)

By

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Jabalpur (MP)

2012

CERTIFICATE- I

This is to certify that the thesis entitled, **"Genetic Studies of Phenological and Yield Components in Promising Lines of Soybean"** submitted in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE IN AGRICULTURE (Plant Breeding and Genetics)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Miss Amrita Badkul** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma (Certificate awarded etc.) or has been published / published part has been fully acknowledged. All the assistance and help received during the course of the investigation has been acknowledged by her.

(Dr. A.N. Shrivastava)
Chairman of Advisory Committee

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

Chairman: (Dr. A.N. Shrivastava) ……………………………………………..

Member: (Dr. M.K. Shrivastava) ……………………………………………..

Member : (Dr. Smt. Rajani Bisen) ……………………………………………..

Member : (Dr. R.B. Singh) ……………………………………………..

CERTIFICATE-II

This is to certify that the thesis entitled **"Genetic Studies of Phenological and Yield Components in Promising Lines of Soybean"** submitted by **Miss Amrita Badkul** to the Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE IN AGRICULTURE** in the Department of **Plant Breeding and Genetics, JNKVV, Jabalpur,** after evaluation has been approved by the Student's Advisory Committee and the External Examiner and by the student's Advisory Committee after an oral examination on the same.

Place : Jabalpur	**(Dr. A.N. Shrivastava)**
Date: …………	Chairman of Advisory Committee

MEMBER OF THE STUDENT'S ADVISORY COMMITTEE

Chairman :	(Dr. A.N. Shrivastava)	……………………
Member :	(Dr. M.K. Shrivastava)	……………………
Member :	(Dr. Smt. Rajani Bisen)	……………………
Member :	(Dr. R.B. Singh)	……………………...
Head of the Department :	(Dr. D.K. Mishra)	……………………
Director of Instructions :	(Dr. P.K. Mishra)	..……………………

TO MY BELOVED

GRAND MA

AND PARENTS

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Prostration and adoration to the lotus feet of God almighty for giving this opportunity to express my heart felt gratitude to all those who have extended help to make this study a success.

Space does not follow to my desired extent and words fails to express adequately, the feeling of my unfathomable sense of reverential gratitude which, I owe to most respected member and the chairman of my advisory committee, Dr. A.N. Shrivastava, Principal Scientist (Soybean), (Department of Plant Breeding & Genetics, JNKVV, Jabalpur) for his inestimable support, preeminent supervision and giving me an opportunity to work under his guidance, valuable suggestions, sustained interest and encouragement which made this research possible.

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I am tempted to individually thank all of my seniors. I am mentioning my unforgettable seniors especially Prabha mam, Sagar sir, Stuti mam, Amita mam, Arpita mam, Varsha mam. I am especially grateful to my colleagues Shubham, Priti, Priti Vanshkar, Pratibha, Vikash, Uma Shankar, Vikash Kumar, Manisha, Purti, Apeksha, Monika, Manshi, Deepak sir, and my loveable juniors Priyanka, Aakansha, Jitendra, Priti and Hemlata.

I also like to thank Sunder bhyia, Kodulal and all the Workers on the field who helped in my field work.

Jabalpur

Dated: (Amrita Badkul)

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VITA

The author of this thesis Miss Amrita Badkul D/o Sh. Ashok Kumar Jain was born on 21 October, 1986 at Tikamgarh (M.P.). She studied in Govt. Girls Higher Secondary School (M.P.) and passed Higher Secondary Examination in year 2004 securing first division.

She joined Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) and successfully completed the degree of B.Sc. (Ag.) from College of Agriculture, Tikamgarh (M.P.) in the year 2010 with first division (7.71 OGPA out of 10.00 point scale)

For further study, she got admission in M.Sc. (Ag.) for specialization in Plant Breeding and Genetics at College of Agriculture, Jabalpur (M.P.). The author sincerely completed all the prescribed course work and now thesis is submitted in partial fulfillment of the requirement of the degree M.Sc. (Ag.) in Plant Breeding and Genetics.

***

i. APPENDIX

Weekly meteorological parameters during crop season (2011-12)

Month	Weeks	Temperature		RH %		Rainfall (mm)	No. of rainy days	Sunshine hours
		Max	Min	Max	Min			
June	23	40.1	26.4	61	28	15.4	1	7.4
	24	39.6	25.2	73	37	23.4	3	6.2
	25	31.0	22.5	89	84	253.2	5	2.8
	26	27.4	22.8	90	80	91.3	4	0.4
July	27	32.8	23.8	86	61	15.2	2	4.9
	28	32.0	23.5	92	71	46.4	3	3.1
	29	30.3	22.8	93	83	429.1	6	2.5
	30	29.9	22.7	90	70	119.2	3	9.4
August	31	31.1	23.6	92	82	140	5	3.9
	32	28.7	22.7	93	85	118.5	6	1.5
	33	29.8	22.7	92	78	57.6	3	4
	34	30.9	22.9	93	70	14.6	3	6.3
September	35	31.5	22.8	96	71	150.6	7	5.8
	36	29.5	22.6	94	80	221.6	4	1.2
	37	29.7	22.4	93	73	92.2	3	3.9
	38	30.8	21.9	93	67	41.0	4	5.1
October	39	31.3	20.8	86	56	00	0	6.9
	40	32.2	18.6	90	54	5.2	1	9.0
	41	32.4	19.1	92	43	00	0	8.3
	42	32.6	15.8	89	31	0	0	9.3
November	43	31.8	13.9	87	30	0	0	8.9
	44	31.0	11.0	86	24	0	0	9
	45	31.8	12.1	89	29	0	0	8.3
	46	30.9	12.4	89	28	0	0	8.0

ii. APPENDIX

Genotype	Vegetative phase(days)	Reproductive phase (days)	Plant height (cm.)	No. of branches/ plant	No.of Pods/plant	No. of seeds/plant	NO. of seeds/pod	Biological yield/plant(g)	Harvest index(%)	100 seed weight(g)	Yield/ plant(g)
Code 1	42.50	56.00	42.90	4.50	80.30	162.50	2.03	25.64	44.77	7.08	11.46
Code 2	40.00	58.00	43.60	2.80	81.60	162.50	1.99	27.77	51.57	8.95	14.25
Code 3	41.00	58.00	32.90	3.30	54.80	93.00	1.71	22.77	48.68	9.29	11.11
Code 4	41.50	55.00	52.30	3.60	68.00	139.50	2.06	22.40	53.02	8.55	11.84
Code 5	43.00	55.50	51.90	3.40	70.90	135.50	1.92	28.67	46.54	9.80	13.29
Code 6	43.00	56.50	53.20	3.90	80.30	162.00	2.02	23.18	48.50	7.02	11.25
Code 7	40.00	58.00	43.90	2.70	61.70	156.00	2.52	26.68	52.32	9.00	14.05
Code 8	41.00	57.50	44.90	3.40	82.90	144.50	1.74	24.59	52.63	8.99	12.94
Code 9	41.50	57.00	52.20	4.60	83.20	148.00	1.77	27.56	58.15	10.07	15.94
Code 10	36.00	59.50	44.30	4.10	57.30	110.50	1.93	21.66	53.57	10.57	11.60
Code 11	44.50	52.00	44.70	4.60	72.40	139.00	1.92	24.25	55.52	9.71	13.49
Code 12	40.00	57.00	37.20	4.40	62.30	125.00	2.01	26.74	51.52	11.08	13.83
Code 13	42.50	52.00	46.40	4.10	60.70	114.00	1.88	17.18	53.65	8.27	9.17
Code 14	46.00	49.50	43.00	4.20	67.90	141.00	2.07	19.32	53.31	7.33	10.30
Code 15	40.00	59.00	56.80	4.60	76.20	144.50	1.89	29.09	49.85	10.40	14.55
Code 16	35.50	57.50	59.30	3.30	60.60	129.50	2.14	29.72	52.40	12.06	15.58
Code 17	36.00	61.00	37.10	3.30	52.70	119.00	2.25	19.26	56.79	9.21	10.92
Code 18	46.00	54.50	50.90	4.00	79.30	191.50	2.43	27.31	49.86	7.11	13.63
Code19	42.00	54.50	55.20	5.00	68.40	144.00	2.11	23.97	56.41	9.39	13.51
Code 20	40.00	58.50	46.30	4.30	70.90	126.00	1.79	22.76	48.97	9.64	11.13
Code 21	37.50	62.00	46.80	4.90	66.40	109.00	1.64	25.94	50.02	11.91	12.97
Code 22	32.50	55.00	32.50	1.10	26.10	46.50	1.79	11.11	52.41	12.47	5.83
Code 23	43.00	55.00	53.30	5.00	83.80	162.50	1.94	29.43	53.12	8.28	15.56
Code 24	35.50	53.00	33.50	2.00	25.35	36.50	1.45	8.39	30.77	7.69	2.56
Code 25	42.00	54.50	44.20	4.30	68.10	131.50	1.93	20.74	49.54	7.64	10.28
Code 26	29.00	59.50	28.50	0.50	21.90	34.50	1.58	8.57	36.82	9.25	3.15

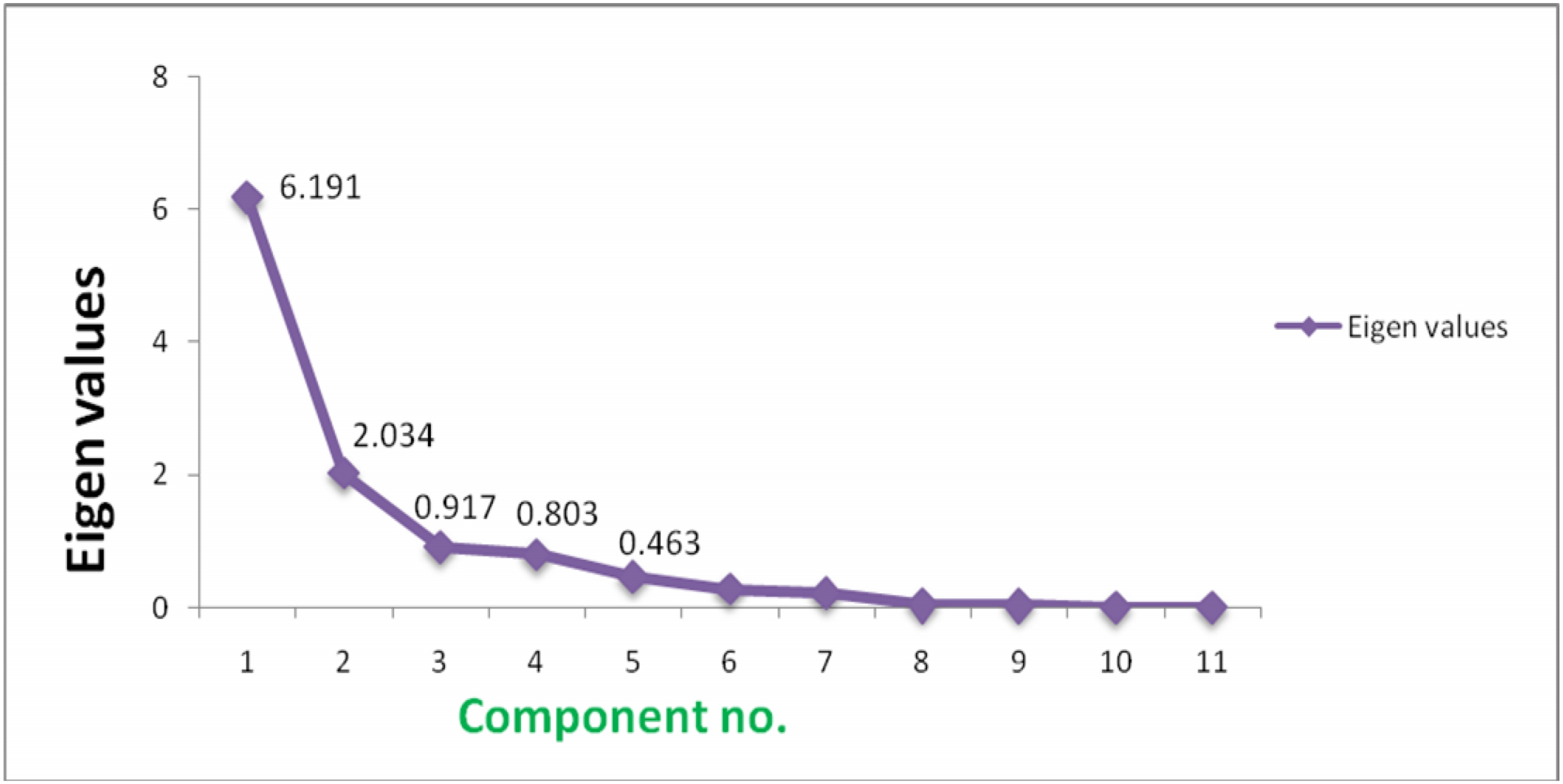

Figure 2: Screen plot of principal component analysis of soybean genotype between eigen value and principal components.

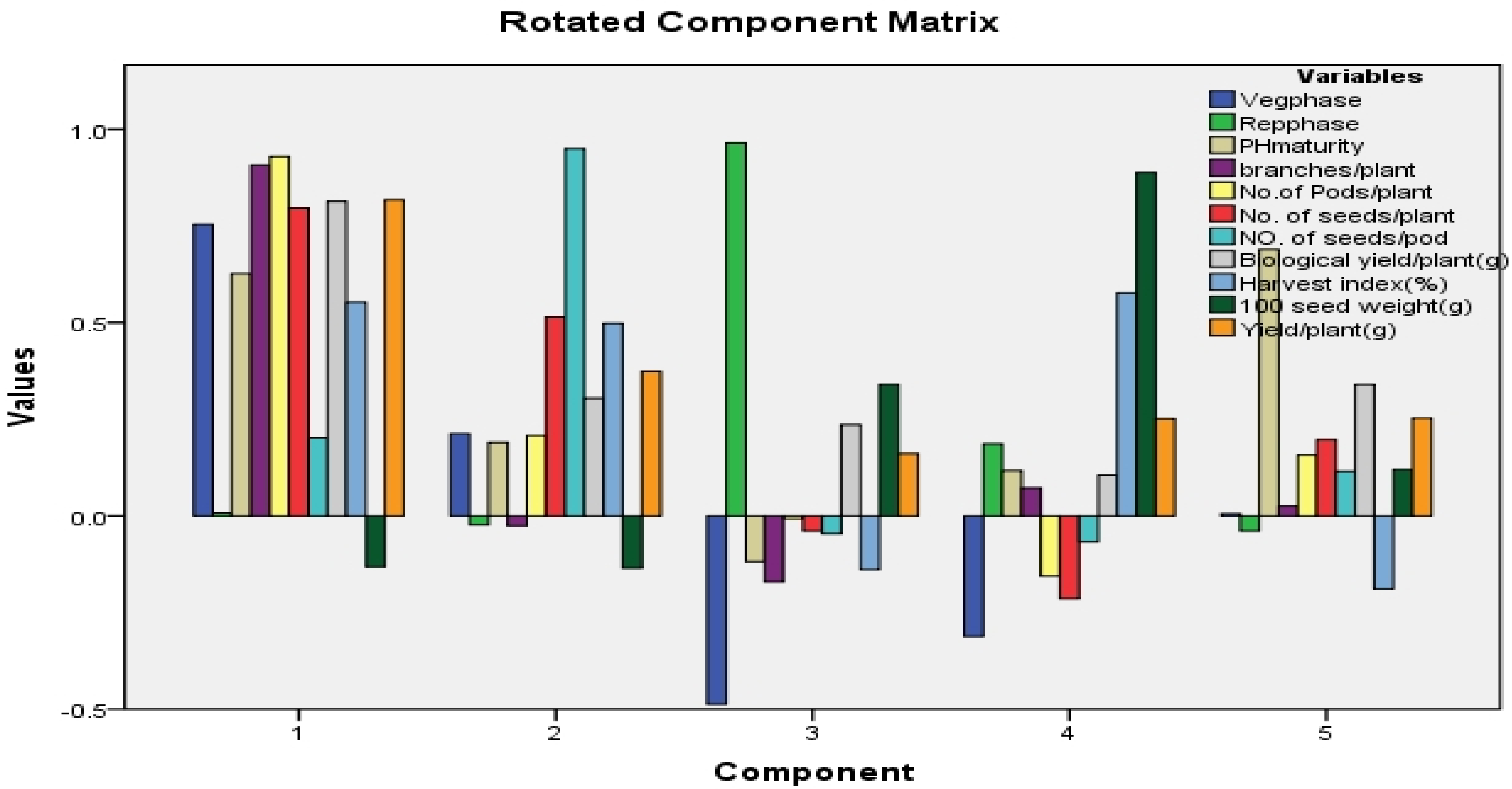

Figure 3: 11 Phenological and yield traits of soybean genotypes showed in bar diagram.

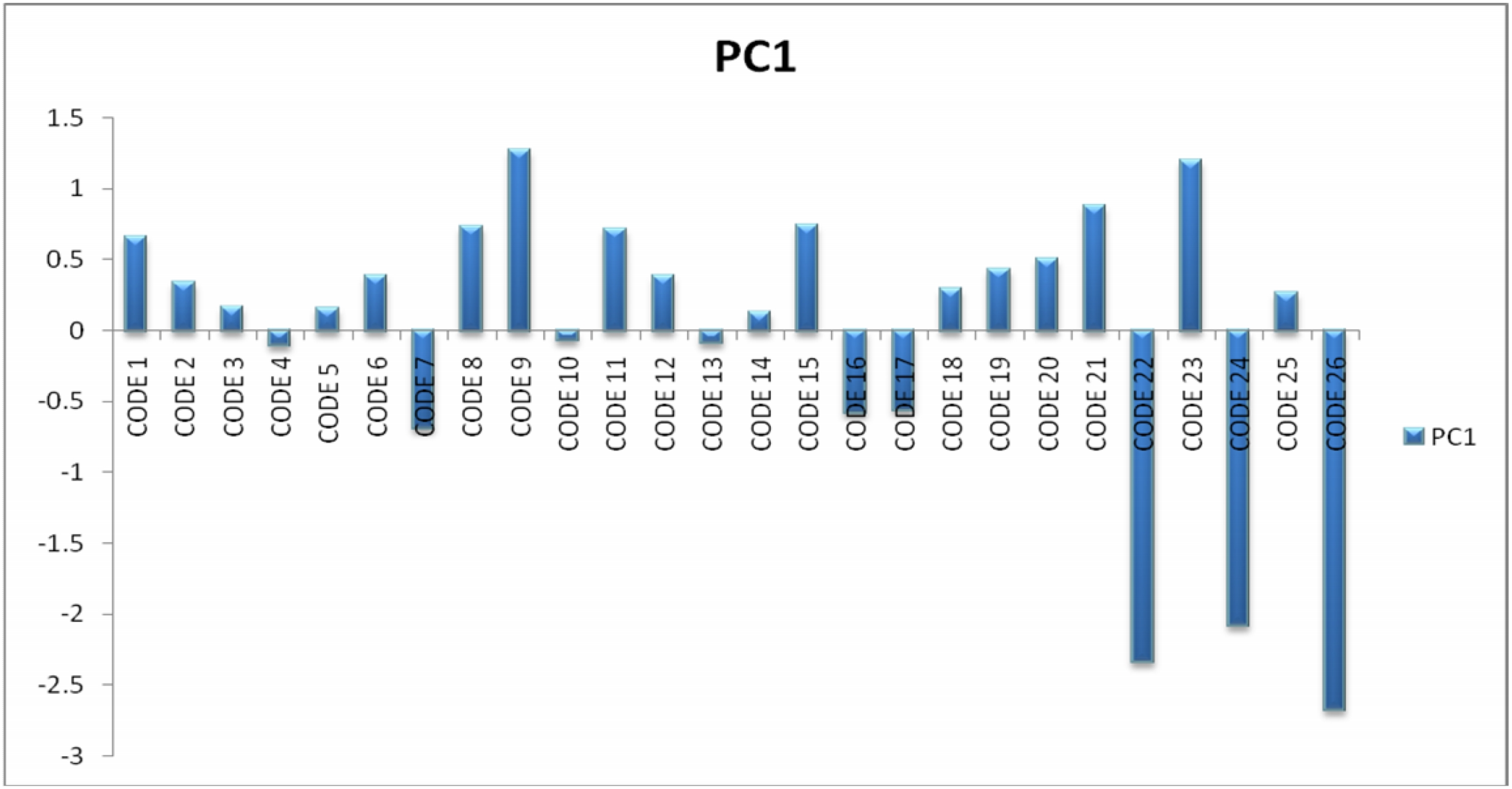

Figure 4: Bar diagram of Principal component 1

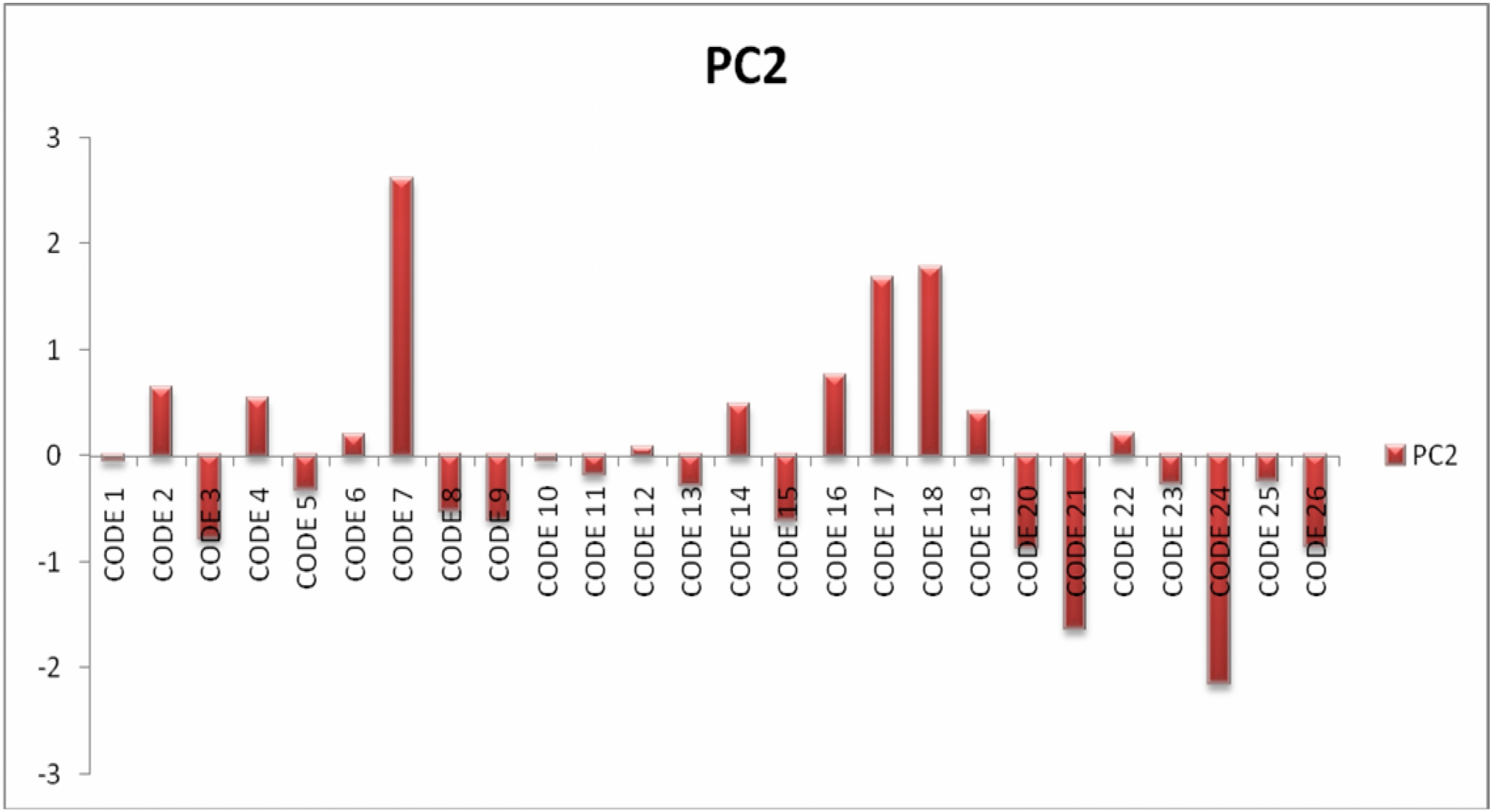

Figure 5: Bar diagram of Principal component 2

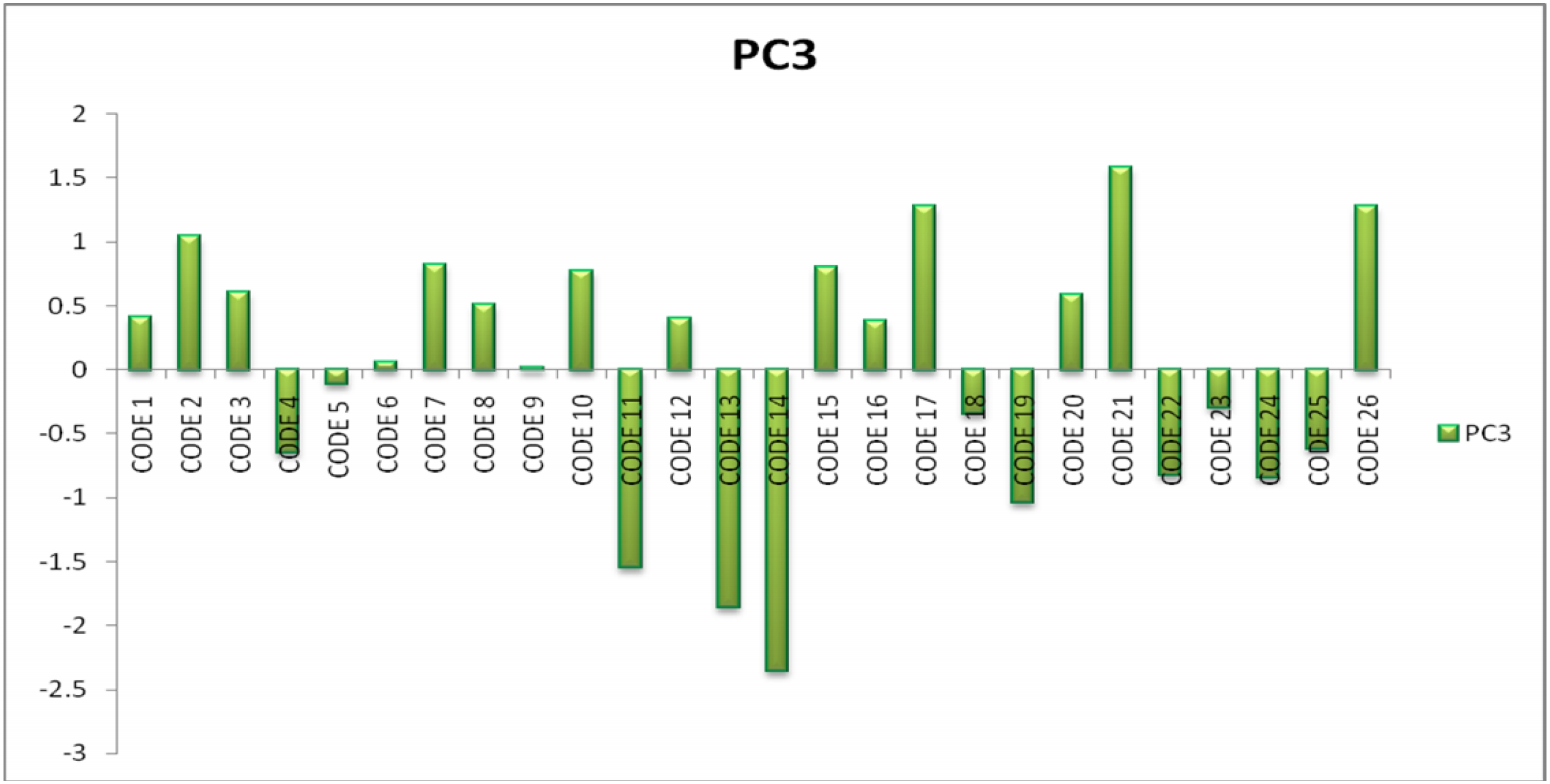

Figure 6: Bar diagram of Principal component 3

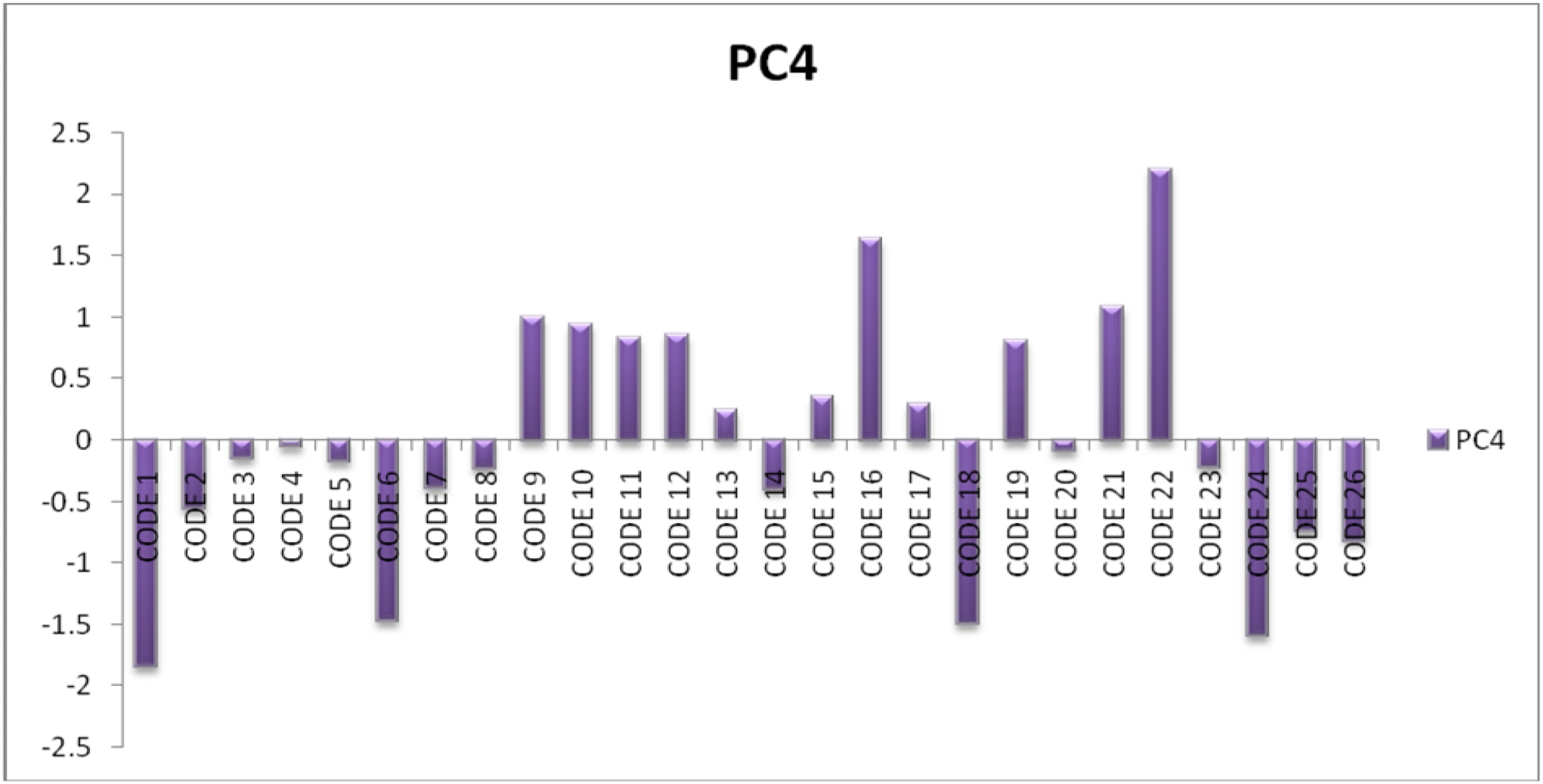

Figure 7: Bar diagram of Principal component 4

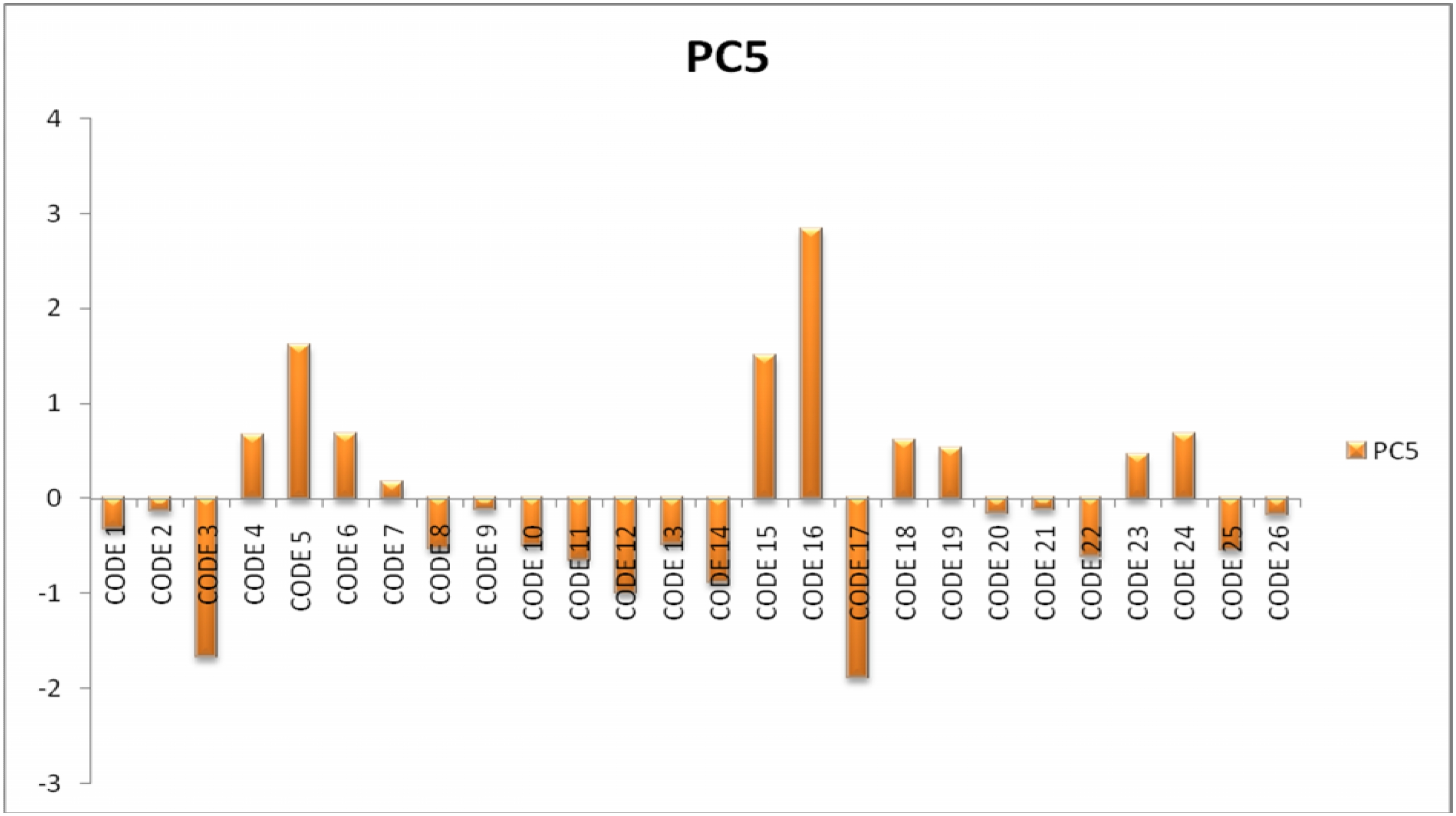

Figure 8: Bar diagram of Principal component 5

CHAPTER-I

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] belongs to family *Leguminosae* syn. *Fabaceae*, subfamily *Papilionoideae,* tribe *Phaseoleae* and sub tribe *Glycininea*. The genus *Glycine* (Willd) is divided into two sub genera, *Glycine* and *Soja* (Moench) F.J. Herm. The subgenus *Glycine* is composed of several wild perennial inbreeding species indigenous to Australia (Hermann, 1962; Newell and Hymowitz, 1980; Tindale and Craven, 1993). The subgenus *Soja* includes the cultivated soybean, *Glycine max* and wild soybean, *Glycine soja*. Both the species are annual and diploid with 2n=40 and hybridize readily. The origin of soybean is in north and central China (Hymowitz, 1970 and Cuzin, 1976). Soybean first emerged as a domestic crop around eleventh century B.C. in the eastern half of northern China and migrated to southern China, Korea, Japan and South-East Asia probably between eleventh to third century B.C. (Hymowitz, 1970). Soybean is under cultivation since 17th century in Europe but it was probably introduced in India in between 1870 and 1880 (Parmar, 1997).

Soybean ranks first amongst oilseed crops in the world and India both. India ranks fourth in terms of soybean area in the world behind only to USA, Brazil and Argentina. However, in terms of total production, India ranks fifth in the world after USA, Brazil, Argentina and China. Within four decades of its introduction to central and southern parts of the country, it has made a phenomenal growth among agrarian community. There are very few examples of any other crop taking such giant strides in terms of adoption among farmers, as soybean has achieved. At present, soybean is being grown in 10.334 million hectare with 11.939

million tonnes of production and 1155 kg ha^{-1}. In Madhya Pradesh, it is grown in 5.730 million hectare with 6.171 million tones of production and 1077 kg ha^{-1}. It plays a pivotal role to meet the demand of the edible oil (25%) and earns huge amount (more than 7000 crore per annum) of foreign exchange through export of soybean de-oiled cake. Soybean has largely been responsible in uplifting socio-economic status of farmers.

Soybean contains all the three macronutrients required for good nutrition along with substantial quantity of minerals, vitamins and essential amino acids. Owing to its oil and protein profile, this crop has an important role in nutritional security of masses. It contains lysine content comparable with cow milk. Soybean oil is either directly used as edible oil or for manufacturing of vanaspati ghee. It is widely used in variety of foods and also in production of different antibiotics. Thus, it is considered as wonder crop.

The yield level in soybean is hovering around 1.2 tonne ha^{-1} which is quite low. Yield is a complex entity influenced by several phenological, physiological, yield traits and environment in soybean as true in other crops also. At J.N.K.V.V., several advanced generation fixed genotypes have been developed of different crosses with concerted efforts mounting appropriate selection pressure. Hence, it becomes imperative to know the status of variability, heritability, genetic advance, association, direct and indirect effect of various traits under study in these isolated lines for the assessment of genetic improvement. In later generations of self pollinated crops like soybean, assessment of different traits is proved to be quite meaningful for the exploitation of additive and positive genes and identification of promising genotypes.

In view of above aspects and looking to the importance of simultaneous genetic information on various important phenological and yield traits, the present investigation was conducted on advanced generation fixed lines of soybean with following objectives:

1. To study the genetic variability of phenological and yield components.
2. To study association among phenological and yield components.
3. To study the direct and indirect effects of various phenological and yield components on yield.
4. Identification of superior genotypes.
5. Characterization on the basis of morphological traits.

CHAPTER-II

REVIEW AND LITERATURE

Soybean is considered as one of the important grain legume, because of high nutritional value and oil content. In India, it is extensively cultivated during *kharif* season. Soybean has witnessed increasing trends in the production and productivity over the years. So there is need to develop high yielding varieties with proper plant architecture, which are resistant to biotic and abiotic stresses. An attempt has been made in the present investigation to understand the variability, correlation, path and principal component between the soybean genotypes. The review of literature pertaining to these aspects are presented in this chapter under the following headings:

2.1 Parameters of genetic variability

Analysis of variance, Mean and range, Genotypic and phenotypic coefficient of variation, Heritability, Genetic advance

2.2 Association analysis

2.2.1 Correlation coefficient analysis

2.2.2 Path coefficient analysis

2.3 Principal component analysis

2.4 Characterization

2.1 Parameters of genetic variability

Fisher (1918) for the first time studied the genetic variability in relation to environmental variability. Later on several workers have also derived different techniques for the estimation of components of variance (Wright, 1921, Robinson *et al*., 1951, Warner, 1952, Kaw and Menon, 1972 and Tawar and Tiwari, 1981).

Frankel (1947) emphasized the importance of heritability of metric traits in plant population; Warner (1952) first developed the detailed method for estimating the heritability in plants.

Johnson *et al*. (1955) defined heritability as a ratio of genotypic to phenotypic variance and stressed its importance in selection programme. He also indicated that estimates for heritability when studied along with genetic advance would provide appropriate information than the study of heritability alone. A brief review of the work done on soybean on this aspect has been given below:

Characters	**Genotypes used**	**Variability parameters**				**References**
		GCV	**PCV**	**h^2**	**GAM**	
(1) Plant height	121	High	High	High	High	Amaranath *et al.,* 1991
	21	Low	High	Low	High	Tiwari & Bhatnagar, 1991
	81	High	High	Low	Moderate	Kalaimagal, 1991
	-	-	-	Moderate	High	Yaduvanshi,1992
	58	High	High	High	High	Ghatge and Kadu, 1993
	70	High	High	High	High	Kumari and Balasubramanian, 1993
	51	High	High	High	High	Mahajan *et al.,* 1994
	50	High	High	High	High	Shrivastava & Shukla, 1998
	-	High	High	High	High	Ramgiry *et al.,* 1998
	30	Low	Low	High	Low	Singh & Singh, 1999
	30	High	High	High	High	Thorat *et al.,* 1999
	285 lines, 5 control varieties	High	High	High	High	Siahsar and Rezai, 1999
	40	High	High	High	High	Ramana *et al.,* 2000
	56	High	High	High	High	Jain & Ramgiry, 2000
	196	High	High	High	High	Agarwal *et al.,* 2001
	03	High	High	High	High	Basavaraja, 2002
	16	High	High	High	High	Bangar *et al*., 2003
	60 (f3)	Moderate	Moderate	High	High	Kausar, 2005
	55	-	-	High	High	Gohil *et al.,* 2006
	-	-	-	High	High	Vishnoi, 2006
	25	High	High	-	-	Sirohi *et al.,* 2007
	30	-	-	High	High	Nag *et al*., 2007

	14	High	High	High	High	Islam and Mian, 2008
(2) No. of branches per plant	121	High	High	High	High	Amaranath *et al.,* 1991
	81	High	High	High	High	Kalaimagal, 1991
	51	High	High	Low	High	Mahajan *et al.,* 1994
	50	High	High	High	Moderate	Shrivastava & Shukla, 1998
	285 lines, 5 control varieties	High	High	-	-	Siahsar and Rezai, 1999
	42	High	High	high	Moderate	Ramana *et al.,* 2000
	196	High	High	high	Moderate	Agarwal *et al.,* 2001
	03	High	High	High	High	Basavaraja, 2002
	16	High	High	High	High	Bangar *et al,.* 2003
	60 (f3)	High	High	High	High	Kausar, 2005
	17	Moderate	Moderate	high	High	Karad *et al.,* 2005
	84	Moderate	Moderate	high	High	Parameshwar, 2006
	31	-	-	High	-	Aditya *et al.,* 2011
(3) No. of pods per plant	21	Low	High	Low	Low	Tiwari & Bhatnagar, 1991
	121	High	High	Moderate	High	Amaranath *et al.,* 1991
	81	Moderate	High	Low	Low	Kalaimagal, 1991
	-	High	High	-	-	Yaduvanshi, 1992
	70	High	High	High	High	Kumari & Balasubramanian, 1993
	-	High	High	-	-	Koniecyny *et al.,* 1994
	51	High	High	High	High	Mahajan *et al.,* 1994
	50	High	High	-	-	Shrivastava & Shukla, 1998
	30	High	High	High	High	Singh & Singh, 1999
	30	High	High	High	High	Thorat *et al.,*1999
	285 lines, 5 control varieties	High	High	High	High	Siahsar and Rezai, 1999
	42	High	High	High	High	Ramana *et al.,* 2000
	56	-	-	High	High	Jain & Ramgiry, 2000
	196	High	High	High	High	Agarwal *et al.,* 2001
	03	High	High	High	High	Basavaraja, 2002
	16	Moderate	Moderate	-	-	Bangar *et al.,* 2003
	17	High	High	High	High	Karad *et al.,* 2005
	56	-	-	Low	-	Vart *et al.,* 2005
	84	Moderate	Moderate	High	High	Parameshwar, 2006
	55	High	High	High	High	Gohil *et al.,* 2006
	25	High	High	-	-	Sirohi *et al.,* 2007
	30	-	-	High	High	Nag *et al.,* 2007
	14	-	-	High	High	Islam and Mian, 2008
	31	High	High	High	High	Aditya *et al.,* 2011
(4) No. of	121	Moderate	High	High	-	Amaranath *et al.,*

seeds per plant						1991
	81	Moderate	High	Low	Moderate	Kalaimagal, 1991
	58	-	-	High	High	Ghatge and Kadu, 1993
	51	High	High	High	High	Mahajan *et al.,* 1994
	-	High	High	High	High	Taware *et al.,* 1997
	49	High	High	High	High	Nehru *et al.,* 1999
	30	-	-	High	High	Nag *et al.,* 2007
	14	-	-	High	High	Islam and Mian, 2008
(5) No. of seeds per pod	121	Moderate	Moderate	Low	High	Amaranath *et al.,* 1991
	81	Low	Moderate	Low	Moderate	Kalaimagal, 1991
	30	Low	Low	Low	Low	Thorat *et al.,* 1999
	42	Low	Moderate	Low	Moderate	Ramana *et al.,*2000
	56	Moderate	Moderate	-	-	Jain & Ramgiry, 2000
	196	Low	Low	Moderate	Moderate	Agarwal *et al.,* 2001
	03	High	High	Moderate	Moderate	Basavaraja, 2002
	60 (f3)	High	High	High	High	Kausar, 2005
	17	Moderate	Moderate	Moderate	Moderate	Karad *et al.,* 2005
	84	Low	Moderate	Moderate	Low	Parameshwar, 2006
(6) Biological yield per plant	50	High	High	High	High	Shrivastava & Shukla, 1998
	38	High	High	High	High	Dixit *et al*., 2002
	25	High	High	-	-	Sirohi *et al.,* 2007
	31	High	High	High	High	Aditya *et al.,* 2011
(7) Harvest index	70	Moderate	Moderate	High	High	Kumari and Balasubramanian, 1993
	38	High	High	High	High	Dixit *et al*., 2002
	56	High	High	High	High	Vart *et al.,* 2005
(8) 100 seed weight	30	High	High	High	Low	Thorat *et al.,*1999
	285 lines, 5 control varieties	-	-	High	High	Siahsar & Rezai, 1999
	56	Moderate	Moderate	-	-	Jain & Ramgiry, 2000
	16	Moderate	Moderate	-	-	Bangar *et al.,* 2003
	14	-	-	Low	-	Islam and Mian, 2008
	31	-	-	High	-	Aditya *et al.,* 2011
(9) Yield per plant	121	High	High	Low	High	Amaranath *et al.,* 1991
	81	Low	High	Moderate	High	Kalaimagal, 1991
	21	High	High	Moderate	High	Tiwari & Bhatnagar, 1991
	70	Low	Low	High	High	Kumari & Balasubramanian, 1993
	58	High	High	-	-	Ghatge and Kadu, 1993
	51	High	High	Low	High	Mahajan *et al.,* 1994
	50	High	High	High	High	Shrivastava &

						Shukla, 1998
	30	High	High	High	High	Singh & Singh, 1999
	30	High	High	Moderate	Low	Thorat *et al.,* 1999
	42	High	High	Moderate	High	Ramana *et al.,* 2000
	56	High	High	High	High	Jain & Ramgiry,2000
	196	High	High	High	High	Agarwal *et al.,* 2001
	03	High	High	-	High	Basavaraja, 2002
	38	High	High	High	High	Dixit *et al*., 2002
	16	Moderate	Moderate	High	High	Bangar *et al.,* 2003
	60 (f3)	High	High	High	High	Kausar, 2005
	17	High	High	High	High	Karad *et al.,* 2005
	84	Moderate	High	High	High	Parameshwar, 2006
	55	High	High	High	High	Gohil *et al.,* 2006
	30	-	-	High	High	Nag *et al.,* 2007
	25	High	High	-	-	Sirohi *et al.,* 2007
	31	High	High	-	-	Aditya *et al.,* 2011

Some other important traits such as genetic variability etc. studied by different workers for the identification of heritable characters are summarizing here:

Devine *et al*. (2002) evaluated that different cultivars of soybean showed significant variability for plant height and days to maturity.

Kumar *et al.* (2005) reported variability for 100 seed weight in Indian soybean.

Sujata and Basavaraja (2011) reported that the analysis of variance and other genetic parameters indicated considerable genetic variability for different characters among the genotype. The characters viz., plant height, days to flowering, days to maturity, specific leaf weight, number of pods per plant, harvest index and 100 seed weight showed very narrow differences between phenotypic and genotypic coefficient of variation in all the four leaflet types.

2.2 Association analysis

2.2.1 Correlation coefficient

The need of correlation coefficient was suggested by Galton (1988). He also described the degree of association between variables. Searle (1961) described the mathematical application of correlation at phenotypic, genotypic and environmental level.

A brief review of traits showing correlation with yield:

S. No.	Characters	Type	Investigator (s)	Year
1	Plant height	+ve	Nimbalkar and Gujar	2000
		+ve	Bangar *et al.*	2003
		+ve	Mukhekar *et al.*	2004
		+ve	Vishnoi	2006
		+ve	Nag *et al.*	2007
		+ve	Sirohi *et al.*	2007
		+ve	Burli *et al.*	2010
2	No. of branches per plant	+ve	Patware *et al.*	2001
		+ve	Jain *et al.*	2002
		+ve	Oneml	2003
		+ve	Mukhekar *et al.*	2004
		+ve	Vishnoi	2006
		+ve	Muhammad *et al.*	2006
		+ve	Aditya *et al.*	2011
3	No. of pods per plant	+ve	Nimbalkar and Gujar	2000
		+ve	Chamundeshwari	2003
		+ve	Mukhekar *et al.*	2004
		+ve	Vart *et al.*	2005
		+ve	Muhammad *et al.*	2006
		+ve	Nag *et al.*	2007
		+ve	Narjesi *et al.*	2007
		+ve	Sirohi *et al.*	2007
		+ve	Islam and Mian	2008
		+ve	Burli *et al.*	2010
		+ve	Aditya *et al.*	2011
4	No. of seeds per plant	+ve	Nimbalkar and Gujar	2000
		+ve	Chamundeshwari	2003
		+ve	Nag *et al.*	2007
		+ve	Narjesi *et al.*	2007
		+ve	Islam and Mian	2008
5	No. of seeds per pod	+ve	Jain *et al.*	2002
		+ve	Oneml	2003
6	Biological yield per plant	+ve	Vart *et al.*	2005
		+ve	Sirohi *et al.*	2007
7	Harvest index	+ve	Aditya *et al.*	2011
8	100 seed weight	+ve	Nimbalkar and Gujar	2000
		+ve	Bangar *et al.*	2003
		+ ve	Shrivastava *et al.*	2005
		+ve	Muhammad *et al.*	2006
		+ve	Narjesi *et al.*	2007
		+ve	Messhenas *et al.*	2011

Review of literature showing correlation among character

S. No.	Characters	Type	Investigator (s)	Year
1	Days to maturity with yield	-ve	Yaduvanshi	1992
		+ve	Bhattacharya and Ram	1994
		+ve	Bangar *et al.*	2003
		-ve	Muhammad *et al.*	2006
2	Plant height with number of branches per plant	+ve	Kumar and Nadarajan	1992
		+ve	Singh	1993
3	Plant height with number of pods per plant	+ve	Kazmi and furhatullah	1991
		+ve	Bangar *et al.*	2003
4	Plant height with 100 seed weight	-ve	Jagtap and Choudhry	1993
		+ve	Bangar *et al.*	2003
5	Number of pods per plant with number of seeds per plant	+ve	Dogney *et al.*	1998
6	Seed weight with no. of pods	+ve	Bangar *et al.*	2003
		+ve	Muhammad *et al.*	2006

2.2.2 Path coefficient analysis

The concept of path coefficient was developed by Wright (1921). Path coefficient analysis is applied for assessment by Dewey and Lu (1959) in crested wheat grass, followed by Ramanujan and Rai (1963) in Brassica, Singh and Malhotra (1970) in Mungbean. The literatures available on path analysis in soybean are listed below:-

S.No.	Characters	Direct effect	Investigators	Year
1	Plant height	+ve	Singh	1993
		+ve	Singh *et al.*	1994
		+ve	Dogney *et al.*	1998
		+ve	Islam and Mian	2008
2	Number of branches per plant	+ve	Mehetre *et al*.	1994
		+ve	Yasin and Yadav	1994
		+ve	Dobhal and Gautam	1995
		+ve	Taware *et al*.	1997
		+ve	Dogney *et al*.	1998
		+ve	Onemal	2003
		+ve	Mukhekar *et al*.	2004
		+ve	Muhammad *et al.*	2006
		+ve	Vishnoi	2006
3	Number of pods per	+ve	Mehetre *et al*.	1994

	plant	+ve	Mishra *et al*.	1994
		+ve	Singh *et al.*	1994
		+ve	Dobhal and Gautam	1995
		+ve	Singh *et al*.	1996
		+ve	Taware *et al*.	1997
		+ve	Shridhara *et al*.	1998
		+ve	Onemal	2003
		+ve	Mukhekar *et al*.	2004
		+ve	Muhammad *et al.*	2006
		+ve	Vishnoi	2006
4	Number of seeds per plant	+ve	Shridhara *et al*.	1998
		+ve	Sudaric *et al*.	2002
		+ve	Nag *et al.*	2007
		+ve	Islam and Mian	2008
5	Harvest index	+ve	Vart *et al.*	2005
		+ve	Narjesi *et al.*	2007
6	100 seed weight	+ve	Dobhal and Gautam	1995
		+ve	Muhammad *et al.*	2006
		+ve	Nag *et al.*	2007
		+ve	Islam and Mian	2008
7	Biological yield	+ve	Sirohi *et al.*	2007

2.3 Principal component analysis

Principal component analysis (PCA) is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. With minimal effort PCA provides a road map for how to reduce a complex data set to a lower dimension to reveal the sometimes hidden, simplified structures that often underlie it. It reduces the dimensionality of the data while retaining most of the variation in the data set. PCA accomplishes this reduction by identifying directions, called principal components, along which the variation in the data is maximal. By using a few components, each sample can be represented by relatively few numbers instead of by values for thousands of variables (Ringer, 2008). Thus, the primary benefit of PCA arises from quantifying the importance of each dimension for describing the variability of a data set. A brief reviews has been summarized below:

In 2006, Miladinovic *et al.* reported three principal components in his investigation and found first one, which explained 58.92% of the total variance included harvest index, reproductive period, seed weight and vegetative period respectively. The second component explained 23.63% of the total variance. The third component, explaining 16.16% of the total variance, included yield and plant height.

Iqbal *et al.* (2008) studied three principal components; first three components accounted 69.77% of the total variance. PC1 included number of filled pods per plant, grain yield and biological yield per plant, while 100-seed weight and harvest index were included in PC2 and days to maturity and number of branches per plant in PC3.

Ojo *et al.* (2012) conducted an investigation and found three principal components, the PC1 had 52%, PC2 showed 26% and PC3 exhibited 10% variability among the genotypes for traits under his study. The first principal component was mostly correlated with the number of pods per plant, pod length, pod yield per plant, 100-seed weight and seed yield per plot. The characters that were mostly correlated with the second principal component were days to 50% flowering and days to maturity.

2.4 Characterization

Kumar and Narayanaswamy (1999) studied ten soybean varieties and evaluated for 7 seed traits. Out of seven, seed coat colour, hilum colour, seed shape and seed size were stable traits and could be used for development of a varietal identification key.

Satyavathi *et al.* (2004) studied seventy five soybean cultivars were characterized based on the National Test Guidelines and the International Union for Protection of New varieties of plants table characteristics for soybean and identification key based on 19 morphological characters, i.e. hypocotyls anthocyanin colour, growth type, growth habit, shape of lateral leaflet, size of lateral leaflet, intensity of green colour, flower colour, presence of hair in pods, colour of hairs, plant height, intensity of brown colour of pods, seed size, seed shape, colour of ground testa, seed coat colour, seed hilum, colour of hilum funicle, and timing of flowering and maturity.

Sawarkar (2010) reported wide range of variation for hilum colour, seed size and shape, leaf shape, flower colour and intensity of brown colour on pod. Seed size, days to flowering and days to maturity are the uniform characters but their expression is altered by the fluctuations of environment. Plant growth type and growth habit were the most stable and distinguishing traits and could be used for development of a varietal identification key.

Lawn and James (2011) reported physiological developments internationally, particularly the discovery of the long juvenile trait and to a lesser extent the semi-dwarf ideotype.

CHAPTER-III

MATERIAL AND METHODS

The present investigation was carried out during the *Kharif* 2011-12. The experimental materials and methods adopted during the course of investigation have been described in this chapter. The information related to climate and soil of experimental site is given ahead.

3.1 Experimental material and other details

3.1.1 Experimental site

The experiment was conducted at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.) during the *Kharif* season 2011-12. The soil of the experiment is medium black with uniform topography and free from water logged conditions.

3.1.2 Climate and Weather

Jabalpur is situated at 23.9^0 N latitude, 79.58^0 E longitudes and at an altitude of 411.87 m above the mean sea level. The region has sub tropical, semi arid climate. The main features are hot and dry summer and cold winter with occasional showers. The average rainfall is about 1200 mm. The minimum and maximum temperatures range between 22 ^{0}C to 35 ^{0}C, respectively during the *Kharif* season.

The climatic condition during the crop period were optimum for a normal plant growth (Appendix-I).

3.1.3 Experimental material

The experimental material was comprised of 26 fixed advanced generation genotypes of soybean.

Table 1: Detailed of the material is given below

S. No.	Genotype	Generation	CODE
1	JS 97-52 X JSM-299	F_6	Code -1
2	JS 97-52 X JSM-299	F_6	Code -2
3	JS 99-76 X JSM-275	F_6	Code -3
4	JS 97-52 X JS 95-60	F_7	Code -4
5	JS 97-52 X JS 95-60	F_7	Code -5
6	JS 97-52 X JSM 120A	F_7	Code -6
7	JS 97-52 X JSM 286	F_7	Code -7
8	JS 97-52 X JSM 286	F_7	Code -8
9	JS 97-52 X JS 20-02	F_8	Code -9
10	JS 97-52 X JS 95-56	F_8	Code -10
11	JS 97-52 X JS 95-56	F_8	Code -11
12	JS 97-52 X JS 95-56	F_8	Code -12
13	JS 97-52 X JSM-52	F_8	Code -13
14	JS 97-52 X JSM-52	F_8	Code -14
15	JSM 146 X JSM-152	F_8	Code -15
16	JSM 146 X JSM-152	F_8	Code -16
17	JSM-240 X JSM-189	F_8	Code -17
18	JS 97-52 X JS(IS) 90-5-12-1	F_9	Code -18
19	JS 97-52 X JSM-52	F_9	Code -19
20	JSM-240 X JSM-189	F_9	Code -20
21	JSM-240 X JSM-189	F_{10}	Code -21
22	JS 98-63 X PK-768	F_{11}	Code -22
23	JSM 110 X JSM-60	F_{11}	Code -23
24	NRC-2007-A-2-3	NRC	Code -24
25	NRC-2008-B-2-6-2	NRC	Code -25
26	NRC-2009-A-1-3-3-1-1	NRC	Code -26

Technical programme of work:

Experimental details are as under:

Experimental Design	-	Randomized Complete Block Design
Number of Replications	-	2
Number of genotypes	-	26
Sowing	-	08-07-2011
Plot size	-	3.0 m x 1.6 m
Number of rows/plot	-	5
Spacing (Row to Row)	-	40 cm

3.2 Observations recorded

For recording the observations, five random competitive plants selected from each line in each replication and following phenological and morphological observations were recorded.

3.2.1 Phenological traits

3.2.1.1 Vegetative phase

Number of days was counted from sowing to flower initiation.

3.2.1.2 Reproductive phase

Number of days was counted from flower initiation to the full maturity (95% pods have reached mature pod colour).

3.2.1.3 Plant height (cm)

The height of five plants was measured at maturity in centimetres from the ground level to the tip of the plant and average was calculated.

3.2.1.4 Number of branches per plant

The number of branches of five tagged plants from each plot was recorded and mean was calculated.

3.2.1.5 Number of pods per plant

The total numbers of pods per plant at maturity were counted on five plants and mean was calculated.

3.2.1.6 Number of seeds per plant

Number of seeds was counted from five plants and mean was calculated.

3.2.1.7 Number of seeds per pod

Number of seeds per pod was calculated by dividing mean by mean number of pods per plant.

3.2.1.8 Biological yield per plant (g)

Dry weight of five tagged plants harvested above the ground level from each plot was taken before threshing.

3.2.1.9 Harvest index

Harvest index was worked out from the following formula:

$$\text{Harvest Index (H.I.)} = \frac{\text{Seed yield}}{\text{Biological yield}} \text{x} 100$$

3.2.1.10 100 seed weight (g)

Weight of 100 normal seeds drawn randomly from each lot was taken in grams.

3.2.1.11 Yield per plant

The tagged five plants were harvested and threshed separately. The seed yield of individual plant was weighed in gram.

3.2.2 Traits for characterization

3.2.2.1 Hypocotyl colour

Hypocotyl was observed in the field, visually in bright sunlight when cotyledons are completely unfolded.

3.2.2.2 Growth type

The plant growth type was observed at time of flowering/ maturity stage visually.

3.2.2.3 Growth habit

The plant growth habit was observed at stage of 50% flowering.

3.2.2.4 Pubescent (present/absent)

Presence or absence of hairs on pods and stem was observed at advanced pod filling stage; about 70 % pods have reached final length (15-20 mm) visually.

3.2.2.5 Pubescent colour

Colour of hairs on pod and stem was observed at maturity.

3.2.2.6 Leaf shape

Shape of the lateral leaflets was observed visually at full flowering stage.

3.2.2.7 Flower colour

The colour of fully developed freshly open flowers was observed visually in morning hours.

3.2.2.8 Pod colour

The pod colour observed at maturity.

3.2.2.9 Seed coat colour

Seed coat colour was observed at maturity in daylight by visual observation.

3.2.2.10 Seed size

The size of seed was observed as the weight of randomly selected 100 ripe seeds (10% moisture) as small (<10 g), medium (10-13 g) and bold/ large (> 13 g).

3.2.2.11 Seed shape

Fully developed and matured seeds were visually observed to classify genotypes based on seed shape.

3.2.2.12 Hilum colour

Hilum colour of all the genotypes was visually observed after the seed threshing.

3.2 Statistical analysis

Statistical analysis was performed for following parameters:

3.3.1 Analysis of variance

3.3.2 Estimation of mean, range, GCV and PCV, heritability, expected genetic advance and genetic advance as percentage of mean.

3.3.3 Estimation of phenotypic and genotypic correlations.

3.3.4 Path coefficient analysis.

3.3.5 Principal component analysis

3.3.1 Analysis of variance

The data were statistically analyzed on the basis of method described by Panse and Sukhatme (1967) to work out existing variance of observed traits.

1. Genotypic variance (σ^2_g) $= \frac{M_2 - M_3}{r}$

2. Phenotypic variance (σ^2_p) $= \frac{M_2 - M_3 + M_3}{r}$

3. Environmental variance (σ^2_e) = M_3

Skeleton of Analysis of Variance for Randomized Complete Block Design

Source of variation	d.f.	Sum of square	Mean sum of square	Expected MSS	F value
Replication	(r-1)	RSS	M_1	$\sigma^2e + g\sigma^2r$	RMS/ EMS
Genotype	(g-1)	TSS	M_2	$\sigma^2e + r\sigma^2g$	TMS/ EMS
Error	(r-1) (g-1)	ESS	M_3	σ^2e	
Total	**(rg - 1)**				

r = Number of replications

g = Number of genotypes

df = Degrees of freedom

RSS = Replication sum of square

TSS = Treatment sum of square

ESS = Error sum of square

M_1 = Mean square due to replication

M_2 = Mean square due to genotypes

M_3 = Mean square due to error

A significant value of F-test 5% and 1% level indicates that the genotypes differ significantly among themselves, which requires computing the critical difference (CD).

$$\text{Standard error of difference } SE(d) = \sqrt{\frac{2EMS}{r}}$$

$$\text{Critical difference (CD)} = t_\alpha \times SE_{(d)}$$

where,

t_α = t-value at 1% and 5% probability level

3.3.2 Parameters of genetic variability

3.3.2.1 Mean

The average of recorded observation was calculated as follows:-

$$\text{Mean } (\bar{x}) = \frac{\sum x_i}{n}$$

Where,

Σx_i = Summation of all values of observation

n = Number of observed values

3.3.2.2 Range

Range is the difference between the smallest and the greatest term of a series of observation and thus provides the information about the variability present in the genotypes.

3.3.2.3 Estimation of phenotypic and genotypic coefficients of variation

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

$$\text{PCV}(\%) = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{GCV}(\%) = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

The estimates of PCV and GCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973).

< 10 per cent = low

10-20 per cent = moderate

> 20 per cent = high

3.3.2.4 Heritability

Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1979):

$$h^2\,(bs)\% = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

3.3.2.5 Genetic advance

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson, Comstock, and Harvey (1951).

$$G(s) = K \times h^2 \times \sigma p$$

where,

K = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

3.3.2.6 Genetic advance as percentage of mean

It was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA was categorized as

< 25 per cent	=	low
25-35 per cent	=	moderate
>35 per cent	=	high

3.3.3 Estimation of correlations

Phenotypic, genotypic and environmental correlation coefficients between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Miller *et al.* (1958).

$$r_{xy} = \frac{\text{Cov.}_{x,y}}{\sqrt{V_x \times V_y}}$$

where,

r_{xy} = Correlation coefficient between character x and y,

$\text{Cov}_{x,y}$ = Co-variance of character x and y,

V_x = Variance of character x, and

V_y = Variance of character y.

To test the significance of phenotypic and environmental correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1963) at n-2 d.f. at two levels of probability, viz., 5% and 1%.

3.3.4 Path coefficient analysis

It is a simple standardized partial coefficient method to detect the direct and indirect effects of the independent variable on dependent variable. It permits separation of correlation into components of direct and indirect effects.

The method of path coefficient was developed by Wright (1921) and modified by Dewey and Lu (1959). The following set of simultaneous equations were formed and used for estimation of direct and indirect effects on seed longevity.

$r_{1y} = p_{1y} + r_{12}p_{2y} + r_{13}p_{3y} + \ldots\ldots + r_{1y}p_{1y}$

$r_{2y} = r_{2y}\, p_{iy} + p_{2y} + r_{23}p_{3y} + \ldots\ldots + r_{21y}p_{1y}$

$r_{ky} = r_{ki} + r_{ki}\, p_{2y} + r_{13}p_{3y} + \ldots\ldots + r_{2iy}p_{iy}$

$r_{xky} = r_{xki}\, p_{iy} + r_{zk2}\, p_{2y} + r_{xk3}\, p_{3y} + \ldots\ldots + p_{ky}$

r_{xky} = Coefficient of correlation between the independent character.

p_{iy} to p_{ky} = Direct effects of character 1 to k on dependent character y.

Direct effect: The direct effects were calculated as follows -

$$P_{Ky} = \sum_{i=1}^{k} C_{Ki}\ r_{Ky}$$

Indirect effect: Indirect effect of any independent traits on the dependent one via other independent traits was computed by multiplying the direct effect (P_{ky}) of that independent variable with the corresponding correlation coefficient as follows:

$$K^{th} \text{ trait via (n-1)} = rk\ (n\text{-}1)\ P\ (n\text{-}1)\ Y$$

Residual effect: Residual effect was obtained as per the formula given below:

$$R = \sqrt{1 - E_{di}\ r_{ji}}$$

where,

d_i = Direct effect of character

r_{ij} = Correlation coefficient of i^{th} character with j^{th} character.

3.3.5 Principal component analysis (Ingebriston and Lyon, 1985)

PCA is a well-known method of dimension reduction (Massay, 1965; Jolliffie, 1986), which seeks linear combinations of the columns of ***X*** with maximal variance, or equivalently, high information. It is routinely applied in chemo metrics with the goal of providing the most compact representation of the data. The original *p* variables ***X*** = [**x**1 *. . .* **x***p*] are transformed in a new predictor set **T** = [**t**1 *. . .* **t***k*], with *k* ≤ min*(n* −1*, p)*. The new variables **t***j,* called *scores*, are a weighted average of the original ***X*** variables. The *principal components* are the eigenvectors, **u***j* from the eigen decomposition of ***X'X*** (and of the sample covariance matrix **S**, up to a constant). PCA sequentially maximises the variance of a linear combination of the original predictor variables

$$\mathbf{U}_j = \arg\max \mathrm{Var}(\boldsymbol{X}\mathbf{u}),$$

$$\mathbf{u}=1$$

Subject to the constraint that $\mathbf{u}'_i \mathbf{S}\mathbf{u}_j = 0$ for all $1 \leq i < j$. This ensures that $\mathbf{t}_j = \boldsymbol{X}\mathbf{u}_j$ is uncorrelated with all the previous linear combinations $\mathbf{t}_i = \boldsymbol{X}\mathbf{u}_i$. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that $\mathbf{t}_1 = \boldsymbol{X}\mathbf{u}_1$ has the largest sample variance among all normalized linear combinations of the columns of $\boldsymbol{X}$. Each subsequent component gives combinations with the largest possible variance which is uncorrelated with those that have been taken earlier.

There are various standard approaches to find the principal components, e.g. taking the singular value decomposition of $\boldsymbol{X}$. In chemo metrics it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (Wold, 1966). This is because the number of required components is usually much less than the total possible number (k _ p). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates $\mathbf{t}_1$ and $\mathbf{u}_1$ from the $\boldsymbol{X}$ matrix. Then the outer product $\mathbf{t}_1\mathbf{u}\_1$ is subtracted from $\boldsymbol{X}$ and the residual $\boldsymbol{X}_2$ is calculated. In turn, this residual can be used to calculate $\mathbf{t}_2$ and $\mathbf{u}_2$.

CHAPTER-IV

RESULTS

The experimental results of the present investigation have been mentioned under following sub-heads.

4.1 Parameters of genetic variability

4.1.1 Analysis of variance

4.1.2 Mean and range

4.1.3 Genotypic and phenotypic coefficient of variation

4.1.4 Heritability

4.1.5 Genetic advance

4.2 Association analysis

4.2.1 Correlation coefficient analysis

4.2.2 Path coefficient analysis

4.3 Principal component analysis

4.4 Characterization

4.1 Parameters of Genetic Variability

4.1.1 Analysis of variance

The ANOVA indicated that the mean sum of squares due to genotypes were highly significant for yield contributing traits viz., vegetative phase, reproductive phase, plant height, number of pods per plant, number of seeds per plant, harvest index, biological yield per plant, yield per plant and significant for 100 seed weight. The analysis of variance for the characters under study has been given in table 2.

Table 2. Analysis of variance for phenological and yield components in promising lines of soybean.

S. No.	Source of Variation	d. f.	MEAN SUMS OF SQUARES										
			Veg. phase (days)	Repro. Phase (days)	Plant height (cm)	No. of branches/ Plant	No. of pods/ Plant	No. of seeds/ plant	No. of seeds/ Pod	Biological yield/ Plant (g)	Harvest index (%)	100 Seed weight (g)	Yield/ Plant (g)
1	Replications	1	5.56	2.33	42.12	0.09	18.84	216.08	0.01	14.85	8.59	0.06	1.16
2	Treatments	25	32.17**	16.74**	129.54**	2.57	604.47**	2972.81**	0.11	71.81**	68.18**	4.70*	23.33**
3	Error	25	0.68	3.09	7.72	0.22	37.98	315.88	0.03	7.58	8.44	0.22	2.35
4	S. Ed ±	-	0.58	1.24	1.97	0.33	4.36	12.57	0.13	1.95	2.06	0.33	1.09
5a	CD 5%	-	1.70	3.62	5.72	0.97	12.69	36.60	0.37	5.67	5.99	0.96	3.16
B	CD 1%	-	2.30	4.90	7.75	1.31	17.18	49.54	0.49	7.67	8.10	1.30	4.28

**Significant at 1% *Significant at 5%

4.1.1 Estimation of parameters of genetic variability

The parameters of genetic variability viz., mean, range, phenotypic and genotypic coefficient of variation (%), heritability in broad sense (%), genetic advance and genetic advance as percentage of mean for each trait are presented in table 3.

4.1.2 Mean and Range

Estimates of mean and range for all the eleven characters have been depicted in table 3. Mean value character wise and genotype wise have been presented in table 3.

Vegetative phase

The degree of dispersion for vegetative phase ranged from 29.00 {NRC-2009-A-1-3-3-1-1 (Code 26)} to 46.00 days {JS 97-52 X JSM 52 (Code 14)} with mean of 40.06 days {JS 97-52 X JS (IS) 90-5-12-1 (Code18)} and CV 2.06%.

Reproductive phase

Reproductive phase recorded minimum of 49.50 days {JS 97-52 X JSM 52, (Code 14)} and maximum of 62.00 days {JSM 240 X JSM 189 (Code 21)} with mean value of 56.37 days and CV 3.12%.

Plant height

The plant height ranged from 28.50 {NRC-2009-A-1-3-3-1-1 (Code 26)} to 59.30 cm {JSM 146 X JSM 152 (Code 16)} with mean value of 45.30 cm and CV 6.13%.

Number of branches per plant

Number of branches per plant recorded minimum of 0.50 {NRC-2009-A-1-3-3-1-1 (Code 26)} and maximum of 5.00 {JS 97-52 X JSM 52 (Code19)} with mean value of 3.69 {JSM 110 X JSM 60 (Code 23)} and CV 12.75%.

Number of pods per plant

Number of pods per plant varied from 21.90 {NRC-2009-A-1-3-3-1-1 (Code 26)} to 83.80 {JSM 110 X JSM 60 (Code 23)} with mean value of 64.77 and 9.51% CV.

Number of seeds per plant

Number of seeds per plant ranged from 34.50 {NRC-2009-A-1-3-3-1-1 (Code 26)} to 191.50 {JS 97-52 X JS(IS) 90-5-12-1 (Code18)} with mean value of 127.23 and CV 13.97%.

Number of seeds per pod

Number of seeds per pod ranged from 1.45 {NRC-2007-A-2-3 (Code 24)} to 2.52 {JS 97-52 X JSM 286 (Code 7)} with mean value of 1.94 and 9.13% CV.

Biological yield per plant

The average value of biological yield per plant was recorded as with 22.87 g degree of dispersion from 8.39 {NRC-2007-A-2-3 (Code 24)} to 29.72 g {JSM 146 X JSM 152 (Code16)} and 12.04% CV.

Harvest index (%)

Harvest index (%) had mean value of 50.41%, CV 5.76% and ranging from 30.77% {NRC-2007-A-2-3 (Code 24)} to 58.15% {JS 97-52 X JS 20-02 (Code 9)}.

100 Seed weight

100 seed weight varied from 7.02 {JS 97-52 X JSM 120A (Code 6)} to 12.47 g {JS 98-63 X PK 768 (Code 22)} while recording mean of 9.26 g and 5.04% CV.

Yield per plant

The yield per plant recorded minimum of 2.56 g {NRC-2007-A-2-3 (Code 24)} while maximum of 15.94 g {JS 97-52 X JS 20-02 (Code 9)} with mean value of 11.70 g and CV 13.12%.

4.1.3 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation for yield and yield contributing characters are summarized in table 3. The phenotypic coefficient of variation was significantly higher in magnitude than that of genotypic coefficient of variation for all the characters under study. Number of branches per plant recorded the highest PCV (32.05%) and GCV (29.40%) followed by number of seeds per plant (31.87% and 28.65%), yield per plant (30.63% and 27.68%), number of pods per plant (27.67% and 25.98%), biological yield per plant (27.55% and 24.78%), moderate for plant height (18.29% and 17.23%), 100 seed weight (16.93% and 16.17%), number of seeds per pod (13.87% and 10.45%), harvest index (12.28% and 10.84%), vegetative phase (10.12% and 9.91%), and low PCV and GCV is of reproductive phase (5.59% and 4.64%).

4.1.4 Heritability (%) (BS)

Heritability was estimated for all the quantitative characters under study. The heritability estimates varied for different morphological and agronomical traits (Table 3). Most of the characters expressed high estimates of broad sense heritability. The highest heritability was obtained (95.87%) for vegetative phase followed by 100 seed weight (91.15%), plant height (88.75%), number of pods per plant (88.18%),number of branches per plant (84.18%), yield per plant (81.66%), biological yield per plant (80.91%), number of seeds per plant (80.79%) and harvest index (77.96%). Moderate heritability was recorded for the traits reproductive phase (68.86%) and number of seeds per pod (56.74%).

Table 3: Parameters of genetic variability for phenological and yield components in promising lines of soybean.

S.No.	Character	Mean	Range		CV%	PCV (%)	GCV (%)	h^2b (%)	GA as % of mean
			Min.	Max.					5%
1	**Vegetative phase (days)**	40.06	29.00	46.00	2.06	10.12	9.91	95.87	19.98
2	**Reproductive phase (days)**	56.37	49.50	62.00	3.12	5.59	4.64	68.86	7.92
3	**Plant height (cm)**	45.30	28.50	59.30	6.13	18.29	17.23	88.75	33.43
4	**Number of branches plant^{-1}**	3.69	0.50	5.00	12.75	32.05	29.40	84.18	55.57
5	**Number of pods plant^{-1}**	64.77	21.90	83.80	9.51	27.67	25.98	88.18	50.26
6	**Number of seeds plant^{-1}**	127.23	34.50	191.50	13.97	31.87	28.65	80.79	53.04
7	**Number of seeds pods^{-1}**	1.94	1.45	2.52	9.13	13.87	10.45	56.74	16.22
8	**Biological yield plant^{-1} (g)**	22.87	8.39	29.72	12.04	27.55	24.78	80.91	45.91
9	**Harvest Index (%)**	50.41	30.77	58.15	5.76	12.28	10.84	77.96	19.72
10	**100 seed weight (g)**	9.26	7.02	12.47	5.04	16.93	16.17	91.15	31.79
11	**Yield plant^{-1} (g)**	11.70	2.56	15.94	13.12	30.63	27.68	81.66	51.53

Classes of Heritability (%): High >70 %, Medium 50-70% , Low < 50 %

4.1.5 Genetic advance as percentage of mean:

The highest genetic advance as percentage of mean (at 5% Selection intensity) were recorded for number of branches per plant (55.57%) followed by number of seeds per plant (53.04%), yield per plant (51.53%), number of pods per plant (50.26%), biological yield per plant (45.91%), medium for plant height (33.43%) and 100 seed weight (31.79%), whereas low for vegetative phase (19.98%), harvest index (19.72%), number of seeds per pod (16.22%) and reproductive phase (7.92%).

4.2 Association analysis

4.2.1 Correlation coefficient analysis

Phenotypic and genotypic correlations between yield per plant and various yield traits viz., vegetative phase, reproductive phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, biological yield per plant, harvest index, 100 seed weight are given in table 4 and 5. The results revealed that the estimates of genotypic correlation coefficients were higher than the phenotypic correlation coefficients.

4.2.1.1 Vegetative Phase

Vegetative phase had highly significant positive association with number of pods per plant (0.761), number of seeds per plant (0.750), number of branches per plant (0.684), biological yield per plant (0.533), yield per plant (0.524), plant height (0.489), harvest index (0.363) and number of seeds per pod (0.359). It showed highly significant negative association with reproductive phase (-0.510) and 100 seed weight (-0.519).

4.2.1.2 Reproductive Phase

It showed highly significant positive association with 100 seed weight (0.422).

4.2.1.3 Plant Height

Plant height showed highly significant positive association with biological yield per plant (0.716), yield per plant (0.712), number of pods per plant (0.711), number of seeds per plant (0.697), number of branches per plant (0.592), harvest index (0.395), and significant positive correlation with number of seeds per pod (0.349).

4.2.1.4 Number of Branches per plant

Number of branches per plant showed highly significant positive association with number of pods per plant (0.733), yield per plant (0.658), number of seeds per plant (0.656), biological yield per plant (0.623) and harvest index (0.505).

4.2.1.5 Number of Pods per plant

This character showed highly significant positive association with number of seeds per plant (0.914), biological yield per plant (0.842), yield per plant (0.826), and harvest index (0.484) and significant association with seeds per pod (0.332).

4.2.1.6 Number of Seeds per plant

Association of this trait was found highly significant positive association with yield per plant (0.825), biological yield per plant (0.823), number of seeds per pod (0.674), and harvest index (0.519). It showed negative significant association with 100 seed weight (-0.341).

4.2.1.7 Number of Seeds per pod

This character revealed highly significant positive association with yield per plant (0.487), harvest index (0.467) and biological yield per plant (0.432).

4.2.1.8 Biological Yield Per plant

Biological yield established highly significant positive association with yield per plant (0.962) and harvest index (0.463).

4.2.1.9 Harvest Index

It showed the highest significant positive association with yield per plant (0.663).

4.2.1.10 100 Seed Weight

100 seed weight showed no correlation with any traits.

Table 4: Genotypic (G) correlation for phenological and yield components in promising lines of soybean.

Character		Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Number of branches plant^{-1}	Number of pods plant^{-1}	Number of seeds plant^{-1}	Number of seeds pods^{-1}	Biological yield plant^{-1} (g)	Harvest Index (%)	100 seed weight (g)	Yield plant^{-1} (g)
Vegetative phase (days)	**G**	**1**	-0.570	0.532	0.743	0.823	0.837	0.465	0.602	0.410	-0.558***	0.588
Reproductive phase (days)	**G**		**1**	-0.067	-0.120	-0.035	-0.065	-0.019	0.274	0.017	0.530	0.237
Plant height (cm)	**G**			**1**	0.692	0.722	0.726	0.432	0.737	0.506	0.012	0.753
Number of branches plant^{-1}	**G**				**1**	0.821	0.718	0.211	0.734	0.546	-0.097	0.742
Number of pods plant^{-1}	**G**					**1**	0.957	0.458	0.856	0.574	-0.278	0.845
Number of seeds plant^{-1}	**G**						**1**	0.689	0.852	0.583	-0.359	0.836
Number of seeds pods^{-1}	**G**							**1**	0.542	0.556	-0.218	0.558
Biological yield plant^{-1} (g)	**G**								**1**	0.598	0.116	0.978
Harvest Index (%)	**G**									**1**	0.286	0.735
100 seed weight (g)	**G**										**1**	0.180
Yield plant^{-1} (g)	**G**											**1**

Significant Levels 0.05 0.01 0.005 0.001 If correlation r = 0.2732 0.3541 0.3836 0.4432

Table 5: Phenotypic (P) correlation for phenological and yield components in promising lines of soybean.

Character		Vegetative phase (days)	Reproductive phase (days)	Plant height (cm)	Number of branches plant^{-1}	Number of pods plant^{-1}	Number of seeds plant^{-1}	Number of seeds pods^{-1}	Biological yield plant^{-1} (g)	Harvest Index (%)	100 seed weigh t (g)	Yield plant^{-1} (g)
Vegetative phase (days)	**P**	**1**	-0.510***	0.489***	0.684***	0.761***	0.750***	0.359**	0.533***	0.363**	-0.519	0.524***
Reproductive phase (days)	**P**		**1**	-0.083	-0.110	-0.058	-0.121	-0.110	0.137	-0.016	0.422**	0.107
Plant height (cm)	**P**			**1**	0.592***	0.711***	0.697***	0.349*	0.716***	0.395**	-0.026	0.712***
Number of branches plant	**P**				**1**	0.733***	0.656***	0.245	0.623***	0.505***	-0.136	0.658***
Number of pods plant^{-1}	**P**					**1**	0.914***	0.332*	0.842***	0.484***	-0.272	0.826***
Number of seeds plant^{-1}	**P**						**1**	0.674***	0.823***	0.519***	-0.341*	0.825***
Number of seeds pods^{-1}	**P**							**1**	0.432**	0.467***	-0.199	0.487***
Biological yield plant^{-1} (g)	**P**								**1**	0.463***	0.091	0.962***
Harvest Index (%)	**P**									**1**	0.239	0.663***
100 seed weight (g)	**P**										**1**	0.148
Yield plant^{-1} (g)	**P**											**1**

Significant Levels 0.05 0.01 0.005 0.001, If correlation r = 0.2732 0.3541 0.3836 0.4432

4.2.2 Path coefficient analysis

Path coefficient analysis measures direct and indirect contribution of various independent characters on the dependent character. It reveals whether the association of these independent characters with yield, the dependent character is due to their direct effect on yield or is consequence of their indirect effect via other component characters.

In the present study path coefficient analysis was carried out using phenotypic correlation, using yield per plant as a dependent variable. Path coefficients are rated as per the scales given by Lenka and Mishra (1973). The estimates of path coefficient are furnished in table 6.

4.2.2.1 Vegetative Phase

Vegetative phase had negative direct effect (-0.092) on yield per plant with positive indirect effect via reproductive phase (0.047), 100 seed weight (0.048), whereas it had negative indirect effect via plant height (-0.045), number of branches per plant (-0.063), number of pods per plant (-0.070), number of seeds per plant (-0.069), number of seeds per pod (-0.033), biological yield per plant (-0.049) and harvest index (-0.034).

4.2.2.2 Reproductive Phase

Reproductive phase had negative direct effect (-0.021) on yield per plant with positive indirect effect via vegetative phase (0.011), plant height (0.002), number of branches per plant (0.002), number of pods per plant (0.001), number of seeds per plant (0.003) and number of seeds per pod (0.002), while it had negative indirect effect via biological yield per plant (-0.003) and 100 seed weight (-0.009).

4.2.2.3 Plant Height

The direct effect of plant height on yield per plant was found positive (0.006) with positive indirect effect via vegetative phase (0.003), number of branches per plant (0.003), number of pods per plant (0.004), number of seeds per plant (0.004), number of seeds per pod (0.002), biological yield per plant (0.004), harvest index (0.002), where as it had negative indirect effect through reproductive phase (-0.001).

4.2.2.4 Number of Branches per plant

This trait exhibited positive direct effect (0.037) on yield per plant. This trait showed two negative indirect effect through reproductive phase (-0.004) and 100 seed weight (-0.005), rest of all indirect effects were positive as via vegetative phase (0.025), plant height (0.022), number of pods per plant (0.027), number of seeds per plant (0.024), number of seeds per pod (0.009), biological yield per plant (0.023) and harvest index (0.019).

4.2.2.5 Number of Pods per plant

Direct contribution of this trait on yield per plant was found positive (0.713) with positive indirect effect via reproductive phase (0.042) and 100 seed weight (0.194). Rest of the indirect effect were negative through vegetative phase (-0.542), plant height (-0.507), number of branches per plant (-0.523), number of seeds per plant (-0.652), number of seeds per pod (-0.237), biological yield per plant (-0.600) and harvest index (-0.345).

4.2.2.6 Number of Seeds per plant

Number of seeds per plant had positive direct effect on yield per plant (0.777). It had positive indirect effect via vegetative phase (0.583), plant height (0.541), number of branches per plant (0.509), number of pods per plant (0.710), number of seeds per pod (0.523), biological yield per plant (0.639) and harvest index (0.403), while it had negative indirect effect via reproductive phase (-0.094) and 100 seed weight (-0.265).

4.2.2.7 Number of Seeds per pod

Number of seeds per pod had negative direct effect on yield per plant (-0.373) with positive indirect effect via reproductive phase (0.041) and 100 seed weight (0.074). It had negative indirect effect via vegetative phase (-0.134), plant height (-0.130), number of branches per plant (-

0.091), number of pods per plant (-0.124), number of seeds per plant (-0.251), biological yield per plant (-0.161) and harvest index (-0.174).

4.2.2.8 Biological Yield per plant

Direct contribution of this trait on yield per plant was found positive (0.944), all the indirect effect were found positive through vegetative phase (0.503), reproductive phase (0.129), plant height (0.676), number of branches per plant (0.588), number of pods per plant (0.795), number of seeds per plant (0.777), number of seeds per pod (0.408), harvest index (0.437) and 100 seed weight (0.086).

4.2.2.9 Harvest Index

Harvest index had positive direct effect on yield per plant (0.369) with positive indirect effect via vegetative phase (0.134), plant height (0.146), number of branches per plant (0.186), number of pods per plant (0.178), number of seeds per plant (0.191), number of seeds per pod (0.173), biological yield per plant (0.171) and 100 seed weight (0.088). Only one indirect effect was found negative through reproductive phase (-0.006).

4.2.2.10 100 Seed Weight

100 seed weight had negative direct effect on yield per plant (-0.064) with positive indirect effect via vegetative phase (0.033), plant height (0.002), number of branches per plant (0.009), number of pods per plant (0.017), number of seeds per plant (0.022) and number of seeds per pod (0.013). Rest of all the indirect effect was negative via reproductive phase (-0.027), biological yield per plant (-0.006) and harvest index (-0.015).

Table 6: Genotypic and Phenotypic path coefficient analysis showing direct and indirect effects for phenological and yield components in promising lines of soybean.

		Veg. phase (days)	Repro. Phase (days)	Plant height (cm.)	Number of branches plant^{-1}	Number of pods plant^{-1}	Number of seeds plant^{-1}	Number of seeds pods^{-1}	Biological yield plant^{-1} (g)	Harvest Index (%)	100 seed weight (g)
Veg. phase (days)	**G**	**0.112**	-0.064	0.060	0.084	0.093	0.094	0.052	0.068	0.046	-0.063
	P	**-0.092**	0.047	-0.045	-0.063	-0.070	-0.069	-0.033	-0.049	-0.034	0.048
Repro. Phase (days)	**G**	-0.115	**0.202**	-0.014	-0.024	-0.007	-0.013	-0.004	0.055	0.003	0.107
	P	0.011	**-0.021**	0.002	0.002	0.001	0.003	0.002	-0.003	0.000	-0.009
Plant height (cm.)	**G**	0.145	-0.018	**0.273**	0.189	0.197	0.198	0.118	0.201	0.138	0.003
	P	0.003	-0.001	**0.006**	0.003	0.004	0.004	0.002	0.004	0.002	-0.000
Number of branches plant^{-1}	**G**	-0.272	0.044	-0.253	**-0.366**	-0.300	-0.263	-0.077	-0.268	-0.200	0.035
	P	0.025	-0.004	0.022	**0.037**	0.027	0.024	0.009	0.023	0.019	-0.005
Number of pods plant^{-1}	**G**	-2.611	0.110	-2.293	-2.606	**3.174**	-3.037	-1.454	-2.717	-1.822	0.882
	P	-0.542	0.042	-0.507	-0.523	**0.713**	-0.652	-0.237	-0.600	-0.345	0.194
Number of seeds plant^{-1}	**G**	1.558	-0.122	1.350	1.336	1.780	**1.861**	1.281	1.586	1.086	-0.668
	P	0.583	-0.094	0.541	0.509	0.710	**0.777**	0.523	0.639	0.403	-0.265
Number of seeds pods^{-1}	**G**	-0.710	0.028	-0.660	-0.323	-0.700	-1.052	**-1.528**	-0.828	-0.850	0.332
	P	-0.134	0.041	-0.130	-0.091	-0.124	-0.251	**-0.373**	-0.161	-0.174	0.074
Biological yield plant^{-1} (g)	**G**	1.337	0.608	1.637	1.630	1.900	1.892	1.203	**2.220**	1.328	0.258
	P	0.503	0.129	0.676	0.588	0.795	0.777	0.408	**0.944**	0.437	0.086
Harvest Index (%)	**G**	0.539	0.022	0.665	0.718	0.755	0.767	0.731	0.787	**1.315**	0.376
	P	0.134	-0.006	0.146	0.186	0.178	0.191	0.173	0.171	**0.369**	0.088
100 seed weight (g)	**G**	0.604	-0.574	-0.013	0.105	0.301	0.389	0.236	-0.126	-0.310	**-1.083**
	P	0.033	-0.027	0.002	0.009	0.017	0.022	0.013	-0.006	-0.015	**-0.064**
Yield plant^{-1} (g)	**G**	0.588	0.237	0.753	0.742	0.845	0.836	0.558	0.978	0.735	0.180
	P	0.524	0.107	0.712	0.658	0.826	0.825	0.487	0.962	0.663	0.148

R Squre = 0.9920 Residual effect = 0.0893

4.3 Principal components analysis

PCA is a well-known method of dimension reduction (Massay, 1965; Jolliffie, 1986), which seeks linear combinations of the columns of ***X*** with maximal variance, or equivalently, high information. PCA provides a roadmap for how to reduce a complex data set to a lower dimension to sometimes hidden, simplified structures that often underlies it. Principal component analysis is appropriate for obtaining measures on a number of observed variables and to developing a smaller number of artificial variables (called principal component) that will account for most of the variance in the observed variables. It is routinely applied in chemometrics with the goal of providing the most compact representation of the data. There are various standard approaches to find the principal components, e.g. taking the singular value decomposition of ***X***. In chemometrics it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (Wold, 1966). The eigenvectors and the corresponding loadings for each individual from the PCA can be used as covariates within a logistic regression framework to account for the underlying structure.

In present research programme, PCA was preformed for phenological and yield component traits in promising lines of soybean. Out of eleven, only five principal components (PCs) exhibited more than 0.5 eigen value, and showed about 94.62% total variability among the traits studied. So, these five PCs were given due importance for further explanation. The PC1 showed 56.29% while, PC2, PC3, PC4 and PC5 exhibited 18.49%, 8.34%, 7.30% and 4.21% variability respectively among the genotypes for the traits under study (Table7).

Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 56.29% variability with eigen value 6.19 which then declined gradually. Semi curve line is obtained which after fifth PC tended to straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other four PCs, which is selected for explain here. So, selection of lines from this PC will be useful (Figure 2 and 3).

Table 7: Eigen values, % variance and cumulative eigen values of promising lines of soybean.

Traits	Principal component	Eigen values	% variation	Cumulative %
Veg. phase	PC1	6.191	56.286	56.286
Repro. Phase	PC2	2.034	18.494	74.780
Plant height	PC3	0.917	8.335	83.115
No. of branches/plant	PC4	0.803	7.296	90.411
No. of pods/plant	PC5	0.463	4.207	94.618
No. of seeds/plant	PC6	0.281	2.554	97.172
No. of seeds/pod	PC7	0.215	1.951	99.123
Biological yield / plant	PC8	0.049	0.446	99.569
HI	PC9	0.042	0.383	99.952
100 seed weight	PC10	0.005	0.041	99.993
Yield/plant	PC11	0.001	0.007	100.000

Rotated component matrix revealed that the PC1 which accounted for the highest variability (56.29%) was mostly related with traits such as vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index and yield per plant. In second PC the traits *viz*., number of seeds per plant and number of seeds per pod were more related. The PC3 was dominated by phenological trait such as reproductive phase which considered from days to first flowering to days to maturity. The principal component PC4 and PC5 were also related to yield components. The fourth component was more related to harvest index and 100 seed weight, whereas PC5 was closely related to plant height.

In soybean genotypes top 5 principal component scores (PC scores) for all the character were estimated in these five components and presented in table 8. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal component. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype.

Table 8: Five PC values of rotation component matrix for eleven variables of twenty six genotypes of soybean.

Traits	Principal components				
	PC1	PC2	PC3	PC4	PC5
Veg. Phase	0.754*	0.213	-0.487	-0.312	0.006
Repro. Phase	0.008	-0.023	0.965*	0.187	-0.038
Plant height	0.627*	0.190	-0.119	0.117	0.689*
No. of branches/plant	0.907*	-0.026	-0.170	0.072	0.025
No. of pods/plant	0.930*	0.208	-0.008	-0.156	0.157
No. of seeds/plant	0.796*	0.515*	-0.039	-0.214	0.197
No. of seeds/pod	0.202	0.950*	-0.046	-0.067	0.115
Biological yield/plant	0.814*	0.305	0.236	0.105	0.340
Harvest index (%)	0.553*	0.498	-0.139	0.577*	-0.189
100 seed weight	0.132	-0.135	0.340	0.889*	0.120
Yield/plant	0.818*	0.374	0.161	0.252	0.253

Extraction method: Principal component analysis
An asterisks (*) represents more related traits in each principal component

Principal Component 1

It includes Code 9 which had the highest PC score 1.27 value followed by Code 23 (1.20), Code 21 (0.87), Code 15 (0.74) and Code 8 (0.73). It indicated that they had high value for phenological and yield related traits such as vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index and yield per plant.

Principal Component 2

It includes the genotypes which had high PC score for Code 7 (2.60), Code 18 (1.77), Code 17 (1.67), Code 16 (0.75) and Code 2 (0.63). It showed they had high value for number of seeds per plant and number of seeds per pod.

Principal Component 3

It includes Code 21 (1.58) followed by Code 26 (1.28), Code 17 (1.27), Code 2 (1.04) and Code 7 (0.81), which exhibited high value for phenological traits *viz*., reproductive phase.

Principal Component 4

In PC4 Code 22 recorded the highest PC score (2.19) followed by Code 16 (1.63), Code 21 (1.08), Code 9 (0.10) and Code 10 (0.93) indicated that they had high value for harvest index and 100 seed weight.

Principal Component 5

It includes Code 16 (2.82) which exhibited the highest PC score followed by Code 15 (1.49), Code 5 (1.61), Code 24 (0.67) and Code 6 (0.67) indicated that they had high value for plant height.

Code 9 was found in PC1 and PC4 and had maximum PC score, where as Code 21 was present in PC 1, 3, 4 and had the highest traits for phenological and yield. On the basis of top 5 PC scores in each principal component, genotypes are selected and presented as summarized form in table 9.

Table 9: Interpretation of rotated component matrix for the traits having values >0.5 in each PCs.

	PC1	PC2	PC3	PC4	PC5
Traits	Veg. Phase	No. of seeds/plant	Rep. phase	HI	Plant height
	Plant height	No. of seeds/pod	-	100 seed weight	-
	No. of branches/ plant	-	-	-	-
	No.of pods/plant	-	-	-	-
	No. of seeds/plant	-	-	-	-
	Biological yield/plant	-	-	-	-
	HI	-	-	-	-
	Yield/plant	-	-	-	-

Table 10: PCA scores of soybean genotypes

Genotype	PC1	PC2	PC3	PC4	PC5
Code 1	0.6569	-0.0435	0.4103	-1.8348	-0.3120
Code 2	0.3356	**0.6315**	**1.0354**	-0.5526	-0.1282
Code 3	0.1596	-0.7777	0.6023	-0.1514	-1.6555
Code4	-0.0999	0.5326	-0.6513	-0.0469	0.6529
Code 5	0.1540	-0.3091	-0.1119	-0.1667	**1.6099**
Code 6	0.3834	0.1861	0.0580	-1.4710	**0.6661**
Code 7	-0.6927	**2.5996**	**0.8129**	-0.3840	0.1643
Code 8	**0.7324**	-0.5128	0.5063	-0.2331	-0.5202
Code 9	**1.2703**	-0.5963	0.0132	**0.9998**	-0.1148
Code 10	-0.0708	-0.0389	0.7674	**0.9301**	-0.4895
Code 11	0.7141	-0.1757	-1.5426	0.8219	-0.6504
Code 12	0.3838	0.0699	0.3960	0.8466	-0.9927
Code 13	-0.0864	-0.2734	-1.8555	0.2410	-0.4744
Code 14	0.1240	0.4794	-2.3543	-0.3955	-0.8790
Code 15	**0.7372**	-0.6008	0.7945	0.3423	**1.4921**
Code 16	-0.5837	**0.7540**	0.3793	**1.6287**	**2.8248**
Code 17	-0.5645	**1.6734**	**1.2748**	0.2818	-1.8739
Code 18	0.2848	**1.7672**	-0.3492	-1.4870	0.6009
Code 19	0.4294	0.3983	-1.0360	0.7993	0.5233
Code 20	0.4972	-0.8563	0.5838	-0.0835	-0.1522
Code 21	**0.8743**	-1.6226	**1.5785**	**1.0788**	-0.1131
Code 22	-2.3368	0.1954	-0.8265	**2.1924**	-0.6046
Code 23	**1.1982**	-0.2559	-0.2988	-0.2231	0.4574
Code 24	-2.0831	-2.1473	-0.8444	-1.5842	**0.6694**
Code 25	0.2571	-0.2307	-0.6195	-0.7358	-0.5378
Code 26	-2.6745	-0.8465	**1.2771**	-0.8129	-0.1627

Table 11: Five genotypes are selected on the basis of PC score in decreasing order in each component and presented below:

	PC1	PC2	PC3	PC4	PC5
Traits	**Code 9**	**Code 7**	**Code 21**	Code 22	**Code 16**
	Code 23	Code 18	Code 26	**Code 16**	**Code 15**
	Code 21	**Code 17**	**Code 17**	**Code 21**	Code 5
	Code 15	**Code 16**	**Code 2**	**Code 9**	Code 24
	Code 8	**Code 2**	**Code 7**	Code 10	Code 6

4.4 Characterization

In this present experiment, soybean genotypes were characterized on the basis of morphological traits viz., hypocotyl colour, growth type, growth habit, pubescent, pubescent colour, leaf shape, flower colour, pod colour, seed coat colour, seed size, seed shape, hilum colour. The categorization of different genotypes on the basis of twelve morphological traits is mentioned in table 12.

Expressions of following morphological traits were observed visually for distinctiveness and variations

4.4.1 Hypocotyl colour

Based on hypocotyl colour of seedling, genotypes were categorized in two groups *i.e.,* Green [1] and violet [2] hypocotyl colour. Twenty two genotypes were identified green hypocotyl colour whereas, four genotypes showed violet hypocotyl colour.

4.4.2 Growth type

On the basis of plant growth type, genotypes were categorized in three groups *i.e.,* determinate [1]; semi-determinate [2] and indeterminate [3]. Six genotypes were observed determinate growth type, while nineteen genotypes exhibited semi determinate growth type and one genotype was indeterminate type.

4.4.3 Growth habit

Based on the plant growth habit, genotypes were categorized in three groups *i.e.,* erect [1]; semi-erect [2] and spreading [3]. Six genotypes were grouped as erect type, eighteen genotypes as semi erect group and two genotypes as spreading type.

4.4.4 Pubescent

On the basis of presence or absence of hair on pod, genotypes were categorized in two groups *i.e.,* glabrous (absence of hairs) [1] and pubescent (presence of hairs) [2]. Twenty-one genotypes showed presence of hairs *i.e*. pubescence and remaining five abscent of hairs *i.e.* glabrous type.

4.4.5 Pubescent colour

Among all the pubescent entries only one type of hair colour was observed *i.e.,* Tawny [1].

4.4.6. Leaf shape

Based on shape of lateral leaflet, genotypes were categorized into three groups *i.e.,* lanceolate [1]; pointed ovate [2]; and rounded ovate [3]. Two genotypes were observed with lanceolate, fourteen genotypes with pointed ovate and remaining ten with rounded ovate types of leaves.

4.4.7 Flower colour

Only two types of classes are formed on the basis of flower colour *i.e.,* white [1] and violet [2]. Four genotypes showed violet flower colour and twenty-two white flower colour.

4.4.8 Pod colour

Considerable variation was observed for the intensity of brown colour on mature pods among the genotypes. The soybean genotypes are categorized as light [1]; medium [2] and dark [3]. Four genotypes showed light pod colour, thirteen genotypes medium pod colour and remaining nine genotypes were having dark pod colour.

4.4.9 Seed coat colour

No variation is observed for seed coat colour among the soybean genotypes. All the genotypes under study had yellow seed coat colour *i.e.,* Yellow [1].

4.4.10 Seed size

On the basis of seed size, genotypes are categorized in three groups *i.e.,* small (<10 g) [1]; medium (10-13 g) [2] and bold/ large (>13 g) [3]. Nineteen genotypes of soybean recorded small seed size, five genotypes medium seed size and remaining two genotypes had bold seed type.

4.4.11 Seed shape

On the basis of seed shape, genotypes were categorized in four groups *i.e.,* spherical [1]; spherical-flattened [2]; elongated [3]; elongated-flattened [4]. Fourteen genotypes were spherical, nine elongated, two elongated-flattened and remaining one was spherical-flattened.

4.4.12 Hilum colour

On the basis of hilum colour, genotypes were categorized in five groups *i.e.,* grey [1]; brown [2]; dark brown [3]; black [4] and dark black [5]. Two genotypes were observed with gray hilum colour, six with brown colour, two genotypes with dark brown hilum colour, four genotypes with black hilum colour and remaining twelve genotype with dark black hilum.

Table 12: Categorization of soybean genotypes based on morphological character.

Character	Classes	Genotypes
1. Hypocotyl colour	Green	Code 1, Code 2, Code 3, Code 4, Code 5, Code 6, Code 7, Code 8, Code 10, Code 11, Code 12, Code 15, Code 16, Code 17, Code 18, Code 19, Code 20, Code 21, Code 22, Code 23, Code 24, Code 26
	Violet	Code 9, Code 13, Code 14, Code 25
2. Growth type	Determinate	Code 2, Code 7, Code 8, Code 17, Code 22, Code 26
	Semi-determinate	Code 1, Code 3, Code 4, Code 5, Code 6, Code 9, Code 10, Code 11, Code 12, Code 13, Code 14, Code 16, Code 18, Code 19, Code 20, Code 21, Code 23, Code 24, Code 25
	Indeterminate	Code 15
3.Growth habit	Erect	Code 4, Code 14, Code 19, Code 22, Code 24, Code 26
	Semi-erect	Code 1, Code 2, Code 3, Code 5, Code 6, Code 7, Code 8, Code 9, Code 10, Code 11, Code 12, Code 13, Code 16, Code 17, Code 20, Code 21, Code 23, Code 25
	Spread	Code 15, Code 18
4. Pubescent	Pubescent	Code 1, Code 2, Code 3, Code 4, Code 5, Code 7, Code 8, Code 9, Code 11, Code 12, Code 13, Code 14, Code 15, Code 16, Code 18, Code 19, Code 21, Code 22, Code 23, Code 24, Code 25
	Glabrous	Code 6, Code 10, Code 17, Code 20, Code 26
5. Pubescent colour	Twany	Code 1, Code 2, Code 3, Code 4, Code 5, Code 7, Code 8, Code 9, Code 11, Code 12, Code 13, Code 14, Code 15, Code 16, Code 18, Code 19, Code 21, Code 22, Code 23, Code 24, Code 25
	Absent	Code 6, Code 10, Code 17, Code 20, Code 26
6.Leaf shape	Lanceolate	Code 1, Code 2
	Pointed ovate	Code 3, Code 5, Code 8, Code 9, Code 11, Code 12, Code 13, Code 14, Code 16, Code 18, Code 22, Code 23, Code 24, Code 25
	Rounded ovate	Code 4, Code 6, Code 7, Code 10, Code 15, Code 17, Code 19, Code 20, Code 21, Code 26,
7. Flower colour	Violet	Code 9, Code 13, Code 14, Code 25

	White	Code 1, Code 2, Code 3, Code 4, Code 5, Code 6, Code 7, Code 8, Code 10, Code 11, Code 12, Code 15, Code 16, Code 17, Code 18, Code 19, Code 20, Code 21, Code 22, Code 23, Code 24, Code 26
8. Pod colour	Light	Code 1, Code 5, Code 10, Code 23
	Medium	Code 3, Code 6, Code 7, Code 8, Code 11, Code 12, Code 16, Code 17, Code 18, Code 20, Code 21, Code 22, Code 26
	Dark	Code 2, Code 4, Code 9, Code 13, Code 14, Code 15, Code 19, Code 24, Code 25
9. Seed coat colour	Yellow	Code 1, Code 2, Code 3, Code 4, Code 5, Code 6, Code 7, Code 8, Code 9, Code 10, Code 11, Code 12, Code 13, Code 14, Code 15, Code 16, Code 17, Code 18, Code 19, Code 20, Code 21, Code 22, Code 23, Code 24, Code 25, Code 26
10. Seed size	Small	Code 1, Code 2, Code 3, Code 4, Code 5, Code 6, Code 7, Code 8, Code 11, Code 13, Code 14, Code 17, Code 18, Code 19, Code 20, Code 23, Code 24, Code 25, Code 26
	Medium	Code 9, Code 10, Code 12, Code 15, Code 21
	Bold	Code 16, Code 22
11. Seed shape	Spherical	Code 2, Code 3, Code 4, Code 8, Code 9, Code 10, Code 13, Code 14, Code 17, Code 18, Code 19, Code 20, Code 21, Code 25
	Spherical-flattened	Code 6
	Elongated	Code 1, Code 5, Code 7, Code 11, Code 12, Code 15, Code 16, Code 22, Code 26
	Elongated - flattened	Code 23, Code 24
12. Hilum colour	Grey	Code 16, Code 17,
	Brown	Code 10, Code 13, Code 15, Code 18, Code 24, Code 26
	Dark brown	Code 2, Code 7
	Black	Code 4, Code 20, Code 21, Code 25
	Dark black	Code 1, Code 3, Code 5, Code 6, Code 8, Code 9, Code 11, Code 12, Code 14, Code 19, Code 22, Code 23

Table 13: Categorization of soybean genotypes based on morphological character.

S.No.	Code	Hypc	GT	GH	Pb	PbC	LS	FC	PC	SCC	SSi	SSh	HC
1.	Code 1	P	SD	SE	Pb	T	Ln	W	L	Y	S	E	DBl
2.	Code 2	P	D	SE	Pb	T	Ln	W	D	Y	S	Sp	DBr
3.	Code 3	P	SD	SE	Pb	T	PO	W	M	Y	S	Sp	DBl
4.	Code 4	P	SD	E	Pb	T	**RO**	W	D	Y	S	Sp	Bl
5.	Code 5	P	SD	SE	Pb	T	PO	W	L	Y	S	E	DBl
6.	Code 6	P	SD	SE	Gl	A	RO	W	M	Y	S	SpF	DBl
7.	Code 7	P	D	SE	Pb	T	RO	W	M	Y	S	E	DBr
8.	Code 8	P	D	SE	Pb	T	PO	W	M	Y	S	Sp	DBl
9.	Code 9	A	SD	SE	Pb	T	PO	V	D	Y	M	Sp	DBl
10.	Code 10	P	SD	SE	Gl	A	RO	W	L	Y	M	Sp	Br
11.	Code 11	P	SD	SE	Pb	T	PO	W	M	Y	S	E	DBl
12.	Code 12	P	SD	SE	Pb	T	PO	W	M	Y	M	E	DBl
13.	Code 13	A	SD	SE	Pb	T	PO	V	D	Y	S	Sp	Br
14.	Code 14	A	SD	E	Pb	T	PO	V	D	Y	S	Sp	DBl
15.	Code 15	P	ID	Sp	Pb	T	RO	W	D	Y	M	E	Br
16.	Code 16	P	SD	SE	Pb	T	PO	W	M	Y	B	E	Gy
17.	Code 17	P	D	SE	Gl	A	RO	W	M	Y	S	Sp	Gy
18.	Code 18	P	SD	Sp	Pb	T	PO	W	M	Y	S	Sp	Br
19.	Code 19	P	SD	E	Pb	T	RO	W	D	Y	S	Sp	DBl
20.	Code 20	P	SD	SE	Gl	A	RO	W	M	Y	S	Sp	Bl
21.	Code 21	P	SD	SE	Pb	T	RO	W	M	Y	M	Sp	Bl
22.	Code 22	P	D	E	Pb	T	PO	W	M	Y	B	E	DBl
23.	Code 23	P	SD	SE	Pb	T	PO	W	L	Y	S	EF	DBl
24.	Code 24	P	SD	E	Pb	**T**	PO	W	D	Y	S	EF	Br
25.	Code 25	A	SD	SE	Pb	T	PO	V	D	Y	S	Sp	Bl
26.	Code 26	P	D	E	Gl	A	RO	W	M	Y	S	E	Br

Note:

Hyp C	Hypocotyl colour	P=Present; A=Absent
GT	Growth type	D=Determinate; SD=Semi-determinate ; ID= indeterminate
GH	Growth habit	E=Erect; SE=Semi-erect ; Sp=Spread
Pb	Pubescence	Pb=Pubescent; Gl=Glabrous
PbC	Pubescent Colour	T=Twany; A=Absent
LS	Leaf shape	Ln=Lanceolate; PO=Pointed ovate; RO=Rounded ovate
FC	Flower colour	V=Violet; W=White
PC	Pod colour	L=Light; M=Medium; D=Dark
SCC	Seed coat colour	Y=Yellow
SSi	Seed size	S=Small; M=Medium; B=Bold
SSh	Seed shape	Sp=Spherical; SpF=Spherical-flattened; E=Elongated; Ef= Elongated flattened
HC	Hilum colour	Gy=Grey; Br=Brown; DBr=Dark brown; Bl= Black; DBl=Dark black

CHAPTER-V

DISCUSSION

Soybean is the most important oilseed crop of India. Over last four decades its introduction to especially central and southern parts of India, it has made a significant inroads among agrarian community. There are few examples of any other crop taking such giant strides in terms of adoption among farmers, as soybean has achieved. Though the average productivity of India have been realized 2.5 times more from 1970-71 (426 kg/ha) to 2011-12 (1155 kg/ha). However, this yield level is low in comparison to other prominent soybean growing countries. Breeders efforts are always to break the yield barriers through genetic improvement. In this regards, at JNKVV, Jabalpur, several fixed advanced genotypes of soybean, developed from diverse crosses, have been isolated. It would be of immense importance to evaluate these genotypes applying biometrical parameters.

Looking to the above aspects, the present investigation was undertaken subject to different genetical studies viz., genetic variability, heritability, genetic advance, association analysis and principal component analysis. On the basis of these studies and assessment, ranking of genotypes can be done and superior genotypes can be promoted as variety and used in further breeding programmes. The experimental findings are discussed under following heads:

5.1 Parameters of genetic variability

- 5.1.1 Genetic variability
- 5.1.2 Genotypic and phenotypic coefficient of variation
- 5.1.3 Heritability and genetic advance

5.2 Correlation coefficient

5.3 Path coefficients analysis

5.4 Principal component analysis

5.5 Characterization

5.1 Parameters of genetic variability

5.1.1 Genetic variability

The estimate of genetic variability was recorded in advanced generation fixed genotypes isolated from different crosses. The ANOVA revealed that the characters viz., vegetative phase, reproductive phase, plant height, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index, yield per plant exhibited highly significant mean sums of square except 100 seed weight which showed significant mean sum of square. This indicates that sufficient variability has been created for most of the important characters among different genotypes developed through hybridization involving diverse parents. However, narrow variability was observed for number of branches per plant and number of seeds per pod.

Similar results have been obtained by Ghatge and Kadu (1993) for plant height and seed yield, Shrivastava and Shukla (1998) for plant height, pods per plant, biological yield and seed yield, Thorat *et al.* (1999) for 100 seed weight, Devine *et al.* (2002) for plant height and Kumar *et al.* (2005) for 100 seed weight.

Contradictory results have been given by Shrivastava and Shukla (1998) for branches per plant.

5.1.2 Phenotypic and genotypic coefficient of variation

To obtain a clear picture about the variability in all the genotypes, the variability was further splited into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). In the present study, the phenotypic coefficient of variability was higher than genotypic coefficient of variability for all the characters. High magnitudes of PCV was observed for the traits *viz.,* number of branches per plant, number of seeds per plant, yield per plant, number of pods per plant and biological yield per plant.

Moderate values of PCV were noticed for characters viz., plant height, 100 seed weight, number of seeds per pod, harvest index, vegetative phase. Reproductive phase showed low value of PCV. This result indicated the greater scope for selection of these traits for further breeding work, because substantial variability exist in advance lines for most of the important traits.

In accordance to the above findings Hina Kausar (2005) for plant height and number of branches per plant, Aditya *et al.* (2012) for number of pods per plant, biological yield per plant and yield per plant, Nehru *et al.* (1999) for number of seeds per plant, Karad *et al.* (2005) and Parameshwar (2006) for number of seeds per pod and Banger *et al.* (2003) for 100 seed weight have reported similar findings.

Contradictory results have been reported by Kumari Nirmala and Balasubramanian (1993) for yield per plant and Singh and Singh (1999) for plant height.

5.1.3 Heritability and Genetic Advance

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and to indicate accuracy with which a genotype can be identified phenotypically. Heritability estimates along with the genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that the character showing high heritability will also exhibited high genetic advance.

If high or moderate heritability is accompanied with high or moderate genetic advance indicates additive gene action involved in the inheritance of concerned traits and selection may be effective. While high or moderate heritability coupled with low genetic advance or *vice versa* indicates predominance of non additive gene action.

Heritability estimates have been broadly classified into low (below 50%), medium (50% and 70%) and high (above 70%) and genetic advance estimates classified into low (below 25%) medium (25-35%) and high (above 35%) in order to draw some conclusions about these parameters.

Heritability is broad sense (h^2) and genetic advance were calculated for each character under study. These estimates varied from character to character. The knowledge of heritability enables to assess the amount of variance due to genetic cause, which is likely to be transferred in the progeny.

High heritability was recorded by all the characters except reproductive phase, number of seeds per pod, which showed moderate heritability.

Number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and yield per plant showed high genetic advance. Plant height and 100 seed weight showed moderate genetic advance, while vegetative phase, reproductive phase, number of seeds per pod and harvest index showed low genetic advance.

Number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, yield per plant showed high heritability and high genetic advance indicated the preponderance of additive gene action.

High heritability with moderate genetic advance was found for plant height and 100 seed weight, indicated the preponderance of additive gene action in the inheritance of these traits.

Vegetative phase, reproductive phase, number of seeds per pod and harvest index recorded high or moderate heritability with low genetic advance, exhibiting non additive gene action in expression of their effects.

These findings are in agreement with the findings of Islam and Mian (2008), Nag et al. (2007) for plant height, number of pods per plant and number of seeds per plant, Parameshwar (2006) for number of branches per plant and number of seeds per pod, Aditya *et al.* (2011) for biological yield per plant, Gohil *et al.* (2006) for yield per plant.

Contradictory reports have been given by Thorat *et al.* (1999) for yield per plant and number of seeds per pod, Islam and Mian (2008) for 100 seed weight, Kalaimagal (1991), Vart *et al.* (2005) and Tiwari and Bhatnagar (1991) for number of pods per plant and plant height.

5.2 Association analysis

5.2.1 Correlation coefficient

Yield is a complex quantitative character governed by large number of genes and is highly influenced by environment. Hence, the selection of superior genotypes based on yield as such is not effective. For a rational approach towards improvement of yield, selection has to be made for the components of yield. Association of yield components and yield thus assumes special importance on the basis of indirect selection. Genetic correlation between different characters of plant often arises because of linkage or pleiotrophy.

Analysis of correlation coefficient revealed that the degree of association between yield and its components or gives the mutual relationship between the yield components. It helps in direct selection of associated characters for the improvement of desirable traits.

In biological system most of the characters are associated with each other by one or more paths. In the present investigation, correlations were worked out at phenotypic and genotypic levels in all possible character combination of all the soybean genotypes.

In general, genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficient. This indicated that although there is strong inherent association between the various pairs of characters studied, phenotypic expression of the correlation becomes less under the influence of environment. The low phenotypic correlation would result from the masking and modifying effects of environment on the association characters at gene level. The important causes of genetic correlations are linkage, pleiotrophy and heterozygosity.

In present study, phenotypic correlation of yield was positive and significant with vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pods, biological yield per plant and harvest index. This suggests while selecting for improvement in seed yield these characters should be kept in mind provided the characters show high variability. None of the characters under study exhibited negative correlation with yield.

Among the other character pairs, high and positive association was found for vegetative phase with number of pods per plant, number of seeds per plant, number of branches per plant, biological yield per plant, plant height, harvest index and number of seeds per pod; reproductive phase with 100 seed weight; plant height with biological yield per plant, number of pods per plant, number of seeds per plant, number of branches per plant, harvest index and number of seeds per pod; number of branches per plant with number of pods per plant, number of seeds per plant, biological yield and harvest index; number of pods per plant with number of seeds per plant, biological yield per plant, harvest index and seeds per pod; number of seeds per plant with biological yield per plant, number of seeds per pod and harvest index; number of seeds per pod with harvest index and biological yield per plant, and biological yield per plant with harvest index. Present findings revealed that by making selection and improvement for a particular character simultaneous improvement in the associated character(s) may be achieved.

In agreement with the present findings Burli *et al.* (2010) for yield with plant height and number of pods per plant, Aditya *et al.* (2011) for yield with number of branches per plant, number of pods per plant and harvest index have reported positive correlation.

Contradictory reports have been reported by Bangar *et al.* (2003) for seed weight with plant height and number of pods per plant.

The negative correlation was observed for vegetative phase with reproductive phase and 100 seed weight; reproductive phase with 100 seed weight, and number of seeds per plant with 100 seed weight.

5.2.2 Path coefficient analysis

Path coefficient analysis is also known as standardized partial regression coefficient which is unitless. The basic assumption of path analysis is that the path diagram utilizes a complete representation of the causal factor involved in determining the end product, the grain yield.

Path coefficient analysis was carried out using genotypic and phenotypic correlation and taking the yield per plant as the dependent variable in order to see the causal factor and to identify the best components, which are responsible for increasing yield per plant.

The path analysis of the present investigation revealed that substantial positive direct effect on yield was exerted by plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and harvest index, while negative direct effect by vegetative phase, reproductive phase, number of seeds per pod and 100 seed weight.

Similar findings have been reported by Islam and Mian (2008) for plant height and number of seeds per plant, Sirohi *et al.* (2007) for biological yield per plant, Vishnoi (2006) for number of pods per plant and number of branches per plant.

Contradictory results have been reported by Muhammad *et al.* (2006), Nag *et al.* (2007) and Islam and Mian (2008) for 100 seed weight.

5.3 Principal component analysis

Owing to lack of knowledge regarding relative importance and usefulness of variables, the investigator tries to include all the possible variables and makes the data matrix perceivably large, complicated and beyond comprehension. Therefore, the investigator requires a technique for systematic reduction and summarization of data sets.

Principal component analysis, basically a well known data reduction technique, initially floated by Pearson (1901) and later developed by Hotelling (1933), offers solution to this complex problem by transforming the original set of variables into smaller set of linear combinations that account for most of the variability of the original data set. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1982) and also to rank genotypes on the basis of PC scores.

In advanced generations of cross JS 97-52 X JS 20-02 (Code 9), the first principal component accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. The first principal component accounted for maximum variability *i.e*., 56.29 per cent which reduced gradually to 4.21 per cent in fifth principal component. The first five principal components having eigen values greater than 0.5 altogether explained 94.62 per cent of the total variation.

Rotated component matrix revealed that each principal component separately loaded with various phenological and yield attributing traits under study. The PC1 was more related to the phenological and yield attributing traits *viz*., vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index and yield per plant. Thus, PC1 allowed for simultaneous selection of phenological and yield related traits and it can be regarded as yield factor. PC2 exhibited positive effect for No. of seeds per plant and No. of seeds per pod allowed for higher seed yield. The third principal component was more related to phenological traits *i.e.,* reproductive phase whereas PC4 was more loaded with yield related traits *viz.,* harvest index and 100 seed weight. The fifth PC was more related to plant height.

Similar results was found by Miladinovic *et al*. (2006) for harvest index, reproductive period, seed weight, vegetative period, yield and plant height. Iqbal *et al.* (2008) for filled pods per plant, grain yield, biological yield per plant, 100 seed weight, harvest index, days to maturity and number of branches per plant. Ojo *et al.* (2012) for number of pods per plant, pod length, pod yield per plant, 100-seed weight and seed yield per plot.

From this study it was cleared that PC1, PC2, PC4 and PC5 found mostly related to yield attributing traits whereas PC3 was related to phenological traits. As PC1 was constituted by most of the yield attributing traits, an intensive selection procedures can be designed to bring about rapid improvement of dependent traits *i.e.,* yield by selecting the lines from PC1.

In PC2 number of seeds per plant and number of seeds per pod are yield related traits. The PC3 exhibited more related to phenological traits (reproductive phase). The PC4 was more related to harvest index and 100 seed weight. In PC5 plant height contributes positive effects on yield attributing traits.

PC scores were calculated for all the advanced lines in 5 principal components and utilized in finding advanced lines, superior for different combination of phenotypic traits. A high value of PC score of a particular advanced line in a particular PC denotes high value for those variables, in that advanced line which the component is representing. Thus these score can be utilized to propose precise selection indices, whose intensity can be decided by variability explained by each of the PC.

According to the first PC score, Code 9 had highest score followed by Code 23, Code 21 and Code 15 etc., indicated that they were more related to vegetative phase, plant height etc. The highest PC scores in advanced lines Code 7, Code 18, Code 17 etc in PC2 was closely related to number of seeds per plant, number of seeds per pod. In PC3 highest PC score exhibited by Code 21 followed by Code 26 and 17 for reproductive phase. At the same time PC scores of advanced line Code 22 followed by Code 16 and Code 21 etc in PC 4 related to harvest index and 100 seed weight. PC scores for PC 5 exhibited plant height characteristics in advanced line Code 16. Thus breeder can select lines having the highest score with desirable combination of quantitative and qualitative traits for further breeding programme.

It can be concluded that PC analysis highlights the characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of yield attributing traits. PCA also help in ranking of genotypes on the basis of PC scores in corresponding component.

From the above discussion it is clear that in the advanced lines Code16 hold the first position followed by Code 7 and Code 22 on the basis of PC score for PC scores in all principal components. When we considered the entire PC with PC scores and character basis then Code 9 ranks first because it present in PC 1 and PC 4 also. Code 9 contributes maximum character because most of the yield related traits are present in PC 1. In PC 4 there are two characters harvest index and 100 seed weight also contribute yield attributing traits, so Code 9 performs best in comparison to other genotypes will be utilized for precise selection to the development of suitable genotypes and also used in best breeding material for the transfer of suitable traits in recipient genotypes. Code 21 also found in PC 1 (this component having maximum characters), PC 3 and PC 4 because PC score of this advanced line is lower in comparison to Code 9, but it present in three principal components and contributes maximum characters in comparison to Code 9. On that basis Code 21 is an ideotype breeding material for selection and utilization in precise breeding programme.

5.4 Characterization

Characterization with distinct morphological markers is essential for identification of genotypes and Intellectual property protection. India has enacted legislation for the Protection of Plant Varieties and Farmer's Right in 2001, in order to provide incentives for development and fulfill obligations under Trade Related Intellectual Property Right (TRIPs). Novelty, Distinctiveness, Uniformity and Stability are the essential requirements for grant of protection to varieties/ germplasm / variation either. Genotypes are characterized on the basis of morphological traits viz., hypocotyl colour, growth type, growth habit, pubescence, pubescence colour, leaf shape, flower colour, pod colour, seed coat colour, seed size, seed shape and hilum colour. From the study of these characters we can easily identify different genotypes of soybean. So, we can use these characters as an identification keys.

Similarly characterization pattern was adopted by Kumar and Narayanaswamy (1999), Satyavathi *et al.* (2004) and Sawarkar (2010) taking distinguished morphological traits.

Overall results revealed that among the newly developed genotypes of soybean, substantial variability exists. On the basis of correlation and path studies of the present investigation, the most important traits identified among the promising genotypes of soybean are plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and harvest index contributing substantially towards yield.

The characters viz., vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index and yield per plant are more important yield contributing traits based on Principal Component analysis. Genotypes namely JS 97- 52 x JS 20-02 (Code 9), JSM 110 X JSM 60 (Code 23), JSM 240 X JSM 189 (Code 21), JSM 146 X JSM 152 (Code 15), JS 97-52 X JSM 286 (Code 8) were found promising, which can be further promoted as variety or may be utilized as further breeding program.

CHAPTER-VI

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

6.1 Summary

The present investigation entitled “Genetic Studies of Phenological and Yield Components in Promising Lines of Soybean” was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur, during *Kharif* 2011-12. This investigation was carried out with 26 advanced generation fixed genotypes of soybean in randomized complete block design in two replications. Observations were recorded on five randomly selected plants from each replication per treatment. Data were recorded on vegetative phase, reproductive phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod, biological yield per plant, harvest index, 100 seed weight and yield per plant. Characterization were recorded on the basis of following characters such as hypocotyl colour, growth type, growth habit, pubescent, pubescent colour, leaf shape, flower colour, pod colour, seed coat colour, seed size, seed shape and hilum colour. The objective of this study was to estimate the genetic variability, heritability, genetic advance, association analysis, path coefficients, principal component analysis for yield and yield components and characterization of genotypes.

Analysis of variance revealed sufficient and desirable amount of variability for most of the characters which indicates that genotypes can be developed with more variability by involving diverse parents in crosses.

High value of PCV were recorded for number of branches per plant, number of seeds per plant, yield per plant, number of pods per plant and biological yield per plant also indicated high variability.

Number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, yield per plant, plant height, 100 seed weight and number of seeds per pod expressed high to moderate heritability and genetic advance revealed the preponderance of additive gene action in the inheritance of these traits, whereas remaining traits viz., vegetative phase, reproductive phase and harvest index were governed by non additive gene action because for them the combination of heritability and genetic advance were found either high heritability with low genetic advance or *vice versa*. In the selection and breeding programme these information should be taken care of for the improvement of these characters in soybean.

The characters viz., plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and harvest index were found more important on the basis of correlation and path analyses. Hence directional selection through these traits will be very effective for improvement of grain yield.

On the basis of principal component analysis only five principal components exhibited more than 0.5 Eigen value and showed about 94.62% total variability. The PC1 showed 56.29%, while PC2, PC3, PC4, PC5 exhibited 18.49%, 8.34%, 7.30% and 4.21% variability, respectively among the genotype for the traits under study. Rotated component matrix revealed that each principal component separately loaded with various yield and physiological traits. The PC1, PC2 PC4 and PC5 mostly related to yield attributing traits where as PC3 related to reproductive phase. Thus, PC1 was more related to most of the yield attributing traits viz., vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index and yield per plant. An intensive selection procedures can be designed to bring about rapid improvement of dependent traits i.e. yield by selecting lines from PC1. It can be regarded as yield factor.

On the basis of principal component analysis, genotypes developed by the cross JS 97- 52 x JS 20-02 (Code 9) was found most important because it was present in PC1 and PC4. Whereas other four genotypes developed from crosses viz., JSM 110 X JSM 60 (Code 23), JSM 240 X JSM 189 (Code 21), JSM 146 X JSM 152 (Code 15) and JS 97-52 X JSM 286 (Code 8) were also found important.

Conclusions

1. Sufficient variability obtained for most of the economic traits through present investigation, reveals that through hybridization extent of variability is possible to increase involving diverse parents in soybean.

2. Most of the important traits viz., branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, yield per plant, plant height, 100 seed weight and number of seeds per pod exhibited the high heritability and genetic advance revealed additive gene action which can be exploited to achieve transgressive segregants adopting appropriate breeding methods.

3. The most important traits identified among the promising genotypes of soybean are plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and harvest index contributing substantially towards yield as per the association and path analyses.

4. On the basis of overall analysis promising genotypes as identified as Code 9 (JS 97-52 x JS 20-02) followed by Code 23 (JSM-110 x JSM-60), Code 21 (JSM-240 x JSM-189), Code 15 (JSM 146 x JSM-152) and Code 8 (JS 97-52 x JSM-286).

Suggestions for further work:

The following suggestions have been made for further study:-

1. The genetic variability analysis of these genotypes should be studied in more than one year to validate the results.
2. Characters showing high heritability with high genetic advance should be exploited to isolate potential genotypes.
3. A better crop ideotype can be developed using findings of association and principal component analysis.
4. Because Code 9 having the highest PC score, so molecular marker can be developed for the identification of the QTLs for important traits including yield.

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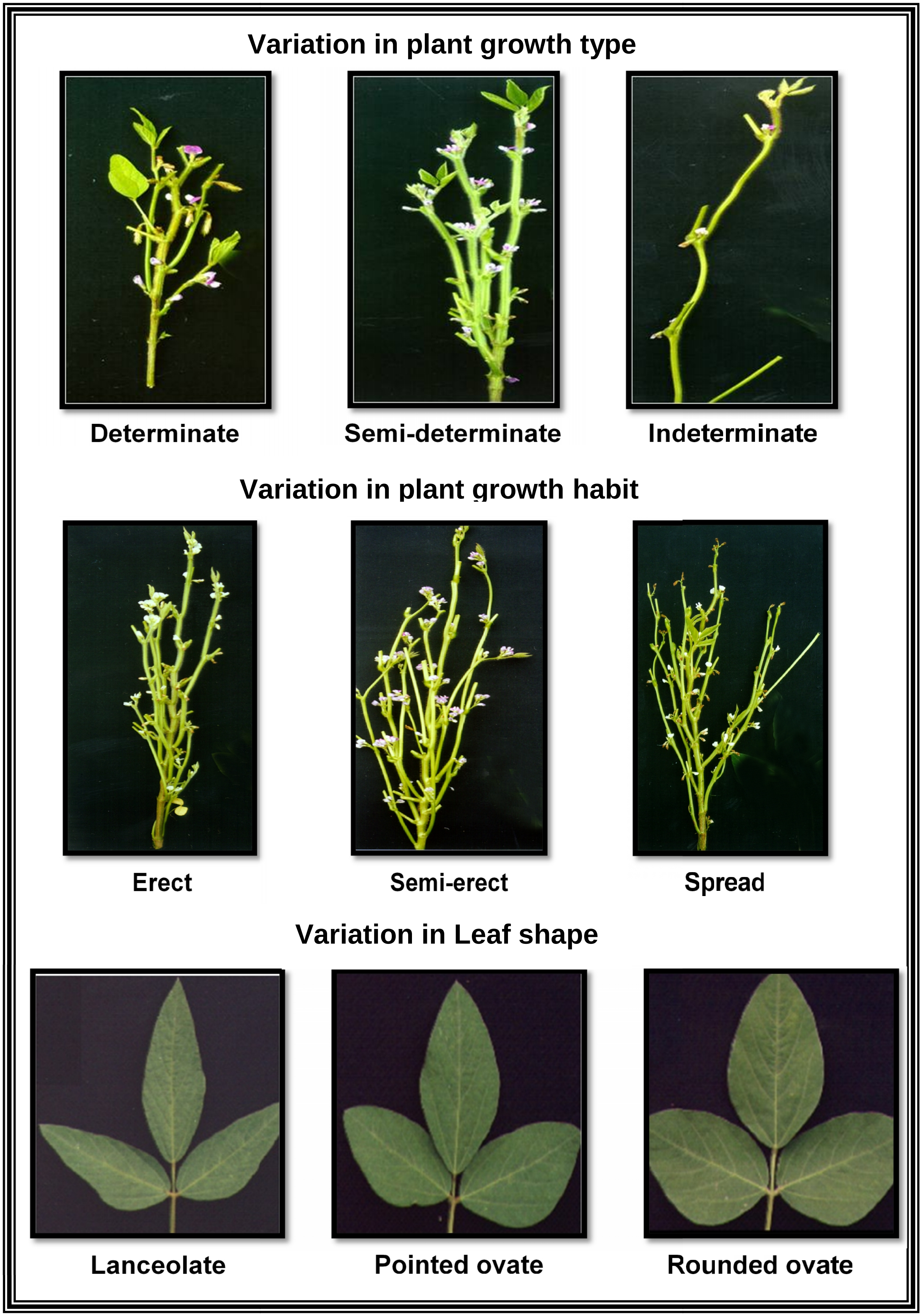
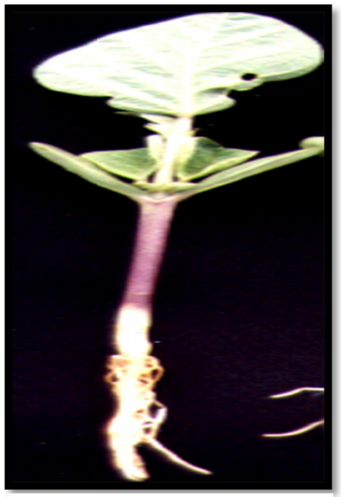


Plate 1: Characterization of soybean genotype

Variation in hypocotyl colour



Present

Absent

Variation in Pubescent

Pubescent

Glabrous

Variation in Flower colour

Violet

White

Plate 2: Characterization of soybean genotype

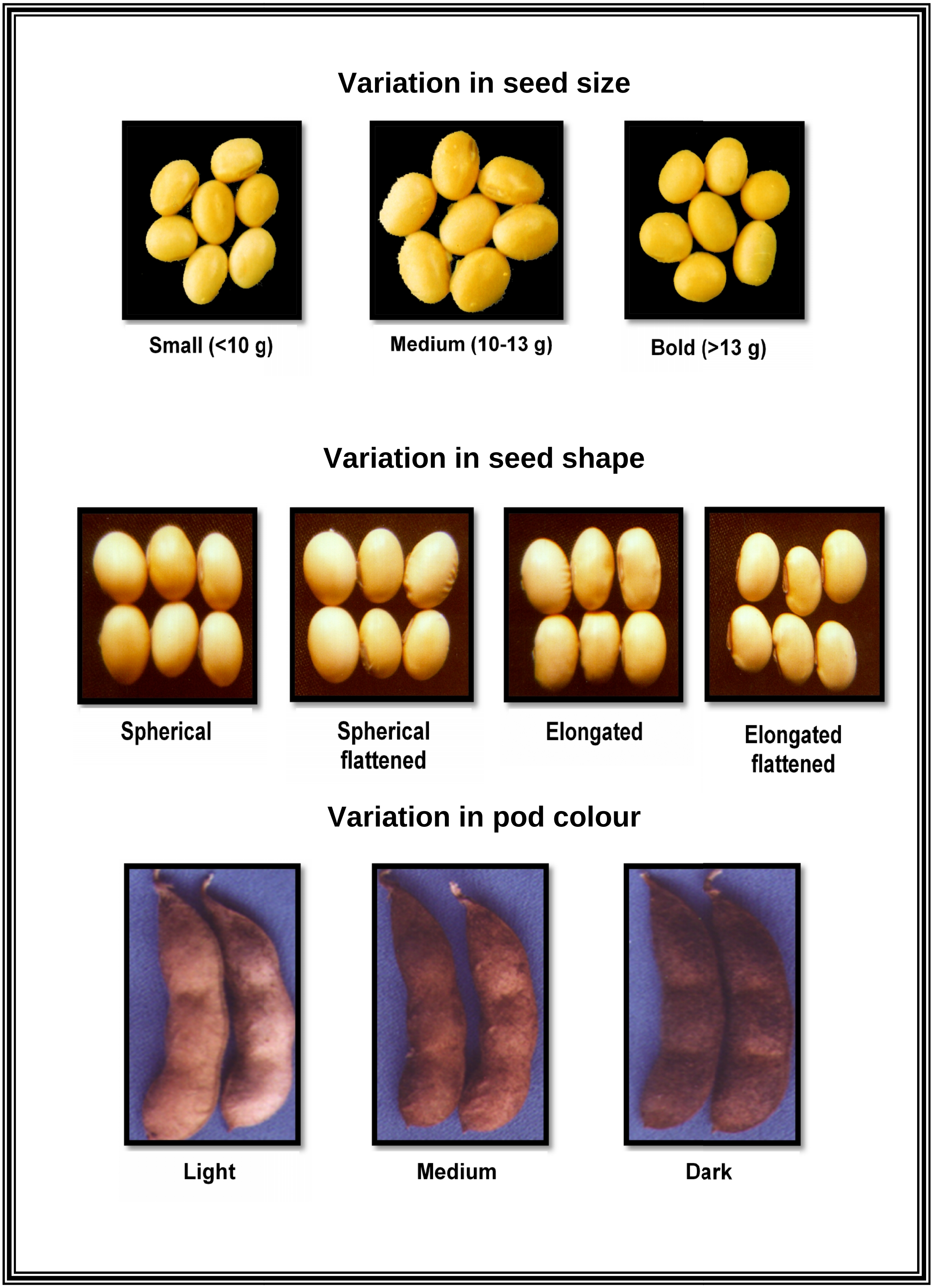


Plate 3: Characterization of soybean genotype

ABSTRACT

1. Title of the thesis	:	**Genetic Studies of Phenological and Yield Components in Promising Lines of Soybean**
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ABSTRACT

The present investigation entitled “Genetic Studies of Phenological and Yield Components in Promising Lines of Soybean” was conducted at Seed Breeding Farm of J.N.K.V.V., Jabalpur, during *Kharif* 2011-12 on 26 advanced generation fixed genotypes of soybean with the objective to estimate the genetic variability, heritability, genetic advance, association analysis, path coefficients, principal component analysis for yield and yield components and characterization of genotypes in randomized complete block design in two replications.

Analysis of variance revealed sufficient and desirable amount of variability for most of the characters which indicates that genotypes can be developed with more variability by involving diverse parents in crosses. High value of PCV were recorded for number of branches per plant, number of seeds per plant, yield per plant, number of pods per plant and biological yield per plant also indicated high variability.

Number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, yield per plant, plant height, 100 seed weight and number of seeds per pod expressed high to moderate heritability and genetic advance revealed the preponderance of additive gene action in the inheritance of these traits, whereas remaining traits viz., vegetative phase, reproductive phase and harvest index were governed by non additive gene action because for them the combination of heritability and genetic advance were found either high heritability with low genetic advance or *vice versa*. In the selection and breeding programme these information should be taken care of for the improvement of these characters in soybean.

The characters viz., plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant and harvest index were found more important on the basis of correlation and path analysis. Hence directional selection through these traits will be very effective for improvement of grain yield.

On the basis of principal component analysis only five principal components exhibited more than 0.5 Eigen value and showed about 94.62% total variability. The PC1 showed 56.29%, while PC2, PC3, PC4, PC5 exhibited 18.49%, 8.34%, 7.30% and 4.21% variability respectively among the genotype for the traits under study. Rotated component matrix revealed that each principal component separately loaded with various yield and physiological traits. The PC1, PC2, PC4 and PC5 mostly related to yield attributing traits where as PC3 related to reproductive phase. Thus, PC1 was more related to most of the yield attributing traits viz., vegetative phase, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, biological yield per plant, harvest index and yield per plant. An intensive selection procedures can be designed to bring about rapid improvement of dependent traits i.e. yield by selecting lines from PC1. It can be regarded as yield factor. On the basis of principal component analysis, genotypes developed by the cross JS 97-52 x JS 20-02 (Code 9) was found most important because it was present in PC1 and PC4. Whereas other four genotypes developed from crosses viz., JSM 110 X JSM 60 (Code 23), JSM 240 X JSM 189 (Code 21), JSM 146 X JSM 152 (Code 15) and JS 97-52 X JSM 286 (Code 8) were found important.